Dimensions of Personality: A Genetic Approach

Irene Rebollo Mesa

Data collection was supported by the following grants:
Health, lifestyle and personality: A study of adolescent twins and their parent (Dutch Heart Foundation NWO-900-562-137); Genetics of alcohol and nicotine use (VU-USF 96/22); The genetic basis of anxiety and depression: mapping quantitative trait loci in humans (NWO 904-61-090); Database Twin register (NWO 575-25-006); Genetics of individual differences in smoking initiation and persistence (NWO 985-10-002) ; Resolving cause and effect in the association between regular exercise and psychological well-being (NWO-MW 904-61-193); CNCR (Centre Neurogenetics/Cognition Research): Genes for ADHD and Depression; CMSB (Center for Medical Systems Biology); Twin-family database for behavior genetics and genomics studies (NWO 480-04-004); Genome-wide analyses of European twin and population cohorts to identify genes predisposing to common diseases (GENOMEUTWIN; EU/QLRT-2001-01254)

I. Rebollo was supported:
In part by NWO (NWO/SPINOZA 56-464-14192), the Borderline Personality Disorder Research Foundation, and the Ministerio de Educacion y Ciencia de España (FPU-AP2001-0016).

Reading Committee:

Dr. S.M. van den Berg
Department of Biological Psychology, Vrije Universiteit Amsterdam

Dr. R. Colom Marañón
Department of Personality, Assessment and Psychological Treatment, Madrid, Spain.

Dr. J. Denollet
Department of Psychology and Health, University of Tilburg

Dr. J.A. Feij
Department of Work and Organizational Psychology, Vrije Universiteit Amsterdam

Dr. J.H. Kamphuis
Department of Psychology, University of Amsterdam

Dr. B. Muthén
Graduate School of Education & Information Studies, Social Research Methodology Division, Los Angeles, CA, USA.

ISBN 90 8659 002 0
Printed by Febodruk b.v. Enschede (www.febodruk.nl)
Cover Peralta (www.peralta.nl)
Lay-out Peralta (www.peralta.nl) & Irene Rebollo

VRIJE UNIVERSITEIT

DIMENSIONS OF PERSONALITY: A GENETIC APPROACH

ACADEMISCH PROEFSCHRIFT

ter verkrijging van de graad Doctor aan
de Vrije Universiteit Amsterdam,
op gezag van de rector magnificus
prof.dr. T. Sminia,
in het openbaar te verdedigen
ten overstaan van de promotiecommissie
van de faculteit der Psychologie en Pedagogiek
op dinsdag 27 juni 2006 om 13.45 uur
in de aula van de universiteit,
De Boelelaan 1105

door

Irene Rebollo Mesa

geboren te Madrid, Spanje

promotor:	prof.dr. D.I. Boomsma
copromotor:	dr. C.V. Dolan

TABLE OF CONTENTS

Chapter 1

GENES, ENVIRONMENT, AND PERSONALITY

Irene Rebollo & Judith R.Harris

This Chapter is based on: Rebollo, I. & Rich Harris, J. (2005) Genes, ambientes e personalidade. In Colom, R. & Flores-Mendoza, C. Introdução à Psicologia das Diferenças Individuais. Porto Alegre: ArtMed (pp. 293-315.) [Genes, Environment and Personality. In Colom, R. & Flores-Mendoza, C. Introduction to the Psychology of Individual Differences.]

INTRODUCTION

Everybody has questions about personality. Why is Susanna so different from her sister Elena? Why is Jimmy so aggressive – is it the neighborhood he lives in, the friends he plays with? Why do I become more like my father, the older I get? The purpose of research in psychology is to answer such questions in a scientific way, rather than to rely on intuition. If intuition were always correct, there would be no need to do research. Since intuition is not always correct, we should expect to sometimes be surprised by the results of research.

The word personality refers to patterns of behavior, attitudes, and emotions that are typical of a given individual. Personality traits or characteristics differ from one individual to another, but within a given individual they show some consistency across contexts and some stability over time.

In the past 20 years, research on personality has produced some surprising findings, which have cast doubt on long-held beliefs. Even today, most psychologists still believe that a child's personality is shaped by two forces: “nature,” meaning the child's genes, and “nurture,” meaning the home environment provided by the child's parents. But often the influence of genes is admitted only reluctantly and thereafter is ignored. Developmentalists (psychologists who study child development) have focused almost all their attention on the influence of the parents.

Because developmentalists have little or no power to modify the way parents rear their children, they look for confirmation of their theories in a traditional type of research called correlational research. They measure some aspect of the parents' behavior (e.g., how often the parent praises or hugs the child) and some aspect of the child's behavior or personality (e.g., how well the child gets along with his or her classmates). If a correlation between the two measures is found – if the parents who give a lot of praise or hugs have children who have good relationships with their classmates – the developmentalists conclude that the affectionate parenting is responsible for the children's social success (Maccoby, 2000; Maccoby & Martin, 1983; Pastor, 1981).

The flaw in these studies is that they provide no way of controlling for the influence of genes; heredity is entirely ignored. The research method is therefore incapable of ruling out other possible explanations of the results. Children and parents share 50% of their genes; perhaps the parents are nice to their children, and the children are nice to their classmates, because they both have genes that predispose them to being pleasant and affectionate. Or perhaps children who have genes that predispose them to being pleasant and affectionate are loved more by their parents, and therefore the parents give them more praise and hugs.

The trouble with correlational studies is that correlations tell us nothing about causes or effects – they only tell us which variables co-vary. Nor does the use of a longitudinal method solve the cause-or-effect problem. For example, research on infant attachment has found that babies who have “secure” attachments to their mothers are more likely to have successful social relationships with other people when they are older. But the fact that the measurement of attachment came first doesn't mean we can conclude that attachment is causal. It is possible that babies with certain inherited personality characteristics are more likely to have secure attachments to their mothers, and that these same characteristics also increase the chances that their other relationships will also be successful.

In short, the methods used in traditional developmental research produce results that are ambiguous and uninterpretable. Some portion of a measured correlation may be due to the influence of the environment; some portion may be due to the influence of genes. But how much of each? Until behavioral geneticists devised ways of separating the two kinds of influences, researchers could only guess.

WHAT IS BEHAVIORAL GENETICS?

The field of behavioral genetics had a stormy start; at first, there was a general rejection of its methods and principles. Simply using words like “genetic” or “heredity” was enough to make these researchers the target of political and moral accusations. But over the years – thanks in part to the increased interest in the human genome – these words have become acceptable. Today the evidence is overwhelming that we cannot ignore the genetic and biological substrates of human behavior and personality.

That is a worrisome idea to some people, but it need not be. The fact that a behavior is influenced by genes does not mean that it cannot be changed. Furthermore, the fact that a behavior is influenced by the environment is not necessarily good. If everything that happened to people, good or bad, had the power to change their personalities, then they would be completely at the mercy of unfair environmental circumstances, such as those that exist in underdeveloped countries.

But the fact that all personality characteristics are influenced to some extent by genes was not the surprising result that came out of behavioral genetics; if some people were surprised by it, they shouldn't have been. The truly surprising result was about the environment. The assumption that “environment” is equivalent to “home environment” or “family environment,” and that the most important influence on children is the way their parents bring them up, was not supported by the evidence. In fact, the research showed that for most traits, the effects of growing up in a particular

family are negligible. It turned out that a substantial portion of the variation in human personality and behavior is accounted for neither by the effects of genes nor by the effects of growing up in a particular family.

The goal of behavioral genetics

The objective of behavioral genetics is to explain individual differences in psychological traits by ascribing them to genetic and environmental sources. The research is focused on differences among people; it has nothing to say about characteristics common to every member of the population. Nor can it explain the personality of a single individual.

Francis Galton, a cousin of Charles Darwin, is usually credited with founding the field. It was Galton who realized that psychological traits that are normally distributed, such as personality and intelligence, must be influenced by several genes, not just one. The fact that most traits are the outcome of a number of genes acting together is the cornerstone of quantitative genetics, because it means that the closer the genetic relatedness of two people, the closer the resemblance between them should be. The methods of behavioral genetics are based on this principle.

Accounting for the variance

The purpose of a behavioral genetic study is to account for the variance – to explain the differences from one individual to another in a given group of people, the subjects who take part in the study. Because we can't measure an entire population, we measure a sample of people drawn, preferably at random, from the population. Then we take measurements of that sample: their height, or IQ scores, or scores on a personality test. Generally the measurements will be distributed in the shape of a normal or “bell-shaped” curve. Next, we compute an average: the mean of our sample for the measured characteristic. In some kinds of research, interest is focused on the mean, but in behavioral genetics the focus is on the variance.

Accounting for the variance means finding the causes of the deviations from the mean. What makes one person score high and another score low?

Separating genetic and environmental sources of variance

Traditional research in psychology also looks for ways to explain the variance; a correlation of .30, for example, “accounts,” in a mathematical sense, for 9% of the variance (you square the correlation to get amount of variance accounted for). But, as we al-

ready noted, a correlation can only tell us whether or not two variables vary together. It cannot tell us anything about causes and effects.

Behavioral genetic methods are intended to solve this limitation. The unique feature of these methods is that subjects are recruited for studies not singly but in pairs – usually pairs of twins or siblings. The pairs may differ in how closely they are related genetically: they may be "identical" or monozygotic (MZ) twins, who share 100% of their genes; "fraternal" or dizygotic (DZ) twins, who on average share 50%; full siblings, who also share 50%; half siblings who share 25%; or step- or adoptive siblings, who have no genes in common. Alternatively or in addition, the subjects may differ in the similarity of their childhood environments. Generally only two levels of environmental similarity are possible: either both subjects grew up in the same family (which means that their childhood environments, though not identical, must have been alike in many ways), or they grew up in different families (which means their environments must have differed in many ways). The use of such pairs gives us the ability to ask questions like these: Are siblings[1] who share many genes more alike in personality than those who share fewer genes? How much more alike? Are siblings who grew up in the same family more alike than similar pairs who grew up in different families? How much more alike?

The three components of the variance

For the purpose of this explanation, we will assume that we have given our subjects a personality test that measures a trait called "aggressiveness" and have calculated an aggressiveness score for each subject. We begin by asking what proportion of the variance in aggressiveness is explained by genetic influences of any kind, and what proportion by environmental influences of any kind. For this purpose, the variance V, is assumed to be the sum of three components:

$$V_T=V_g+V_C+V_E$$

Where V_g stands for genetic variance, and V_C+V_E stand for environmental variance. The variance components can be standardized by estimating the proportion of variance accounted for by each of them, by dividing each variance component by the total variance. The standardized components are represented as:

1 We will use the word "siblings" in this chapter to mean all kinds of sibling pairs, including twins and adoptive siblings.

$$h^2 + c^2 + e^2 = 1$$

where h^2, known as heritability, is the genetic variance; c^2 is the variance we will attribute to the environment shared by siblings who grow up in the same family; and e^2 is the variance we will attribute to the "unique" environment – the environment not shared by siblings in the same family.

Of the three, heritability is the easiest to understand. People differ in part because they have different genes. Close relatives are less likely to have different genes than distant relatives; the closer the relationship, the greater the genetic similarity. Thus, to the degree that a trait is influenced by genes, the trait should be more similar in MZ twins than in DZ twins and more similar in biological siblings than in adoptive siblings.

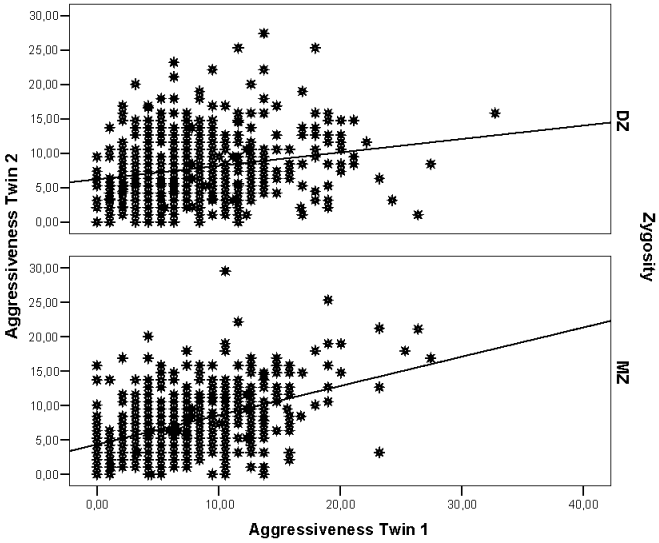

Figure 1.1

Scatterplot of MZ and DZ twins for Aggressive Behavior. (r_{MZ}=.446, r_{DZ}=.214). (Data from the Netherlands Twin Register)

Calculating the second component, c^2 or shared environment (SE) is based on similar reasoning for environment. To the degree that a trait is influenced by the environment, the trait should be more similar in two subjects raised in the same family than in two raised in separate families. Thus, the more similar the environment, the more similar a

pair of subjects should be on a given trait. Two people raised in the same family – even though they undoubtedly have different experiences within the family – will have environments that are more similar than two raised in different families, because the environments of the two raised in different families can differ in so many more ways. For example, a family can be headed by one parent, by two parents who get along well, or by two who are always fighting. These circumstances are likely to differ for people raised in different families but are the same for people raised in the same family. All the stable aspects of the home environment, including many factors (e.g., parents' education and socioeconomic status) that are commonly believed to be important to developmental outcomes, may differ for two people reared in different homes but are the same for those reared in the same home. Two people raised in the same family are likely to have similar environments outside the home as well: they share a neighborhood, schools and teachers, and often (especially in the case of twins) a peer group.

That leaves the last component, e^2, usually called nonshared environment (NSE). This is the variance that is left over after we have subtracted all the variance we can attribute either to shared genes or to shared environment. Another way of describing it is “unexplained variance.” It is not genetic and we cannot attribute it to any aspect of the environment that is the same for both members of a sibling pair and that influences them both in the same way. It includes the effects of any experiences that siblings share but that fail to make them more alike in the measured trait, as well as the effects of any experiences they do not share.

The variance attributed to the NSE is itself made up of three components. First, measurement error: any inaccuracies in our measurements will increase this component of the variance. It is estimated that about 20% of the variance in personality measures and 10% of the variance in IQ is due to measurement error (Plomin, 1990).

The second component is the variance that results from random physiological processes in development, before or after birth. There is not enough room in the genome to specify every detail; thus, the brains of MZ twins differ slightly for the same reason that their fingerprints do. In the uterus, one twin might be in a better position than the other. After they are born, one twin might experience a serious accident or illness. All these factors can lead to physical differences between twins (or ordinary siblings) that are caused neither by their genes nor by their shared environment.

The third and most interesting part of the NSE is the unique experiences that twins or siblings have. Their environments may differ in a number of ways and for a number of reasons. Their mother may love one of them more than the other. They may have different friends or different teachers. If they are ordinary siblings rather than twins,

they differ in age, so one of them grows up with a bossy older sibling while the other grows up with a pesky younger one. If they belong to the same peer group, one of them might have higher status in the group than the other. They might be characterized by their peers in different ways or assigned different roles within the group.

We currently have no way of estimating the amount of NSE variance attributable to random physiological processes or to unique experiences.

Making use of the resemblances between siblings

The first step in estimating the amount of variance that can be attributed to h^2, c^2, and e^2 is to calculate the resemblance in the trait – aggressiveness, in our example – between the pairs of siblings in our study. Each subject is given a test and receives an aggressiveness score. One member of the pair may score high and the other low, or the two may be very similar. On a scatter plot we can plot a point for each subject, with the position on the vertical axis determined by one sibling's score, the position on the horizontal axis by the score of the other sibling. We can calculate a correlation for each group or subgroup of subjects, expressing how similar the pairs are in aggressiveness.

By dividing our subjects into subgroups, we can compare the correlations in aggressiveness between pairs who vary in their genetic relatedness and/or those who did or did not grow up in the same family. According to principles of quantitative genetics, if people who share more genes are more alike, that means that genes must account for some part of the variance among our subjects. Following the same reasoning, if siblings who grew up in the same home are more alike, then the shared environment must account for some part of the variation, The remaining variance, the portion not accounted for by genes or shared environment, will be attributed to the nonshared (unexplained) environment – a component that, as we said, includes measurement error. Thus, we are dividing the total variance into two parts, attributed to two different kinds of causes: (1) causes that produce similarities or correlations between siblings (genes or environment shared by them), and (2) causes that do not produce similarities between pairs but that contribute to the variance among our subjects. Causes of the second kind make the members of a pair neither more alike nor less alike than any two subjects picked at random from our group of subjects.

The design of behavioral genetic studies

Among the lessons taught by behavioral genetic research, perhaps the most important is that no conclusions can be reached about parents' effects on children by studying

only one child per family. It is mandatory to study at least two members of the same family in order to control for genetic influences and to determine whether environmental influences are shared or non-shared.

Adoption designs

Adoption is a natural experiment that creates pairs of individuals in which environment and genes are separated. The most interesting condition is the one in which MZ twins are adopted by different families soon after birth and reared in different homes; the abbreviation MZA is used for these rare pairs. Because they share 100% of their genes and none of their rearing environment, any correlation between them can be attributed entirely to their shared genes. Thus, the correlation between MZA twins is a direct estimate of h^2:

$$h^2 = r_{MZA}$$

The design becomes stronger if our subject pairs include MZ twins reared together (MZT), as well as those reared apart. Now we can estimate the effect of c^2 by subtracting the MZA correlation from the MZT correlation, because the MZT correlation is due to the joint effects of shared genes and shared environment, whereas the MZA correlation is due only to genes:

$$c^2 = r_{MZT} - r_{MZA}$$

Finally, we can subtract c^2 and h^2 (everything that makes siblings more alike) from 1 to estimate the remaining variance or e^2 (everything that fails to make siblings more alike):

$$e^2 = 1 - (c^2 + h^2)$$
$$= 1 - r_{MZT}$$

Similar comparisons can be done with other kinds of family arrangements. The correlation between adoptive parents and their adopted children provides a direct estimate of shared environment effects; that between biological parents and their adopted-away children gives another way of estimating heritability. Note that correlations between parents and children are likely to be lower than correlations between siblings, even though the proportion of genes shared is the same, because parents and children belong to different generations and any generational differences (e.g., due to

cultural changes) will increase the differences between them, moreover the expression of genes may be age dependent as well. For this reason, behavioral geneticists prefer to estimate environmental effects by making comparisons between two adoptive siblings reared in the same home, rather than between adopted children and their adoptive parents.

Twin design

With this design, reared-together MZ twins are compared to reared-together DZ twins. MZ twins share 100% of their genes; DZ twins share, on average, 50%. Because they are the same age, reared-together twins not only share the stable features of their rearing environment (such as parents' education); they also experience changes in family circumstances (a change of residence, a parental divorce) at the same stage of their lives.

$$h^2 + c^2 + e^2 = 1 = S\tan dardized\ \ Variance$$
$$r_{MZ} = h^2 + c^2;$$
$$r_{DZ} = \frac{h^2}{2} + c^2;\ \ thus$$
$$h^2 = 2(r_{MZ} - r_{DZ})$$
$$c^2 = r_{MZ} - h^2;\ \ and$$
$$e^2 = 1 - r_{MZ}$$

Box 1.1

Equations to estimate the components of variance through a twin design (all twins are reared together)

For almost every trait, MZ twins are more similar than DZ twins. We can use this difference in similarity to estimate the different portions of the variance, using the equations in Box 1.1 (Plomin, DeFries, McClearn, & McGuffin, 2001):

These equations are based on the following reasoning. MZ twins share twice as many genes as DZ twins, so if the MZ correlation is about twice the DZ correlation, there must be some effect of genes. If the MZ and DZ correlations are about the same, then no effect of genes has been demonstrated. If the MZ correlation is noticeably smaller than 1, there must be some effect of the non-shared environment. When the DZ correlation is more than half the MZ correlation, that is evidence for a shared environment effect, because it means that the DZ twins are more alike than we would

expect on the basis of their shared genes. This method of estimating the different variance components was described by Falconer (1989). It is assumed that dominance genetic effects are absent, that mating occurs at random in the population, that the within family environments of MZ and DZ twins are equally variable, and that there are no interactions between genes and environment.

However, if the DZ correlation is less than half the MZ correlation, that is an indicative of the presence of dominance genetic effects (d^2). With the classic twin design, the effects of c^2 and d^2 can not be simultaneously estimated because shared environmental effects and non-additive genetic effects have opposite consequences in the difference between MZ and DZ correlations (reducing and increasing the MZ-DZ differences in correlation, respectively). In order to estimate d^2 the MZ and DZ correlations are redefined as follows:

$$r_{MZ} = a^2 + d^2$$
$$r_{DZ} = 1/2\, a^2 + 1/4\, d^2$$

Where a^2 stands for additive genetic effects and d^2 stands for dominance genetic effects. DZ twins share 50% of the additive genetic variance, and 25% of the dominance genetic variance. Therefore, a^2 and d^2 can be estimated as follows:

$$a^2 = 4r_{DZ} - r_{MZ}$$
$$d^2 = 2r_{MZ} - 4r_{DZ}$$

The estimate of $a^2 + d^2$ is known as broad heritability. The heritability is a property of a given population under certain environmental circumstances, and it might not generalize to a different population or after a change in the environmental conditions. Nowadays, more complex data analysis methods like Structural Equation Modeling, and extended family designs allow the study of other sources of variation from non-additive genetic effects, to assortative mating or gene-environment interactions (Neale & Cardon, 1992).

Family designs

In recent years twin and adoption designs have been extended; all kinds of family arrangements and kinship relationships can now be included in a behavioral genetic study. Some critics have objected to the twin and adoption studies by saying that the

lives of twins and adoptees may be different from those of other children. Including ordinary families gets around this objection. It also provides more information, thus improving the accuracy and reliability of the results. Many behavioral geneticists now use complex mathematical models so that kinships of several types can be included in the same analysis. In addition to MZ and DZ twins, these studies may include full siblings and half siblings. Families with adopted children have become harder to find, so an alternative is to use step-siblings: two biologically unrelated children reared in the same home by parents who produced these children in previous partnerships.

Data analyses for such complicated designs consist of finding the solution (the estimates of h^2, c^2, and e^2) that provides the best fit to all the data. This kind of complex design has recently been used by Reiss and his associates (Reiss, Neiderhiser, Hetherington, & Plomin, 2000), in a study we will discuss later in this chapter.

The basic results of behavioral genetic studies

In many areas of psychology, effects tend to be small and unreliable; a result found in one study may fail to be replicated in the next. This is not the case in behavioral genetics. The results found in this field have the quality that statisticians call "robustness." In addition, as we previously noted, the results found in this field are surprising – or were surprising when they were first announced in the 1970s (Loehlin & Nichols, 1976). In fact, the results were so surprising that for a long time they were ignored by most psychologists outside the field of behavioral genetics. It was writers like Plomin and Daniels (1987), Scarr (1992), Rowe (1994), and Harris (1995; 1998) who forced developmentalists and other psychologists to pay attention to the work of the behavioral geneticists.

The results can be summarized quickly. When it comes to personality, genetic effects generally account for 30% to 60% of the variance or around 45% on average. To put it another way, heritability is usually around .45. Shared environment accounts for zero to 10%; the most common result in recent studies is that estimates of shared environmental variance do not differ significantly from zero (Bouchard & Loehlin, 2001). The remainder, about 50%, is non-shared or unexplained environmental variance (NSE). Since this last component includes measurement error, and measurement error accounts for about 20% of the variance in personality scores, this means that genes – more precisely, genetic differences among the subjects – account for a little more than half of the reliable variance (see Figure 1.2).

What is surprising about these results, of course, is the lack of effect of SE. None of the aspects of the environment that siblings share – including most of the factors that were long believed to be important to personality development – have measurable

effects. If they do have effects, the effects are not consistent; perhaps a given environmental factor, such as divorced parents, affects one sibling one way, the other sibling a different way. But bear in mind that many of the subjects in these studies are MZ twins. Why should one twin react one way and the other, the same age and with the same genes, react a different way? Furthermore, though there are some environmental factors, such as divorced parents, that one can imagine might have different effects on different children, there are other factors for which that explanation is less plausible. Consider our example of aggressiveness. Why should having aggressive parents make one child more aggressive and the other more pacific? Traditional theories of personality development would not lead us to expect such an outcome. The whole idea of giving advice to parents is based on the premise that parental behaviors have predictable effects on children. What the behavioral genetic results showed is that parental behaviors such as a tendency to be aggressive either have unpredictable effects or no effects at all.

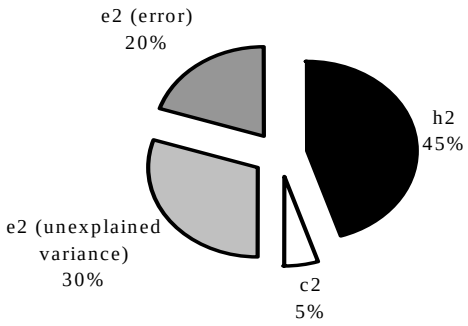

Figure 1.2

Average decomposition of personality variance

At first glance the behavioral genetic results seem to conflict with the results of the thousands of correlational studies produced by developmentalists. But there is no conflict if you look more closely. Developmental studies find correlations between parental behaviors and child outcomes that tend to be small – seldom above .30 and often much smaller. This is inconsistent with the .45 heritability for personality traits found by behavioral geneticists. The correlation between parents and their offspring would approach a maximum of $\frac{1}{2}h^2$ if parents and children where matched for age, no cohort effects were present, and $h^2 = 100\%$.

There are two other things to keep in mind at this point. First, remember that we are talking about proportions of variance explained by anonymous or unknown genes (though, as we will see, efforts are now being made to identify specific genes). Second, estimates of the components of the variance obtained in a given study apply only to the population that the subjects come from. Until the results are replicated in other populations with different demographic features, these estimates cannot be generalized. But most of the results found in behavioral genetic studies have already been replicated in more than one sample, and in some cases in more than one part of the world. The results are remarkably consistent, regardless of the measures used (self-report questionnaires, observations, etc.) or the method (twin, adoption, or family studies). There is no mathematical necessity for a study of reared-apart twins and a study of reared-together adoptive siblings to both give the same result – no effect of shared environment – but they do.

With estimates of the three components of variance in hand, we can now begin to look for potential specific sources of influence: specific genes and specific environmental variables.

GENETIC SOURCES OF VARIANCE

A principle of quantitative genetics is that the inheritance of a given psychological trait depends on the effects of multiple genes. Genes are composed of a sequence of bases: four different molecules situated along the two strands that roll around each other to form the double helix of the DNA (desoxyribonucleic acid) molecule. The bases on one strand are paired with the bases of the other as a result of their structural properties: C (cytosine) pairs with G (guanine), and A (adenine) pairs with T (thymine). The sequence and pairing of base pairs is the language of the DNA that allows it to replicate itself and to direct the synthesis of proteins. Generally, genes are transcribed into RNA (Ribonucleic Acid) that is subsequently translated into protein. The human genome is composed by 3200 Mb (million base pairs) divided over 22 pairs of autosomal chromosomes and 2 sex chromosomes (XX female, XY male). The total number of genes estimated by the Human Genome Project, ranges from 30 000-50 000. The position of a single gene on a chromosome is called a locus.

Genes can be polymorphic, which means they can have various base sequences, called alleles. These variations in sequence are caused by a change, insertion or deletion of bases and are called polymorphisms. The specific combination of two parental alleles in a given person is his or her genotype. Of course a

person has various genotypes across genes. These polymorphic genes are potential sources of observed individual differences in personality traits. The observed or measured characteristics of an individual (which are the result of environmental influences as well as genes) are called the phenotype.

Additive and non-additive genetic effects

There are two kinds of genetic effects. Additive effects are directly transmitted from parents to children. The action of additive polymorphic genes is a consequence of the sum of the allelic effects. They increase parent-offspring resemblance and resemblance between biological siblings.

Non-additive genetic effects depend on a specific combination of alleles; they are not inherited in the usual way; these are genes that do not "breed true." The parents may have characteristics that the children do not have, and vice versa. The reason that they do not breed true is that the combination of alleles is not inherited as a package. Instead, its components are split up during the recombination that occurs during sexual reproduction, and thus the offspring receives only one of two alleles from each parent. Only MZ twins have exactly the same genes – that is, the same alleles, and thus they share the totality of the non-additive genetic effects.

Two different processes may lead to non-additive effects: dominance and epistasis. Dominant genes are not additive because having one allele (at a given locus) is as good as having two, so they break the rule that the more alleles you have of a given trait, the more of that trait you have. Epistasis is when the action of a gene in one locus is to increase the effects of a gene in another locus; in other words, there is an interaction between genes at different loci.

In partitioning the variance, behavioral geneticists often leave out non-additive genetic effects and analyze their data using the "ACE model": A for additive genetic effects, C for shared environment, and E for the non-shared environment. To calculate non-additive effects requires large data sets. The assumption is that non-additive effects are generally too small to seriously affect the results. However, the pattern of MZ-DZ correlations can indicate if the ACE model is appropriate or if an ADE model (with dominance genetic effects) would explain the data better; DZ correlations lower than half the MZ correlations are indicative of the presence of non-additive genetic effects, whereas DZ correlations half or larger than half the MZ correlations are indicative of shared environmental effects. Heritability based on the ACE model (additive effects only) is called narrow_heritability. When non-additive effects are included, the result is called broad heritability.

Heritability is sizable for most traits

In two reviews of the evidence on genetic and environmental sources of personality (Bouchard et al., 2001; Bouchard & McGue, 2003), Thomas Bouchard and his colleagues summarized the evidence from four large twin studies on the "Big Five" dimensions of personality (see Table 1). Also included in this table are the results of two previous summaries of evidence, by Bouchard himself (1997) and by John Loehlin (1992).

Table 1.1

Broad heritabilities of self-report measures of the Big Five factors

	New Studies				Summaries		
Trait	(Jang, Livesley, & Vernon, 1996) Canada	(Waller, 1999) US	(Loehlin, McRae, Costa, & John, 1998) US	(Riemann, Angleitner, & Strelau, 1997) Germany	Mean of the four recent studies	(Loehlin, 1992) Review of Kinships	(Bouchard, 1997) Summary of Literature
Extraversion	.53	.49	.57	.56	.54	.49	.54
Agreebleness	.41	.33	.51	.42	.42	.35	.52
Conscientiousness	.44	.48	.52	.53	.49	.38	.40
Neuroticism	.41	.42	.58	.52	.48	.41	.58
Openness	.61	.58	.56	.53	.47	.45	.52
number of MZ pairs	123	313	490	660			
number of DZ pairs	127	91	317	304			

The reported results show the broad heritabilities (additive plus non-additive) for the five most general personality traits. Heritabilities between .40 and .60 are consistently found, with minor differences between traits. One curious result on the right side of the table is that studies based only on twins (Bouchard, 1997) lead to higher h^2 estimates than those based on other kinships (Loehlin, 1992). This is probably due to the presence of non-additive effects, always shared by MZ twins. In a recent publication, Keller and colleages (2005) used an extended families design analyzing data on the Eysenck's and Cloninger's personality dimensions, from 9672 twins and 3241 of their siblings. They found that the non-additive genetics effects explained 12-36% of the variance, and generally accounted for more variation than did additive genetic variance. Thus, differences in personality seem to have a genetic origin, but they are not shared by parents and their offspring.

Other psychological characteristics often included under the heading of personality, such as social attitudes, religiousness, and psychological interests have also been explored with genetically informative designs. You probably would expect lower heritabilities and stronger environmental influences for such characteristics. E.g. Boomsma et al. (1999) found that family resemblance in religious attitude could be entirely explained by the shared environment in adolescent Dutch twins. However, although genetic factors hardly influenced social attitudes during the first few years of life, the contribution of genetic factors to differences in attitudes rises to the same proportions as in personality later in adulthood. This is what Eaves and colleagues (1999) found in a study of extended kinships of adult twins, with their parents, siblings, spouses and adult children. However, the authors found that a high degree of marital resemblance (assortative mating), as well as the impact of parental attitudes on offspring attitudes (cultural inheritance) are also relevant sources of family resemblance for social attitudes, as opposed to personality.

The search for specific genes

Now that we know that genetic differences account for a substantial part of the variation in personality, we are ready to look for specific gene variations (alleles). The researcher's job is to look for genes that could be related to psychological differences – genes that act in the brain. (Such genes may also have actions elsewhere in the body.) Finding such genetic variations would, in turn provide us with a new and valuable research tool. Correlations between genotypes and behavioral characteristics are unambiguous with regard to causality: DNA can cause personality traits but changes in personality traits cannot cause changes in DNA, although they could change gene expression.

Because all personality traits are influenced by a number of genes acting together, the potential size of the effect of the variation in a single gene is likely to be small – perhaps only 1% to 4% of the total variance in a given trait. An individual gene that combines with other genes to influence a given trait is called a Quantitative Trait Locus or QTL.

The search for specific variations in the genetic code that could account for genetic variance in personality began only recently, in 1996 (Benjamin et al., 1996). Ebstein, Benjamin, and Belmaker (2002) have listed some of the criteria that researchers use to select one polymorphism for the study of personality traits:

- Do the alleles differ in their physiological action?
- Are the base pairs of the gene responsible for the coding of proteins?
- Is the gene expressed in an appropriate brain region?

- Is the gene implicated in the functioning of some relevant neurotransmission?

If the answer to most of those questions is positive, then a given polymorphic gene can be selected as a target for further study. We will describe two polymorphisms that have been selected as promising candidates in personality studies.

DRD4. This gene is related to the functioning of dopamine in brain reward and approach systems. Chromosome 11 (see Figure 4), contains a repetition of a sequence of 16 bases. The alleles vary in the number of times that the sequence is repeated, from 2 to 10. Personality scores are compared between people with long versions of the gene (7 repeats or more) and people with short versions (5 repeats or less). There is some evidence that people with the long alleles tend to show higher scores on sensation-seeking. The long alleles have also been related to disorganized attachment in children, attention deficits, and addictive behaviors such as alcoholism and heroin addiction. However, the results are not always replicated. A recent quantitative review (McGue, 2002) concluded that, although the mean effect size of the long allele is significant, there is substantial variability in the results across studies that is still unexplained.

Figure 1.3.

Locus of the DRD4 polymorphism on chromosome 11

5-HTT. This gene, also called serotonin transporter (SERT), on chromosome 17 (see Figure 5), was targeted because it is related to the functioning of the serotonin system. Serotonin is the neurotransmitter that is targeted by antidepressants such as Prozac; like Prozac, the 5-HTT gene is involved in regulating re-uptake of serotonin in brain synapses (Lesch et al., 1995). This neurotransmitter has effects on moods and emotions, cognition, sensory processing, motor activity and circadian rhythms (Lesch, 2002). A polymorphism in the promoter region of the gene consists of 2 alleles, the short allele, associated with lower efficiency of the serotonin system, has 14 repeats of a particular series of bases; the long one has 16 repeats. The short allele has been related to higher scores on neuroticism and various measures of anxiety, but the results are variable (Middeldorp et al., 2006) and the effect sizes are rather small (3% to 4%

of the total variance). McGue (2002) concluded that the mean effect size of the short allele on neuroticism was not statistically significant.

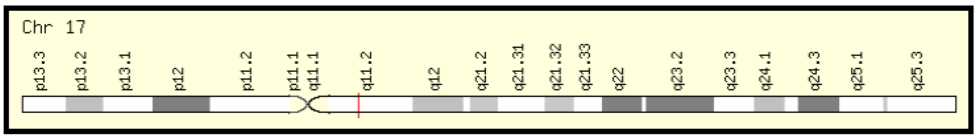

Figure1.3

Locus of the 5-HTTPLR on chromosome 17

Though failures to replicate preliminary findings are discouraging, the search for genes has just begun. New data produced by the Human Genome Project will lead to the identification of more target genes. To prepare for the future, researchers in the behavioral sciences – and eventually mental health practitioners in the clinic – will have to accustom themselves to the use of DNA analyses and results.

ENVIRONMENTAL SOURCES OF VARIANCE

As we explained, behavioral genetic methods divide the environmental variance into two components, that shared by siblings who grow up in the same family (SE, for shared environment) and that not shared by siblings who grow up in the same family (NSE). By definition, SE influences are anything that makes the siblings more alike. NSE influences do not make the siblings more alike but also do not make them more different: in regard to the variance attributed to NSE, siblings are neither more alike nor less alike, on average, than any two subjects drawn from the same population. This is an important point to keep in mind, because the NSE is sometimes misleadingly defined as “the environment that makes siblings different,” which makes people think that there must be some factor – children's desire to differentiate themselves from their siblings, or the parents' efforts to treat them as separate individuals – that causes them to become less alike. If that were the case, however, then the correlations between siblings reared together should be lower than those between siblings reared apart, and there should be negative correlations between adoptive siblings. That is not what is found. There is no evidence that growing up together makes siblings less alike. In some ways, at least during childhood and adolescence, siblings reared together are slightly more alike than siblings reared apart. Table 2 shows estimates of SE and NSE from Rowe (1994).

Table 1.2

Environmental effects for the Big Five personality traits (Rowe, 1994)

	SE	NSE
Extraversion	.02	.49
Agreeableness	.09	.52
Conscientiousness	.05	.55
Neuroticism	.07	.52
Openness	.06	.49
Mean	.06	.51

Other studies have yielded even lower estimates for SE. In a large sample of 4298 pairs of twins over the age of 17, no significant SE effects were found for any aspect of personality as assessed by the Multidimensional Personality Questionnaire (Finkel & McGue, 1997).

Efforts to find the sources of shared environment effects

Since SE effects are so low for most aspects of personality, it almost seems pointless to look for their source. The startling fact about SE is how little it matters. The lack of significant effects of SE means, for example, that people who grew up in tidy, well-organized homes run by conscientious parents are, on average, no higher in conscientiousness than people who grew up in homes run by happy-go-lucky slobs. If there were any tendency for people reared in well-organized homes to be more conscientious as adults, then two people reared in the same home would be more alike in conscientiousness than two reared in different homes.

However, there are a few characteristics that do show some SE effects. There is a modest correlation in IQ between young siblings growing up together – even adoptive siblings – but this correlation declines to zero by the time they reach adulthood (Plomin, Chipuer, & Neiderhiser, 1994). More relevant to our interests here are certain similarities in behavior, especially in adolescent delinquency and the use of substances such as alcohol and tobacco. To understand these effects, it is important to remember that the “shared” environment for siblings includes the environment they share outside the home. In fact, it does appear to be the environment they share outside the home that causes siblings to resemble each other in delinquency and substance use. Rowe (1997) has shown that non-twin siblings who are close in age and who spend a lot of time together outside the home are more likely to resemble each other in the extent to which they commit delinquent acts during the teenage years. Breaking laws and using alcohol or drugs are activities that teenagers engage in outside the home, in the company of their friends. We interpret the SE effects on delinquency and substance use as neighborhood or peer group effects.

Efforts to find the sources of non-shared environmental effects

The fact that growing up in a particular home seems to have little or no lasting effect on personality should not be misunderstood: it does not mean that the environment is unimportant, and it certainly does not mean that everything is genetic. It means that we do not yet know what aspects of the environment are the important shapers of personality, which means that we do not yet know how personality is shaped. The aspects of the environment that were formerly thought to be important have been shown to have negligible effects, so the search is now on for something to take their place.

The 1987 article by Plomin and Daniels titled "Why are the children in the same family so different from one another?" was the first in a chain of articles and books that eventually led to greater interest in the non-shared kind of environment and to research programs designed to search for specific sources of NSE. On theoretical grounds, five areas appear to offer the most promise:

- Structural characteristics of the family (e.g., birth order, age and gender differences between siblings)
- Differential parental treatment (the fact that a parent might behave differently to different children – e.g, give one more affection than the other)
- Differential sibling interaction (e.g., one sibling might be dominated by the other)
- Differential experiences outside the home (e.g., two siblings might be treated differently by peers or teachers)
- Differential life events (e.g., one sibling has an experience, such as a serious injury, that changes the course of his or her life)

Within-family differences in environment

The first reaction to the surprising findings about SE and NSE was rather conservative. If those aspects of the family environment shared by siblings do not matter, then maybe what matters is those aspects of the family environment not shared by siblings – for example, birth order. Two studies were specifically designed to look for sources of NSE effects.

The first was a meta-analysis by Turkheimer and Waldron (2000). Turkheimer and Waldron collected all the relevant studies they were able to find, 43 in all. The results were disappointing. The mean effect size was 0.041, which means that the environmental measures studied explained, on average, only 4% of the NSE variance in psychological traits (including intelligence and adjustment, as well as personality). Of the factors that were examined, the smallest effects were found for family constella-

tion variables, including birth order and sex of siblings; on average these variables accounted for only 1% of the variance. The largest effects – though still quite small – came from studies that examined the effects of interactions with peers and teachers; these studies accounted, on average, for 5% of the variance.

Table 1.3 summarizes the findings of Turkheimer and Waldron.

Table 1.3

Amount of variance (in percent) accounted for by various environmental measures, as reported by Turkheimer and Waldron (2000)

Environmental measure	% of variance explained
Family constellation	1.1
Differential parental behavior	2.3
Differential sibling interaction	2.4
Differential peer or teacher interaction	5.3
All measured environmental variables put together	13.3

The second major attempt to find the sources of NSE effects was a well-designed longitudinal study by Reiss and his colleagues (2000). This was a powerful study because it included six different types of sibling pairs: MZ twins, DZ twins, full siblings, half-siblings, and step-siblings, growing up in the same family. All the families were headed by two parents. The 708 pairs of siblings were examined twice, about two years apart. The study spanned the years of adolescence; the average age of the participants was around 13 years on the first occasion and 15 on the second, but the range of ages was wide: 10 to 21.

Reiss and his colleagues collected a large number of measures of the environment and a large number of measures of the behavior, personality, and adjustment of the adolescents. Most of the measures were based on separate reports from two or more individuals, averaged together. For example, the amount of conflict between a given parent and a given child was judged by each parent separately, and also judged by the child. Sibling conflict was judged by both parents and by both siblings. The result of all this work was summarized by Reiss et al. in a few sentences:

> "*We can say with confidence that, on the basis of the data we collected, the following family characteristics do not reflect nongenetic, nonshared influences on the adolescent: differential marital conflict about the adolescent versus the sib, differential parenting toward siblings, and asymmetrical relationships the sibs construct with each other. . . . Given that our very large twelve-year study was designed to identify nonge-*

> *netic, nonshared factors, this dearth of findings is not only disappointing but galvanizing.*" (Reiss et al., 2000, pp. 406-407)

Reiss and colleagues found differences between the siblings, and found differences in the way their parents behaved toward them. The reason that their data did not account for the effects of the NSE was that the differential behavior by parents appeared to be a response to, rather than the cause of, the personality differences between the siblings. The parents were responding to genetic differences between their children. In other words, what Reiss et al. found was a gene-environment correlation, which we will now explain.

GENE-ENVIRONMENT CORRELATIONS AND INTERACTIONS

Until now we have been talking about the independent or main effects of genes and environment. But these factors do not always act independently: for example, measures of the environment, such as how a parent behaves to a child or what kind of home the parent provides, may be affected in various ways by genetic factors. We've just mentioned one example of this: the parent's behavior is, in part, a reaction to the genetic characteristics of the child.

Three kinds of gene-environment correlations

A gene-environment r(G,E) correlation is found when differences in people's genotypes produce differences in their environments. Because of their genetic characteristics (or the genetic characteristics of their parents, which they may inherit), children experience different environments. Because of their genetic characteristics, children choose different environments for themselves. There are three kinds of r(G,E)correlations.

Passive r(G,E)correlations. One reason why genes are correlated with the rearing environment is that parents provide both to their children: genes and environment. Since parents and their biological children share genes, and since the parents' genes have an influence on the kind of environment they provide, the home environment that children experience is likely to be somewhat concordant with their genetic propensities. For example, parents who love to read are likely to provide their children with a home full of books. Their children are likely to become adults who love to read – a finding that traditional developmentalists generally attribute to the book-filled envi-

ronment provided by the parents. But if we controlled for genes using behavioral genetic methods, we would find that the love of reading is mostly or completely explained by genetic factors: the children inherited their love of reading from their book-loving parents.

It is important to remember that a parent's child-rearing style is influenced by the parent's personality (Losoya, Callor, Rowe, & Golsmith, 1997); for example, parents with warm, outgoing personalities tend to give their children more affection. Since the parent's personality is in part a function of genes, and since each parent passes on 50% of his or her genes to each offspring, we would expect to find correlations between the parents' child-rearing styles and the children's personalities. Interestingly, Losoya et al. (1997) found that when adopted children grow up and have children of their own, they show no signs of SE effects on their own child-rearing styles. Two adoptees reared in the same home are as unalike in their child-rearing styles as two adoptees picked at random.

Reactive (also called evocative) r(G,E)correlations. Another explanation of the book-loving children is possible: perhaps their parents provide them with lots of books because that is what the children want and ask for. The way parents (and other people) act toward a given child is in part a function of the child's genetic characteristics. People are more affectionate with an agreeable child than with one who is irritable or obstinate. They are likely to use harsher disciplinary techniques with a very active or defiant child. The associations that Reiss et al. (2000) found between differential parenting and genetic differences between siblings were reactive r(G,E) correlations.

Active r(G,E)correlations. As children get older, they become more able to select and modify their environments according to their genetic predispositions and their genetically influenced abilities and interests. The kid who likes reading will frequent libraries and bookstores, will gravitate toward a peer group with an academic orientation, and will seek out a mate who also enjoys reading.

Can r(G,E)correlations account for the unexplained variance?

Some psychologists have tried to use r(G,E) correlations to account for the lack of effects of shared environment and to explain why virtually all of the nongenetic variance is of the non-shared sort. The idea is that “people make their own environments” and that the environments they make cause them to “grow up to be individually different” (Scarr, 1992, pp. 1-2). Both statements are true but unfortunately they do not explain the NSE variation in personality. People make their own environments because they are genetically different; it is their genotypes that cause them to choose certain environments (e.g., studious friends) and that cause people to react to them in

certain ways (e.g., by buying them books or taking them to museums). To the extent that an individual's non-shared environment is correlated with his or her genes, the effects of that environment will contribute to genetic variance (Purcell, 2002). That is why Harris (1998, p. 30) calls r(G,E) correlations “indirect genetic effects.” They are the effects of the effects of the genes.

The standard methods of behavioral genetics cannot separate the effects of r(G,E) correlations from the genetic portion of the variance. Researchers are currently working on new methods to do so – for example, by looking for new ways to measure the environment (Purcell, 2002). Eventually, though, the solution to the problem will come from the study of the genes themselves. Once researchers have discovered the effects of various genes or combinations of genes, they will be able to calculate “pure” genetic effects and thus separate the direct effects of the genes from the indirect effects.

GxE Interactions

Currently, many developmentalists are pinning their hopes on GxE interactions. They are hoping that these interactions will solve the problem of the unexplained NSE variance in a way that will preserve the importance of the family environment, in which they strongly believe. These hopes are based on the fact that GxE interactions, unlike GxE correlations, do contribute to the nonshared nongenetic variance. However, interactions between genes and the rearing environment contribute to the genetic variance, i.e. when the effect of the shared environment depends on the genotype of the child.

A GxE interaction occurs when individuals with different genotypes react differently to a given environmental condition or experience. Thus, if parents use a harsh, authoritarian method of child-rearing, their children may react in different ways. A timid child might be afraid of punishment and become passive and obedient, whereas a bolder one might be motivated to rebel.

Can GxE interactions account for the unexplained variance?

There is no question that GxE interactions occur. But there are three problems with trying to use them to explain the NSE variance. The first is that none of the GxE interactions that have been found and replicated are of the sort in which a child with one genotype reacts one way and a child with a different genotype reacts in a completely different way. The replicable GxE interactions that have been reported are all of the kind in which children with a particular genotype are more sensitive to a particular environmental condition. The children with a different genotype either don't react at all or show a milder reaction (Caspi et al., 2002; McGue, 2002).

The second problem with using GxE interactions to account for NSE effects is that they cannot explain the differences between MZ twins. MZ twins have the same genotype; thus, they should react in the same way to a given environmental condition. If they don't react in the same way, it cannot be because of a GxE interaction. A GxE interaction requires that there be a difference in genes; thus, another explanation is required to account for the differences between MZ twins. The study by Reiss et al. (2000) showed that the nongenetic differences in personality and adjustment between MZ twins are about as large as those between other sibling pairs; the researchers found no important differences in SE or NSE across the six different kinds of sibling pairs in their study. This implies that whatever nongenetic influences make DZ twins, ordinary siblings, and step-siblings differ from each other also make MZ twins differ from each other. And, as we noted, GxE interactions can not account for the nongenetic differences between MZ twins.

GxE interactions are difficult to study. When found, they tend to be small (McGue, 2002). The interactions that turn up in one study often fail to be replicated in the next study.

One reason the effects are so small and unreliable is that until recently researchers have had no way to directly measure an individual's genotype. A recent study published in the journal Science (Caspi et al., 2003) offers hope that the identification of specific genes might aid in the search for GxE interactions. The researchers compared adults (age 26) with short and long alleles for the 5-HTT gene, which, as we previously mentioned, regulates the serotonin system. The researchers also asked the subjects about stressful life events, relating to jobs, relationships, health, and so on, that had occurred in the past five years. The results showed that people with the short 5-HTT allele were significantly more likely to develop a serious depression in response to stressful life events. In the absence of stressful life events, these people were hardly distinguishable from those with the long allele, but their genetic vulnerability showed up when their lives became stressful. There was a statistical interaction between alleles, life events, and depression; subjects with long alleles were less likely to get depressed if they experienced stressful events.

An important point, often overlooked, is that the tendency to have stressful life events has itself been shown to have significant heritability (Plomin & Bergeman, 1991). Some people evidently have a genetic predisposition for getting themselves involved in potentially stressful situations. This means that a statistical interaction between the 5-HTT genotype, stressful life events, and depression could be a GxG interaction (an interaction between the 5-HTT gene and other, unknown genes), rather than a true GxE interaction. However, Caspi et al. (2003) ruled out that possibility by

showing that the environmental variable (stressful life events) correlated with depression in subjects with the short allele only if the stressful life events came first, before the depression. Having stressful life events between the ages of 21 and 26 was not related to depression before the age of 21. If it were a GxG interaction, having the short allele plus stressful life events should be related to depression at any age.

The heritability of the tendency to have stressful life events shows how difficult it is to find "pure" measures of environment. Genes influence virtually all of the choices people make in life and the outcomes of these choices: whether they get married and whether their marriages are successful, what career they pick and how well they do in it, whether they are prone to having accidents, and so on. This means that some of the variation in the environments that parents provide to their children can be attributed to the parents' genes (passive GxE correlations) or to the genes of the children themselves (reactive GxE correlations).

SOURCES OF STABILITY AND CHANGE

The word personality refers to aspects of behavior that are relatively stable over time and across situations or contexts – relatively stable, not perfectly stable. To some extent, behavior is the product of an individual's stable tendencies; to some extent it is a product of the specific context. Thus, there is always a mixture of change and stability. But even for the portion of behavior that is due to stable personality, there are changes during development. The stability that does occur is of two kinds, differential and absolute

Differential *continuity* refers to the consistency of differences between individuals in a given trait. For example, although an introverted person may behave in a more extraverted way at a party, an extravert will behave in an even more extraverted way, and thus the differences between them will be maintained. Evidence from longitudinal studies shows high levels of differential continuity across the life span (Caspi & Roberts, 2001).

Absolute *continuity* is related to the stability or change in the mean scores, averaged across many individuals of the same age. It is a function of the way people change as they get older. Evidence suggests that there are small changes in the mean levels of some personality traits with age: extraversion and agreeableness tend to increase, while neuroticism tends to decrease. These changes are about equally experienced by everybody (Caspi et al., 2001).

Since behavioral genetics is more concerned with variation between individuals than within individuals, its main object of study is the differential kind of continuity.

Stability and change across the life span

The standard way to study the differential stability of personality is to measure a sample of subjects at two points in time and calculate the correlation between the two scores of each individual. This correlation is called the stability coefficient (also known as test-retest reliability). A review (Roberts & DelVecchio, 2000) showed that stability coefficients increase with age and decrease as the interval between the two measurements grows longer. This can be interpreted as showing that, as we grow older, our behavior becomes more a function of our stable personality and less influenced by our immediate context. The stability coefficient keeps increasing until middle age. It is around .30 in childhood, .65 in early adulthood, and .75 at age 50.

Few longitudinal studies have attempted to disentangle the genetic and environmental sources of stability and change in personality. We will summarize the available evidence.

Child and adolescent samples. The study by Reiss et al. (2000), with an adolescent sample, found that genetic factors were the strongest mediators of stability, accounting, on average, for 58% of the stable variance in measures of adolescents competence (e.g.. sociability, autonomy, self worth). Shared and non-shared environment accounted for a negligible part of stability (SE, 15%; NSE, 9%). On the other hand, the NSE was important in explaining developmental changes, explaining an average of 35% of the change, whereas genes explained 37% of the variance in developmental changes. This means that a significant part of the changes that occur during development are foreordained by the genes.

Adult samples. Early studies with various personality scales, and a more recent study with the Multidimensional Personality Questionnaire (McGue, Bacon, & Lykken, 1993) show the same pattern: over 80% of the stable component of personality is explained by genetic factors, and over 70% of the personality change is attributable to the NSE. The heritability of change is much smaller but is also significant. The SE does not account for either stability or change. Thus, it appears that genetic propensities are largely responsible for the stable personality differences among people. The environment, while accounting for a great part of variability, mainly has only temporary effects on behavior and personality.

Mechanisms of genetic and environmental stability and change

The mechanisms producing stability and change have so far been anonymous. Can we draw any conclusions about them, or at least make any guesses?

Genetic mechanisms. According to Reiss et al. (2000), genetic effects on stability might act in three ways. First, the biological effects of some genes could continue to act during the entire life span. Second, some genes could influence the early development of neurobiological systems in the brain, which thereafter remain stable. Third, the effects of genes could be perpetrated and reinforced through GxE correlations. With regard to developmental changes, genes could be responsible in at least two ways. First, cellular mechanisms might produce changes in the gene's expression due to natural developmental processes – genes turn on and off during development – or to changes in the environment. Second, GxE interactions might occur, causing genes to be expressed in some environments (e.g., the home environment of early childhood) but not in others.

Environmental mechanisms. The NSE seems to produce changes through some environmental influences that are differently experienced by siblings and that have a strong impact for a period of time but then fade and disappear. These experiences may be part of daily life (e.g., school, work, or leisure activities) or come from life events differently perceived by siblings (e.g., the loss of a parent through divorce or death).

These findings on stability and change in personality should lead to a reconsideration of methods used to explore the environment. Not only does the method need to control for genetic effects, but more longitudinal studies are needed, given that the major effects of the environment are responsible for changes rather than long-term stability in personality.

ENVIRONMENT AND PERSONALITY: CURRENT EXPLANATIONS AND FUTURE DIRECTIONS

What do we know at present? We know that the environment accounts for 50% of the variation in personality at a given point in time, but this result applies mostly to the big 3 or the big 5 personality traits, say neuroticism, extroversion, psychoticism, agreeableness, openness and conscientiousness. We know that the environment that matters is the one not shared by siblings growing up in the same family. We know that environmental forces outside the home are more likely to account for part of that vari-

ance. And we know that the influential forces of the environment will change over time, because the evidence indicates that the NSE mainly accounts for change.

What do we not yet know? We still have no clear idea of the specific characteristics of the environment that produce differences in personality, or of the causal mechanisms leading to those differences. We do not know if the general results apply to other personality traits that have received less attention from psychologists, but that have been found to be related with socially relevant factors like health or delinquency, e.g., sensation seeking, anger, aggressive behavior or hostility.

What do we think? The present state of the art has produced diverse reactions. Authors such as Turkheimer and Waldron (2000) argue that the effects of the environment could be all interaction and little main effect, and that we do not have the statistical power or appropriate methodologies to detect these interactions. Along the same lines, Roberts and Caspi (2002) have argued that the effects of a single environmental factor is too small to lead to significant differences in a single point in time and that the environment acts continuously in a cumulative manner.

Other authors believe that the explanation of the NSE may be randomness – environmental or biological or both. Environmentally oriented writers (e.g., Reiss et al, 2000) state that environmental factors act randomly and it is unlikely that we will ever find consistent effects on psychological traits. Biologically oriented authors (Molenaar, Boomsma, & Dolan, 1993) believe that the NSE may not really be environmental at all, but rather the result of random and chaotic processes involved in the early development of the nervous system.

Still other writers (McGue et al., 1993; Scarr, 1992) argue that differences in environments do not have long-lasting effects on personality as long as they are within the normal range – the kinds of environment typically provided by members of our species to their infants and children – but that extreme circumstances, outside the normal range, might have noticeable effects.

Finally, Judith Harris (1995, 1998) proposes an integrative "Group Socialization Theory" in which the main environmental agent is the peer group, which shapes personality differences through a process of within-group differentiation. The backbone of her proposal is that learning is context-specific; thus, a change of group or context may lead to a change in personality, depending on the norms of the new group, the way the individual is characterized by the new group, or the social demands of the new context.

These proposals are responses to overwhelming evidence pointing to the need of a change in our concept of environment. None of them have been proved but they all give clues that may point us toward the true answer or answers.

FUTURE RESEARCH ON THE ENVIRONMENT

Future research on the environment will have to take into account all available evidence and be meticulous in the design and methods applied. Here are some suggested guidelines for those future designs:

- It is mandatory to use designs that control for genetic effects in order to correctly study environmental effects. We cannot tell what the environment does to the child without taking into account what the child brings to the environment.
- The environmental forces we are looking for are, in general, not shared by siblings in the same family.
- Better measures of the environment should be developed, and the individual should be considered as an active participant.
- More longitudinal studies should be conducted, because such studies may have a better chance of detecting the mechanisms that underlie NSE effects.
- We should be cautious about generalizing results from studies done on specific developmental periods. Effects found in children often vanish by adulthood. Adolescence seems to be a special period of life when results may differ from other periods. More studies should be conducted with adult samples or with different generations of the same family (e.g. twins and their parents or children).
- Outside-the-family variables appear to be more promising than the family ones. Only 8 out of the 43 studies analyzed by Turkheimer and Waldron (2000) included such variables. We should move our research interests out of the family.
- Reports from parents do not always agree with reports from children or from observers outside the family. We should explore these differences and be careful about pooling reports.

There are two aspects of research on which up-to-date developmentalists and behavioral geneticists are now in agreement: both acknowledge that children are active participants in shaping their own environments, and both recognize the necessity to develop new measures of environment. In addition to objective measures of the environment, there is now more interest in the subjective environment: the possibility that a given environment may be perceived differently by different individuals. Though a variable under study may appear to be shared, it may be experienced differently by each member of the family.

There is much that we already know about the environment, but much more that we do not yet know.

OUTLINE OF THE THESIS

The present thesis represents a contribution to the identification of the basic dimensions of personality from a psychobiological perspective (Eysenck, 1992a; Zuckerman, 1992). To this end, we made use of the personality data from the ongoing longitudinal study of the Netherlands Twin Register (Boomsma et al., 2002). Data from close to twenty thousand individuals from twin families have been collected in six survey studies over twelve years from 1991 to 2002. The sample size, the composition, and the longitudinal character of these data make of them an invaluable resource for the study the structure of personality and its sources of variance. Chapter 2 contains a simulation study that gauges the degree of bias produced by the dependency of family data on the estimates of standard errors and chi-squared, when they are treated as independent observations in a phenotypic model. In addition chapter 2 assesses the efficiency of an estimator, which corrects for dependency. This estimator is applied in subsequent chapters. In Chapter 3, following an overview of the leading psychobiological theories of personality (the theories of Eysenck, Gray, Cloninger and Zukerman) contains an empirical study of the structure of personality. The aim of this study is to shed light on the composition and characteristics of the third factor (or factors) beyond Extroversion and Neuroticism, by making use of a longitudinal design to control for inter and intra-individual differences in personality due to age. The remainder of this thesis addresses the genetics of three components of this third factor, namely Type A Behavior, Anger, and Aggression. These studies provide the beginning of the study of the characteristics of this third factor as a possible basic dimension of personality. In chapter 4 the genetic and environmental influences of Type A Behavior are studied using an extended twin design (twins and their parents) in an attempt to identify the presence of non-additive genetic effects and sibling interaction effects. Chapter 5 addresses the same issues with respect to the trait anger, by incorporating a repeated measures design that increased the power to detect replicable effects. Finally, in chapter 6, we used the analysis of individual growth curves to study individual changes in aggression as well as the genetics of aggression at age 18, in a sample of twins from 11 to 40 years old who participated in four survey studies between 1991 and 2000. The last chapter offers a general discussion of the findings and future directions.

Chapter 2

PHENOTYPIC FACTOR ANALYSIS OF FAMILY DATA: CORRECTION OF THE BIAS DUE TO DEPENDENCY

Irene Rebollo, Marleen H.M. de Moor, Conor V. Dolan & Dorret I. Boomsma

This Chapter is based on: Rebollo, I., de Moor, M.H., Dolan, C.V. & Boomsma, D.I. (In Press). Phenotypic factor analysis of family data: correction of the bias due to dependency. Twin Research and Human Genetics.

Twin registries form an exceptionally rich source of information, which is largely unexploited for phenotypic analyses. One obstacle to straightforward phenotypic statistical analysis is the inherent dependency, which is due to the clustering of cases within families. The present simulation study gauges the degree of the bias produced by the dependency of family data on the estimates of standard errors and chi-squared, when they are treated as independent observations in a phenotypic model, and assess the efficiency of an estimator, which corrects for dependency.

When family-clustered data are used for phenotypic analysis, in treating individuals as independent, and using standard Maximum Likelihood estimation, there is a tendency for the chi-square statistic to be overestimated and the standard errors of the parameters to be underestimated. The bias increases with family resemblance, due to heritability or shared environment. The source of family resemblance –either heritability (h^2) and/or shared environment (c^2)- interacts with the composition of the sample. In the absence of c^2, samples with twins, parents and spouses show the lowest bias, whereas in the presence of c^2 samples with only twins show the lowest bias. In all conditions the bias remained below 15%. The use of the 'complex option' available in Mplus (clustering corrected Robust Maximum Likelihood estimation) reduces the bias to the levels observed when only independent cases are considered. Thus with the use of robust estimates the bias due to family dependency becomes practically negligible in all conditions of dependency.

In conclusion, the present study shows that the bias due to dependency in family data does not form a serious obstacle to phenotypic data analysis.

INTRODUCTION

Twin registries form an exceptionally rich source of information due to a unique combination of characteristics. First, they generally comprise many thousands of cases. Second, the variety of measured phenotypes is large, including many psychological, biological, and clinical traits as well as important sociological and demographical information. In addition, increasingly, next of kin of twins are included (i.e., parents, siblings, spouses, children of the twins, etc.). This allows for the study of cohort effects, cultural transmission, and rater bias, and also increases the generalizability of the results to the general population. Finally, a very useful aspect of registries is that they often include longitudinal data. As Busjahn stated: "The virtue of a twin register is not so much determined by the existing database of measures but by the ability to get back to the twins to add phenotypes in a hypothesis-driven manner" (Busjahn, 2002, p.vi). At present twin registries have been

established in several countries around the world (see Boomsma, 1998; Martin, 2002), and more often than not these registries include similar or even identical phenotypic measures, which facilitates replication, and allows for cross-cultural comparisons.

Twin registries were established primarily to advance the study of genetic and environmental contributions to phenotypic individual differences. However, given the amount of information and the sample sizes, they form a rich, yet largely unexploited, source of information for phenotypic analyses (i.e., not addressing genetic or environmental sources of variance). One obstacle to straightforward phenotypic statistical analysis is the inherent dependency, which is due to the clustering of cases within families. It is generally known that simply treating dependent data as independent in phenotypic analyses results in bias in standard errors and other test (e.g., goodness of fit) statistics (Laplante & Hebert, 2001).

Published articles in which family data serve purely phenotypic analyses are scarce (Brown et al., 2002; Kirk, Hickie, & Martin, 1999), whereas it is quite common to apply some kind of phenotypic factor analysis (i.e. exploratory factor analysis, principal components analysis, or confirmatory factor analysis) to the measures studied, prior to the intended genetic modeling (Edwards, Austin, Newman, Mayer, & Selby, 1994; Eley et al., 2003; Jonnal, Gardner, Prescott, & Kendler, 2000; Tozzi et al., 2004; Wade, Wilkinson, & Ben Tovim, 2003). When confronted with the problem of non-independence of the data, the researchers usually either ignore it, adopt complicated (yet still approximate) methods for accommodating dependency (van der Sluis et al., 2005), or opt for splitting the sample and analyzing data of independent individuals only. In most cases, splitting the sample may amount to discarding as much as half of the data. This is clearly a drawback, which is exacerbated when data on multiple family members is available, since not only the size of the sample is reduced, but also the representativeness of the sample may be diminished.

The aim of the present simulation study is to gauge the degree of the bias produced by the dependency of family data on parameters, standard errors and chi-square estimates, when they are treated as independent observations in a phenotypic model, and to assess the efficiency of an estimator, which corrects for dependency. The study was designed to be representative of large and small twin registers, with and without extended family data. We consider a common factor model, with two correlated latent factors; such a model is often employed in preliminary data reduction to investigate the structure of the measures under study, and the relationship between latent constructs. We consider the effects of heritability,

shared environment, family size, and estimation method on the accuracy of the parameter estimates (factor loadings, residual variances, and variance-covariance structure of the latent factors), their standard errors, and the chi-square (likelihood ratio) goodness of fit test. We hypothesized that 1) larger family resemblance due to heritability or shared environment will produce a decrease in the accuracy of the estimates of SE (standard errors) and chi-square; 2) when family resemblance is exclusively due to heritability, including other members of the family besides the twins, like parents or spouses, will decrease the similarity among the members of each cluster, and thus reduce the dependency and subsequent bias in the estimates of SE and Chi-square; and 3) the use of Normal Theory Maximum Likelihood estimation (Azzelini, 1996; Bollen, 1989) will lead to less accurate estimates than Robust Maximum Likelihood estimation corrected for clustering (Muthén & Satorra, 1995).

METHOD

The procedure that we followed consists of two steps: (1) Simulation of family (clustered) data using a common pathway model; and (2) Phenotypic analysis of the simulated data, fitting a phenotypic factor model with two correlated latent factors.

Simulation of family data

A common pathway model (Neale et al., 1992) with two common factors was used to generate family (clustered) data. Figure 2.1 shows the path diagram of the simulated model, for a family of DZ (dizygotic) twins, their parents and spouses.

In the simulated model, the covariance between six observed variables (V1-V6) is explained by two phenotypic correlated latent factors (F_1-F_2). The first three variables are indicators of the first factor, and the last three variables are indicators of the second factor. The values of the factor loadings and residual variances were chosen in order to have reasonable and varying signal-noise ratios: the percentage of variance explained by the latent factors was 83% for V1 and V4, 60% for V2 and V5 and 40% for V3 and V6. The same measurement model was generated for all family members: Twin 1 (T1), Twin 2 (T2), Father (F), Mother (M), and spouses of the twins (S1 and S2).

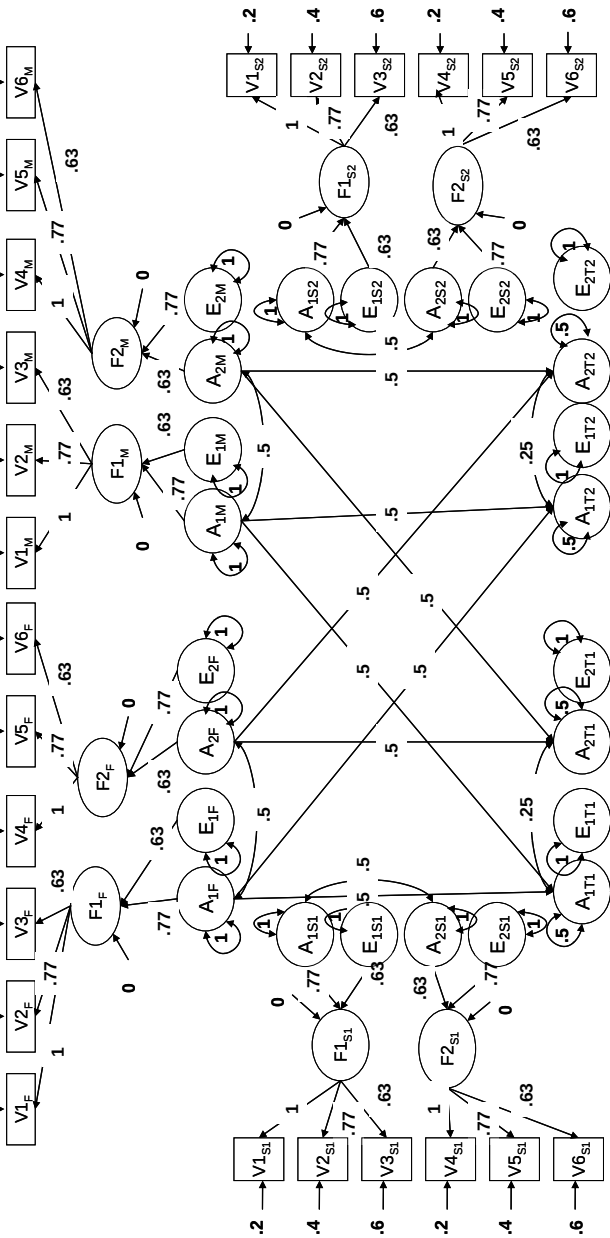

Figure 2.1

***Simulated common pathway model**: Path diagram depicted for conditions: FS = 6 (Twins, parents and spouses), Heritability = 60-40. Model depicted for DZ twin families. DZ twins share 50% of their additive genetic variance inherited form their parents, as showed in the figure. MZ twins share 100% of their additive genetic variance and thus, the MZ model includes and additional correlation path of 0.5 across genetic factors $A_{1T1} \leftrightarrow A_{1T2}$ and $A_{2T1} \leftrightarrow A_{2T2}$. T1: twin 1, T2: Twin 2, F: Father, M: Mother, S1: Spouse of twin 1, S2: Spouse of twin 2. V1-V6: observed variables, F1, F2: Common factors 1 and 2, A: Additive genetic effects, E: Non-shared environmental effects.*

In the first set of simulations familial clustering of the data was explained by an additive genetic component (A_1 for F_1 and A_2 for F_2). The variance of each latent factor was additionally explained by a unique environmental component (E_1 for F_1 and E_2 for F_2). A genetic correlation of 0.5 between the two additive genetic components of the two phenotypic factors was modeled, assuming that both latent factors are correlated due to common genetic variance. Parents and offspring share 50% of the additive genetic variance, as do DZ twins on average (Falconer, 1989). MZ (monozygotic) twins share the totality of the genetic variance, and thus the MZ model contains an additional correlation of 0.5 between the genetic factors of the twins $A_{1T1} \leftrightarrow A_{1T2}$ and $A_{2T1} \leftrightarrow A_{2T2}$ (not depicted in the figure), which, added to the 0.5 shared through the parents, makes the expected additive genetic correlation of 1.

In a second set of simulations, a general shared environmental factor 'C' was added to the variance components A and E. This factor was meant to represent environmental conditions such as socio-economic status, or diet that might increase family resemblance across parents and their offspring, and between spouses. The general latent factor C had loadings on all the phenotypic factors F1 and F2 in all the family members.

The means of the observed variables (intercepts) as well as the means of the latent factors were fixed to zero in the simulated model. The observed variables and latent factors were multivariate normally distributed.

The simulated model includes a number of features that affect the dependency generated among family members. These features were chosen so as to resemble the empirical results found for most psychological variables studied in adult samples. Specifically, in the first set of simulations family resemblance is due to genetic factors, and effects of shared environment are absent. Under these conditions parents and twins, and the twins pairs themselves form dependent cases, whereas the spouses are mutually independent. These conditions apply to personality variables measured in adult samples (Bouchard et al., 2003). In the second set of simulations, the possible effects of shared environment and assortative mating were added to the model through a general shared environmental factor. Under this condition all family members, including the spouses, form dependent cases. The results of this condition apply to cognitive abilities (Bouchard et al., 2003), and to social attitudes (Eaves et al., 1999).

Two factors were varied in the simulation study: (1) The degree of family resemblance through the heritability of the latent factors, and the inclusion of the C factor, and (2) family size and composition. (1) In the first set of simulations three levels of heritability were chosen: A40-A40 (0.40 for both F1 and F2), A60-A40 (0.60 for F1 and 0.40 for F2) and A60-A60 (0.60 for F1 and F2). In the second set of simulations

heritability was chosen to equal 0.35 for both factors, and the amount of variance explained by the C factor was 0.25 for both factors (A35-C25). In this second set of simulations the degree of resemblance between twins was equivalent to that of the A60-A60 condition, with the difference that part of it is due to shared environment, which also produces resemblance across the other family members. (2) Three levels of family size (FS) were chosen: FS = 6 (twins, parents and spouses of the twins), FS = 4 (twins and parents), and FS = 2 (twins).

For the first set of simulations sample size was also varied to represent typical sample sizes of large and small twin registries (Martin, 2002). Simulations that represented large twin registries had a sample size of 2000 families (1000 MZ, 1000 DZ), and included 9 conditions (3 conditions of heritability X 3 conditions of FS). Simulations that represented small twin registries had a sample size of 500 families (250 MZ, 250 DZ), and included the 3 levels of heritability -family size was not varied as small twin registries often do not include other family members-.

First, we carried out 1000 replications for each heritability condition with FS = 6 and sample size = 2000. We created conditions FS = 4 and FS = 2 by selecting a subset of the generated sample, as would be done with a real data set. Secondly, we carried out 1000 replications for each heritability condition with FS = 2 and sample size = 500. Finally, we carried out 1000 replications for the A35-C25 condition with FS = 6 and sample size = 2000. We created the conditions FS = 4 and/ FS = 2 by selecting a subset of the generated sample. We created missing data in percentages similar to those observed in the adult sample of the Netherlands Twin Registry (NTR) as a function of family membership: 5% for twins, 35% for parents, and 60% for spouses.

The datasets were generated[2] using a Monte Carlo procedure in Mplus Version 3.13 (Muthén & Muthén, 2005). The same model used to generate the data was fitted to the 1000 data sets using the internal Monte Carlo procedure in Mplus to ensure that the parameter values were correctly recovered. Replications that did not converge or gave inadmissible parameter estimates were excluded from further analyses.

Phenotypic analysis of family data: analysis of bias

First, the generated data sets were re-structured so that each member of the family was treated as an independent case, while retaining information about family membership. Thus, the new data sets contained six observed variables (V1-V6), and a cluster variable (family identification number). The sample size for each condition is equal to the

2 The Mplus scripts used to generate and analyze the data are available upon request to the first author.

number of families times the family size (e.g., number of families = 2000 and FS = 6 gave rise to a new sample size of 12000).

Subsequently, we analyzed these newly created datasets in Mplus using the Monte Carlo procedure. A phenotypic factor model with two correlated latent factors was fitted using two types of estimation. The first was Normal Theory Maximum Likelihood (ML) estimation, which assumes that the data are normally, identically, and independently distributed. The second type of estimation used was Robust Maximum Likelihood (MLR) in combination with the "Complex" option in Mplus, which takes into account clustering of the data. The parameter estimates are ML estimates, whereas the standard errors are corrected for the dependency in the data. The correction is made by using a weight matrix that involves fourth-order moments and contains cluster information. The chi-square statistic is scale-corrected. The scale is a function of the same weight matrix and the degrees of freedom of the model (For further details about the correction, see Muthén & Satorra, 1995) (For further details about the correlations, see Muthén et al., 1995). The family was used as the cluster unit for the correction.

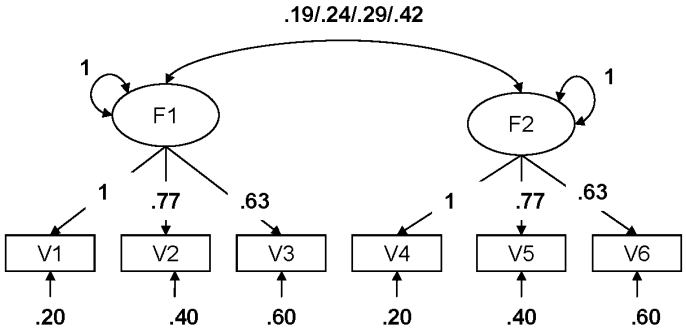

Figure 2.2.

Phenotypic two correlated latent factor model*: the diagram contains the true population values based on the simulation model. The three correlations between the latent factors correspond respectively to the conditions A40-A40, A60-A40, A60-A60 and A35-C25.*

We compared the bias produced in the parameter estimates, standard errors, and chi-square statistic by the dependence of family data across heritability and FS conditions, and across the two types of estimation methods. For the first set of simulations, we expected the largest bias for the condition A60-A60 and FS = 2, and the smallest bias for the condition A40-A40 and FS = 6. For the second set of simulations, for condition

A35-C25, we expected the bias for FS=2 to be equivalent to that of the condition A60-A60. However, we expected the bias for FS=4 or 6 to be larger than in the first set of simulations, due to the family resemblance produced by the general C. Given that the assumptions of the ML estimation are not met, we expected that it would provide biased estimates of SE and Chi-square statistic. We expected the MLR estimation with correction for clustering to reduce the bias in all conditions.

The percentage relative bias was used to evaluate the accuracy of the chi-square statistic, parameter estimates, and standard errors. The percentage relative bias is computed as $\left({(\hat{\theta} - \theta)}/{\theta} \right) * 100$, where $\hat{\theta}$ is the mean estimated value of chi-square, parameter estimates and standard errors across replications and θ is the true population value. Figure 2.2 shows the fitted model including the true parameter values (factor loadings, residual variances, and variance-covariance of the latent factors) as chosen in the simulation study. The latent factors were scaled by fixing the first factor loading to 1, and the variances of the latent factors were freely estimated. The means of the observed variables were zero in the model. The expected value of the chi-square statistic equals the number of degrees of freedom (DF) asymptotically. The DF of the model equal 14, i.e., 27 (observed statistics) - 13 (estimated parameters). To assess the effects of the standard errors, we compare the means of the standard error over replications with the standard deviations of the parameter estimates over replications. The mean standard deviation provides the criterion in assessing the accuracy of the standard errors, because given that the assumptions of the ML estimation are satisfied, the latter should equal the former asymptotically.

We considered both the mean chi-square, and the distribution of the chi-square by comparing the proportion of replications for which the critical values are exceeded with the expected proportions (0.05 and 0.01) under a chi-square distribution, when fitting the correct model.

Finally, we fitted the phenotypic factor model to the data of a single member of the family (twin 1). This enables the comparison of the results for data with different degrees of dependency with the results for data that are independent.

RESULTS

The Monte Carlo procedure in Mplus (which both simulates and analyzes the data) showed that the true parameter values were correctly recovered in more than 95% of the replications in all simulation conditions. For the replications with sample size equal to 2000, 4.5% of the replications of the 40-40 heritability condition, 3.7% of the

60-40 condition, 4.1% of the 60-60 condition, and 2.3% of the A35-C25 condition were excluded from further analyses, because of non-convergence or inadmissible estimates. For replications with family size equal to 500 all replications converged and gave acceptable parameter estimates.

Table 2.1 shows the relative bias in the estimation of the chi-squared statistic. The analyses of dependent family data as independent using ML result in an overestimation of the chi-square statistic. In addition, the probability of the true model being rejected (error type I) tends to be larger than expected under a central chi-squared distribution. For the first set of simulations, the bias increases with higher heritability, and it tends to be larger when twins and parents are analyzed. For the second set of simulations, with a general C component, the size of the bias in the chi-square for FS=2 was equivalent to that of the A60-A60 condition. However, the pattern of results for FS was inverted, so that the amount of bias increased with the inclusion of parents and spouses in the sample. However, it should be noted that overall the bias in the chi-squared statistic is quite small, ranging from 2%-11% across all conditions. The same pattern of results is shown for sample sizes 2000 and 500, although the overestimation of the chi-square for FS = 2 appears to be larger for the smaller sample size. This result does not seem to be a consequence of the sample size, but probably a random product of the simulation process. This can be inferred from the observation of the relative bias when only twin 1 was analyzed (FS=1). For all heritability conditions, for N = 500 and FS = 1 the relative bias was slightly positive, whereas for N = 2000 and FS = 1 the relative bias was negative. The difference in relative bias between conditions FS = 2 and FS = 1 is equivalent for N=2000 and N=500 (4.1/4.1, 4.9/5.2, 6.1/6.3 for the three heritability conditions respectively).

When the clustered data are analyzed using the complex estimation in Mplus, the bias due to dependency is corrected for all conditions, and the estimates of the chi-square return to the levels obtained under independent sampling (see FS=1 in table 2.1), and the distribution of the chi-square, in terms of nominal and observed error rates, is well approximated.

Table 2.2 shows the percentage of relative bias of the parameter estimates. In all, 13 parameters were freely estimated in the factor model (6 residual variances, 4 factor loadings, 2 latent factor variances and one correlation). The tables show the mean bias across all parameter estimates in relative and absolute values. The parameter estimates were perfectly recovered across all conditions, with percentages of absolute bias always below 1%.

Table 2.1

Bias on Chi-square statistic and its distribution: Percentage Relative Bias on the Chi-square (14 Degrees of Freedom) statistic over the replications and proportion of replications for which the critical value is exceeded.

Family Size	Estimation Method (Mplus)[a]	Percentage Relative Bias on Chi-square				Observed proportion for Expected proportion= .05				Observed proportion for Expected proportion= .01			
		A40-A40	A60-A40	A60-A60	A35-C25	A40-A40	A60-A40	A60-A60	A35-C25	A40-A40	A60-A40	A60-A60	A35-C25
N(families)=2000													
6: Twins, Parents & Spouses (N=11806)[b]	General	2.600	3.807	4.914	11.143	.067	.070	.079	.110	.022	.022	.022	.038
	Complex	-1.907	-1.829	-1.829	-2.400	.057	.054	.057	0.50	.016	.015	.012	0.12
4: Twins & Parents (N=7992)	General	4.314	5.836	7.300	9.350	.072	.078	.086	.094	.021	.022	.023	.032
	Complex	-1.757	-1.743	-1.764	-2.271	.045	.051	.052	.052	.016	.017	.016	.022
2: Twins (N=4000)	General	2.221	3.000	3.950	3.936	.060	.062	.069	.068	.013	.014	.017	.016
	Complex	-1.264	-1.364	-1.321	-1.457	.044	.047	.048	.046	.009	.013	.012	.009
1: Twin 1 (N=2000)	General	-1.907	-1.943	-2.143	-1.764	.044	.046	.043	.049	.015	.015	.013	.015
N(families)=500													
2: Twins (N=1000)	General	4.279	5.436	6.500		.071	.076	.079		.008	.010	.015	
	Complex	0.643	0.779	0.764		.062	.058	.057		.006	.008	.008	
1: Twin 1 (N=500)	General	0.179	0.150	0.129		.047	.046	.045		.011	.011	.010	

[a] *General: ML. Complex: MLR with cluster correction.*

[b] *Actual sample size, smaller than number of families X family size due to missingness.*

Table 2.3 shows the percentage of relative bias on the standard errors (SE) averaged across all parameter estimates. When the family data are analyzed using ML the SE of the parameter estimates tend to be underestimated, judging by the mean relative values. For the first set of simulations, the bias is larger when the heritability is greater, and when only twins are analyzed, compared to conditions where parents and spouses are included. For the second set of simulations, the pattern is again inverted so that the bias is lowest when only twins are analyzed. The size of the bias for the A35-C25 condition for FS=2 is similar to that for the A60-A60 condition, whereas the size of the bias gets larger for FS=4 or 6. However, again the bias is quite small: in no condition does the average exceed 15%, or the maximum exceed 20%. The bias fluctuates across parameter estimates, as it can be appreciated in the difference between the relative and the absolute value of the mean bias. Furthermore, the pattern of results and the size of the bias are comparable for sample sizes equal to 2000 and 500.

When the complex estimation method of Mplus is used to estimate the factor model, the negative bias in the SE is corrected across all conditions, so that the mean percentage relative bias shows values close to zero or slightly positive, i.e., comparable to the values obtained when the data are independent, i.e., data of single family members.. However, the size of bias of the SE was not equal across all parameter estimates. The estimates of the variances and covariance of the common factors display the largest bias. Table 2.4 shows the mean percentage relative bias and the percentage of total bias in these 3 parameters.

Table 2.2

Percentage relative bias on parameter estimates (not affected by estimation method)

	Mean Bias (Mean |Bias|)[a]			
Family Size	A40-A40	A60-A40	A60-A60	A35-C25
N(families)=2000				
6: Twins, Parents & Spouses (N=11806)[b]	-0.126(0.231)	-0.119(0.234)	-0.122(0.234)	0.021(0.077)
4: Twins & Parents (N=7992)	-0.129(0.253)	-0.117(0.255)	-0.119(0.256)	0.026(0.089)
2: Twins (N=4000)	-0.095(0.248)	-0.089(0.268)	-0.093(0.263)	0.054(0.115)
1: Twin 1 (N=2000)	-0.167(0.234)	-0.154(0.262)	-0.156(0.267)	-0.002(0.103)
N(families)=500				
2: Twins (N=1000)	-0.267(0.288)	-0.276(0.297)	-0.283(0.309)	
1: Twin 1 (N=500)	-0.388(0.472)	-0.394(0.489)	-0.412(0.514)	

[a] *Mean Bias: Mean of Parameter Bias across all parameter estimates. Mean |Bias|: Mean of Parameter Bias in absolute value across all parameter estimates.*

[b] *Actual sample size, smaller than number of families X family size due to missingness.*

When the family clustered data are analyzed using ML estimation, the SE of the parameter estimates of the latent factors are consistently underestimated between 2.7 and 7.5% across conditions in the first set of simulations, and between -8.9 and 11.45 in the second set of simulations. The pattern across heritability and family size conditions resembles the one observed for all the parameters. In the first set, the bias is larger for higher heritability values and for FS=2 or 4. For the second set, the bias is smallest for FS=2. When the Mplus complex estimation method is used to correct for clustering, the bias is reduced to values comparable to those obtained with FS=1, remaining under 2%.

Table 2.3

Percentage relative bias on Standard Errors across all parameter estimates

Family Size	Estimation Method (Mplus)[c]	Mean Bias(Mean |Bias|)[a] A40-A40	A60-A40	A60-A60	A35-C25
N(families)=2000					
6: Twins, Parents & Spouses (N=11806)[b]	General	-0.496(2.011)	-0.408(2.182)	-0.689(2.581)	-2.206(4.243)
	Complex	0.125(1.996)	0.345(1.734)	0.541(1.813)	0.519(2.208)
4: Twins & Parents (N=7992)	General	-0.405(2.335)	-0.744(2.722)	-1.055(3.007)	-2.567(4.120)
	Complex	0.382(1.548)	0.416(1.562)	0.406(1.423)	0.155(1.508)
2: Twins (N=4000)	General	-0.786(2.448)	-1.122(2.664)	-1.429(3.013)	-1.932(3.367)
	Complex	-0.086(2.172)	-0.132(2.234)	-0.172(2.167)	-0.289(2.137)
1: Twin 1 (N=2000)	General	-0.581(1.748)	0.024(1.837)	-0.053(1.976)	-0.194(2.131)
N(families)=500					
2: Twins (N=1000)	General	-0.609(1.494)	-0.902(1.844)	-1.065(2.155)	
	Complex	-0.029(1.546)	0.005(1.673)	0.208(1.764)	
1: Twin 1 (N=500)	General	-0.999(1.930)	-0.969(1.927)	-0.952(1.972)	

[a] *Mean Bias: Mean Bias across SE of all parameter estimates. Mean |Bias|: Mean Bias in absolute value across SE of all parameter estimates.*

[b] *Actual sample size, smaller than number of families X family size due to missingness.*

[c] *General: ML. Complex: MLR with cluster correction.*

DISCUSSION

The results of the simulation study indicated there is a tendency for the chi-square statistic to be overestimated, and the standard errors of the parameters underestimated. when standard ML estimation is used to analyze family clustered data, and dependent individuals are treated as independent cases. Furthermore, the distribution of the chi-square is affected, resulting in an increase in Type I errors. When fitting a model with common latent factors, most of the bias is localized in the SE of the variances and covariances of the common factors.

Table 2.4

Percentage relative bias on Standard Errors for variances and covariance of the latent factors

Family Size	Estimation Method (Mplus)[c]	Mean Bias(Mean |Bias|)[a]				%of SE Bias in the model due to the bias on variances and covariance of the latent factors			
		A40-A40	A60-A40	A60-A60	A35-C25	A40-A40	A60-A40	A60-A60	A35-C25
N(families)=2000									
6: Twins, Parents & Spouses (N=11806)[b]	General	-2.743(2.743)	-3.526(3.526)	-5.240(5.240)	-11.452(11.452)	31.48%	37.28%	46.84%	62.28%
	Complex	0.145(2.480)	-0.031(1.813)	0.088(1.911)	0.354(2.636)	28.67%	24.12%	24.32%	27.54%
4: Twins & Parents (N=7992)	General	-4.107(4.107)	-5.847(5.847)	-7.517(7.517)	-12.665(12.665)	40.58%	49.57%	57.68%	70.94%
	Complex	-0.956(0.956)	-0.823(0.823)	-0.920(0.920)	-0.868(1.346)	14.25%	12.15%	14.92%	20.60%
2: Twins (N=4000)	General	-3.625(4.638)	-5.093(5.093)	-7.192(7.192)	-8.912(8.912)	43.73%	44.11%	55.09%	61.08%
	Complex	-0.803(3.234)	-1.028(3.000)	-1.756(3.542)	-1.612(3.403)	34.36%	30.99%	37.71%	36.74%
1: Twin 1 (N=2000)	General	-1.040(1.295)	-0.495(1.033)	-1.047(1.047)	-0.974(0.974)	17.079%	12.97%	12.23%	10.55%
N(families)=500									
2: Twins (N=1000)	General	-1.537(1.537)	-2.729(2.729)	-4.081(4.081)		23.73%	34.14%	43.70%	
	Complex	1.171(1.559)	1.416(1.986)	1.644(2.218)		23.28%	27.38%	29.01%	
1: Twin 1 (N=500)	General	1.566(1.566)	1.701(1.701)	1.834(1.834)		18.73%	20.37%	21.46%	

[a] *Mean Bias: Mean Bias across SE of variances and covariance of the latent factors. Mean |Bias|: Mean Bias in absolute value across SE of variances and covariance of the latent factors.*

[b] *Actual sample size, smaller than number of families X family size due to missingness.*

[c] *General: ML. Complex: MLR with cluster correction.*

Figure 2.3 shows an overview of the results across conditions. It can be observed how, under ML estimation, the positive bias in the chi-square and the negative bias in SE increase with family resemblance. Family size and the source of family resemblance interact. In the absence of C, samples with twins, parents and spouses show the lowest bias, whereas under the presence of C, samples with only twins show the lowest bias. The effect of family resemblance on the bias is independent of sample size. The results for A60-A60 and A35-C35 conditions suggests that it is the total amount of family resemblance, and not its nature, that determines the amount of bias produced in the SE when only twins are analyzed.

Figure 2.3 clearly depicts how the use of the corrected MLR (complex) estimation reduces the bias across all conditions to the levels observed when only independent cases are considered.

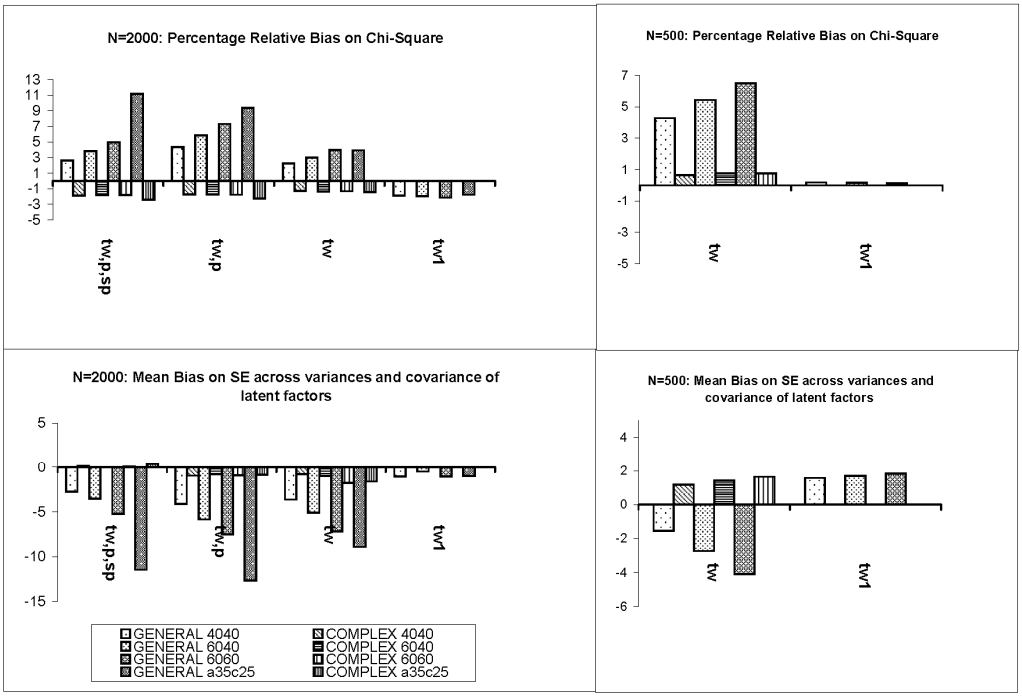

Figure 2.3

***Summary of results**: Percentage relative bias on Chi-squared statistic, and Mean bias on SE of parameter estimates of the latent factors F1 and F2 are depicted across conditions. Tw: twins, p: parents, sp: spouses, tw1: twin 1.*

These results were concordant with the hypotheses, except for the bias on the chi-square across family size conditions in the first set of simulations. We expected the largest bias in both SE and Chi-Square in the FS=2 condition. Whereas the SE bias follows the predicted pattern, the Chi-square bias turned out to be lowest in this condition, and highest for FS = 4. However, with such a small amount of bias, we do not consider these slight differences between FS conditions to be a cause of concern.

It must be noted that the scope of the present study is somewhat limited by the assumptions of the simulated model and sampling conditions. Further simulations will reveal whether varying certain conditions will give rise to significantly different results. Such condition may pertain to different kinds of phenotypic analysis or theoretical models, larger number of observed variables, the inclusion of other kinds of relatives (siblings, children of twins, etc.), or unbalanced number of MZ and DZ families. On the other hand, the good outcome of the MLR correction due to clustering, might be due to aggregatability. According to Muthén & Satorra (1995) a 2-level factor model is aggregatable if the factor loading matrices are equal on the within-cluster and between cluster levels. In the present paper we have used a common pathway model that assumes that the measurement model for E and A has the same structure. The results might not apply when the variance decomposition of the phenotype is better explained by an independent pathway model, for which the factor structures of A and E differ significantly.

Although the results appear to be quite acceptable, the method for correcting for dependency (i.e., the 'complex' option in Mplus) is approximate as the cluster unit used is the family. This implies that the correction is undertaken assuming that the dependency is homogeneous across family members, so the same correction is applied, for example, to MZ and DZ families, or to spouses, parents and twins. However, the problem of different model structures for different family members could to some extent be handled in a multiple group analysis. Alternative strategies to obtain adjusted estimates are possible: e.g. replication methods like bootstrap (Laplante et al., 2001), or treating each family as a case and fitting the model in the diagonal within person part of the matrix, estimating the off diagonal elements as nuisance parameters (for a detailed explanation of this method using Mx (Neale, Boker, Xie, & Maes, 2003), (see van der Sluis et al., 2005). However, the complex option in Mplus does arguably provide the easiest, if approximate, way to correct for dependency.

Multilevel structural equation modeling and hierarchical linear mixed modeling is often used to handle data clustering (Hox & Maas, 2001; Muthén et al., 1995). With these methods the variance-covariance matrix is decomposed into within and between cluster components. Using the family as a cluster implies that all the variance due to

the differences among the members of the same family is analyzed in the within level part of the model, whereas the variance due to the differences between different families is analyzed in the between level part of the model. In real settings the exact sources of resemblance between family members may be unknown, and therefore it is also unknown which components of the variance (genetic, shared environment, non-shared environment, assortative mating etc.) are placed in the within and between parts of the model. Under these conditions, it is unclear how the parameter estimates within each level can be interpreted, or how they can be related to the true values obtained under phenotypic analysis with independent sampling. This problem is exacerbated when data from extended pedigrees are analyzed, because the sources of differences and resemblance between each pair of members of the family are different, and the family is treated as a homogeneous cluster in multilevel modeling. Therefore, multilevel modeling assumes that the family members are statistically equivalent, whereas with the multivariate approach it would be possible to give different parameter values to different family members.

Summing up, through the use of robust estimates the bias due to family dependency becomes practically negligible. Even if no correction is applied, the point estimates are correct, and if the chi-square statistic indicates a good model fit ($p>.05$), it is certain that the same conclusion would be attained with independent data. However certain precautions should be taken when interpreting the results of uncorrected solutions. It is possible that certain parameters appear to be statistically significant, whereas they may actually be non-significant in the analysis of truly independent observations. If the chi-square statistic indicates poor model fit ($p<.05$), there is a small probability that a good model fit would have been obtained with independent data, because of the increase in type I error due to dependency. If family data are used for phenotypic analysis with no correction for the inherent dependency, one should take into account that the nature of the family resemblance for the given trait, and the family composition of the sample interact to result in larger or smaller amounts of bias in the SE. When variation in the phenotype under study is exclusively due to genetic and non-shared environmental effects, an extended family sample will result in a smaller bias, whereas if family resemblance in the phenotype under study is also due to shared environment, cultural transmission or assortative mating, the use of an extended family sample will result in a larger amount of bias.

In conclusion, the present study shows that the gains of using the richness of family data from twin registers for phenotypic analysis outweighs the relatively small drawbacks of slight bias in SE and chi-square statistic. More importantly, it shows that irrespective of the source of family resemblance or dependency, the bias is successfully corrected by the MLR estimation with clustering correction of the Mplus program.

Chapter 3

Basic Dimensions of Personality Revisited on a Sample of 17557 Individuals from the Netherlands Twin Register: The Third Factor in Psychobiological Theories

INTRODUCTION

Personality and psychobiological theories

In order to describe, explain, and predict consistent patterns of behavior, psychologists and others have used different terms, such as personality, temperament, or character. The observation of consistent specific responses across different situations and over time supports the inference of habitual reactions, which may be intercorrelated. The term trait is invoked to denote a cluster of correlated habitual reactions. Examples include sociability, responsibility, aggressivity, or thoughtfulness. From the analysis of correlations among a variety of traits, *supertraits or personality types* emerge, such as Neuroticism or Extroversion (Eysenck, 1982). The objectives of assessment may dictate whether specific responses, or habitual reactions are of greater interest. Whether a trait-level or type-level analysis is preferable depends on the aims of the assessment. Traits and types are known to be more consistent, reliable, and replicable across culture, sex, and age, and may therefore be viewed as a more suitable level of analysis for the development of explanatory theories (Zuckerman, 1991).

The number and the nature of the basic dimensions or personality types required to explain major behavioral differences have been a matter of debate for a long time. Recent numbers have varied from Cattel's 16 (1957), to Eysenck's 3 (Eysenck & Eysenck, 1985) or Gray's 2 (Gray, 1987), passing through the five factor model (FFM), originally proposed by Norman (Norman, 1963), and recently the focus of increasing interest, thanks to the research of Costa and McRae (McCrae & Costa, 1997). From the perspective of differential psychology, a given trait should be reliably identified and replicated in factor structures, and should show certain stability across time, if it is to be considered a basic dimension of personality. From this perspective, the FFM has received a good deal of support, and its factor analytic structure is considered to be well established. However, its support originates largely in factor analytic results, and the FFM model is based on classification of trait adjectives in natural language (Eysenck, 1992a; Tomita et al., 2000). From a psychobiological perspective, basic personality traits are considered the outcome of evolutionary processes, and therefore must be based on differences in the functioning of certain biological structures that are, at least, partially heritable (Zuckerman, 1991). According to Eysenck (Eysenck, 1992a) and Zuckerman (Zuckerman, 1992; Zuckerman, Kuhlman, Joireman, Teta, & Kraft, 1993), the definition of a *basic* trait of personality cannot be established solely by factor analysis. In this paper, we focus on three influential psychobiological theories of personality, that is, the theories of Eysenck (1985), Gray (1987), and Cloninger (1993). We also consider Zuckerman's revision of Gray's

theory (Zuckerman, 1991), which represents an attempt to reconcile findings from animal and human studies.

Eysenck (1985) posited three basic personality types defined by positions on three orthogonal dimensions of personality: *Extroversion-Introversion (E), Neuroticism-emotional stability (N),* and *Psychoticism (P).* Extroverts are sociable, dominant and assertive, optimistic and vital, with a tendency to enjoy activity, to be aggressive, anger easily, and to lack control over their emotions. In contrast, introverts tend to be quiet, withdrawn, and reserved. They are reticent and enjoy order, carefully control their emotions, and are frustrated by difficulty, but rarely behave aggressively. Individual differences in E are associated with arousability of the reticulo-cortical circuit, through which perceptual stimuli influence the brain activity. People seek a moderate 'ideal' level of arousal through their behavior, i.e., by regulating, seeking or avoiding, stimulation. Introverts are generally over-aroused, whereas extroverts are under-aroused; therefore the levels of arousal influence conditionability, and so the higher threshold of introverts renders them more susceptible to conditioning, compared to extroverts, who need more stimulation.

Individuals, who are highly neurotic, are anxious, emotional, unstable, prone to depression, irrational, and tense. Stable individuals are organized, and like routine and careful planning, they are unconcerned and well-balanced. N is associated with differences in arousability of the limbic circuit, such that high neuroticism is characterized by a higher sensitivity to emotional stimulation. Emotional stability facilitates conditioning.

The P dimension comprises a combination of impulsivity, lack of empathy, aggressiveness, sensation seeking, and lack of interest in others. Eysenck (1992b; 1997) suggested that it might be related to the serotonergic or dopaminergic functions.

Gray (1987), working in an experimental psychology tradition, developed his theory on the basis of a modification of Eysenck's E and N dimensions, in which he emphasized the importance of the interaction between innate personality differences and the type of stimulation. Gray developed the Conceptual Nervous System (CNS), composed of different behavioral systems, which determine the behavioral reaction to different kinds of stimuli. Differences in basic personality traits are a reflection of differences in the sensitivity of these systems.

In his discussion of these systems, Gray (1987) distinguishes between unconditioned and conditioned stimuli, and between appetitive and aversive stimuli. Each behavioral system within the CNS responds to a certain combination of these types of stimuli: (1) The Fight Flight System (FFS) responds directly to unconditioned punishment or absence of reward by activating behavior either through flight or fight (i.e.,

aggressive) reaction. Differences in the sensitivity of the FFS have been linked to the medial hypothalamus and the amygdala. (2) The consumatory mechanisms respond to unconditioned reward with approach behavior. (3) The Behavioral Activation System (BAS) is activated by conditioned signals of reward and non-punishment, and increases the probability of approach behavior. Individual differences in the BAS are associated with differences in impulsivity. The functioning of the BAS is associated with mesolimbic dopaminergic pathways. (4) The Behavioral Inhibition System (BIS) responds to fear that is elicited by conditioned signals of punishment, non-reward, or novel stimuli. Sensitivity of the BIS supports individual differences in anxiety, Gray's second personality dimension, and is associated with the functioning of the septo-hypocampus. Gray's dimensional model focuses mainly on the systems that respond to conditioned stimuli, which give rise to differences in anxiety (Anx) and impulsivity (Imp).

Cloninger (1986) developed his psychobiological theory based on twin and family studies, studies of longitudinal development, psychometric studies, and on learning in humans and research on neurotransmitter systems. Cloninger and colleagues (1993) emphasize that behavioral variation is the result of the interaction of genetic and environmental influences. The authors make a distinction between *temperament factors* and *character dimensions*. The former involve automatic responses that reflect heritable differences in the processing of perceptual information by the memory system, whereas the latter are attributable to learning and development of new adaptive responses as a consequence of experience. They defined the following four basic dimensions of temperament. (1) *Novelty Seeking (NS)*, which defined as a heritable tendency to respond strongly to novelty and cues of reward with exploratory activity, and is hypothetically related to a low basal dopaminergic activity. NS is manifest in impulsivity, quick loss of temper, or active avoidance of frustration. (2) *Harm Avoidance (HA)* is the heritable tendency to respond strongly to aversive stimuli, leading to learned inhibition of behaviour, and is related to high serotonergic activity. It is manifest in passive avoidance, such as fear, shyness, and fatigability. (3) *Reward Dependence (RD)* is the heritable tendency to react strongly to rewards, maintaining behaviors previously associated with reward, and is hypothesized to be associated with low basal noradrenergic activity. It is manifest in sentimentality, social attachment, and dependence on approval of others (Cloninger, 1986). (4) *Persistence* is defined as persistence, despite frustration or fatigue. Persistence was originally hypothesized to be a component of RD, but later reassigned the status of an independent dimension (Cloninger, Svrakic, & Przybeck, 1993).

Cloninger et al. defined the following three dimensions of character. (1) *Self Directedness* is related to the acceptance of the individual self, and the individual's ability to control, regulate, and adapt behavior to suit the situation at hand, in accordance with the individual's goals and values. (2) *Cooperativeness* is expressed in individual differences in identification with, and acceptance of, other people, and is related to agreeability, tolerance, empathy, and compassion at the positive pole, and to aggressive behavior, hostility, intolerance, or revenge at the negative pole. (3) *Self Transcendence* concerns the acceptance of nature in general, and is related to spirituality and self-consciousness (Cloninger et al., 1993).

Which factors are basic, how are dimensions of the different models interrelated: Previous reviews.

Cross-theoretical investigations of the structure of personality are few in number. The majority of the available studies addressed the structure of personality within a given theory by factor analysis of the subscales or traits of the questionnaires developed by the authors of the theories (Cloninger et al., 1993; Garcia, Aluja, & Garcia, 2004; McCrae & Terracciano, 2005; Stallings, Hewitt, Cloninger, Heath, & Eaves, 1996; Tomita et al., 2000). At best, these studies addressed the superiority of one of two competing models (big three vs. big five) by factor analyzing the subscales of the questionnaires associated with the given theories (Church & Burke, 1994; Costa & McCrae, 1995; Draycott & Kline, 1995; Heath, Cloninger, & Martin, 1994; Saggino, 2000). However, the personality *types*, which are described by psychobiological theorists are supposed to be *basic* features of individual differences in human behavior, which should be reflected in more specific, less holistic personality traits (Eysenck, 1991). The identification of such factors should be independent of the method of measurement and the specific questionnaires used, as long as the measures are reliable and cover a sufficient number and variety of personality characteristics in order to capture variation in the higher order factors. The questionnaires developed to measure personality types or traits were constructed and adapted, with the aim of satisfying a given preconceived theoretical structure. Although, the structure is supposed to exist, and to be open to replication, the scope of the model is limited if the same general personality *types* are not identifiable (i.e., explain variance) in different tests. This applies to the measurement of individual differences in general, but more strongly to biological theories, with their roots in evolved heritable biological structures.

Arguable the most impressive work in reviewing and identifying the *basic* factors of personality across theories and measurement instruments is that of Zuckerman (Zuckerman, 1992; Zuckerman & Cloninger, 1996; Zuckerman, Kuhlman, & Camac,

1988; Zuckerman et al., 1993; Zuckerman, Kuhlman, Thornquist, & Kiers, 1991). Zuckerman et al. (1988; Zuckerman, Kuhlman, Thornquist, & Kiers, 1991) measured forty-six personality traits to study the relationship and hierarchical structure of personality dimensions. Based on this work, Zuckerman et al. argued that the 5 and 3 factor models are compatible, albeit at different levels in the hierarchy. They first fitted a 7 factor model, in which the factors were interpretable as *sociability, activity, aggression, impulsivity, neuroticism-anxiety (N-anx), autonomy, and anger-restraint.* In the 5 factor model anger and N-anx merged to form a *general emotionality* factor (N-emot), and autonomy and impulsivity merged to form a *P- impulsive unsocialized sensation seeking (P-ImpUSS)* factor. Finally, in the three factor solution, the aggression factor merged with P-ImpUSS. Zuckerman (1991) identified this last three factor solution with Eysenck's PEN, but with certain reservations: The E factor was mainly formed by the sociability scales, and part of activity, and it was negatively correlated with N, despite of Eysenck's attempts to maintain them as independent dimensions. Furthermore, although the aggression and anger traits each loaded on the N and P factors, the subscales of hostility, anger, aggression, and lack of inhibition were "close in factorial space and anger-hostility and aggression actually form a cluster intermediate between N and P". Conformity and inhibition traits appeared to fall on the opposite extreme of the dimension. The impulsivity and sensation seeking scales all clustered together within the P factor, which did not correlate with the E factor. In light of these results, Zuckerman et al. (1993) proposed an alternative FFM, in which the basic traits are *ImpUSS, Aggression-Hostility (Agg,Host), activity (Act), Sociability (Sy), and N-Anx.* Zuckerman et al. tested their new structure by pooling their own scale (ZKPQ) with Eysenck's EPQ and Costa & McCrae's NEO. Their results replicated the previous results in terms of the identification of N-anx and P-ImpUSS as basic factors. The independence of the activity scale from the E-Sy dimension was not supported. The fourth Aggressive-Hostility factor was found to be clearly differentiated from the other three. The authors commented on this that "the distinction between Aggression-Hostility and anxiety is important because aggression and anxiety have distinctive psychobiological bases and should not be confounded within a single factor" (p.763).

In a recent study, Aluja et al. (2004) replicated Zuckerman's results by factor analysing the EPQ, ZKPQ, and NEO subscales. They extracted 3, 4, and 5 factors. The results supported the Agg-host factor as a higher order factor at the same level as N-Anx, E-Sy and P-ImpUSS.

In a subsequent publication, Zuckerman and Cloninger (1996) studied the relationships across their own and Eysenck's dimensions of personality. The results showed a great deal of overlap between Zuckerman's and Cloninger's dimensions, whereas Ey-

senck's scales showed a more complex pattern. Harm Avoidance with N-Anxiety and N formed a congruent and homogeneous cluster, with a large negative correlation with E. The authors considered Harm Avoidance to be a "fundamental dimension of temperament" (p.284), close to Gray's (1987) anxiety dimension. Similarly, novelty seeking and ImpUSS were highly correlated, but correlated only moderately with P and E. This result was consistent with previous research, which showed the relationship of the novelty and sensation seeking scales with common socially relevant phenomena and a common biological substrate. The authors argued that ImpUSS should also be considered as a "fundamental dimension of temperament", instead of a second order trait, as it is usually defined in 3 and 5 factor models. The rest of the correlations were moderate to low, except for a large negative correlation between the Agg-host scale and Cloninger's cooperativeness.

In the light of his reviews of theories of personality, the empirical structure of personality, and the biological and physiological bases of behaviour, Zuckerman (1991) developed a psychobiological model for personality. Zuckerman established five super-traits or personality types: *extraversion, P-impulsive unsocialized sensation seeking, aggression-hostility, activity and N-emotionality.* Zuckerman's psychobiological model follows a hierarchical structure moving from the genotype, to neuropsychological structures, to the biochemical and psychophysiological level, to the behavioral, and finally to the trait level. For Zuckerman "traits do not cause behavior; they are generalizations based on past behavioral and cognitive events", and we try to explain those generalizations based on differences in biological mechanisms. He argues, contra Gray's conceptual nervous system, that there is little empirical support for an isomorphic equivalence between the structure of personality and the organization of the nervous system. Biological systems involving neurotransmitters or brain structures do not act independently from one another, and therefore may well interact to produce individual differences in behavior. One biological system can also have diverse effects in more than one personality trait. Zuckerman (1991) described a variety of sources of differences in personality: 1) the neurotransmitters involved in the serotonin, dopamine, and norepinephrine pathways in the brain; 2) the enzymes regulating the production and degradation of neurotransmitters, e.g., Monoamine Oxidasa (MAO), or dopamine-beta-hidroxilase (DBH); 3) hormones, such as androgens, estrogens or testosterone; 4) endorphins; and 5) benzodiazepine receptors, e.g., gamma-aminobutyric acid (GABA). Specifically, high levels on the traits involved in the *P-impulsive sensation seeking* dimension are associated with deficits in MAO regulation, low levels of serotonin, high norepinephrine, and high levels of testosterone. *Activity, positive mood, and social interaction* are influenced by dopamine activity, and the balance

between serotonergic and catecholaminergic systems. Decreased serotonin levels are associated with higher levels of *aggression*, where serotonin acts in an antagonistic way to dopamine. The traits from the *N-emotionality* dimension are regulated by the responsivity of GABA, concentrations of benzodiazepine receptors and endorphins, and the functioning of the amygdala. Behavior associated with the *E-sociability* dimension is defined in terms of the interplay between the activity of the dopamine systems, behavioral activity, and the active pursuit of reward. High levels of dopamine activity are associated with high levels of behavioral activity and reward pursuit.

While Zuckerman's line of research focused mainly on Eysenck's and Cloninger's systems, another long research tradition has addressed the comparison and possible combination of the personality theories of Eysenck and Gray. Matthews and Gilliland (1999) reviewed the extensive literature on this matter, in which they compared the strengths and weaknesses of these theoretical frameworks. The theories were found to differ not only in the definition of the basic factors of personality and their position in a hierarchical structure, but also in the nature of the relevant moderators, i.e. level of stimulation vs. type of stimulation. According to their review, psychometric evidence provided stronger support for Eysenck's structural model. Eysenck's predictions (1985) regarding the relationship of electrodermal activity and evoked potentials with extraversion have been supported empirically, but the relationship between the level of arousal and performance is still unclear. With respect to N, it is correlated with sensitivity to emotional states, and with sensitivity to associative conditioning, but its relationship with levels of autonomic activity also remains unclear. In general, Eysenck's theory appeared to provide a better account of human behavioral tendencies than Gray's. On the other hand, the major support for Gray's theory (1987) stems from its predictions regarding the interaction between the effects of different types of motivational stimuli and the effects of personality on behavior. Furthermore, in psychophysiological research, impulsivity has more predictive validity than Extroversion, and it also predicts behavioral activation. In conclusion, both theories suffer the limitation of not being able to predict differences in performance on experimental tasks from differences in brain functioning.

Personality is not perfectly stable: stability and change

Personality is far from perfectly stable (Caspi et al., 2001). In an extensive review of longitudinal studies of personality, Roberts and DelVecchio (2000) found that overall rank-order trait consistency increases in a linear, yet steplike, pattern, reaching a peak at 50 to 59 years old. Trait consistency increased at three points of life: from infancy to toodlerhood (from .35 to .50 approximately), from college years to early adulthood

(from .50 to .60), and from early middle age to late middle age (to .70). These results were recently replicated by Bazana and Stelmack (2004) in a meta-analysis on the stability of personality across the life span. They emphasized that age has a systematic influence on personality traits, raising the level of some, and lowering the level of others traits. The authors of both meta-analyses concluded that, given the effect of age on trait consistency, the construct validity of the measurements might be affected by the age of the sample, and thus "aggregating over as many situations and occasions as possible increases both the magnitude of the test-retest correlations and, because measurement error is reduced, the validity of the measure" (Bazana & Stelmack, 2004, p.128).

The recent evidence on the rank order stability of personality suggests that studies of the relationships among personality traits, and of the structure of personality should take age and developmental changes into account in their measurements and their factor models. If the rank order with respect to different personality traits is subject to change over time, and that change varies as a function of age, the intercorrelations between the measured traits might change depending on the age composition of the sample.

With respect to the structure of personality, it appears that the self reported personality trait structure is clearly recognizable at the age of 12, and well developed by about the age of 14. It is practically indistinguishable from the adult personality by age 16 (Allik, Laidra, Realo, & Pullman, 2004).

McGue et al. (1993), in a study of the genetic and environmental basis of stability and change, showed that the stable component of individual differences in personality is associated largely with enduring genetic influences. Personality change is largely associated with non-shared environmental factors, although there is also a moderate genetic influence on change. This result suggests that obtaining several measurements of personality traits over time, instead of single-measurements, might improve the chances of finding reliable relationships between personality and biological substrates. Eysenck (1991) stated that "Person-significant behaviors are organized in a hierarchical fashion, from the most specific (level 1) to the most general (level 4). (…) The lower the level, the more it is a measure of state; the higher the level, the more it is a measure of trait. (…) hence level 4 concepts are the most far-reaching aggregating behaviors characteristic of a given person over many years" (p.776). Therefore, if we want to capture variance on the fourth level, variance on personality types, it is not enough to measure personality at one single occasion. Rather we should measure it a repeated number of times to ensure that we capture differences in behavioral tendencies that remain stable across time and age.

The present study

In the light of the above, there seems to be two main gaps in the field of personality research. First, there is agreement that the 16 factor model of Cattel is too extensive and too specific, and that two *basic* factors are not sufficient either to explain the wide variety of behavioral differences (Cloninger, 1986; Eysenck, 1992a; Zuckerman, 1991; Zuckerman et al., 1993). However, the number, the nature, and the hierarchical position of the additional factor(s) is still a matter of debate. Second, it seems that personality research has generally neglected the fact that personality is far from stable, and that along the life span there can be changes in personality traits, not only in the mean levels, but also in the rank order. These changes might affect both the correlation pattern across a given set of personality variables, and the predictive validity of a score obtained in a given developmental period.

In the present study, we analyzed the latent structure underlying 13 measures of personality in a sample of 17557 individuals, who participated in a longitudinal study over 12 years, which comprised 6 surveys. We used the longitudinal character of the data and the age differences to take into account intra and inter-individual changes in personality across time. This method allowed us to obtain a more reliable estimation of the *trait* comparable across individuals, so that differences in age do not influence correlations across traits. In this manner, we have tried to shed some light on the possible nature of the "third factor" of personality.

What might be the nature of the third factor(s)? We can establish a fairly straightforward equivalence between Cloninger's and Gray's two main personality types, i.e., HA-Anx (BIS) and NS-Imp (BAS). The identification of Eysenck's types with these two clusters is less straightforward. Eysenck's Neuroticism would certainly be identified with the first cluster (BIS). Given the latest modifications of Eysenck's theory and questionnaires (Aluja, Garcia, & Garcia, 2002), and according to previous reviews (Zuckerman, 1991) and genetic research (Eaves, Eysenck, & Martin, 1989), Eysenck's E is no longer related with impulsivity. E would now seem to be related with sociability factors at the positive pole, and with negative emotionality factors related with the BIS at the negative pole. The same modifications in Eysenck's theory lead to the most likely identification of the P factor and the BAS cluster. This overview is consistent with the early review of Zuckerman et al. (1988), which identified two clear clusters that were related with the activation and inhibition of behavior, plus a sociability component.

However, all three theories admit the necessity of at least one additional personality type or *basic* personality trait, but the theories differ in the posited nature of this *third factor*. Furthermore, in the three theoretical frameworks, the definition and etio-

logical mechanisms of the third factor remains underdeveloped, in comparison to the extensive work on the other dimensions. These third dimensions are left unexplained after clustering together the commonalities across the three theories: RD and the three character scales from Cloninger, the FFS of Gray, and the antisocial or un-socialized component of Psychoticism (Heath, Jardine, Eaves, & Martin, 1988; Pickering, 2004). The third factor (or factors), which we hope to identify in our data, should present a certain combination of these three unexplained dimensions.

Up to this point we have described the main psychobiological theories of personality, say those of Eysenck, Gray, Cloninger and Zuckerman. We have identified two main limitations in basic personality research. First, the negligence of intraindividual differences across time, and second the underdevelopment of personality dimensions beyond the first two. In this article we used a repeated measures design, along an interval of 12 years, in order to capture the trait variance. A factor analysis on this trait variance from a pool of diverse personality variables was intended to clarify the structure of personality with regard to the third personality factor (or factors).

METHOD

Participants and Procedure

The participants in this study were registered by the Netherlands Twin Registry (NTR) of the Department of Biological Psychology at the Vrije Universiteit in Amsterdam. They were included in the cohort of adolescents and young adults, who were recruited through the city councils in 1990-1991 and in 1992-1993, and are participating in an ongoing longitudinal study. After 1995 an effort was also made to recruit adult and older twins. The twins, their parents, siblings, and spouses participated in surveys that were conducted approximately every 2 years. Six surveys concerning lifestyle, personality, and psychopathology were conducted in 1991, 1993, 1995, 1997, 2000, and 2002. In the present study we will analyze personality data collected in all 6 surveys. Further details on response rates, response bias, and demographic characteristics of the sample can be found elsewhere (Boomsma et al., 2002; Koopmans, Slutske, Heath, Neale, & Boomsma, 1999; Stubbe, Posthuma, Boomsma, & de Geus, 2005; Vink et al., 2004).

The total sample with personality data comprises 17557 individuals. These are the twins and their family members, who returned the survey, which included the personality questionnaires, and completed at least one of the personality questionnaires, in at least one of the six surveys. Table 3.1 shows the distribution of the sample as a function of data points available.

Table 3.1

Distribution of the sample by survey

Number of times subjects participated						
	1	2	3	4	5	6
Total N=17557	6324	4305	3428	2222	819	459
Chronological distribution [a]						
AND	1991	and 1993	and 1995	and 1997	and 2000	and 2002
1991	1586	412	866	183	118	459
1993		719	968	150	116	324
1995			7	203	113	291
1997				380	228	531
2000					1078	134
2001						2554

[a] *Each column on the right implies participation on the previous surveys. E.g., 116 participants returned personality questionnaires in 1993, 1995, 1997 and 2000 inclusive, but not in 1991 or 2002. The cells are exclusive. This distribution does not cover the entire sample. Participants who participated in intermediate surveys are not listed here, but counted above.*

The first part of the table shows the number of individuals, who returned the questionnaires at occasions ranging from 1 to 6. A total of 459 individuals returned personality questionnaires in all six surveys, and about two thirds of the sample contribute to longitudinal data. Note that not all subjects were invited at each occasion. The second part of the table shows the distribution of the sample by consecutive participation. The diagonals contain the number of individuals, who participated only once, and the off-diagonal the number of individuals, who participated in the subsequent years. In 1995, only families that had participated previously were invited to participate.

Table 3.2 shows the age composition of the sample, and the family members who took part in each survey. The mean age of the sample changed only slightly in the first 5 surveys, but it did increase considerably in 2002, mostly due to the addition of a large number of adult participants (spouses), and the re-introduction of the parents. The percentiles also show how the age distribution varies substantially more than the mean age. Especially in 1995 and 1997, the last centile is lower, which is probably due to the absence of the parental generation. Data from participants under 13 years old were discarded, as the structure of personality does not mature until about this age (Allik et al., 2004).

Surveys 1 and 2 comprised the twins and their parents. In survey 3, in 1995, the other siblings of the twins were invited to participate, but did not receive personality questionnaires. In 1997 the siblings participated and received personality questionnaires. In 2000 the spouses of the twins, who at that time had reached young adulthood, were also invited to participate. In the last survey in 2002 all the members

of the family were invited to collaborate. Thus, not only the passing of the time, but also the inclusion of new individuals in the study, can affect the age distribution of the sample.

Table 3.2

Composition of the sample by age and family members

Descriptive statistics for Age									Composition by family members			
						Percentiles for age						
	Mean	SD	Min	Max	Skewness	25	50	75	Twins	Parents	Siblings	Spouses of twins
1991	31.51	15.04	13	71	0.281	17	21	46	3379	3009	-	-
1993	33.25	14.97	14	73	0.061	18	39	46	3635	3678	-	-
1995	33.29	14.60	16	75	0.348	20	25	48	3172	3209	948	-
1997	27.73	10.14	18	83	1.82	21	25	29	2923	5	1272	-
2000	31.65	10.46	21	91	1.67	24	28	35	4085	3	1261	685
2002	40.48	14.07	23	93	0.45	28	34	54	4037	2770	1226	1388

Measures

From the pool of available data on personality and psychopathology (Boomsma et al., 2002), we selected a total of 13 variables. We did not use variables that overlapped with others, because a similar construct was measured with two different questionnaires (e.g., anxious depression and depression). We discarded these because they are redundant, and to avoid computational problems deriving from correlations close to 1. In addition, we discarded variables that were closely related to cognitive abilities (e.g., attention problems). The 13 selected measures, which cover a wide range of personality characteristics, are: neuroticism, extraversion, somatic anxiety, thrill and adventure seeking, experience seeking, boredom susceptibility, disinhibition, trait anger, trait anxiety, depression, type A behavior, aggression, and rule breaking behavior.

Neuroticism (N), extraversion (E), and somatic anxiety (SomAnx) were measured with the Amsterdamse Biografische Vragenlijst (Wilde, 1970), which is a Dutch questionnaire based on the Eysenck Personality Questionnaire (Eysenck et al., 1985). The neuroticism scale includes 30 items (Cronbach's α=0.89 –averaged over surveys), the extraversion scale 21 items (α=0.84), and the somatic anxiety scale 17 items (α=0.66). The four dimensions of sensation seeking were measured with the Dutch translation of Zuckerman's Sensation Seeking Scale (SSS; Feij, Dekker, Koopmans, & Boomsma, 1997; Feij & Van Zuilen, 1984; Zuckerman, 1971). The dimension thrill and adventure seeking (Tas) includes 12 items (α=0.87), experience

seeking' (Es) 14 items (α=0.69), boredom susceptibility (Bs) 13 items (α=0.66), and disinhibition' (Dis) 12 items (α=0.79). The Dutch adaptation of Spielberger's State-Trait Anger Scale- (STAS; Spielberger, Jacobs, Russell, & Crane, 1983; van der Ploeg, Defares, & Spielberger, 1982) was used to measure trait anger (Ang). The STAS includes 10 items (α=0.86). Depression (Dep) was measured with the short version of the Beck's Depression Inventory (BDI; Beck, Ward, Mendelson, Mock, & Erbaugh, 1961), a 13 item scale (α=0.80). Anxiety (Anx) was measured with the Spielberger State-Trait Anxiety Inventory trait version (STAI; Spielberger, Gorsuch, & Lushene, 1970), which includes 20 items (=0.91). The Dutch adaptation of the Jenkins Activity Survey (Appels & Jenkins, 1985; JAS; Appels, Jenkins, & Rosenman, 1982) was used to measure Type A Behavior Pattern. This included 24 items (α=0.84). Finally, aggressive behaviour (Agg) and rule breaking behavior (Rbb) were measured with the Young Adult Self Report (YASR; Achenbach, 1990). The Rbb scale includes 11 items (α=0.43), and the Agg scales include 19 items (α=0.77).

Table 4 shows samples sizes by questionnaire and survey. The questionnaires ABV, SBL, and STAI were included in 5 of the 6 surveys, but not in 1995. The Agg and Rbb from the YASR were administered on four occasions, with the exceptions of 1993 and 2002. Depression from the BDI and anger trait were administered on two occasions, Ang in the two first surveys, and Dep in 1993 and 1997. TAB was administered exclusively in 1991.

Analyses

Structural equation modeling (SEM), in addition to exploratory factor analysis (EFA), was used to study the structure of personality underlying the selected pool of measures. The use of SEM has three advantages here. First, it allows us to create a measurement model to make the best use of the longitudinal information, i.e., a model that takes into account intraindividual variation. Second, it allows us to model the effects of covariates like age, i.e., to control for interindividual differences in developmental stage. And it allows the analyses of complete data with any pattern of missingness, assuming the data are missing at random (Schafer & Graham, 2002).

Mplus v 3.13 (Muthén et al., 2005) was used to fit the various models. In view of the missingness, we analyzed the raw data, rather than the summary covariance matrix, so as to make use of all the available data. In the NTR, those families that did not participate in a second survey, were invited to participate in subsequent surveys. The fact that participants were allowed to return to the study, in combination with the analysis of complete data, in opposition to the exclusive use of complete cases, minimizes the effects of sample attrition and provides unbiased estimates.

Family clustered data do not fulfill the assumption of independence of observations for phenotypic statistical analysis, and treating dependent data as independent may result in bias in standard errors and goodness of statistics (Laplante et al., 2001). To correct for this, we used the Robust Maximum Likelihood (MLR) in combination with the "Complex" option in Mplus. The latter corrects the effect of clustering. The parameter estimates are ML estimates, but the standard errors are corrected for the dependency in the data. The correction is done by using a weight matrix that involves fourth-order moments and contains cluster information. The chi-square statistic is scale-corrected. The scale is a function of the same weight matrix and the degrees of freedom of the model (Muthén et al., 1995). Family was used as the cluster unit in the correction. A previous simulation study showed the efficiency of this method to correct he effects of dependency due to family resemblance (Rebollo, de Moor, Dolan, & Boomsma, 2006).

The AIC (Akaike's information Criterion; Akaike, 1987) and the RMSEA (Root Mean Squared Error of Approximation; Steiger, 1990) were used to evaluate the fit of the models. The AIC compares the models on the basis of parsimony, taking into account the χ^2 and the degrees of freedom (Joreskog, 1993) . The lower the AIC, the better the fit of the model to the data and the more parsimonious it is. The likelihood ratio test is performed under the assumption that the model holds exactly in the population. Models that are assumed to hold approximately in the population will always be rejected in large samples. The RMSEA is a measure of closeness of fit, and provides a measure of discrepancy per degree of freedom. A value of 0.05 indicates a close fit, and values up to 0.08 represent reasonable error of approximation of the model (Joreskog, 1993).

Growth models as measurement model

Previously, models have been proposed to estimate stable "trait-like" parameters from longitudinal data, modeling intraindividual variability (Nesselroade, 2001). In these previous models a factor model was used as a measurement model for each survey, and the longitudinal trends were modeled at a higher order latent level. The focus of these previous attempts was to study variability in changes over time. The focus of the present study was to estimate, and factor analyze the portion of variance that is comparable across participants independently of their age and the survey in which personality was measured. This is what we view as "trait-like" variance. To this end, instead of fitting a factor model directly to the observed scores, we employed a growth curve model (Hertzog & Nesselroade, 2003; McArdle, 1988), as a measurement model

for those variables that were measured 4 or 5 times. This model is depicted in figure 3.1a.

The figure 3.1a shows a variable that was measured in all surveys except for 1995. In a growth model, the individual differences on the five repeated measures are explained by two latent factors, denoted the level (l) and the shape (s). The model involves fitting a linear function throught the data of each case. The level factor may be viewed as representing a random intercept (i.e., a general level). The shape factor may be viewed as a random slope, which accounts for individual differences in linear change over time. The shape factor was defined by assigning to each survey a consecutive number as a loading, i.e., 1991 (0), 1993 (1), 1995(2), 1997 (3), 2000 (4), and 2002 (5). These loadings (0,1,2,3,4,5) may be interpreted as a defining linear contrast, as in a repeated measured ANOVA. By fixing the first shape loading to zero, the 1991 measurements define the level or intercept. The observed means are modeled as linear function of the means of the level and shape factors. The mean of the level represents the mean initial trait level; the mean of the shape represents the average change over time. The variance of the level factor accounts for the individual differences in level, and the variance of the shape accounts for the individual differences in the slope of the linear growth function. The level and shape factors are allowed to correlate so that the change may covary with the initial level. This model implies that people may vary in the amount and rate of change that they underwent over the years, but they do not vary in the functional form of the growth (Hertzog et al., 2003).

The variation in age, at which the participant entered the study (e.g., twins were adolescents, and their parents obviously adults) may render the variance of level and shape, as well as the means difficult to interpret. To control for these age differences, and obtain estimates of the level and shape variances that are independent of individual differences among the subjects in developmental stage, we introduced age in 1991 as a covariate. Thus, the model implies that part of the variance on initial level and shape is explained by age differences. In other words, depending on how old a person is, he or she might have entered the study with a given initial level that might be lower or higher than if the same person had entered the study 10 years earlier. Intraindividual variance due to error, or developmental growth, and interindividual differences due to age are regressed out of the variance of the level factor. In other words, if we computed a factor score for each participant on the level factor, without re-incorporating the contribution of age, every individual in the sample could be compared with it. This is the variance that we used to study the structure of “trait-like” personality.

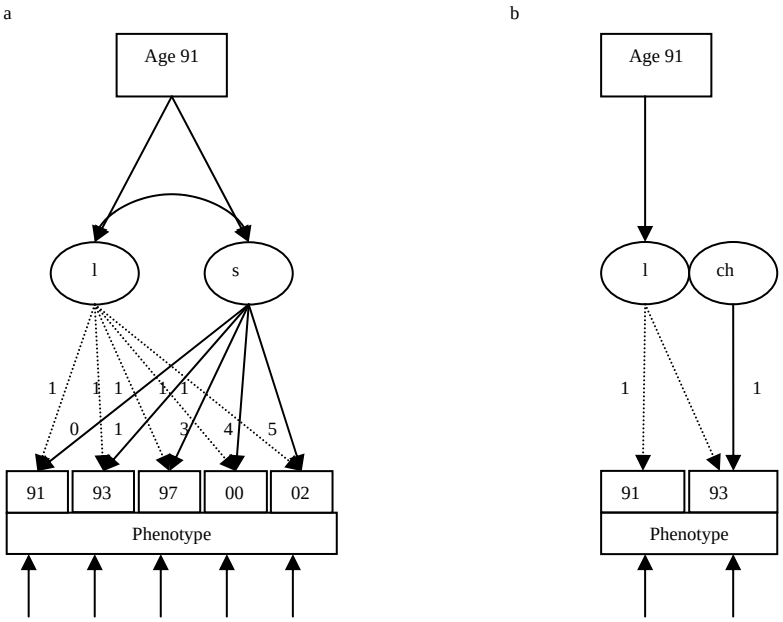

Figure 3.1.

a) Linear growth model with age covariate for a variable measured in 5 surveys. l-level, s-shape b) Latent change model with age covariate applied to those variables that were measured twice. l-level, ch-change.

Of course, several other models of growth or change may be considered. However, the purpose of the present model is not to study or model in detail developmental stability and change, but to control for it in a parsimonious and efficient way that is consistent and comparable across variables. Consistent with previous studies on stability and change in personality (Bazana et al., 2004; Caspi et al., 2001; Roberts et al., 2000; Robins, Fraley, Roberts, & Trzesniewski, 2001), the present model is adequate to correctly separate inter-and intraindividual variance. Furthermore, this approach to modeling change has the advantage of optimal correction for measurement error (Hertzog et al., 2003).

For those variables that were measured twice, i.e., Dep and Ang, a latent change model (Hertzog et al., 2003) was used as a measurement model. Figure 3.1b shows the corresponding path diagram. The latent factor, denoted L, represents the common variance between the two repeated measures or initial level, whereas the factor denoted Ch represents the change in the second measurement. Age is specified as a covariate of the initial level. This model is used to capture the most reliable variance underlying the two available measurements.

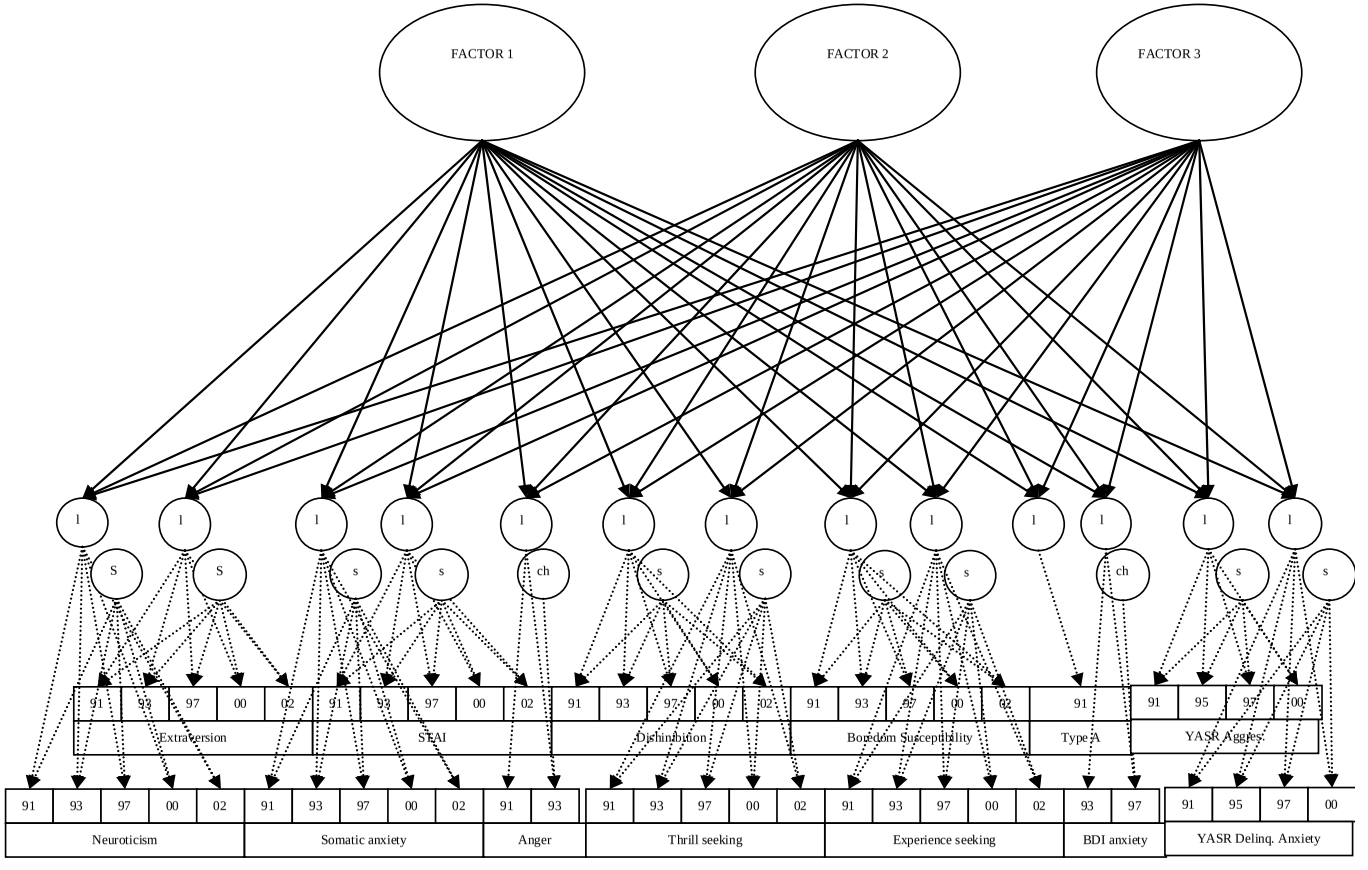

Figure 3.2

Path diagram of 3 factor model estimated in Mplus. Residual variances (not depicted) are freely estimated. Variances of the three higher order factors are fixed to 1. Three path coefficients, one from Factor 2 and two from Factor 3, are constrained to zero in order to identify the exploratory factor model.

The factor model

The structure of personality was investigated by subjecting the covariance matrix of the level factors to factor analysis. These are the latent levels that were specified in latent growth model for each variable to capture stable trait-like inter-individual differences. We carried out an exploratory factor analysis (EFA) in Mplus by introducing minimal identifying constraints (Raykov, 1998; van Prooijen & van der Kloot, 2001). Figure 3.2 shows the complete path diagram for a three factor model.

The model was identified by constraining 9 parameters: the variance of the latent factors was fixed to equal 1, the covariances between the latent factors were fixed to equal 0, and 3 factor loadings were also fixed at zero. In order to find a sensible combination of loadings to fix (Millsap, 2001), we factor analyzed using SPSS (Maximum Likelihood , Norusis, 2005) the correlation matrix across the levels, which was obtained from Mplus. The lowest loadings obtained in the SPSS solution were fixed to zero in the Mplus analysis. As for the number of factors extracted, the initial analysis in SPSS indicated that the maximum number of factors to be extracted was three. Four and five factor solutions did not converge due to communalities larger than 1. Therefore 3 and 2 factor models were tested in Mplus. The exploratory factor solutions obtained from Mplus were then rotated in R (Ihaka & Gentleman, 1996) using promax (i.e., oblique) rotation.

Finally, to investigate the effects of the longitudinal method, and the data analysis chosen in the present article, we extracted three alternative solutions with EFA in SPSS. We first factor analyzed the correlation matrix across the latent levels obtained from Mplus. This solution differs from the CFA solution in the absence of control of age effects. Secondly, we factor analyzed the mean scores across surveys, which is another possible approach to obtain trait-like individual differences. Third, to compare the longitudinal perspective with the usual cross sectional design, we factor analyzed only the scores obtained in 1991 –with the slight difference that Dep was not included in the pool of variables. If the approach chosen in the present paper is correct, where developmental changes are controlled and modeled, the solution obtained through CFA should give a clearer composition of the factors.

RESULTS

Description of the sample

Table 3.3 show the descriptive statistics by scale and survey.

Table 3.3

Descriptive statistics

		N	Mean	Standard Deviation	Skewness	Kurtosis
Extraversion	1991	6318	56.19	16.21	-0.32	-0.67
	1993	7495	57.76	16.77	-0.36	-0.69
	1997	4174	61.45	16.42	-0.64	-0.35
	2000	5879	60.81	16.62	-0.61	-0.38
	2001	9107	57.49	17.39	-0.39	-0.67
Neuroticism	1991	6306	54.66	24.06	0.35	-0.66
	1993	7468	48.41	24.16	0.63	-0.36
	1997	4174	46.54	23.96	0.73	-0.16
	2000	5871	46.92	24.47	0.74	-0.17
	2001	9106	47.02	24.81	0.73	-0.23
Somatic Anxiety	1991	6330	13.39	5.64	1.16	1.36
	1993	7504	17.84	5.50	1.33	1.97
	1997	4174	17.35	5.18	1.51	2.76
	2000	5883	17.59	5.19	1.43	2.45
	2001	9139	17.46	5.37	1.47	2.39
Thrill & Adventure Seeking	1991	6340	32.65	11.74	0.08	-0.99
	1993	7502	31.87	11.92	0.15	-1.01
	1997	4173	35.79	11.39	-0.15	-0.82
	2000	5958	33.55	11.12	-0.01	-0.82
	2001	9216	30.84	11.11	0.19	-0.88
Experience Seeking	1991	6330	33.09	7.68	0.28	-0.01
	1993	7491	32.75	7.84	0.34	0.10
	1997	4173	33.23	8.42	0.43	0.15
	2000	5937	32.88	8.43	0.41	0.14
	2001	9305	32.97	8.03	0.37	0.59
Boredom Susceptibility	1991	6329	37.40	7.35	0.09	-0.04
	1993	7485	36.58	7.37	0.13	-0.03
	1997	4173	35.91	7.43	0.12	0.03
	2000	5942	35.10	7.53	0.19	0.15
	2001	9311	34.90	7.12	0.21	0.88
Disinhibition	1991	6334	30.05	7.95	0.22	-0.38
	1993	7492	29.51	8.21	0.28	-0.03
	1997	4173	30.79	8.45	0.20	-0.42
	2000	5943	29.74	8.35	0.29	-0.46
	2001	9316	29.33	7.99	0.27	-0.37
Type A Behavior	1991	6291	11.39	4.44	0.21	-0.53
Rule Breaking Behavior	1991	3322	3.65	2.44	1.02	2.28
	1995	3075	3.04	5.11	1.11	1.75
	1997	4161	2.60	1.95	1.01	2.41
	2000	5934	1.80	2.11	1.55	3.42
Aggressive Behavior	1991	3322	7.65	4.54	0.88	1.23
	1995	3075	6.45	4.21	1.01	1.64
	1997	4161	5.25	3.91	0.89	0.68
	2000	5934	5.50	3.78	0.88	0.86
Anxiety	1991	6319	34.21	8.52	0.82	0.56
	1993	7485	33.67	8.77	0.96	1.04
	1997	4168	32.43	9.05	1.07	1.27
	2000	6003	32.72	8.78	1.11	1.47
	2001	9335	33.54	8.49	0.88	0.97
Anger	1991	6341	16.69	4.96	1.26	2.28
	1993	7466	16.54	4.78	1.33	2.43
Depression	1993	7477	1.96	2.75	2.65	10.43
	1997	4178	1.78	2.80	2.98	13.48

Mean levels of most of the phenotypes seem to decrease over the years, except for extraversion. Somatic anxiety and anxiety do not show clear patterns of change. With respect to the distribution, Rbb, SomAnx, and especially Dep were positively skewed, and showed a pronounced kurtosis. We did not transform this variables to reduce this non-normality, because the estimation method MLR is robust given deviations from normality (Muthén et al., 2005).

The means and standard deviations suggest quite large differences in scale between the different questionnaires. As this may cause computational problem in the SEM, we rescaled the variables to reduce the differences in variance. Rescaling involves a linear transformation, which does not otherwise affect the covariance structure.

Stability and change

Table 3.4 shows the stability coefficients for those phenotypes that were measured more than once. Subsequent measures were correlated with the first one, i.e., the measures obtained in 1991 (except for Dep). Therefore, the coefficients show stability from a 2 to 11 years interval.

Table 3.4.

Stability coefficients

	1991 with:					
	1993 (2yrs)	1995 (4yrs)	1997 (6yrs)	2000 (9yrs)	2002 (11yrs)	2002 (without parents)
Extroversion	0.754		0.572	0.557	0.672	0.564
Neuroticism	0.714		0.514	0.521	0.579	0.475
Somatic Anxiety	0.646		0.440	0.416	0.475	0.406
Thrill and Adventure Seeking	0.852		0.690	0.684	0.764	0.608
Experience seeking	0.690		0.579	0.511	0.611	0.511
Boredom susceptibility	0.606		0.677	0.621	0.438	0.347
Disinhibition	0.732		0.570	0.533	0.635	0.525
Rule Breaking Behavior		0.382	0.436	0.301		
Aggressive behavior		0.515	0.436	0.424		
Anger	0.616					
Anxiety	0.663		0.444	0.486	0.529	0.417
Depression			0.464[a]			

[a] *correlated with first measurement in 1993 (4 years stability)*

The coefficients show high levels of stability in general, with the largest for the sensation seeking scales Tas and Dis, and for E and N, and the lowest for Dep and the YASR's Agg and Rbb. Consistent with previous findings (Bazana et al., 2004; Roberts et al., 2000), the stability decreases with larger intervals of measurement. However, for most phenotypes, the coefficients rise again in 2002. This result is probably due to the re-introduction of the parents in that specific survey. The mean age of the parental generation in the 6th survey was 56.32 years, i.e., the age at which previous studies have shown the largest rank order stability for personality (Roberts & Caspi, 2002). The last column of table 4 shows the stability coefficients for 2002 estimated without the parents. These coefficients follow the tendency of the previous ones with smaller values than those obtained in 2000.

Table 3.5

Results of the latent growth models: means, residual variances, and correlation between the latent factors level and shape, proportion of variance of the latent factor level explained by the factor model, and regression coefficients of the level and shape factors on age.

	Mean Level	Mean Shape	Residual S^2 Shape	Residual S^2 Level	σ Level-shape	R^2 Level 3F	R^2 Level 2F	Age β on l	Age β on s
Extroversion	12.588	0.188	0.147	4.821	-0.240	0.419	0.229	-0.194	-0.169
Neuroticism	5.947	-0.239	0.073	0.321	-0.258	0.927	0.933	-0.158	0.229
Somatic Anxiety	9.906	-0.222	0.133	2.501	-0.380	0.536	0.538	-0.157	0.196
Thrill & Adv. Seeking	15.676	-0.350	0.079	3.214	ns	0.746	0.702	-0.621	0.294
Experience Seeking	18.109	-0.141	0.143	2.954	ns	0.717	0.533	-0.233	0.146
Boredom Suscep.	19.864	-0.457	0.112	2.943	ns	0.600	0.627	-0.206	0.300
Disinhibition	18.006	-0.191	0.128	4.089	ns	0.645	0.686	-0.421	0.156
Rule Breaking Behavior	4.886	-0.698	ns	0.741	ns	0.707	0.637	-0.501	0.351
Aggressive Behavior	5.670	-0.614	ns	0.132	ns	0.971	0.762	-0.700	0.351
Anxiety	16.722	ns	0.256	1.527	ns	0.882	0.877	0.032	-0.045
Anger	8.863			3.584	ns	0.441	0.313	-0.085	
Depression	1.063			4.915	ns	0.194	0.194	0.174	
Type A Behavior	10.529			13.171	ns	0.329	0.229	0.091	

[a] *ns: non significant*

Table 3.5 shows the estimates of the linear growth models. The mean of the shape latent factors shows that mean scores of most personality measures tends to decrease

with time, with the largest changes seen in Rbb, Agg, Bs, and Es. Anxiety does not show any significant change, whereas E tends to increase. Level and shape were negatively correlated for E, N and SomAnx, which implies that, for these variables, larger initial levels are associated with smaller shapes. However, this interpretation is made conditional on the choice of shape factor loadings. This correlation may vary with a different choice of shape factor loadings (Stoel & van den Wittenboer, 2003). Age explains a significant amount of variance of both initial level and shape for all variables. For the majority of phenotypes the regression coefficient on the level is negative, whereas the coefficient on the shape is positive. Thus, older individuals show lower initial levels and larger slopes. The effect of age on the slope should be interpreted carefully, as larger slope here does not imply more change given that the shapes are negative and thus, older people show a less steep decrease in the mean scores over time. The effect of age on the shape of extraversion was negative, which reflects the pattern of less change with age, given that Extraversion's slope was positive. Putting together the results of the growth models and the age moderation, we could say that most personality traits show a decrease (or increase) on mean scores with a negative acceleration with aging.

Anx, Dep, and TAB show the opposite pattern for the effect of age on the level, such as for these phenotypes older individuals show higher initial scores.

The factor structure of personality

Appendix I shows the estimated correlations across the level latent factors as estimated in Mplus. This correlations matrix was used as input in SPSS to identify reasonable identification constraints. For the 3 factor solution, Dep showed the lowest loading on the second and third factors, and Es showed the second lowest loading on the third factor. These loadings were constrained to zero in Mplus to arrive at an identified exploratory model.

Table 3.6 shows the three and two factor solutions from Mplus after promax rotation. In the 3 factors solution F1 shows large loadings from the Neuroticism-anxiety dimension, a moderate loadings from Dep, and a negative loading from extraversion. The second factor is determined largely by Es, and includes the sensation seeking scales, and a secondary loading of Rbb. Aggression is the major marker of the third factor. Anger, TAB, and Rbb have their largest loadings on this factor. Extraversion shows a moderate secondary loading on the third factor as well. The first factor can be identified with the Anxiety / Neuroriticsm/ BIS / Harm-Avoidance dimensions. The second factor has features of Impulsive Sensation Seeking / Impulsivity-BAS/

Psychoticism/ Novelty seeking dimensions. The interpretation of the third factor, as expected, is less straightforward. We discuss this factor in detail below. The third factor shows moderate correlations with F1and F2, whereas F1 and F2 are practically independent.

Table 3.6

Factorial solutions (Promax rotation)

	Three Factors			Two factors	
	F1	F2	F3	F1	F2
Depression	**0.405**	0.057	-0.004	**0.404**	-0.002
Anger	**0.291**	-0.170	**0.545**	**0.498**	0.145
TAB	0.164	-0.047	**0.506**	**0.335**	**0.253**
Anxiety	**0.921**	0.063	0.046	**0.943**	-0.036
Neuroticism	**0.915**	0.062	0.082	**0.955**	-0.012
Somatic anxiety	**0.706**	0.044	0.026	**0.725**	-0.038
Exttroversion	**-0.535**	0.061	**0.491**	**-0.395**	**0.437**
Disinhibition	0.003	**0.565**	0.200	-0.036	**0.721**
Experience seeking	0.139	**0.905**	-0.208	-0.072	**0.705**
Boredom suscep.	0.064	**0.559**	**0.277**	0.053	**0.749**
Thrill and ss	-0.134	**0.597**	-0.051	-0.253	**0.566**
Rule breaking	0.089	**0.226**	**0.503**	0.213	**0.552**
Aggressive behavior	0.138	-0.106	**0.674**	**0.373**	**0.294**
Factor correlations					
F2	-0.048			0.245	
F3	0.349	0.499			

In the two factors solution, the third factor merges with the first, and E and Rbb have primary loadings on the second factor. In this solution, F1 contains different expressions of general emotionality and behavioral inhibition, whereas F2 comprises expressions of behavioral activation.

Both models show an excellent fit to the data, according to the RMSEA, i.e., 0.034 and 0.035 for the 3 and 2 factor solutions, respectively. The AIC can be used to compare the fit of the models to the data. The AIC was 1543833 for the 3 factor solution, and 1546494 for the 2 factor solution, indicating that, although the 3 factor solution contains 11 additional parameters, it provides a better and more parsimonious explanation of the covariance structure of the personality traits.

Table 3.5 shows the proportion of variance explained in the 2 and 3 factor models of the latent level factors (R^2). The comparison of both columns shows how the switch from 3 to 2 factors reduces considerably the explained variance of the indicators of the third factor, especially that of Agg, E and Ang. Taken together, the 3 factor solution

provides a better explanation of the variances and covariances of the present personality variables.

Table 3.7 shows three alternative 3 factor solutions obtained with SPSS. The first one shows the promax rotated structure obtained from the correlation matrix across initial levels estimated by Mplus. The main difference between the SPSS and the Mplus solutions, in this case, is that the latter controls for the effect of age in the covariation across traits in the confirmatory model, whereas the former does not. The second one shows the promax rotated factor structure obtained from factor analyzing phenotypic scores averaged across surveys. The last solution represents the most common kind of structure reported in the literature, and it is that obtained from a single pool of cross-sectional data, that of 1991. In the first solution, when compared to the structure obtained from the CFA, we observe complex patterns for Ang, TAB, E and Agg. Ang and TAB have comparable loadings in F1 and F2, E shows similar loadings on the 3 factors as well as Agg. Furthermore, all variables, except Dep, show moderate to high loadings on F3. A similar complex structure can be observed on the second solution, with even larger loadings of the Anxiety/ Neuroticism dimension on the third factor. The last solution shows a slightly different pattern, in which F1 and F2 could be identified with the previous F1 and F3, respectively. However all variables with large loadings on F1 also show moderate to large loadings on F2.

The SPSS solutions illustrate how the choice of the method used to analyze longitudinal data, or the decision to analyze exclusively cross sectional data can greatly affect the interpretation of the results. The part of the solution most affected by it is the nature of the *third factor*, and its possible differentiation from the Anxiety/Neuroticism and Impulsivity/Psychoticism dimensions. The pattern of loadings from E on the second and third factors also varies considerably across methods.

DISCUSSION

We have shown how the combination of SEM and EFA of longitudinal data can serve to clarify the factor structure of a pool of personality traits. In addition, we have demonstrated how the structure, especially of the *third factor*, can be affected by the longitudinal nature of the data used and the data analysis strategy. In the present paper, repeated measures in a time interval of 11 years on 13 personality variables were analyzed. We used a confirmatory factor model to isolate individual differences independent of intra-individual changes over time, and inter-individual differences due to age. Those individual differences were considered to express mainly *"trait-like"* variance, i.e., the variance that is the focus of trait theories of personality. The results of the higher order factor model showed that 3 latent factors or personality types are

required to adequately explain individual differences in personality, as assessed in this study.

Table 3.7.

SPSS solutions

	Three Factors from the correlation matrix of the Intercepts[a]			Three factors extracted from averaged phenotypes across surveys			Three factors extracted from factor -analysing exclusively cross-sectional data from 1991		
	F1	F2	F3	F1	F2	F3	F1	F2	F3
Depression	**.411**	-.035	.016	**.683**	.009	**.329**			
Anger	**.484**	-.146	**.488**	**.431**	.172	**.515**	**.469**	**.625**	.125
TAB	**.350**	-.156	**.323**	.305	.148	**.515**	**.430**	**.463**	.219
Anxiety	**.942**	.053	.320	**.889**	.058	**.526**	**.805**	**.432**	.086
Neuroticism	**.931**	.155	**.481**	**.855**	.128	**.586**	**.876**	**.477**	.107
Somatic anxiety	**.707**	.114	**.369**	**.656**	.091	**.409**	**.610**	**.324**	.092
Exttroversion	**-.361**	**.381**	**.317**	**-.371**	**.364**	.173	-.259	.221	**.414**
Disinhibition	.060	**.785**	**.575**	.024	**.703**	**.366**	.089	**.331**	**.627**
Experience seeking	.057	**.829**	.281	.039	**.644**	.176	.119	.158	**.536**
Boredom suscep.	.157	**.710**	**.491**	.110	**.553**	**.383**	.183	**.320**	**.571**
Thrill and ss	-.174	**.769**	**.508**	-.191	**.687**	.163	-.122	.170	**.549**
Rule breaking	.251	**.667**	**.790**	.203	**.488**	**.498**	.221	**.512**	**.371**
Aggressive behavior	**.354**	**.546**	**.974**	**.375**	**.410**	**.805**	**.437**	**.915**	**.357**
Factor correlations									
F2	.014			-.007			.456		
F3	.296	.562		.487	.450		.053	.430	

[a]*See appendix I*

With respect to the factor solution itself, the interest of the debate here is not so much to decide if 2, 3, 4 or 5 factors are necessary to explain temperament differences, as this has been discussed in detail in the past, and it is generally agreed that the number of factors, and the type of factors will vary depending on the purpose of measurement (prediction, diagnosis, or theoretical interest), as well as on the measurement level (behaviours, habits, personality, temperament). Five, four, or three factor models are the most generally accepted solutions. Furthermore, the number of factors extracted and their nature is directly a result of what is put into the analysis. Of greater interest here is the nature of the actual factors detected, and their identification with the theoretical factors entertained by biological theorists. In this respect, the present solution is particularly useful, as it was based on a large amount of information, and using a methodology that uses that information to arrive at an accurate assessment of trait-like individual differences. This ensures that the correlations due to unstable components

of behavior, developmental changes, or measurement error were corrected. The most striking feature of the final 3 factor structure is the clarity of the composition of the third factor, especially when compared with the SPSS solutions, which were extracted with alternative strategies that are more in line with the usual practice.

In view of the pattern of loadings observed, the first of the 3 factor solution can be identified with the Neuroticism/Anxiety/BIS/Harm Avoidance dimensions. The second factor can be labeled as the Impulsivity/ Impulsive Sensation Seeking/ Psychoticism/ BAS dimension. Finally, the third factor can be interpreted as a combination of characteristics of the dimensions of cooperativeness/FFS from Cloninger's and Gray's theoretical frameworks. In the two factor solution, both first and third factors merge to form a general negative emotionality or behavioral inhibition factor identified with the negative emotionality/Anxiety-BIS dimension, whereas the F2 maintains most of the characteristics of the previous second factor identified with behavioral activation and the psychoticism/Impulsivity-BAS dimension.

Although the interpretation of first and second factors seems quite straightforward and in concordance with Zuckerman's previous research (Zuckerman, 1991), the identification of the third factor is less clear and open to debate. Considering that Agg, Rbb, Ang, and TAB are the markers of this factor, and leaving out the theoretical dimensions already identified with the first two factors, two theoretical designations appear possible for the *third factor*. The first one is Cloninger's *cooperativeness*. In this interpretation, emotions and behaviors associated with the third factor would be categorized as related to character rather than temperament, as mainly environmentally determined, and as closely related to ontogeny and learning processes. Cloninger et al. (1993) define this dimension as the reflection of individual differences in people's ability to identify with others. The third factor could represent the negative pole of cooperativeness, if one interprets it as negative behavioral and emotional reactions to others, rather than just the inability to relate with others. A second plausible theoretical identification for the third factor is Gray's FFS, i.e., bound to unconditioned responses, and the recognition and manifestation of basic emotions controlled by the amygdala. This interpretation is consistent with Zuckerman's studies in which measures of anger, aggression, hostility, and lack of inhibitory control form a coherent cluster within the N+ and P+ quadrant (Zuckerman, 1991; Zuckerman et al., 1988). Zuckerman interprets this cluster as a different kind of negative emotionality, distinguishable from Neuroticism/Anxiety. When Zuckerman et al. (1988; Zuckerman et al., 1991) extracted a more reduced factor solution the Neurotic/anxiety factor and the anger/hostility factor merged into a single general emotionality factor, as it was the case in the present study.

We have interpreted the two factor solution as composed by two general factors of behavioral inhibition and behavioral activation. However, the presence of Ang, TAB, and Agg in the first factor might call for a refinement in the definition of that factor, and may even the question of the convenience to actually merge F1 and F3 in a two factors solution. According to Gray (1987), the responses to conditioned and unconditioned stimuli, although both related with punishment, can be radically different. Whereas the BIS induces inhibition and a nervous stop of any kind of behavior, the FFS provokes the activation of aggressive approach, defensive attack, or the attempt to escape. Both systems also differ in the kinds of emotions with which they are associated. The BIS is related with anxiety and negative affect, whereas the FFS is associated with rage and panic. Gray (1987) demonstrated that anxiolytic drugs reduce anxiety and passive avoidance, but not flight behavior.

A possible theoretical point of conflict with respect to the interpretation of the third factor as the FFS comes from the prediction of Gray (1987) that the BIS inhibits, when necessary, ongoing behaviors activated by any of the other two systems, i.e., BAS or FFS. Thus, some authors (Diaz & Pickering, 1993) would expect a negative correlation between F1 and F2 and F3, and a positive correlation between F2 and F3. However, as explained by Gray (1987), this interaction between the systems concerns the resolution of the approach-avoidance conflict that a given individual suffers when confronted with a situation with multiple stimuli, which activate multiple systems. The resolution of this conflict and consequent behavior displayed in that situation will depend on the trait levels of that individual and the intensity of each stimulus, considering that the activation of the BIS can inhibit the activation of the other systems. However, the trait levels of a given person on any of the three systems are independent and therefore individuals with an overactive BIS (high anxiety) are not necessarily expected to tend towards an under-active BAS (low impulsivity).

From the point of view of Eysenck's theory (1991; 1985), and Heath et al.'s (1988) results regarding the multidimensionality of P, the F3 might be interpreted as impulsiveness, and the F2 as aggressive-unsocialized sensation seeking. Both factors would be considered sub-traits of Psychoticism. The next logical prediction would then be that those two factors should merge in a two factor solution to form a Psychoticism factor. However this is not the case, as in the two factor solution, except for rule breaking behaviour, the rest of the markers of the third factor –aggressive behaviour, anger and Type A- have their principal loadings on the first factor of negative emotionality.

A puzzling result in the factor structure is the position of Extraversion in the factor space. E shows a complex pattern with loadings of similar size, but opposite sign in

more than one factor, in the 3 and 2 factor solutions. Extraversion is a primary dimension that has been replicated in studies of the structure of personality (Aluja, Garcia, & Garcia, 2004; Zuckerman, 1991). The E factor has not been obtained in the present study. This may be because no other indicators such as sociability or activity were included in the pool of variables. However, its complex pattern of loadings suggests that it is not a unidimensional measure. The negative loading of E on the F1 was obtained in previous studies. N and E are not orthogonal as Eysenck defined them, as they seem to be negatively correlated (Diaz et al., 1993; Matthews & Gilliland, 1999; Zuckerman, 1991): introverts are more likely to show high scores in anxiety and neuroticism than extroverts. According to Eysenck (1985) and Gray (1987), we would expect a positive loading of E on F2. However, Eysenck renounced to the dual nature of extraversion, and shifted all the impulsivity items either to the P scale, or deleted them. Thus, Extraversion is more related to sociability and agreeableness than to impulsivity or sensation seeking. Eysenck (1982) showed that the correlation between impulsivity and sociability was mostly due to environmental factors, and both traits might be well considered genetically distinct. Eysenck's suggestion was later supported by Heath et al. (1989) in a genetic analysis of the EPQ. The authors showed that family resemblance in extroversion was mainly explained by non-additive genetic variance, whereas family resemblance in psychoticism was exclusively explained by shared environmental factors. The original rotation of Eysenck's axes proposed by Gray was based on the EPI, where the extroversion scale still comprised impulsivity. Thus, the absence of a loading of E on the second factor is in theory expected. However, consistent with results from previous studies (Zuckerman et al., 1996), the correlations (see appendix I) suggest that E is as related to the markers of F2 as it is to the markers of F3. The loading of E on F2 of the SPSS solutions suggests that the correlation between E and the SS scales is mostly due to age.

We can offer two explanations for the loading of E on the third factor: 1) Gray (1987) argues that Extroverts are both hardly conditioned to fear responses, and more easily conditioned by rewarding unconditioned stimuli. According to Eysenck (1982), extraverts, because of their low arousal and poor conditioning capabilities, would have difficulties forming conditioned responses that are reflective of a conscience. In other words, they are more likely to behave in an un-socialized manner. If we interpret the third factor as a possible outcome of the FFS, a positive relationship between this factor and extroversion makes theoretical sense, as the FFS leads responses to unconditioned stimuli and to aggressive responses characteristic of un-socialized behavior. 2) The second explanation is related to the identification of the third factor with Cloninger's cooperativeness. For Cloninger, Cooperativeness reflects individual

differences in identification with and acceptance of other people. According to Eysenck, extroverts are more often exposed to social situations. If the third factor is identified with the negative pole of cooperativeness, the positive loading of E implies that extroverts are more likely to suffer angry and hostile emotions, and react aggressively, than introverts in social situations.

The resolution of the controversy surrounding the "*third factor*" of personality is one step closer with the results of the present study due to the information obtained from longitudinal data through the modeling of intra and inter-individual differences over time. Whether this third factor is indeed a consistent personality type, and whether it is more consistent with Gray's or Cloninger's theoretical frameworks is a subject for further research. A combination of both might also be plausible given the large negative correlation between Agg-Host and cooperativeness (Zuckerman et al., 1996).

The results of the measurement-growth models showed that most personality variables show a negatively accelerated decrease in mean levels over time and age. That is, trait levels decrease over time, but the rate of decrease gets less steep with aging. Most of them show moderate (0.301) to high (0.852) stability coefficients that decrease with larger time intervals, but seem to increase again when individuals reach middle age.

The residual variances of the majority of shape factors were significant, which means that there are individual differences in change over time that are not explained by age. However, the sizes of the residual variances were small compared to those of the level factors. To test if this variability could produce a significant change in rank order that could affect the intercorrelations across variables, we re-estimated the model changing the coefficients of the shape so that the initial level was fixed in 1997 instead of in 1991 (coefficients -3 -2 -1 0 1 2). This resulted in negligible changes in the factor structure, which did not affect the interpretation of the solution. This is expected, given the implication of the growth curve models that the shape of the change is equal across individuals, while allowing for quantitative differences (Hertzog et al., 2003).

In general, the results of the growth models and the age moderation show that, although there is a large amount of stability over time in personality, the amount of intra-individual change is not negligible, and should be taken into account.

The present modeling strategy also made possible to correct inter-trait-correlations for possible deviations due to variations in the inclusion of different questionnaires in different surveys. E.g., it might be that variables measured by the ABV correlated more strongly with the variables measured by the SBL than with the variables measured by the YASR, because the former two were measured in the same surveys. The

estimation of an initial level latent factor regressed by age can be mathematically compared to the regression of all scores to the score that they would have showed if all of them had been measured at the same time and the same age. This kind of bias in the correlations might especially affect the solution when repeated measure scores are averaged to obtain a single score for factor analysis (see table 7).

LIMITATIONS AND FUTURE DIRECTIONS

A limitation of the present study is the relatively small pool of variables, especially with respect to Extroversion. The inclusion of new measures of sociability or activity might clarify nature of E. The inclusion of some indicators that represent the positive and negative poles of the third factor, i.e. responsibility, restraint, rage, or hostility may well help to further resolve this factor.

The *third factor* estimated in the present study, might be associated with several socially relevant factors, from delinquent behavior to health outcomes, such as coronary heart disease (Chang, Ford, Meoni, Wang, & Klag, 2002; Eaker, Sullivan, Kelly-Hayes, D'Agostino, & Benjamin, 2004; Slaton, Kern, & Curlette, 2000). The first factor has been studied extensively, because of its relationship with several emotional disorders. The third factor might comprise emotions of a different nature and origin. We speculate that the disorders or deviant behaviors that result from these emotions are less socially accepted and attract less attention, and less research or theoretical interest (DiLalla, 2002). According to Eysenck (1991; 1992a) and Zuckerman (1992), the relevance, coherence, and independence of a personality type can not be determined exclusively with factor analysis. Whether the third factor constitutes a basic personality *type*, should be addressed through the study of the biological basis of the cluster of traits that form the factor, and their predictive validity. There should be a basic common biological and/or genetic mechanism underlying individual differences on the cluster of traits, which differs from that of other personality *types*. The combination of traits that defines the third factor should also predict socially relevant phenomena, which differ from those predicted by other personality *types*.

Previous studies have addressed the genetic and environmental basis of anger, type A behavior, and aggression (Ligthart, Bartels, Hoekstra, Hudziak, & Boomsma, 2005; Sims, Boomsma, Carroll, & Hewitt, 1991). Sluyter et al. (2000) found common genetic variance across measures of anger, hostility, and aggression. In a recent publication Keller and colleagues (Keller, Coventry, Heath, & Martin, 2005) replicated and discussed the evidence for additive genetic effects in major personality traits, and stated that “high levels of non-additive genetic variation suggest that personality has probably not been neutral to selection” (p.716). Thus, evidence from behavior genetic studies might tip the balance towards a more biological explanation of the third factor, such as that of Gray’s FFS.

Nonetheless, biological bases of basic personality factors are rather uncertain. Over the years researchers used a variety of strategies to study the biological bases of personality, from experimental psychology with physiological measures (Eysenck, 1997; Gray, 1987), to the study of genetic markers (Gillespie, Cloninger, Heath, & Martin, 2003; Heath et al., 1994). But the results remain rather equivocal, as positive results are rarely replicated (Herbst, Zonderman, Mccrae, & Costa, 2000; Matthews et al., 1999). Zuckerman (1991; Zuckerman et al., 1991) argued that the physiological measures employed are not sufficiently precise, and are more measures of states than of traits. He emphasized that the role of the enzymes, which regulate the production and degradation of neurotransmitters, and ensure the return the system to a homeostatic level, may be more essential than the fluctuating levels of the neurotransmitter activity, which are more sensitive to a given situation. On the other hand, these studies do not sit well with the very definition of personality, as they associate single assessments, either from experimental settings or from questionnaires, with biological measures, without taking into account age differences or change over time. As it has been stated, human significant behaviors are organized in a hierarchical fashion, and only the high levels of the hierarchy are likely to show consistent relationships with biological systems. We contend that both the theory (Eysenck, 1991), and the research methods should take into account the fact that personality changes over time and with age. Individual differences in personality that remain after accommodating those changes can be considered as manifestations of the personality *types* in the higher levels of the hierarchy defined by Eysenck.

Behavior genetic studies of the causes of individual differences is moving more and more towards the study of gene-environment (Purcell, 2002; Purcell & Sham, 2002) and gene-gene interactions (Eaves, Heath, Neale, Hewitt, & Martin, 1998; Keller et al., 2005; Reuter, Schmitz, Corr, & Hennig, 2005), as behavior is the result of a constant interplay between genetic and environmental effects. The identification of the *basic* factors that explain differences in behavior may require the acknowledgement of the dual nature of behavior. Individual differences in human behavior are characterized by a stable component, and by a component that changes over time and situations; they are explained by genetic diversity, and by variation in environmental circumstances. The study of personality should benefit from longitudinal studies that incorporate different family members. Statistical models that separate variance due to stability and variance due to change, and variance due to genetic differences and environment for several personality measures are available thanks to the advances in statistical modeling. Only through longitudinal family studies, while employ the appropriate methodology, it is possible to study reliably the possible biological and physiological bases of personality traits as defined by biological theories of personality.

Appendix

Estimated correlation matrix across intercepts

	DEP	ANG	TAB	ANX	NEU	SOM	EXT	DIS	ES	BS	TAS	RBB	AGG
DEP	1.0000												
ANGER	.1860	1.0000											
TAB	.1640	.3530	1.0000										
ANX	.3850	.4800	.3570	1.0000									
NEU	.3560	.5140	.3570	.8860	1.0000								
SOM	.2620	.3770	.2510	.6660	.7030	1.0000							
EXT	-.1650	.0360	.0760	-.3070	-.2570	-.2050	1.0000						
DIS	-.0180	.2000	.1830	.0940	.1900	.1400	.3350	1.0000					
ES	.0130	.0510	.0940	.0780	.1310	.0950	.2260	.6030	1.0000				
BS	.0560	.2540	.2640	.1880	.2460	.1720	.2950	.5930	.5760	1.0000			
TAS	-.1490	.0110	-.0120	-.1400	-.0150	.0000	.3510	.6260	.6020	.4960	1.0000		
RBB	.0400	.3890	.3020	.2780	.3950	.2950	.3080	.6070	.4470	.5640	.5270	1.0000	
AGG	.0420	.4970	.3280	.3720	.5270	.4040	.2760	.5570	.2810	.4800	.4840	.7730	1.0000

Chapter 4

Genetic and Environmental Influences on Type A Behavior Pattern: Evidence from Twins and their Parents in the Netherlands Twin Register

Irene Rebollo & Dorret I. Boomsma

This Chapter is based on: Rebollo, I. & Boomsma, D.I. (In Press). Genetic and Environmental influences on Type A Behavior Pattern: Evidence from twins and their parents on the NTR. Psychosomatic medicine.

Background: There is a dose response positive relationship between Type A Behavior (TABP) and cardiovascular disease related symptoms. Estimates of heritability for TABP from previous studies vary; this might be explained by limitations in the sizes and compositions of the samples.

Methods: This study combines: a large sample size, twin and parental, data from males and females, two generations of young adults and older adults, and the use of SEM (Structural Equation Modeling) and FIML (full information maximum likelihood) estimation.

To asses TABP the Jenkins Activity Survey (JAS) was collected from MZ and DZ twins and their parents (N=1670 twin families). Structural Equation modeling is used to evaluate and estimate the effects of additive and non-additive genetic effects, non-shared environmental effects, and competitive sibling interaction.

Results: 45% of the variance in TABP was due to genetic factors, (28% were additive and 17% were non-additive). The remaining 55% of the variance was explained by environmental factors not shared by the members of the same family. Competitive sibling interaction effects were not significant. There was no evidence of sex differences either in variances or means.

Conclusion: Understanding the sources of variance on TABP is important for therapy and prevention. According to the present results the relevant environmental factors for the development of TABP are not shared by the members of the same family. The genetic portion of the variance is also worth to consider for therapeutic purposes. Although the genetic code can not be altered, its effects on behavior may be modifiable through the treatment of the biological mediators

INTRODUCTION

The Type A Behavior Pattern (TABP) was defined by Rosenman and Friedman (1974) to describe a behavioral style to cope with stressful situations in life. The original concept comprises physical, psychological as well as behavioral characteristics. These include anger, hostility, aggressiveness, competitiveness, time urgency, behavioral alertness, impatience, loud voice, facial muscle tension, achievement motivation or work involvement. Several studies tried to demonstrate that TABP increases the risk of cardiovascular and coronary heart disease (CVD and CHD) (e.g. Matthews & Jennings, 1984; Rosenman, Friedman, & Strelau, 1964; Zyzanski, Wezesniewski, & Jenkins, 1979). An accumulation of contradictory results raised some doubts about the reliability of TABP to predict CHD incidence (Matthews, 1988; Siegman & Dembroski, 1989). Recent research has tried to solve the controversy by studying different

components of TABP and outcome CHD or CVD as well as related symtoms and precursors (i.e. blood pressure (BP), angina pectoris, heart rate period and variability, atrial fibrillation or hypertension) (Chang et al., 2002; Eaker et al., 2004; Kawachi, Sparrow, Spiro, Vokonas, & Weiss, 1996; Palmero, Diez, & Asensio, 2001; Sloan et al., 2001; Williams et al., 2000; Yan et al., 2003). When sex differences and age effects are taken into account and large samples are employed, most studies find dose response positive relationships between Type A related characteristics and cardiovascular disease related symptoms. It is suggested that type A behavior pattern might predispose people to suffer coronary disease through both unhealthy daily lifestyle behaviors –obesity, alcoholism, social isolation, smoking- and pathophysiological effects –higher blood pressure and heart rate responses, hypercortisolemia, high circulating catecholamines and increased platelet reactivity- (Rozanski, Blumenthal, & Kaplan, 1999; Shah, White, White, & Littler, 2004).

The relationship between TABP and health is of great importance as it can have therapeutic implications (Kawachi et al., 1998; Rozanski et al., 1999; Shah et al., 2004). Two meta-analyses (Linden, Stossel, & Maurice, 1996; Nunes, Frank, & Kornfeld, 1987) have found that psychosocial interventions can reduce mortality and morbidity associated with coronary heart disease. But to be able to modify a given behavioral or psychological characteristic it is necessary first to understand what causes variation among individuals. Behavioral genetics research can help to disentangle the different genetic and environmental sources of variance on Type A Behavior (Siegman & Smith, 1994).

Previous twin studies have explored the genetic and environmental influences on TABP (Carmelli et al., 1988; Duffy et al., 1994; Koskenvuo, Kaprio, Langinvainio, Romo, & Sarna, 1980; Matthews & Krantz, 1976; Meininger, Hayman, Coates, & Gallagher, 1988; Pedersen et al., 1989; Rahe, Hervig, & Rosenman, 1978; Raynor, Pogue-Geile, Kamarck, McCaffery, & Manuck, 2002; Tambs, Sundet, Eaves, & Berg, 1992).These studies tend to find significant heritability estimates with values around .40, but point estimates are quite variable ranging from .032 (Koskenvuo et al., 1980) to .62 (Duffy et al., 1994). This variability of results can be due to differences in the study design, the assessment instrument, or the composition of the samples. Some authors have suggested that heritability might be larger for interview measures than for self reports (Carmelli et al., 1988). Koskenvuo (Koskenvuo et al., 1980) showed that heritability estimates are markedly larger in younger samples. Given that TABP is considered a coronary prone behavior, it is worth to take into account the well known sex differences existent in CAD (Coronary Artery Disease) incidence. These differences could be due to sex differences in the biological and/or environmental factors

influencing TABP. Some factors that have been suggested as possible sources of sex differences are protective effects of estrogens in women, or unhealthier life style in men (Rozanski et al., 1999). However, the majority of studies on the heritability of TABP only include males in their samples (Bortner, Rosenman, & Friedman, 1970; Carmelli et al., 1988; Koskenvuo et al., 1980; Meininger et al., 1988; Rahe et al., 1978; Sims et al., 1991). Four studies included male and female twins, but only two of them studied sex differences in the genetic architecture systematically. Pedersen et al. (1989) found no sex differences in heritability estimates for the Framingham questionnaire, while Tambs et al. (1992) found larger heritability estimates for females on the JAS (Jenkins Activity Survey).

Large differences between MZ and DZ twin resemblances and DZ correlations close to zero are a common finding across studies of TABP and related traits. This pattern of results can be explained by the presence of non-additive genetic effects, competitive sibling interaction or unequal environments for MZ and DZ twins (Loehlin, 1986), but few studies have considered the presence of such effects (Duffy et al., 1994; Sims et al., 1991), and none of them had sample sizes large enough to have power to detect either dominance or sibling interaction effects (Rietveld, Posthuma, Dolan, & Boomsma, 2003).

The present study is intended to disentangle the sources of variance on TABP. Data from a large sample of 1670 twin families are analyzed which provides strong statistical power; male and female MZ and DZ twins, and opposite sex DZ twins are included, and sex differences are explicitly tested. The addition of parental data into the study increases the power to detect and distinguish between additive genetic and dominance genetic effects and competitive sibling interaction effects -under the assumption that the same genes are expressed in both generations-.

METHOD

Participants and Procedure

Participants were registered by the Netherlands Twin Register (NTR), kept by the Department of Biological Psychology at the Vrije Universiteit in Amsterdam. They are part of the adolescent and adult cohort that was recruited through the city councils in 1990-1991. They participate in longitudinal survey studies roughly every two years. The data analyzed here were collected in the 1991 survey. Questionnaires on health and lifestyle were sent by mail to 2375 families who were willing to participate (Boomsma et al., 2002). Completed questionnaires were returned by 1670 families.

The complete sample consists of 1670 families for which data on the phenotypes of the twins and their parents were collected in 1991: 270 MZM (Monozygotic Males), 253 DZM (Dyzigotic Males), 372 MZF (Monozygotic Females), 294 DZF (Dyzigotic Females), 481 DOS (Dyzigotic Opposite sex). There are complete data for 1289 families. For 1605 families there are data for both members of the twin pair. In 62 families data from one of the twins is missing. For 1334 there are data for both parents, and for 271 families data for one of them is missing.

The mean age of the twins was 17.72 (S.D. = 2.37, range = 12-25 years). The mean age of the parents was 46.67 (S.D. = 5.49, range = 35-71 years).

Zygosity for 314 same sex pairs was based on DNA polymorphisms, and for the remaining pairs zygosity was assigned by discrimination analysis using questionnaire items (see Boomsma et al., 2002 for further details). The correspondence between DNA and questionnaire based zygosity was 97%.

The Ethics Committee of the Vrije Universiteit University Hospital approved the study.

Measures

The Dutch adaptation of the JAS (Jenkins Activity Survey) (Appels et al., 1985; Appels et al., 1982) was used to measure TABP. The JAS is one of the most widely used instruments to measure TABP across twin and family studies because it is a reliable instrument with a reasonable amount of items to apply to a large sample. The reliability of the Dutch adaptation measured by the alpha coefficient was .84. The test retest reliability after 6 months was .91. The questionnaire comprises 24 items that give an overall score on TABP. At the moment of collection of the data the Dutch translation of the JAS did not include subscales as their validity had not been established (Appels et al., 1985).

ANALYSES

Structural Equation Modeling (SEM)

Analyses are conducted using SEM as it permits the simultaneous analysis of multiple groups, and the possibility of imposing parameter constraints across groups. The statistical software package Mx was used for this purpose (Neale et al., 2003). To be able to use all the data available even when some member of the family was missing, Full Information Maximum Likelihood estimation (FIML) with raw data was used to fit the models. Twice the negative log-likelihood (-2LL) of the data for each family is calculated, and parameter estimates are produced that maximize the likelihood of the raw

data. Submodels were compared using a likelihood ratio test computed by subtracting -2LL for the restricted nested model from that for the baseline model ($\chi^2 = (-2LL_0) - (-2LL_1)$). The resulting test statistic has a χ^2-distribution with degrees of freedom equal to the difference of the degrees of freedom (DF) between the two models.

The fit of the genetic models is evaluated relative to the fit of a saturated model, were the covariance matrix and the mean structures are estimated without any restriction. The saturated model reproduces the data perfectly and thus, a significant χ^2 difference between the saturated model and a genetic model means that the genetic model does not fit the data adequately, whereas a non-significant χ^2 value means that the model provides a good fit to the data. Given the large sample size, an α value of .01 was used.

The saturated model was used as a reference to test for (1) age and sex effects on the mean levels of TABP; (2) differences in variance across generations; and, (3) the presence of assortative mating (i.e. a significant association between TABP of spouses).

Genetic Modeling

The path diagram in Figure 4.1 represents the general genetic model that is being tested. The diagram represents an "ADEi" model for an opposite-sex twin pair and their parents where the first born twin is a male and the second born twin is a female. The variance of TABP is explained by additive genetic factors, dominance genetic factors and environmental factors not shared by the members of the same family. At first, different parameters are estimated for males and females. Given that the DZ correlations were less than twice the MZ correlations, the shared environment was left out of the model, and dominance genetic effects were modeled instead, as their presence is consistent this pattern of correlations.

It is assumed that the amount of variance explained by each component is proportional in the parental and offspring generations. The parameter γ is placed in the model to account for any differences of variance between them. Resemblance between parents and offspring is explained by the additive genetic variance that they share. In the absence of assortative matting, each parent shares with each twin 50% of the additive genetic variance.

DZ twins resemble each other because they share 50% of their genetic variance, inherited from their parents. They also share 25% of the dominant genetic variance. MZ twins share the totality of both, the additive and the dominant genetic variance.

Thus, the model for the MZ twins includes an additional correlation of 0.5 (not depicted in the figure) between their additive genetic factors (A); this 0.5 plus the 0.5 shared through the parents adds up to 1.0. Additionally, in the model for the MZ twins, the correlation between the dominance genetic factors (D) equals 1.0 instead of 0.25.

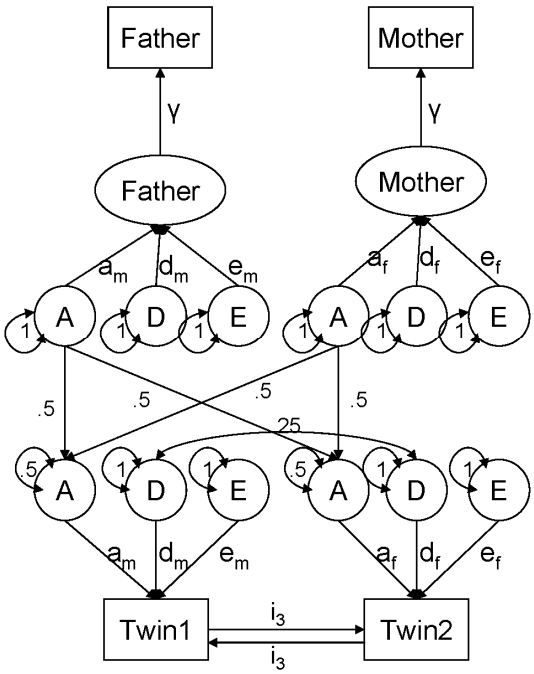

Figure 4.1 Parent-offspring genetic ADEi model

The figure represents an opposite sex DZ pair where the first born is a male and the second born is a female. Measured phenotypes are represented into rectangles: Twin1-first born, Twin2-second born, Mother, and Father. Latent variables representing sources of variance are depicted into circles: A-Additive genetic effects, D-Dominance genetic effects, E-Non-shared environment. γ- represents the scalar parameter to account for the difference in variance in the parental generation. Path coefficients with the subscript m are those for males, and the subscript f is for female parameters. The arrows connecting the twins represent the sibling interaction parameter, i_3 in the diagram is the sibling interaction for opposite sex twin pairs; i_1 would be the interaction parameter for males, and i_2 for females. Parents and offspring are connected by paths with a .5 that represents the 50% of genetic variance that they share.

The phenotypes of the twins are connected through reciprocal paths in the diagram. Those paths and their corresponding parameters represent the direct phenotypic effects that the twins have on each other, that is to say sibling interaction effects. Competitive

sibling interaction effects imply that the twins interact or influence each other in such way that their phenotypes develop in opposite directions.

This would predict DZ correlations close to zero or negative, and lower than half the MZ correlations. In the model tested, it is assumed that the amount of influence that the twins exert on each other is equal, but different interaction effects are estimated for same sex male twins (i_1), same sex female twins (i_2), and opposite sex twins (i_3). This allows sex differences in the amount of interaction between the twins. Further details about the derivation of the expected variances and covariances and the effects of the presence of sibling interaction (Eaves, 1976) on the model expectations can be found in Neale and Cardon (1992).

RESULTS

The saturated model

Tests based on the saturated model showed a significant difference in the means between parents and their offspring ($\chi^2(1)=21.74$, $p<.001$). The mean values estimated are 13.87 for the parents and 9.19 for the twins, thus the parental generation shows higher levels of TABP than the offspring.

The effects of age (twins: $\chi^2(1)=5.76$, $p=.016$, and parents: $\chi^2(1)=.058$, $p=.810$) and sex (twins: $\chi^2(1)=.000$ $p=1.000$, and parents: $\chi^2(1)=.000$, $p=1.000$) on the means were not significantly different from zero for either parents or twins. Thus, mean levels of TABP were equal for males and females and stable across age, within each generation.

The parental generation showed a significantly larger variance than the twins ($\chi^2(6)=74.36$, $p<.001$).

Summary correlations and their confidence intervals (CI) are shown in table 4.1. The DZ correlations are lower than half the MZ correlations, and all of them have a lower bound close to zero or negative; this suggests the presence of dominance genetic effects and/or competitive sibling interaction effects. The size of the parent offspring correlations is indicative of additive genetic effects of roughly .20 to .30.

The last two columns of table 1 show the correlations constrained to be equal for male and female pairs, and the corresponding confidence intervals. The MZ correlations were not significantly different for male and female pairs ($\chi^2(1)= .112$, $p=.737$). The DZ correlations could also be considered equivalent across males, females and opposite sex pairs ($\chi^2(2)= 1.033$, $p=.596$). The joint estimate of the DZ correlation is still less than half the MZ correlation, with a lower bound close to zero. Correlations between mother and female or male twins, and between father and female or male twins were not significantly different from each other ($\chi^2(3)= 2.92$, $p=.404$). The

common estimate of the parent-offspring correlation was .148, and significantly different from zero ($\chi^2(1)= 104.94$, $p<.000$). The spouse correlation (.015) was not significant ($\Delta\chi^2(1)= .311$, $p=.577$), and thus random mating was specified in the genetic models. This implies that spouses do not select each other on the bases of their type A personality pattern, and resemble each other as much as random individuals picked from the population.

Table 4.1

Summary correlations estimated from a constrained saturated model

	N (pairs)	Correlation	99% Confidence Interval	Correlation equated across sexes	99% Confidence Interval
MZM	270	0.493	0.396,0.578	0.480	0.398,0.555
MZF	372	0.472	0.389,0.547		
DZM	253	0.063	-0.063,0.188		
DZF	294	0.120	0.008,0.230	0.118	0.036,0.197
OS	481	0.142	0.054,0.229		
Father-Son (FS)	1259	0.117	0.059,0.176		
Father-Daughter (FD)	1483	0.178	0.124,0.232	0.148	0.111,0.185
Mother-Son (MS)	1407	0.133	0.106,0.208		
Mother-Daughter (MD)	1678	0.157	0.078,0.187		
Spouses	1359	0.015	-0.038,0.068		

Genetic modeling

The full ADEi model provided an excellent fit to the data when compared to the saturated model ($\Delta\chi^2(50)=50.123$, $p=.469$, AIC -49.87). This complete model allowed different amounts of variance explained by A, D and E for males and females (a_m^2, a_f^2, d_m^2, d_f^2, e_m^2 and e_f^2); sibling interaction effects where also allowed to differ for same sex males and females, and for opposite sex pairs (i_1, i_2, i_3); and, variance differences between generations are accounted for by γ in the model.

Departing from the estimates of this full model we tested different hypothesis. The model fitting results are shown in table 4.2. First, in model 2, we tested if the same amount of variance was explained by A, C and E across sexes, by constraining them to be equal for males and females. This constraint did not produce a significant decrease on the fit, and thus A, D and E explain the same amount of variance for males and females. Secondly, in model 3 the three sibling interaction effects were constrained to be equal for same sex male and female pairs and for opposite sex pairs. As this model explained the data as well as the full model, we concluded that twin pairs interact and influence each other to the same extent, irrespective of their gender.

Table 4.2

Genetic model fitting results: First the fit of the general ADEi model is shown, and then several submodels are fitted and compared with the general model to test specific hypothesis

	$\Delta\chi^{2*}$	ΔDF^{*}	p
1. Full ADEi			
2. ADE♂=ADE♀	7.46	3	.058
3. $i_1=i_2=i_3$	.654	2	.721
4. D=0	21.402	2	.000
5. A=0	105.07	2	.000
6. $i_1=i_2=i_3=0$	5.061	3	.167
7. $\gamma = 1$	60.729	1	.000
Final model ADE♂=ADE♀ $i_1=i_2=i_3=0$	12.472	6	.052

[*] *All sub-models are compared with the Full ADEi model.*

Models 4 to 6 were intended to test if additive and dominance genetic variance, and sibling interaction effects are necessary to explain differences in TABP. In models 4 and 5 additive and dominant genetic effects were alternatively fixed to zero. In both cases the constraint produces a significant decrease of fit of the model to the data, which means that both additive and dominant genetic effects are significantly different from zero and thus necessary to explain the variance of TABP. In model 6 sibling interaction effects are fixed to zero without any significant deterioration of the fit, and thus interaction between siblings is not a significant source of variance on TABP.

Finally, we tested for differences in variance across parental and offspring generations by fixing the scalar γ to 1. This model assumes that parents and offspring have the same variance. Model 7 fits the data significantly worse that the full model where the scalar is freely estimated and thus, variances of the parental and offspring generations are significantly different.

Pooling all the previous results together we estimated a final model where familial resemblance is explained by additive and dominance genetic effects, no sibling interaction effects or sex differences are present, and the relative amount of variance explained by each component is proportional for parents and offspring but their total variances differ through the scalar parameter. This model explains the data as well as the full ADEi model (p= .052) and it provides a good fit to the data when compared with saturated model ($\Delta\chi^2(56)=62.58$, p=.254, AIC -49.41). According to this final model 28%(C.I.23,34) of the variance on TABP is explained by additive genetic factors, 17% (C.I. 10,25) by dominance genetic factors, and the remaining 54% (C.I. 48,60) by the non-shared environment. The estimated scalar equals 1.17, indicating a larger total variance in the parental generation.

DISCUSSION

The present study was intended to disentangle the variance of TABP, making use of a powerful design to surpass some of the limitations of previous studies. The results indicate that 45% of the variance is due to genetic factors, among which 28% are additive and 17% are non-additive. The remaining 55% was explained by environmental factors not shared by the members of the same family. No evidence for shared environmental effects was found, as DZ correlations were distinctly lower than half the MZ correlations. Competitive sibling interaction effects were considered as possible explanation for this pattern of correlations but found to be non-significant.

Age and sex did not have significant effects in the mean levels of TABP within each generation. However, the parental generation showed larger means and variances than the offspring twin generation.

The results of the present study are closest to the two studies with the largest sample sizes published so far (Koskenvuo et al., 1980; Pedersen et al., 1989). The twin correlations and the estimates of the broad heritability of both studies are in the same range as here, and no sex differences were found by Pedersen et al.(1989) either. The main discrepancy is relative to the relevance of non-additive genetic effects. Koskenvuo et al. (1980) applied Falconer's formula to estimate heritability, despite the DZ correlations close to zero. Had those authors used SEM, it is likely that they would have found dominance genetic effects. To explore this possibility, we reanalyzed the twin correlations reported by Koskenvuo et al. (1980) using SEM. The results showed that, for age ranges between 18 and 49, 23-32% of the variance is due to dominance genetic effects. However, additive genetic effects were not significantly different from zero, which is a symptom of lack of power to differentiate between additive and dominance genetic effects without the use of information from other family members.

Pedersen et al. (1989) used SEM and considered the presence of non-additive genetic effects. They analyzed data from 6 components of TABP, and found evidence for dominance in 3 of them. But, when dominance effects were found, additive genetic effects were zero and non significant, which is an indicator of lack of power to differentiate between A and D in their models, probably as a consequence of the insufficient sample size, and the fact that they only included MZ and DZ twins.

In the present study, the solid correlations between parents and offspring, consistent for mothers and fathers, and across male and female twins, adds more support to the relevance of additive genetic effects on TABP, and their stability across generations. The information obtained from the resemblance between parents and their offspring, increases the power to distinguish between additive and dominance genetic effects. A reliable estimation of the dominance genetic variance, facilitates a reliable

estimation of possible competitive sibling interaction effects (Rietveld et al., 2003), as both effects increase the difference in resemblance between MZ and DZ twins. Previous genetic studies of the Type A personality and related traits have benefited from the inclusion of parental data, finding results consistent with the ones found here (Sims et al., 1991). In Sims et al.'s (1991) study the sibling interaction effects were discarded as an explanation of the low DZ correlations when parental data where taken in consideration.

Other studies have explored the familial aggregation for TABP beyond the classic twin design. Tambs et al. (1992) studied 150 families of MZ twins, their spouses and children. Consistent with the literature and our own results, their estimate of broad heritability was close to 0.40, and cultural transmission could be deleted from the model. However, no dominance genetic effects were found.

Previous family studies also found familial resemblance for TABP, but disagreed on their interpretation of their results. (Bortner et al., 1970; Matthews et al., 1976; Sweda, Sines, Lauer, & Clarke, 1986). None of them did any genetic modeling besides reporting correlations among different kinship pairs, and the largest study had 221 families (Sweda et al., 1986).

Generally, the pattern of correlations for twins and other family members replicates with slight differences throughout studies. The estimates of broad heritability and the absence of shared environmental effects are also consistent throughout the literature. The differences come when other sources of variance are contemplated and more complex statistical analyses are done, where the results are more sensitive to the size and composition of the sample. This study has a combination of characteristics that increases the reliability of the results obtained: a large sample size, parental data added to the classic twin design, males and females in the sample, two generations of young adults and older adults, and the use of SEM and FIML estimation on raw data to make use of all the information available.

However, TABP as measured by the JAS is a multidimensional construct that comprises a broad range of characteristics, from which only the emotional and attitudinal components such as anger, hostility or aggressiveness actually contribute to the prediction of incidence of CHD (Palmero et al., 2001; Siegman, 1994c). Thus, the results of the present study should be replicated on these toxic components of TABP. Sluyter et al. (2000) explored the genetic and environmental influences on anger, hostility and aggressive behavior, and found comparable results concerning broad heritability estimates within 9 different indicators of TABP. However, the authors lacked enough power to detect dominance genetic effects as the small sample was composed by twins only (45MZ and 37DZ).

Further interesting developments could be the replication of the present results with older twin samples, as well as the use of longitudinal data to clarify the source of the generational differences.

With regard to the implications of our results, the fact that a bit more than half of the variance is explained by environmental effects is valuable information for prevention and therapy. But therapists and researchers should keep in mind that those environmental factors are not shared by the members of the same family.

Not only the environmental, but also the genetic portion of the variance is worth to consider for therapeutic purposes. The emotional component of TABP, anger, has been associated with a polymorphism on the tryptophan hydroxylase gene (Manuck et al., 1999). Moreover, Hostility has been associated with high catecholamine reactivity and diminished brain serotonin functions (Siegman et al., 1994). Although the genetic code can not be altered, its effects on behavior may be modifiable through the treatment of the biological mediators. Similarly, the expression of the genes can be moderated by the environment e.g. gene-environment interaction or correlation.

Further research will extend our understanding of the specific environmental and genetic factors that influence the TABP and how to apply that knowledge for prevention and therapy. The present study provides reliable results on which new findings can be built.

Chapter 5

GENETIC ANALYSIS OF ANGER: GENETIC DOMINANCE OR COMPETITIVE SIBLING INTERACTION

Irene Rebollo & Dorret I. Boomsma

This Chapter is based on: Rebollo, I. & Boomsma, D.I. (In Press). Genetic analyses of Anger: Genetic Dominance or competitive sibling interaction. Behavior Genetics. (Published online ahead of press)

The knowledge of the causes and development of anger is still scarce. Previous studies on the sources of variance on TABP (Type A Behavior Pattern) related measures found variable heritability estimates ranging from .12 to .68, and large differences between MZ and DZ correlations. Some authors considered dominance genetic effects, competitive sibling interaction and sex differences as possible mechanisms to explain the results, but most studies lacked power. The present study uses a large sample of more than 2500 families, with longitudinal data from MZ and DZ pairs as well as their parents, to disentangle the sources of variance on anger. Model Fitting results showed that the sources of variance differ across sexes. For males 23% of the variance is due to additive genetic effects, and 26% to dominance genetic effects. For females 34% of the variance is due to additive genetic effects, and no dominance effects are found. There was no consistent evidence to confirm the presence of competitive sibling interaction as an alternative explanation for the low correlations in DZ males. The focus of research on the prediction of CHD (Coronary Heart Disease) risk through psychological characteristics has recently changed from the multidimensional TABP to its emotional component: Anger. Understanding the sources of individual differences on anger can help to clarify the mechanisms that link it with CHD and its possible implications for treatment and prevention.

INTRODUCTION

Anger is defined by Spielberger et al. (1983) as an emotional state that consists of feelings of variable intensity, from mild irritation or annoyance to intense fury and rage. The study of the sources of individual differences in anger has focused mainly on the contribution of psychological factors to the development of coronary heart disease (CHD). Friedman & Rosenman (1974)identified and defined the Type A Behavior Pattern (TABP) as a pool of characteristics that increase the risk of CHD. As a multidimensional construct, TABP comprises physical components, motivational and cognitive aspects, behavioral tendencies, attitudes and emotions; including loud voice, facial muscle tension, hostility, anger, aggressiveness, achievement motivation, competitiveness, alertness, work involvement, or necessity of environmental control. A number of studies showed a significant relationship between TABP and CHD (eg. : Matthews et al., 1984; Obrist, 1976; Rosenman et al., 1964; Zyzanski et al., 1979). Subsequent research has shown that, among the multiple elements encompassed in the TABP, only the emotional and attitudinal components such as anger, hostility and aggressiveness (‘the AHA syndrome’) contribute to the prediction of CHD incidence; and so the focus of research has changed from TABP to hostility, and to anger (Dem-

broski, MacDougall, Costa, & Grandits, 1989; Matthews, 1988; Palmero et al., 2001; Siegman et al., 1994).

Anger has been related to several phenomena in behavioral medicine and psychological research. High levels of trait anger and internal expression have been associated with increases in blood pressure and induced hypertension (Crane, 1981; Markovitz, Matthews, Wing, Kuller, & Meilahn, 1991; Schneider, Egan, Johnson, Drobny, & Julius, 1996). Some studies show positive correlations between external expression of anger and cardiovascular reactivity in irritated patients (Engebretson & Matthews, 1989; Siegman, 1994b). Furthermore, high levels of anger have been found to be good predictors of risk to coronary disease is several studies (Atchison & Condon, 1993; Bishop & Quah, 1998; Chang et al., 2002; Eaker et al., 2004; Julkunen, Salonen, Kaplan, & Chesney, 1994; Kawachi et al., 1996; Mendes de Leon, 1992; Williams et al., 2000). Others have found a positive relationship between the anger trait and anger held in and chronic symptoms suffered by patients of posttraumatic stress (Lasko, Gurvits, Kuhne, Orr, & Pittman, 1994; Tschannen, Duckro, Margolis, & Tomazic, 1992). High levels of anger have also been associated with psychological disorders like anorexia and bulimia nervosa (Fassino, Daga, & Piero, 2001), or borderline personality disorder (Nothmann, 1999). Finally, different patterns of anger expression have been studied in relation to socially relevant issues like criminal personality (Slaton et al., 2000), sexual offense (Dalton, Blain, & Bezier, 1998), aggressive behavior in adolescents (Peters, 1998), drug addiction (De Moja & Spielberger, 1997) or marital maltreatment (Barbour, Eckhardt, Davison, & Kassinove, 1998).

The present study is intended to explore the extent to which environmental and genetic factors underlie variation in trait anger. Trait anger is conceptualized as the frequency with which an individual experiences the emotional state of anger over time and in response to a variety of situations (Eckhardt, Norlander, & Deffenbacher, 2004). Sluyter et al. (2000) studied the genetics of trait anger as a component of the AHA syndrome, and its relation with testosterone. Additive genetic effects explained 25% of the variance of anger, all common to other measured traits such as TABP, irritability or hostility. Among the nine personality traits considered by the authors in an independent pathway model to define the AHA syndrome, trait anger and indirect hostility showed the lowest heritability estimates (respectively .25, C.I.=.07,.50 for anger and .23 C.I.= .04,.46 for hostility). Both anger and hostility showed quite low DZ correlations (.07 & -.03). Non-additive genetic effects were not included in the model, in spite of its possible relevance suggested by the large difference between the MZ and DZ correlations.

Carmelli et al. (1988) considered thirteen different variables in a study of the genetic and environmental influences on TABP. They found low DZ correlations ranging from -.09 to .32. Only 4 out of 13 DZ correlations were significantly different from zero. Four were measures of anger (anger-in, anger-discuss, anger-symptoms and Framingham anger), among which only anger-symptoms showed a DZ correlation significantly different from zero. The heritability estimate for anger was .36, but no distinction was made between additive and non-additive genetic effects.

Other studies about the sources of variance on TABP obtained similar results (Duffy et al., 1994; Finkel, Pedersen, Plomin, & McClearn, 1998; Koskenvuo et al., 1980; Matthews et al., 1976; Meininger et al., 1988; Pedersen et al., 1989; Rahe et al., 1978), with DZ correlations close to zero and heritability estimates in the order of .40 (ranging from .12 to .68).The heritability was larger for younger samples (Koskenvuo et al., 1980; Meininger et al., 1988).

Loehlin (1986) noticed the same pattern of low DZ correlations for the Thurstone Temperament Schedule. Loehlin proposed three mechanisms that could produce DZ correlations markedly lower than half the MZ correlations (Loehlin, 1986, p. 66):

Firstly, *'MZ twin environments may be relatively more similar than DZ twin environments'*. This could happen through a gene-environment correlation process, but that would appear in genetic models as genetic variance, and would still predict larger DZ correlations. Other authors have suggested that the DZ environment could be less similar than the MZ environment beyond the genetic indirect effects, suggesting some violation of the Equal Environments Assumption (EEA) (Meininger et al., 1988; Rahe et al., 1978). Some studies have found that sociodemographic factors like education, occupation, health behavior, or social support are significantly related with TABP related measures (Carmelli et al., 1988; Koskenvuo et al., 1980; Raynor et al., 2002). They also find that MZ twins tend to be more similar in those variables than DZ twins. Nevertheless, partial correlations between those sociodemographic variables and twin resemblance for TABP related traits, controlling for zygosity, tend to be small and non-significant (Raynor et al., 2002). Furthermore, adjusting the heritability estimates by those covariates, barely changes the results (Carmelli et al., 1988).

Secondly, the presence of genetic dominance and epistasis could also account for DZ correlations lower than half the MZ correlations. Most of the above studies did not test for the presence of non-additive genetic effects. Three studies (Duffy et al., 1994; Sims et al., 1991; Tambs et al., 1992) found non-significant dominance genetic effects, and one (Pedersen et al., 1989) found that actually most of the genetic variance was non-additive. It must be noted that detecting dominance requires large samples, and preferably including pairs of varying genetic relatedness –e.g. twins reared to-

gether and twins reared apart, full siblings, half siblings, and step-siblings- (Posthuma & Boomsma, 2000; Rietveld et al., 2003). Only the study by Pedersen and colleagues fulfilled some of those conditions.

Secondly, *sibling interaction or contrast effects* occur when a high-scoring sibling influences the behavior of the other inhibiting his development, and thus incrementing the within pair difference for a given trait (Eaves, 1976). The within pair difference can also be increased when the twins exaggerate their differences using each other as a reference to define themselves. Two studies have found significant sibling interaction effects on TABP measures (Duffy et al., 1994; Sims et al., 1991). However, in order to reliably detect a relatively large interaction effect (-.20) with the classic twin design, at least 300 twin pairs are necessary (Rietveld et al., 2003). Neither Duffy's or Sims' studies fulfilled this condition and thus, in their results, additive and dominance genetic effects and, dominance and sibling interaction may be confounded. To increase the power of the study, Sims et al. (1991) included parent-offspring data, where the sibling interaction parameters became small and non-significant. In this vein, other authors have suggested that if competitive sibling interaction were to explain the low DZ correlations, then DZ twin pairs reared apart should be more similar than DZ twin pairs reared together, as they do not interact or compare to each other. But in most cases, correlations for DZ twins reared apart are equal or lower than correlations for DZ reared together (Pedersen et al., 1989; Tellegen et al., 1988).

The present study is intended to disentangle the sources of variance of anger trait as a relevant component of the TABP. As other authors have already suggested, the scope of the research on TABP as a multidimensional concept must be better directed to the study of each of its components separately for clearer results and understanding of the mechanisms linking personality and CHD (Eysenck & Fulker, 1983; Palmero et al., 2001). Some of the limitations of the previous studies are surpassed by the study design and methodology applied in the current paper: a large sample, a repeated measures design and the inclusion of data on parents of twins increase the power to detect stable and replicable effects. The combination of twin and parental data increases the power to distinguish between additive and dominance genetic effects, and between dominance and sibling interaction effects.

The focus of this article will be on the clarification of previous contradictory results concerning the presence of dominance genetic effects and/or competitive sibling interaction, as well as sex differences on the sources of individual differences in anger, as a relevant component of TABP. For that purpose, longitudinal data will be used as an instrument of replication, and all parameters will be simultaneously estimated using the data from the two surveys. Based on the results of previous studies it is expected

that additive genetic effects explain a significant portion of the variance, and that either sibling interaction or dominance genetic effects account for the large difference between MZ and DZ twin correlations.

METHOD

Participants and Procedure

Participants were registered by the Netherlands Twin Registry (NTR), kept by the Department of Biological Psychology at the Vrije Universiteit in Amsterdam. They are part of the adolescent and adult cohort that was recruited through the city councils in 1990-1991 and in 1992-1993. They participate in longitudinal survey studies roughly every two years. The data analyzed here were collected in the 1991 and 1993 surveys. The questionnaires were sent to the families and returned by mail (Boomsma et al., 2002) .

The complete sample consists of 2664 families for which data on the phenotypes of the twins and their parents were collected: 438 MZM (Monozygotic Males), 401 DZM (Dizygotic Males), 612 MZF (Monozygotic Females), 454 DZF (Dizygotic Females), 759 DOS (Dizygotic Opposite sex). 750 complete families (both twins and both parents) participated both in 1991 and 1993, 514 did so only in 1991, and 764 participated only in 1993. For the remaining families, some data were missing randomly e.g. only one twin participated, data for one twin is missing in one year, the mother but not the father participated (the randomly incomplete families comprise 5% of the twins and 20% of the parents). Complete and incomplete families were used in the analyses.

The mean age of the twins was 17.68 in 1991 (S.D. = 2.23, range = 12,25 years) and 17.76 in 1993 (S.D. = 3.06, range = 12-25 years). The mean ages of fathers and mothers were 47.77 (S.D. = 5.62, range = 35-71 years) and 45.64 (S.D. = 5.15, range = 33-63 years) respectively in 1991, and 48.07 (S.D. = 5.52, range = 29-73 years) and 45.95 (S.D. = 5.09, range = 32-63 years) respectively in 1993. The SES distribution for this sample is 22.1% of low, 43.8% of middle and 34.1% of high SES (Boomsma et al., 2002). The religious background of the families is comparable to the Dutch population (Boomsma, de Geus, van Baal, & Koopmans, 1999).

The similarity in age in both surveys is due to those families who participated in either 1991 or 1993 but not in both. Appendix A summarizes the information about the age of parents and twins by survey participation. The table shows a tendency for the families that joined in 1993 for the first time to be a bit younger compared to those who where participating for the second time.

Zygosity for 726 same sex pairs was based on DNA polymorphisms, and for the remaining pairs zygosity was assigned by discrimination analysis using questionnaire items (see Boomsma et al., 2002 for further details). The correspondence between DNA and questionnaire based zygosity was 97%.

Measures

The Dutch adaptation of Spielberger's STAS -State-Trait Anger Scale- (Spielberger et al., 1983; van der Ploeg et al., 1982) was used to measure anger trait. The Trait Anger scale is designed to assess the frequency an individual experiences state anger over time and in response to a variety of situations. Reliability measured by the alpha coefficient was 0.86. The STAS is considered a strong measure of anger, based on a solid theoretical model, with excellent psychometric properties across several normative groups. It has shown good discriminant and convergent validity, as well as clinical utility, and it has been administered across a wide range of subject populations and psychological domains (Eckhardt et al., 2004).

ANALYSES

Genetic analyses were conducted using Structural Equation Modeling (SEM) as it permits the simultaneous analysis of multiple groups, and the possibility of imposing parameter constraints across groups. The statistical software package Mx was used (Neale et al., 2003). Full information Maximum Likelihood estimation (FIML) was used to fit the models. Twice the negative log-likelihood (-2LL) of the data for each observation is calculated, and parameter estimates are produced that maximize the likelihood of the raw data. Sub models were compared using a likelihood ratio test computed by subtracting -2LL for the restricted nested model from that for the baseline model ($\chi^2 = (-2LL_0) - (-2LL_1)$). The resulting test statistic has a χ^2-distribution with degrees of freedom equal to the difference of the degrees of freedom between the two models. The fit of the genetic models is evaluated against the fit of a saturated model, were the covariance matrix and the mean structures are computed without any restriction. Besides the χ^2 test statistic, the AIC (Akaike's information Criterion) and the RMSEA (Root Mean Squared Error of Approximation) are used to evaluate the general fit of the models (the difference against the saturated model). The AIC compares the models on the basis of parsimony, taking jointly into account the χ^2 and the degrees of freedom (Jöreskog, 1993). The lower the AIC, the better the fit of the model to the data and the more parsimonious it is. The likelihood ratio test is

performed under the assumption that the model holds exactly in the population (Loehlin, 2004). As a consequence, models that hold approximately in the population will always be rejected in large samples. The RMSEA is a measure of closeness of fit, and provides a measure of discrepancy per degree of freedom. A value of 0.05 indicates a close fit, and values up to 0.08 represent reasonable errors of approximation in the population (Jöreskog, 1993). Besides the estimation of the covariance structure, the mean structure is included as well in all models.

An alpha level of .01 was chosen. Given the power provided by a large sample size; this conservative criterion prevents interpreting slight differences between the models as relevant effects.

According to Neale & Cardon (1992), pooling across sexes is inappropriate unless it is known that there are no sex differences in means, variances or twin pair covariances. For this reason, zygosity groups will be separated by sex and possible sex differences are checked in a saturated model. Furthermore, age is considered as a covariate in the model for the means, with different *regression coefficients* for the parental and offspring generations. This way, age effects on anger are regressed out, and the covariance structure is fitted on the residuals.

RESULTS

The saturated model

First, a saturated model is fitted in which variances, covariances and means are estimated without any constraint. The likelihood associated with the unconstrained saturated model was -2LL(DF)=78542.056 (13271). The estimation of a saturated model also allows for a thoughtful exploration of the descriptive data through a progressive imposition of constraints on the means and variances, testing the effect on the likelihood of the model through the χ^2 statistic. The results of the saturated model guide the selection of the most appropriate genetic model to be fitted.

Constraints on the mean structure showed that there are significant differences in the means across zygosity groups, time point, and parents and offspring. Differences across zygosity groups are not conspicuous -all the means of the twin sample were within the range of 22.65,27.36- and did not show any clear pattern. There is a slight tendency for the means to be smaller in 1993 than in 1991, but still the largest difference is .92. However, there is a remarkable difference between parents and offspring where the former score lower (within the range of 13.97,17.14) than the latter. These differences were taken into account in the mean part. The genetic models include different means for 1991 and 1993, across zygosity groups, and for parents and offspring.

The saturated model against which the genetic models are compared includes these restrictions, so that the mean structure does not affect the selection of the models.

The age regression effects on the means were significantly different from zero for twins ($\chi^2(1) = 53.46$, p<.001) and parents ($\chi^2(1) = 21.82$, p<.001). The unstandardized age effect is -.19 for the twins and .05 for the parents. Standardizing the effects using the SD of anger and age in both groups, age explains 8% of the variance of anger in the offspring generation and 6% of the variance on the parental generation. The direction of the effects appears to change so that during adolescence and young adulthood anger tends to decrease with age, while during the adult years there appears to be a slight increase of anger with aging.

Differences of variance were found across zygosity groups ($\chi^2(16) = 47.38$, p<.001). There is a slight tendency for the same sex DZ twins to show the largest values, followed by the OS twins. MZ pairs show the smallest values. If the variances are constrained separately for males and females, the differences only remain significant in the male sample. Further constraints show that the differences are due to two specific comparisons: DZM in 1991 show a larger variance than OSM, and DZM and OSM in 1993 show a larger variance than MZM. Taking a closer look at the variances, it is clear that the three differences are due to two isolated low variances in the data when compared to the variances of the complete sample (24.59 in 1991 and 23.43 in 1993): that of first born MZM in 1993 (19.37), and that of OS second born in 1991 (16.82). Differences in the variance across zygosity groups can be an indicator of sibling interaction effects (Rietveld et al., 2003), but the differences must show a consistent pattern of larger variances for DZ twins compared to the MZ twins, whereas the present results do not appear to indicate such consistent pattern.

There were also significant differences in the variance between males and females ($\chi^2(12) = 42.08$, p<.001). These differences were due to those comparisons that involved the two outlier variances (MZM93 vs. MZF93, and OSM91 vs. OSF91).

There is a significant difference in the variance between parents and offspring ($\chi^2(12) = 133.10$, p<.001). The parental generation shows a smaller variance (21.88 in 1991 and 19.46 in 1993) than the offspring generation (26.96 in 1991 and 26.63 in 1993). This difference was incorporated in the genetic models by a scalar parameter (see fig.1).

Comparisons between first and second born twins yielded 3 out of 12 significant differences for MZM93 -1st born larger than 2nd-, DZF91 and OSMF91 -2nd born larger than 1st-. There was not a clear or consistent pattern, and this small number of differences is consistent with chance fluctuation.

The saturated model against which the genetic models are tested, that comprises the restrictions on the means, and includes two age regression parameters shows the following fit: -2LL(DF)=78574.99(13285).

Based on the constrained saturated model, Mx was used to estimate the familial correlations (and confidence intervals) shown in table 5.1.

Table 5.1

Twin, parent-offspring and spouse correlations for anger, within time in 1991 and 1993 and across time. Confidence intervals are shown between brackets.

	1991	1993	Cross Time
MZM	0.452 (0.315,0.571)	0.451(0.321,0.563)	0.324(0.140,0.476)
DZM	0.139 (-0.021,0.294)	0.003(-0.115,0.157)	0.076(-0.125,0.269)
MZF	0.400 (0.284,0.504)	0.417(0.313,0.434)	0.356(0.210,0.483)
DZF	0.063 (-0.082,0.206)	0.132(-0.009,0.268)	0.072(-0.093,0.233)
OS	0.145 (0.030,0.255)	0.124(0.015,0.231)	0.027(-0.116,0.170)
Father-Son*	0.148 (0.071,0.224)	0.111(0.039,0.181)	0.164(0.079,0.245)
Father-Daughter	0.175 (0.108,0.240)	0.114(0.047,0.178)	0.172(0.101,0.240)
Mother-Son	0.152 (0.079,0.223)	0.084(0.016,0.151)	0.103(0.018,0.185)
Mother-Daughter	0.150 (0.085,0.213)	0.159(0.098,0.219)	0.146(0.074,0.146)
Spouses	0.058 (-0.008,0.126)	0.078(0.078,0.141)	0.055(-0.020,0.129)

**Parent offspring and spouse correlations constrained to be equal across zygosity groups.*

The MZ correlations are more than twice the DZ correlations. Only one DZ correlation, the one for OSMF in 1993, is larger than zero ($p<.01$). This result is consistent with previous studies and it can be explained by dominance genetic effects and/or competitive sibling interaction. These possibilities are tested in the genetic analysis. Furthermore, the parent-offspring correlations show a very consistent picture with correlations around .150 that point to the presence of additive genetic effects. The low spouse correlations indicate that there is not assortative mating for trait anger. The large difference between MZ and DZ cross time correlations imply that the stability of trait anger across years is probably due to genetic factors, with dominance genetic effect among them. However, it must be noted that both MZ and DZ correlations across time are lower than those within time; whereas the parent-offspring correlations are very similar within and across time. This shows that the cross time correlations of the twin pairs are also affected by the lower stability of the trait during adolescence.

Means, standard deviations and stability coefficients for the parental and offspring samples are summarized in table 5.2.

Genetic analyses

The path diagram in Figure 5.1 represents the general genetic model that is being tested. The diagram represents the model for an opposite sex twin pair and their parents where the first born twin is a male and the second born twin is a female. This is an ADE model where the variance of anger is assumed to be explained by additive genetic factors, dominance genetic factors and environmental factors not shared by the members of the same family. At first, different parameters are estimated for males and females. The latent factors placed above the phenotypes from 1991 are those sources of variance common to 1991 and 1993 or, in other words, the stable sources of variance. The latent factors placed above the phenotypes from 1993 represent the sources of variance specific to 1993 that were not present in 1991. The phenotype in 1991 is explained by the influence of the common factor, and the phenotype in 1993 is due to the sum of the influences of the common factor and the specific 'novelty' factor. i.e. the variance of anger for T191 is decomposed as follows $S^2_{T191} = a^2_{11} + d^2_{11} + e^2_{11}$, while the variance of anger for T193 is partitioned as $S^2_{T193} = a^2_{21} + a^2_{22} + d^2_{21} + d^2_{22} + e^2_{21} + e^2_{22}$.

Table 5.2

Descriptives. Mean and standard deviations within time in 1991 and 1993 for Anger and Age. The cross time correlation or stability coefficient is also shown for anger.

		Twins		Parents	
		Mean	SD	Mean	SD
Anger	1991	16.87	5.19	16.49	4.67
	1993	17.08	5.20	16.19	4.41
	Cross time Correlation	.573		.671	
Age	1991	17.69	2.24	46.68	5.49
	1993	17.76	3.06	46.98	5.42

It is assumed that the amount of variance explained by each component is proportional in the parental and offspring generations. The parameter γ is placed in the model to account for the difference of variance between them observed in the saturated model. Resemblance between parents and offspring is explained by the additive genetic variance that they share. Each parent shares with each twin 50% of the additive genetic variance. Dominance genetic effects are those due to the interaction or combination of alleles at a particular locus. Offspring receive only one allele from each parent, not a combination of two alleles (Plomin et al., 2001). For that reason dominance is not

transmitted from parents and offspring and thus, there is not a D path from parents to offspring.

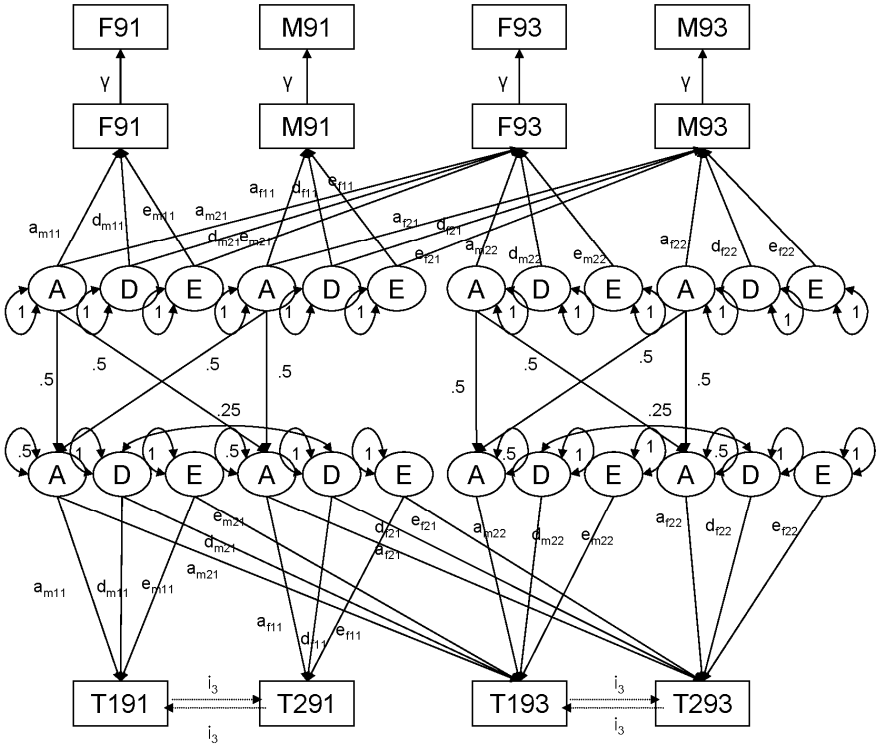

Figure5.1

Parent-offspring genetic ADEi model. The figure represents an opposite sex DZ pair where the first born is a male and the second born is a female. T1-first born, T2-second born, M-Mother, F-Father. 91 and 93 indicate the surveys from 1991 and 1993. γ- represents the scalar parameter to account for the difference in variance in the parental generation. Path coefficients with the subscript m are those for males, and the subscript f is for female parameters. The arrows connecting the twins represent the sibling interaction parameter, i_3 in the diagram is the sibling interaction for opposite sex twin pairs; i_1 would be the interaction parameter for males, and i_2 for females.

Given that the DZ correlations are less than twice the MZ correlations, and that most of them are not significantly different from zero, the shared environment is not included in the model.

DZ twins resemble each other because they share 50% of there genetic variance, inherited from their parents. They also share 25% of the dominant genetic variance. MZ twins share the totality of both the additive and the dominant genetic variances.

The phenotypes of the twins are connected through reciprocal paths. Those paths and their corresponding parameters represent the direct phenotypic effects that the twins have on each other, and thus the sibling interaction effects. It is assumed that the amount of influence that they exert on each other is equal, but different interaction parameters are estimated for same sex male twins (i_1), same sex female twins (i_2), and opposite sex twins (i_3). Further details about the derivation of the expected variances and covariances and the effects of the presence of sibling interaction on the model expectations can be found in Neale and Cardon (1992) and Eaves (1976).

Two constraints are imposed in the model: 1) Sibling interaction effects are constrained to be equal in 1991 and 1993; and 2) the total amount of variance explained by each component A, D, and E is also constrained to be equal in 1991 and 1993 (i.e. $a_{11}^2 = a_{21}^2 + a_{22}^2$). This constraint ensures that the estimates are stable and replicable effects. The 750 families that participated two times provide the information relative to stability. Those families that participated once in 1991 or in 1993 provide information relative to replication across samples.

Table 5.3 shows the results of the model fitting sequence. The general model shows an excellent fit according to the negative AIC and the RMSEA below .05. Departing from the general model, model 2 is fitted to test for sex differences in the variance components of anger, constraining the male's and female's parameters to be equal (i.e. $a_{m11} = a_{f11}; a_{m21} = a_{f21}; a_{m22} = a_{f22}$ for additive genetic effects, and likewise for the dominance and non-shared environmental factors). There was a significant decrease of fit as a consequence of the constraint and thus, it can not be assumed that the same proportion of variance is explained by each component in males and females.

Models 3 and 4 test for sex differences in the sibling interaction parameter, first equating it for same sex male and female pairs, and subsequently equating them to the opposite sex pairs. Both models fit the data as well as the general model, so it can be assumed that there are not significant differences in the amount of sibling interaction effects across sexes.

Models 5 to 8 are intended to test for the significance of certain parameters. In model 5, all dominance genetic effects for males are fixed to zero (i.e. $d_{m11} = d_{m21} = d_{m22} = 0$), and model 6 does the same with the female's dominance components. Table III shows the χ^2 change produced in models 5 and 6 with respect to the general model. Model 5 suffers a significant decrease of fit, while model 6 can be considered as good as the general model. Thus, dominance genetic effects are necessary to explain the variance of anger for males, but not for females.

Table 5.3

Model Fitting Results

MODEL	-2LL	DF	C.T.*	X^2	df	p	X^2,DF (vs SAT)**	AIC	RMSEA
1/ General Model	78938.80	13485					363.81,200	-36.18	.018 (.014, .021)
Tests of sex differences: parameters are constrained to be equal across males and females within zygosity groups									
2/ 1+ADE♂=ADE♀	78966.61	13494	1	27.81	9	.001			
3/ 1+i♂♂=i♀♀	78942.62	13486	1	3.82	1	.051			
4/ 1+i♂♂=i♀♀=i♂♀	78945.22	13487	3	2.60	1	.106			
Significance tests: parameters are constrained to be zero (the scalar is constrained to equal 1)									
5/ 1+D♂=0	78974.66	13488	1	35.85	3	.000			
6/ 1+D♀=0	78943.46	13488	1	4.65	3	.199			
7/ 4+i=0	78950.39	13488	4	5.17	1	.023			
8/ 1+Scalar=1	79116.57	13486	1	177.72	1	.000			
Specific effects in 1993: Novelty effects only present in 1993 are constrained to be zero									
9/ 1+d22=0 ♂&♀	78957.62	13487	1	18.81	2	.000			
10/ 9+a22=0 ♂&♀	78970.50	13489	1	31.70	4	.000			
Combination of constraints: Parameter constraints which did not produce a deterioration of the fit are put together progressively to obtain a final model									
1/ General model	78938.80	13485					363.81,200	-36.18	.018 (.014, .021)
2/ 1+ i♂♂=i♀♀	78942.62	13486	1	3.82	1	.051	367.63,201	-34.37	.018 (.014, .021)
3/ 2+i♂♂=i♀♀=i♂♀	78946.22	13487	2	3.59	1	.057	371.23,202	-32.77	.018 (.014, .021)
4/ 3+ i=0	78950.39	13488	3	4.17	1	.041	375.40,203	-30.60	.018 (.014, .021)
5/ 4+ D♀=0	**78955.62**	**13491**	**4**	**5.23**	**3**	**.156**	**380.63,206**	**-31.37**	**.018 (.014, .021)**

**C.T.= Compared to model #*

*** Chi-squared and degrees of freedom of the model compared to the saturated model. Indicates the goodness of fit of the model.*

Under the label of model 7, departing from model 4, where a single sibling interaction parameter was estimated for all pairs, the sibling interaction effects are fixed to zero ($i_1 = i_2 = i_3 = 0$). The change of fit compared to model 4 is not significant (p>.01) indicating that the constraint can be held and thus, the sibling interaction effects are zero in the population.

Model 8 constrains the scalar 'γ' to one. Such a model implies the assumption that the parental and the offspring generations have the same variance. The large decrease

in the goodness of fit indicates that the difference in variability between generations is not negligible, and must be included in the model.

Models 9 and 10 are intended to find out whether there are novel genetic effects active in the second survey in 1993 that were not present during the first survey in 1991 (d_{22}=0 & a_{22}=0). The results show that neither dominance nor additive genetic effects specific to 1993 can be dropped from the model.

Finally, a series of models are fitted accumulating the previous results with the purpose of finding the most parsimonious explanation of the data. Each of these models is compared to the saturated model to obtain general indices of goodness of fit, as well as to the immediately previous model. Table 5.4 shows the parameter estimates of these five models.

Model 1 is the general model. Models 2 and 3 constrain the sibling interaction effects across sexes. In model 4 the sibling interaction effects are removed. In model 5 dominance genetic effects are removed for the female sample. All five models show a satisfactory fit to the data with negative AIC and a RMSEA lower than .05. According to the χ^2 comparisons with the immediately previous models, none of the progressive constraints produce a significant decrease of fit (p>.01). Choosing among the 5 models following strict statistical criteria would lead to the selection of the general model as the best explanation of the data, as it shows the lowest AIC. But the differences between the models are so slight that the RMSEA does not even change from one to another. It can also be observed in table IV how the parameter estimates for the variance components and the partitioning of the cross time correlation barely change from one model to another (they all fall within the 95% confidence interval of the last model). Clearly the most controversial part of the model fitting sequence in terms of goodness of fit and parameter estimates is the sibling interaction, in line with previous literature (eg. Sims et al., 1991). It is clear from models 2 and 3 that the effects can be equated across sexes. The overall estimate of the sibling interaction effects in model 3 is -.03. Following a strict statistical argument based on the p value (p>.01), sibling interaction effects should be removed from the model. Furthermore, previous analysis showed that, one by one the interaction effects are estimated as: i♂♂91=-0.03 (p=.332), i♂♂93=-0.12 (p<.001), i♀♀91=-0.04 (p=.155), i♀♀93= 0.01 (p=.649), i♂♀91= 0.02 (p=.301), i♂♀93= 0.03 (p=.226). Only the effect for males in 1993 is significantly different from zero. That might be a spurious estimate due to the low MZM first born 1993 variance. When the effects are combined across the 1991 and 1993 samples, the effect does not differ significantly from zero. There is no theoretical reason to support an interaction effect that is observed exclusively in 1993, but not

in 1991, especially given that the mean age of both samples is the same. The effect is neither stable (in those pairs who participated two times) nor replicable (in those pairs who participated once).

Table 5.4

Parameter estimates for models 1-5 where relevant constraints are progressively accumulated. Model 5 is the final selected model and includes confidence intervals between brackets.

MODEL		1	2	3	4	5
Variance	A91	.26	.25	.25	.24	.23(.145,.324)
Decomposition	A93	.26	.25	.25	.24	.23(.145,.324)
Males	D91	.34	.31	.29	.25	.26(.126,.377)
	D93	.34	.31	.29	.25	.26(.126,.377)
	E91	.39	.44	.46	.51	.51(.429,.613)
	E93	.39	.44	.46	.51	.51(.429,.613)
Variance	A91	.29	.30	.30	.29	.34(.279,.406)
Decomposition	A93	.29	.30	.30	.29	.34(.279,.406)
Females	D91	.11	.15	.13	.09	-
	D93	.11	.15	.13	.09	-
	E91	.59	.54	.57	.62	.66(.594,.720)
	E93	.59	.54	.57	.62	.66(.594,.720)
Cross time	A♂	.40	.38	.39	.37	.35(.225,.499)
Correlation	A♀	.40	.41	.40	.40	.47(.363,.499)
Decomposition	D♂	.31	.29	.26	.24	.26(.032,.463)
	D♀	.14	.18	.16	.12	-
	E♂	.29	.33	.35	.39	.39(.227,.566)
	E♀	.45	.41	.43	.48	.53(.422,.636)
Genetic and	A♂	.97	.98	.99	.98	.98
Environmental	A♀	.87	.86	.87	.88	.88
Correlations across	D♂	.58	.59	.59	.62	.65
time	D♀	.82	.79	.80	.89	-
	E♂	.47	.47	.48	.48	.48
	E♀	.49	.48	.49	.50	.51
Sibling	Males	-.08	-.05	-.03	-	-
Interaction	Females	-.02	-.05	-.03	-	-
	Opp Sex	-.00	-.01	-.03	-	-
Scalar		.85	.85	.85	.85	.85

Model 5 is selected as the best and most parsimonious explanation of the data. The broad heritability of anger is .49 for males and .34 for females. About half of the genetic variance in males is due to dominance interaction, whereas no dominant effects are found in the female population. The decomposition of the cross time correlations shows that stability across time is due, 61% to genetic effects, and 39% to non-shared environmental effects for males, while for females genetic effects explain 47% and non-shared environmental effects explain 53% of the stability. The genetic correlation shows that additive effects on anger are very sta-

ble, as 88% for females , and 98% for males of the genes that explain the variance in 1991 are still effective in 1993. The dominance genetic correlation is a bit lower (.65 for males), as well as the environmental correlation (.48 for males.51 for females), which implies that although a large part of the dominance genetic and environmental effects present in 1991 are also present in 1993, a great deal of new dominance genetic effects and environmental sources of variance become relevant two years later.

DISCUSSION

The present study has explored the genetic and environmental sources of variance on anger through a powerful design. It includes a large sample of families of MZ and DZ twins and their parents, and the repeated measurement of the trait, leading to a clarification of previous contradictory results. A review of previous studies revealed that the finding of low DZ correlations compared to the MZ correlations has been a common factor in the field. The explanations provided for this phenomenon vary from study to study. Loehlin (1986) proposed three possible mechanisms to explain such pattern of results. Non-additive genetic effects and competitive sibling interaction are two of the candidate explanations that have been considered and tested in this article. The large sample size and the availability of parental data make this study a unique opportunity to detect and distinguish between those two mechanisms.

The results show that the sources of variance on anger differ across sexes. For males 23% of the variance is due to additive genetic effects and 26% to dominance genetic effects. For females 34% of the variance is due to additive genetic effects, and the remaining is explained by non-shared environmental influences. There was no consistent evidence to confirm the presence of competitive sibling interaction effects. The estimation of the broad heritability lies within the range of previous studies. Variations in the precise estimates might be due to the failure of most studies to consider sex differences and/or and dominance genetic effects (i.e. Carmelli et al., 1988; Koskenvuo et al., 1980; Meininger et al., 1988; Pedersen et al., 1989; Rahe et al., 1978; Sims et al., 1991; Tambs et al., 1992). The main problem of previous studies is the lack of power. Detecting and distinguishing between dominance and sibling interaction effects, while testing for sex differences, requires large samples and, preferably different kinds of relatives (Rietveld et al., 2003).

In the present study genetic variance explains 15% more variance of anger in males than in females. The study of sex differences in the causes of personality traits that increase the risk to CHD might be relevant and informative, as the risk to suffer

coronary problems is larger in males than in females (Dolan, Molenaar, & Boomsma, 1992). A lower heritability in females is consistent with previous studies on genetic markers where serotonin gene polymorphisms have been found to be related with anger on males, but not in females (Manuck et al., 1999). These results could imply different prevention and therapeutic programs for males and females, with the former more focused on biological genetic related sources of variance, and the later more directed to environmental factors e.g. life style.

Although the present study has helped to clarify some issues, there are still some characteristics of the data that need to be explained. Observing the summary correlations under the light of the model fitting results can raise some questions. The presence of dominance genetic variance in males is mostly expressed in larger MZ correlations in males than in females. That increases the MZ/DZ ratio and suggests dominance effects. But there is still the fact that most DZ correlations are not significantly different from zero, and that parent-offspring correlations are in the order of the DZ correlations, pointing to the need of other explanations for the large MZ correlations or low DZ correlations besides dominance genetic effects. The present study has raised serious doubts over the competitive sibling interaction hypothesis. Reed et al. (1991) studied the effects of placentation on a set of Type A personality measures. The authors found greater similarity in monochorionic pairs than in dichorionic pairs, so that correlations in MZ dichorionic pairs were similar to the DZ correlations, less than half the MZ monochorionic correlations. Reed et al. interpret this result as a special violation of the equal environments assumption. Future studies could differentiate between monochorionic and dichorionic MZ pairs, and take that into account into the genetic models. In that vein, Loehlin (1986), modeled a MZ specific latent factor that improved significantly the fit of the genetic model. Loehlin interpreted the factor as either configurational genetic effects and/or shared environments specific to MZ twins. In a study where data on chorionicity are available, Loehlin's MZ factor could be included for the monochorionic MZ pairs, but not for the dichorionic.

The main limitation of the present study to generalize the results might be the age of the twins. During adolescence and young adulthood personality traits are still quite unstable and more sensitive to changes in the non-shared environment (Caspi et al., 2001; Reiss et al., 2000). Such instability could be responsible for the unclear pattern of variances. During adulthood, between 30 and 50 years of age personality stabilizes and the effects of genes gain importance. However, the inclusion of parental data in the sample has helped to reach a strong conclusion regarding the effect of additive genetic effects, as the parent-offspring correlations showed a very consistent picture. Furthermore, it can be observed in table A of the appendix, that among the complete

pairs, there are 2549 twin pairs from 12 to 24 years old, and 2108 parental couples from 33 up to 73 years old. Thus, the adult generation comprises close to half of the sample, and the variance components can be assumed to be equal between the two generations, after a difference in variance is accounted for by a scalar. Future longitudinal studies that cover adolescence and adulthood will advance the understanding of dominance genetic effects and their stability thorough the life span, and distinguish between developmental and generational changes in the variance architecture. With that purpose, we are planning to collect data on anger within the 7th survey of the NTR.

The current tendency to move from the molar idea of TABP to a more elementary level will also help to disentangle the sources of variance and mechanisms that increase the risk of suffering CHD. The present study has shown that the use of large samples and family designs facilitates the reliable detection of important factors like sex differences or dominance genetic effects, and rule out negligible factors like sibling interaction, otherwise detected by weaker designs. To explore the nature of the TABP, several studies like this that consider different molecular characteristics from personality variables to biological endophenotypes or environmental factors -i.e. anger, hostility, blood pressure, serotonin levels, or work overload- will lead to the possibility to select a multivariate phenotype that comprises the *toxic* configuration prone to suffer CHD and its genetic and environmental determinants.

Table A Appendix:

Descriptive statistics for age distribution by survey participation

		1991					1993				
		N	Mean	SD	min	max	N	Mean	SD	min	max
Twins	91&93	913	17.37	2.24	13.08	22.46	913	19.63	2.27	15.00	24.82
	91	697	18.07	2.21	12.60	24.55					
	93						939	15.97	2.58	12.00	24.62
Father	91&93	768	47.41	5.30	35.81	71.14	768	49.49	5.32	37.91	73.76
	91	529	48.07	5.9	35.37	38.46					
	93						811	46.31	4.82	35.91	72.58
Mother	91&93	768	45.28	4.75	34.08	60.41	768	47.57	4.78	36.46	63.16
	91	529	45.80	5.53	33.79	63.65					
	93						811	44.16	4.49	34.17	61.73

** Data from complete twin pairs and parents who participated in 1991, 1993 or both are summarized in detail here. Those families that have random missing values (115 twin pairs, and 556 parents) are not reported in this table but were used in the analyses.*

Chapter 6

Genetics of aggression at age 18 based on individual growth curves in aggression from age 11 to 40

Although individual differences in aggression are quite stable, intraindividual change in aggression has also been established. Most change takes place during the school years, with aggressive behavior becoming more stable after adolescence. Longitudinal studies on the development of aggression are scarce, and the majority of them focus on the period from infancy to about the end of adolescence. In the present study we employed analysis of individual growth curves to study individual changes in aggression occurring within a nine year interval in a sample comprising individuals from 11 to 40 years old. We then compared the rate of change in aggression before and after 18 years old and investigated the genetic and environmental sources of individual differences in aggression at age of 18, as well as the sources of variation in rates of change in aggression. The results showed that mean scores on aggressive behavior decrease during adolescence. By the age 18, aggressive behavior stabilizes. The genetic analysis showed that most of the variance on the slope between 11 and 18 years old was explained by additive genetic effects. The results also showed that 26% of the variance on aggression at the age 18 is explained by additive genetic effects (A), 40% by non-additive genetic effects (D), and 34% by the non-shared environment (E). There were no sex differences in the amount of variance explained by A, D and E.

INTRODUCTION

Aggression involves overt verbal or physical behavior that causes, or threatens to cause, physical or psychological harm to others (Loeber & Hay, 1997; Sluyter et al., 2000). Aggressive behavior in childhood and adolescence is associated with various negative outcomes in adulthood, such as antisocial behavior, low educational attainment, and alcohol abuse (Pulkkinen & Pitkanen, 1993; Schaeffer, Petras, Ialongo, Poduska, & Kellam, 2003).

Aggressive behavior shows moderate rank order stability with age, as indicated by longitudinal studies from childhood to adulthood (Kokko & Pulkkinen, 2005; Loeber et al., 1997). Kokko and Pulkkinen (2005) found a stability coefficient of 0.42 between childhood and middle age. Thus individual differences are quite stable, but also leave room for intraindividual change in aggression. Most change takes place during the school years, while after early adolescence aggressive behavior becomes more stable. Longitudinal studies on the development of aggression are scarce, and the majority of them focus on the period from infancy to about the end of adolescence (Van den Oord, Boomsma, & Verhulst, 1994). According to Loeber et al. (1997) temperamental differences in frustration toleration and in the expression of anger are already present in infants. The actual behavioral expression of aggression starts in the second

and third years of life. However from the preschool years onwards, there is a decrease in aggression and a rise in interpersonal skills. Aggression, as expressed in the mean scores on psychometric measures, decreases from age 4 to age 18, and from preschool to elementary school the prevalence of aggressive behavior declines (van Beijsterveldt, Bartels, Hudziak, & Boomsma, 2003). In the West, the end of adolescence, approximately between the ages 16 and 18 represents a milestone that marks the end of schooling, and the beginning of adult life. A significant percentage of adolescents has finished school at the age of 16, and the greater majority will have completed their basic education by the age of 18. The transition from adolescence to young adulthood is associated with significant changes in the parent-child relationships (Loeber et al., 1997), as young adults assume more responsibility for their own lives, and greater independence, e.g., by leaving the parental home (Ferdinand, Verhulst, & Wiznitzer, 1995). This transition may affect the stability of behavior problems, such as aggression, and the sources of variation in those problems.

The sources of variation in aggression: genetic studies

Rhee & Waldman (2002) presented a meta-analysis of genetic studies on antisocial and aggressive behavior. They included 10 studies of physical aggression, five with childhood samples, and five with adult samples. The best fitting model over all aggression studies was an ACE model (A, C, and E stand for additive genetic, shared environmental, and non shared environmental effects, respectively). Additive genetic effects explained 44% of the variance in aggression, shared environmental effects explained 6%, and non-shared environment effects explained 50%. For antisocial behavior, the results were 47%, 22%, and 31%, for the effects of A, C, and E, respectively. As a general trend concerning both antisocial and aggressive behavior, Rhee & Waldman (2002) observed that C and A decreased with the age of the sample, whereas E increased.

Other studies, not considered by Rhee & Waldman (2002), addressed the genetic and environmental contributions to individual differences in aggression, making use of measures that either combined physical and relational aggression (Eysenck et al., 1983; Hudziak et al., 2003; Rushton, Fulker, Neale, Nias, & Eysenck, 1986; van Beijsterveldt et al., 2003), or made specific distinctions between different emotional and behavioral expressions of aggression, e.g., physical vs. social aggression (Brendgen et al., 2005; Coccaro, Bergeman, Kavoussi, & Seroczynsky, 1997; Ligthart et al., 2005; Sluyter et al., 2000). Five of these studies were performed with children from 3 to 12 years old (Brendgen et al., 2005; Hudziak et al., 2003; Ligthart et al., 2005; van Beijsterveldt et al., 2003; Vierikko, Pulkkinen, Kaprio, Viken, & Rose, 2003). Most

children, who were studied participated in ongoing longitudinal studies, and constituted samples that were homogeneous with respect to age. Between 3 and 12 years genetic influences on aggression are found to be large and stable (van Beijsterveldt et al., 2003). The estimates of the variance explained by A range from 17% to 71%, with an average of 52%; estimates of the effects of C range from 17% to 75%, and average 23%; and the variance explained by the non-shared environment ranges from 7% to 60%, with an average of 21%. The estimates vary as a function of the informant, with parental reports showing larger effects of the shared environment. Teacher reports show lower, or zero effects of the shared environment, or even effects of genetic dominance (Hudziak et al., 2003; Vierikko et al., 2003). Sex differences were often found in heritability estimates for children, with a tendency for females to show larger effects of genes (Hudziak et al., 2003; Ligthart et al., 2005; van Beijsterveldt et al., 2003; Vierikko et al., 2003). Differences in heritability of different kinds of aggression have yet to be resolved, as at present the results are contradictory. Brendgen et al. (2005), in a sample of 6 year old twins, found evidence for shared environmental effects on social aggression, but none for physical aggression, for which family resemblance was entirely genetic. Ligthart et al. (2005), on the other hand, found shared environmental effects on both relational and physical aggression, with larger genetic effects on relational or social aggression in 7 year old twins.

Four studies, not included in the Rhee and Waldman (2002) review, looked at adult samples (Coccaro et al., 1997; Rushton et al., 1986; Sluyter et al., 2000; Tellegen et al., 1988). The results indicate that the estimates of additive genetic effects in adult samples tended to be smaller than those in children, with heritability estimates ranging from 0% to 48% with an average of 26%. Shared environmental effects were absent in all four studies, and the estimates of the non-shared environment increased (25%-72%, average 59%), as also noted by Rhee and Waldman (2002). Non-additive genetic (i.e., dominance) effects were found in two of these studies, ranging from 0% to 40%. Non-additive genetic effects were most evident in Coccaro et al's (1997) study of emotional or indirect expressions of aggression, in contrast to direct assault, which was not characterized by dominance effects. It should be noted that, regardless of the model fitting results, the DZ correlations in the four studies were either close to zero or negative, suggesting the presence of non-additive genetic effects (Eaves, 1988). Possibly, the power to detect such effects was low. There were no sex differences in heritability in any of the adult samples, which is consistent with Rhee and Waldman (2002), who did not find any sex differences in the relative magnitude of genetic and environmental effects on aggressive and antisocial behavior.

The present study looks at aggression occurring within a nine year interval in a sample comprising individuals from 11 to 40 years old, who participated in an ongoing longitudinal study at four different occasions. We employed analysis of individual growth curves to study individual changes in aggression along that age range, from adolescence to adulthood. We selected the age of 18 as a marker of the end of adolescence, and the transition to young adulthood. We then compared the rate of change in aggression before and after 18 expecting, in view of previous results, a stabilization of the rate of change after 18 years old.

We also investigated the genetic and environmental sources of individual differences in aggression focusing on the age of 18, based on the growth curve. Considering the important changes associated with the end of adolescence, and with the previous results obtained in adult samples, we expected the influence of shared environmental effects to be minor and possibly non-additive genetic effects to be in evidence.

METHOD

Participants and procedure

The participants in this study were registered by the Netherlands Twin Registry (NTR) of the Department of Biological Psychology at the Vrije Universiteit in Amsterdam. They were included in the cohort of adolescents and young adults, who were recruited through the city councils in 1990-1991 and in 1992-1993, and are participating in an ongoing longitudinal study. After 1993 an effort was also made to recruit adult and older twins. Surveys were conducted approximately every 2 years. In the present study we analyze the aggression data collected from the twins in 4 survey studies that took place in 1991, 1995, 1997 and 2000. Further details on response rates, response bias, and demographic characteristics of the sample can be found elsewhere (Boomsma et al., 2002; Koopmans et al., 1999; Stubbe et al., 2005; Vink et al., 2004) .

Of the individuals who returned the surveys, at least one, we selected those between 11 and 40 years old. Sixty percent of the selected twins participated in at least two surveys: 635 individuals participated in the four surveys, 1314 in three occasions, 1766 in two, and 2467 once. Table 6.1 shows detailed frequencies of the participation of the sample, and the descriptive statistics for age at each survey.

The total sample comprises 3090 complete and incomplete twin pairs: 500 monozygotic males (MZM), 385 dizygotic males (DZM), 874 monozygotic females (MZF), 529 dizygotic females (DZF), and 802 dizygotic opposite sex pairs (DOS). Table 1 shows the number of complete and incomplete pairs per survey. For same-sex twin pairs, zygosity was based on DNA typing for 522 pairs. For the remaining twins,

zygosity was determined by questionnaire items about physical similarity and frequency of confusion of the twins by family and strangers. The questionnaire-based zygosity was correct for nearly 95% of the cases (Willemsen, Posthuma, & Boomsma, 2005).

Table 6.1

Descriptive statistics for age and Aggression and sample sizes by survey

	Age				Aggression			
	Mean	SD	Minimum	Maximum	Mean	SD	Skewness	Kurtosis
1991	17.71	2.25	12.60	24.58	7.65	4.53	0.88	1.23
1995	19.79	3.12	14.27	28.25	6.50	4.24	0.97	1.63
1997	22.27	4.39	11.50	39.67	5.55	3.90	0.84	0.67
2000	25.72	5.19	12.50	39.98	5.89	3.87	0.84	0.77

Chronological participation[a]					Number of complete and incomplete twin pairs in each survey		
	1991	1995	1997	2000	Complete Pairs	Incomplete Pairs	Total Pairs
1991	991	526	355	635	1615	16	1631
1995		400	263	533	1595	90	1685
1997			216	432	1161	363	1524
2000				860	1328	614	1942

[a] *Each column on the right implies participation on the previous surveys. E.g., 533 participants returned personality questionnaires in 1995, 1997 and 2000 inclusive, but not in 1991. The cells are exclusive. This distribution does not cover the entire sample. 971 individuals who participated in intermittent surveys are not listed here.*

Aggression was measured with the Youth Self Report, which was translated and validated for the Dutch population by Verhulst (1997). Ferdinand, Verhulst & Wiznitzer (1995) argued that it is advantageous in longitudinal studies to use the same scales at each assessment. They tested the applicability of the YSR scales to the data obtained with the Young Adult Self Report (YASR, Achenbach, 1997), by means of confirmatory factor analysis of the items that are similar for the YSR and the YASR. The authors concluded that the YSR factor structure holds in the YASR scores of individuals older than 18 years old. The items of the aggression scale are given in Appendix 1. Ferdinand et al (1995) removed the item “I am disobedient at school” of the YSR, which is not present in the YASR, as it specifically directed at school-attending children and adolescents. This item was also excluded in the present study. The Aggression scale includes 18 items which are scored on a 3 point scale (0=not true, 1=somewhat or sometimes true, 2=very true of often true) and has an alpha coefficient of 0.77. Descriptive statistics pertaining to each survey are shown in table 6.1.

ANALYSES

Data were analyzed with an individual growth curve approach using Structural Equation Modeling (SEM). SEM allows one to test specific theoretical models including random effects about the individual growth in aggression. Random effects in such models are important to account for the expected interindividual differences in the development of aggressive behavior. We fitted various models using the program Mplus v3.13 (Muthén et al., 2005). We analyzed raw data, rather than the summary covariance matrix, in order to make use of all the available data. The analyses of complete data with any pattern of missingness is possible in Mplus, assuming the data are missing at random (Schafer et al., 2002).

The families that did not participate in a second survey were invited to participate in subsequent surveys. The fact that participants were invited to return to the study, in combination with the analysis of all data, rather than the exclusive use of complete cases, minimizes the effects of sample attrition, and ensures unbiased estimates.

Phenotypic Analyses: Latent Growth Modeling

In the phenotypic analyses, we used all individual data. Family clustered data violate the assumption of independence of observations, and treating dependent data as independent may result in bias in standard errors and goodness of fit statistics (Laplante et al., 2001). To correct for this, we used the Robust Maximum Likelihood (MLR) in combination with the "Complex" option in Mplus. The latter corrects the effect of clustering. The parameter estimates are ML estimates, but the standard errors are corrected for the dependency in the data. The correction is made by using a weight matrix that involves fourth-order moments and contains cluster information. The chi-square statistic is scale-corrected. The scale is a function of the same weight matrix and the degrees of freedom of the model (Muthén et al., 1995). The twin pair was used as the cluster unit in the correction. A previous simulation study showed the efficiency of this method to correct the effects of dependency due to family resemblance (Rebollo, de Moor, Dolan, & Boomsma, 2006).

To study the changes in aggression from early adolescence at age 11 to adulthood at age 40, a series of latent growth models (LGM) were fitted. LGM generally specify random intercept and slope latent factors. The mean and variance of the intercept represent the mean level and variation of the true score at a given time point, and the slope factor represents individual differences in rates of change on the true scores over time. The functional form of the change is determined by the values of the fixed loadings of the observed variables on the slope factor or factors (Hertzog et al., 2003).

Equation 1 expresses the model that relates the observed score for person *i* at a given time (or age) *t*, $Y_i(t)$, with the true score in terms of a linear growth model.

$$Y_i(t) = \xi(t^*) + \theta(t - t^*) + \varepsilon_i(t) \quad (1)$$

In equation 1, t^* is the origin of time (or age), a fixed value of time (or age) relative to which time (or age) is scaled. It is a particular value chosen for its theoretical interest. $\xi(t^*)$, the intercept, is the level of person *i*´s true score at t^*. $\theta(t - t^*)$, the slope, is the linear rate of change on the true score over time (or age). $\varepsilon_i(t)$ is the residual term, not accounted for by the growth model, for person *i* at time (or age) *t*.

The conventional SEM approach to growth models makes the assumption that data are collected at an identical set of fixed ages (*t* in equation 1) for all individuals in the sample (Mehta & West, 2000); that is, it is assumed that t is the same for all individuals in each survey. However, in the present dataset each measurement occasion or survey is heterogeneous with respect to age of the participants. Age at the first measurement varies across individuals in a continuous fashion and thus, there is a large number of age cohorts. Fitting a common model of growth to different cohorts implies that the model-implied means and covariances for the observed variables are expected to be identical for all individuals at each measurement point. That is, they are assumed to be equal for individuals who entered the study at, say, age 11 or at age 25. If the developmental curve is defined by processes related to chronological age then the standard LGM produces biased estimates of mean and variance of the shape function (Hertzog et al., 2003). To address this problem, we followed the individual data vector approach for fitting growth curves described by Mehta and West (2000).

Figure 6.1A shows a linear growth curve model in which age is scaled with respect to a common origin across all individuals. This is achieved by fixing the factor loadings of the slope (s) factor to represent a deviation from a common age (this is age 12 in the figure, as an example). The factor loadings of the intercept equal 1 for all individuals in the four surveys. The factor loadings of the slope, represented within diamonds, indicate that the parameter is fixed at a different value for each individual in the sample, depending of their age at each survey (1991, 1995, 1997, and 2000). The factor loadings of the slope can be identified with $(t - t^*)$ in equation 1, where t^* is the origin of age (12 in the figure) and t is age at each survey. E.g., an individual who was 18 in 1991 would have a 6 $(18 - 12)$ as factor loading on the slope from the observed measurement at the first survey; indicating that this individual, in 1991, was

6 years older than a 12 year old, the origin of the scale. According to Mehta and West (2000), once the origin of the time variable is set to a common age across all individuals, a common set of growth parameters can be estimated across individuals.

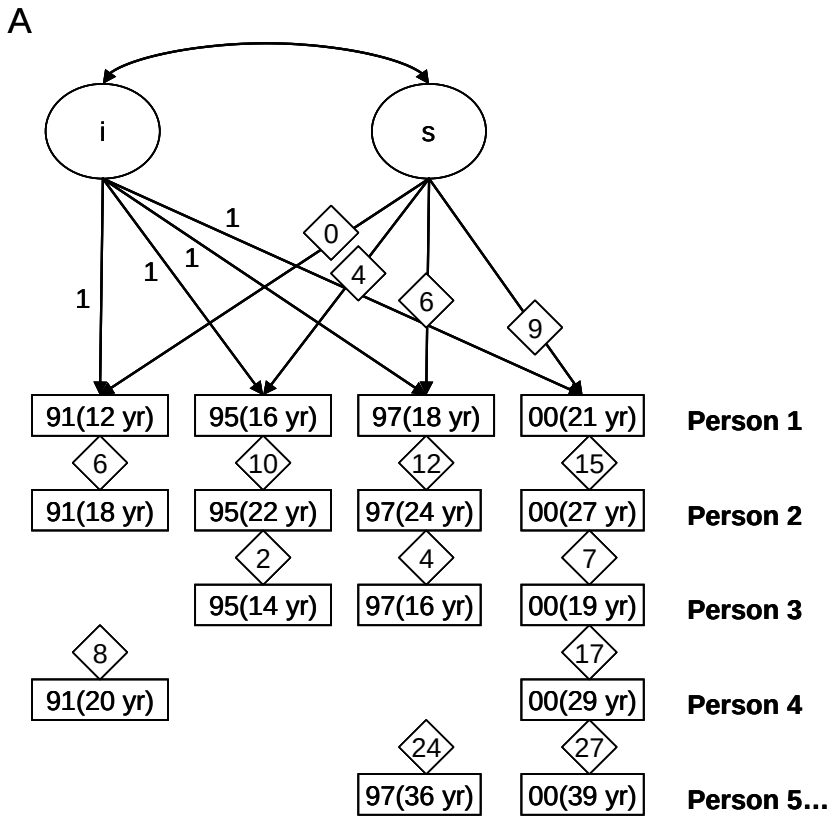

Figure 6.1A

Linear Growth Model with individually varying ages of observation. Factor loadings of slope factor vary across individuals, and represent deviation from a common age (12 in the figure).

To investigate the possible presence of different rates of change in different developmental periods we selected a piecewise linear model to describe the growth in aggression between 11 and 40 years old. The piecewise modeling allows us to model the growth trajectories using two separate linear components. Figure 6.1B shows a piecewise model with individually varying factor loadings on the two slopes, scaling the intercept at age 18. For those individuals below the age of 18, at any of the four surveys, the value of the factor loading on the first slope equals age-18. In other words, it represents the number of years left until the individual becomes 18. For indi-

viduals of 18 years old or over, the loading on the first slope equals 0. The factor loadings on the second slope equal zero for individuals of 18 years or younger. For those individuals over 18 years old, the factor loadings on the second slope equal age-18. Thus, the first slope in figure 1B represents the rate of change in aggression between 12 and 18 years old, whereas the second slope represents the rate of change between 18 and 40 years old. The latent intercept factor represents mean level and variation in aggression at the age of 18. In terms of equation 1, the piecewise model in figure 1B can be expressed as in equation 2.

$$\begin{aligned} Y_i(11 \le t \le 18) &= \xi(18) + \theta_1(t-18) + \theta_2(0) + \varepsilon_i(t) \\ Y_i(18 \le t \le 40) &= \xi(18) + \theta_1(0) + \theta_2(t-18) + \varepsilon_i(t) \end{aligned} \tag{2}$$

Different nested models were fitted to test for sex differences in the growth factors. The Akaike Information Criterion (AIC, Akaike, 1987) and the Bayesian Information Criterion (BIC, Schwarz, 1978) were used to compare the fit of alternative models. BIC and AIC are information theoretic criteria designed to emphasize minimizing the amount of information required to express the data and the model. Thus, those models that are the most parsimonious or efficient representations of the data are selected. Models producing smaller values of AIC and BIC can be thought of as more efficiently approximating the true model, (Markon & Krueger, 2004). A more parsimonious model is preferable to less parsimonious model, if these criteria associated with the former are smaller than those associated with the latter.

Genetic Analyses

With the phenotypic piecewise model in place, with the intercept scaled at age 18, the variances of the intercept and slope were decomposed into genetic and environmental components using the twin method. Through the twin method the variance of a given trait is partitioned into different components explained by genetic and environmental factors. This is possible through the comparison of the resemblance between pairs of relatives who differ in the amount of genetic variance that they share. Monozygotic twins (MZ) share all genetic variance, whereas dizygotic twins (DZ) share on average half of their additive genetic variance, and one quarter of their non-additive genetic variance. To the degree that a trait is influenced by genes, MZ twins are expected to be more similar than DZ twins. If the twins grew up in the same family, they are assumed to share the totality of the shared environmental variance (C). The amount of shared environmental variance is assumed to be equal in MZ and DZ twins. The variance that

is not shared by the twins within the same family is called non-shared environmental variance (E) and do not contribute to the twin resemblance.

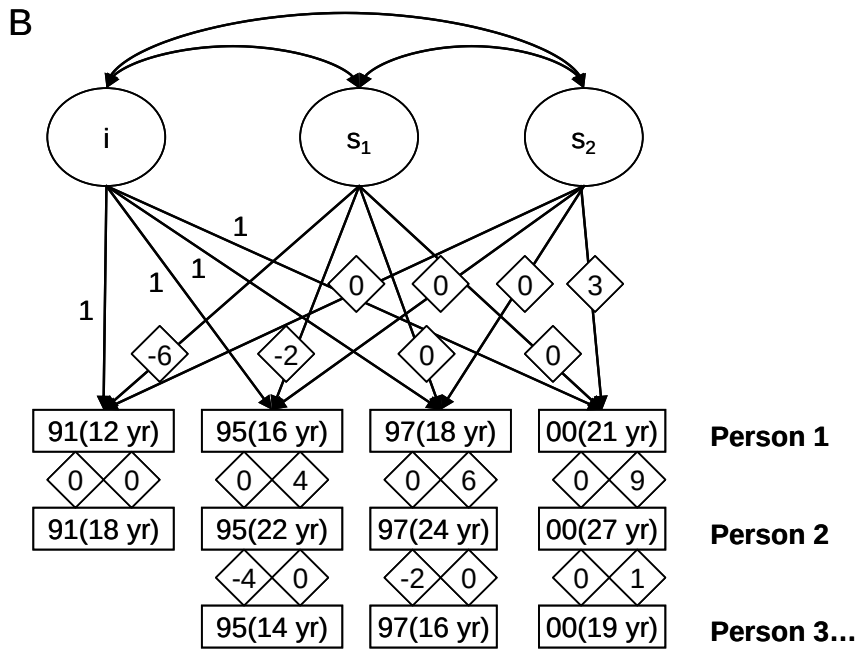

Figure 6.1B

Piecewise Growth model: Factor loadings of slope factors vary across individuals, and represent deviation from a common age (18 in the figure). The first slope factor represents rate of change from 12 till 18 years old, and the second slope factor represents rate of change from age 18 till 40.

In order to obtain an impression of the appropriate genetic model, the twin correlations on the latent growth factors were inspected. MZ correlations on the intercept were more that twice the DZ correlations, which suggests the presence of non-additive genetic effects (D). In a model including A, D, and E effects, variance due to shared environmental effects (C) can not be estimated because this component is not identified. Based on these results we favor a model including D rather than C for the intercept. For the Slope, the female twin correlations were also suggestive of non-additive genetic effects, but the DZM correlation was more than half the MZ correlation, suggesting the possible presence of C. Shared environmental effects and non-additive genetic effects have opposite consequences in the difference between MZ and DZ correlations (reducing and increasing the MZ-DZ differences in correlation, respectively). The presence of D does not necessarily imply the absence of C, but just larger effects of D , and vice versa (Neale et al., 1992). We first fitted and ADE model for intercept and slope, and we finally tested the presence of C on the slope.

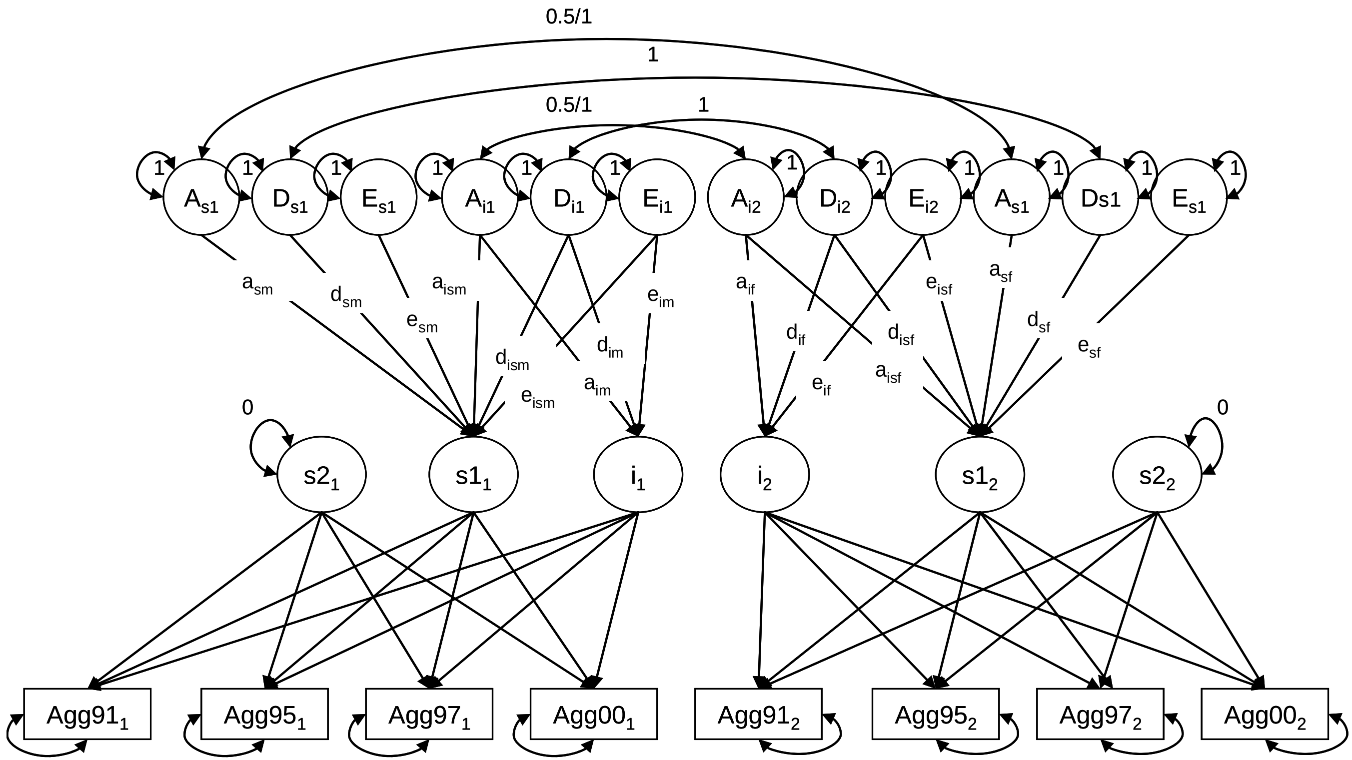

Figure 6.2

Genetic ADE model on intercept and first slope for an opposite sex twin pair. Variables with subscript 1 represent the first born twin; variables with subscript 2 represent the second born twin. Parameters with the subscript m belong to males, and parameters with sub-script f belong to males. A: Additive genetic effects, D: Dominance genetic effects, E: Non-shared environmental effects. The variance of the second slope was estimated as zero in all phenotypic models, and was fixed at zero in the genetic models.

Different submodels were compared to a saturated model to test for specific hypothesis. First we constrained the variance of MZ and DZ twins to be equal. Differences in variance across zygosity are indicative of sibling interaction effects. Next, we fitted two models, in which the variance of the first slope factor, in males and females, was fixed to zero, to test for its statistical significance. Next, a series of genetic models were fitted.

Figure 6.2 shows the ADE model for an opposite sex twin pair where the first born is a male and the second born is a female. The variances of the intercept and the first slope are explained by additive genetic effects (A), dominance genetic effects (D), and unshared environmental effects, i.e., environmental effect not shared by the members of the same family (E). (Note that the variance of the second slope was estimated as zero in the phenotypic analyses, and fixed to zero in the genetic modeling.) The A factors correlate 1 in MZ twins and 0.5 in DZ twins. Dominance effects correlate 1 in MZ twins, and .25 in DZ twins (Falconer, 1989).

In terms of the model parameters depicted in figure 2, the proportion of variance explained by A on the intercept is estimated as $a_i^2 / \left(a_i^2 + d_i^2 + e_i^2\right)$, and similarly for D and E. The proportion of variance explained by A on the slope is estimated as $(a_s^2 + a_{is}^2) / (a_s^2 + a_{is}^2 + d_s^2 + d_{is}^2 + e_s^2 + e_{is}^2)$, and similarly for D and E.

We fitted alternative models, nested under the general ADE model, to test for sex differences in genetic architecture, and to test the significance of the D component.

Maximum Likelihood (ML) estimation was used in the genetic models. Nested models were compared using the AIC and the BIC, and using a likelihood ratio test, which is constructed as: $-2*(\log likelihood_{\mathrm{mod}el1} - \log likelihood_{\mathrm{mod}el2})$. If the restrictions of the more parsimonious model are tenable, this statistic is chi-squared distributed with degrees of freedom equal to the difference in the number of free estimated parameters between the two models. If the chi-square is not significant, given a prior choice of alpha (0.05), we concluded that both models explain the data equally well, and that the more parsimonious is preferred.

RESULTS

Phenotypic Analyses

Table 6.2 shows the model fitting results and parameter estimates of the phenotypic piecewise growth model.

Table 6.2

Results of phenotypic growth models

Model fitting results[a]				
	$LL_{(MLR)}$	AIC	BIC	Δ Parameters from Model 1
Model 1: Full Piecewise (variance of s_2=0)	-36063.1	72166	72302	
Model 2: slope 1 equal to slope 2	-36081.5	72199	72321	2
Model 3: Mean of intercept equal ♂&♀	-36067.0	72172	72302	1
Model 4a: Mean of slope 1 equal ♂&♀	-36067.4	72172	72302	1
Model 4b: Mean of slope 2 equal ♂&♀	-36063.7	72165	72295	1
Model 5: Variance of intercept equal ♂&♀	-36063.3	72164	72294	1
Model 6: Variance of slope equal ♂&♀	-36063.1	72164	72293	1
Parameter Estimates Model 1				
	Males	Females		
Mean intercept	6.737	7.094		
Mean slope1[a]	-0.590	-0.318		
Mean slope2[a]	-0.155	-0.174		
Variance intercept	9.405	9.032		
Variance of slope 1	0.802	0.846		
Variance of slope 2	0.000	0.000		
Correlation intercept-slope 1	-0.301	0.517		

a. All models are nested to model 1: each model incorporates a new constraint that is not included in the next model.

The estimates of the means of first and second slope suggest that aggression decreases at a greater rate between ages 11 and 18 years, and keeps decreasing after 18, but at a lower rate. In model 2, the mean of the first and the second slopes were constrained to be equal. Both the AIC and the BIC increase considerably, indicating that there is a significant difference in the rate of change in aggression between the two, age periods 11-18 and 18-40. Furthermore, there are significant individual differences in the rate of change between 11 and 18, but the variance in the slope between 18 and 40 is estimated at zero, and it was therefore fixed at zero in all the subsequent analyses. There also was significant variation in the intercept, or level of aggression at the age of 18.

In model 3, the mean of the intercept was constrained to be equal in males and females. The AIC of model 2 was larger than that of model 1, and the BIC remained equal. The increase in the AIC suggests that females have a slightly larger mean on aggression at age 18 than males. In model 4a, the mean of the first slope was constrained to be equal across sexes. The AIC increased, whereas the BIC remained the same compared to model 1. The larger AIC suggests that decrease in aggression between 11 and 18 years old is steeper in males than it is in females. In Model 4b the mean of the second slope was constrained, producing a decrease in both AIC and BIC. Thus, the decrease in the mean of aggressive behavior after 18 is the same in males

and females. In models 5 and 6, the variance of intercept and the variance of the slope were constrained to be equal in males and females. Both constraints resulted in a decrease in AIC and BIC, indicating that males and females show the same amount of variation in aggression at age 18, and the same variance on the slope from 11 to 18.

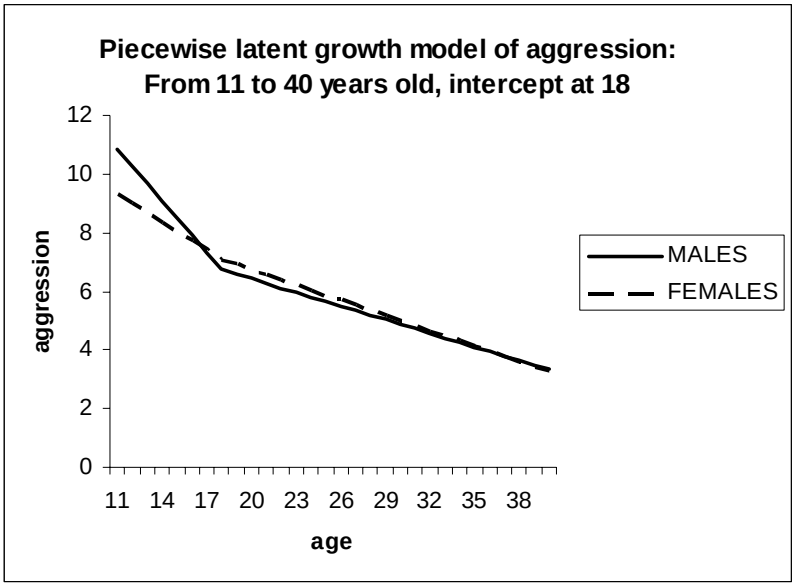

Figure 6.3

Mean levels of aggression from 11 to 40 years old, implied by the piecewice LGMs.

Figure 6.3 shows the graphic representation of the mean slopes of aggression between 11 and 40 years old implied by the piecewise growth model with the intercept at the age of 18, as estimated in model 1. In this figure, it is clear how the males depart from larger values in aggression at the beginning of adolescence compared to the females. The aggressive behavior of males decreases at a higher rate until the age of 18, at which age females show slightly higher levels of aggression. Subsequently, the aggressive behavior of both sexes continues decreasing at a lower rate and the values of males and females approximate to each other. Mode 1 was the phenotypic model used in the genetic modeling.

Genetic Analyses

Table 6.3 shows the estimates of the twin correlations on the growth factors, intercept and first slope (the second slope was a fixed effect). The first column shows the MZ

and DZ twin correlations on the intercept. The MZ correlations are large, and more than twice the DZ correlations. The second column shows the twin correlation on the first slope. The MZ correlations were again large, with the DZM and DOS correlations larger than half the MZ correlation, and the DZF correlation non significantly different from zero. Thus, the twin correlations on the intercept suggest the presence of dominance genetic effects, as do the twin correlations of the females for the slope. The male and DOS correlations on the slope rather suggest the presence of shared environmental effects. The third column shows the phenotypic correlation between intercept and slope. Most of these correlations did not differ significantly from zero. The fourth column shows the cross twin correlation between intercept and slope. Most of these correlations, except for that of DZM, were not significantly different from zero.

Table 6.3

Twin correlations and variances on the growth factors

	i_1 with i_2	s_{11} with s_{12}	s_{11} with i_1 & s_{12} with i_2	s_{11} with i_2 & s_{12} with i_1	Variance i	Variance s_1
MZM	0.694	0.985	0.150[a]	0.096[a]	9.960	1.070
DZM	0.174	0.762	-0.293	-0.439	9.242	0.841
MZF	0.659	0.824	0.174[a]	-0.019[a]	8.873	0.754
DZF	0.200	0.236[a]	0.131[a]	-0.117[a]	9.108	0.919
DOS	0.281	0.695	equal to DZ	-0.037[a]	equal to DZ	equal to DZ

a. non statistically significant p>0.05

Large differences between MZ and DZ correlations, with low DZ correlations are compatible with the presence of competitive sibling interaction and with non-additive genetic effects (Loehlin, 1986; Lykken, McGue, Tellegen, & Bouchard, 1992) . Most support has been obtained for the presence of non-additive genetic effects (Eaves et al., 1998; Keller et al., 2005). The competitive sibling interaction effects are also indicated by DZ variances larger than MZ variances (Rietveld et al., 2003). The variances of intercept and slope across zygosity groups are shown in the last two columns of table 6.3. The variances of female DZ twins seem to be larger than those of MZ twins. To test if this difference was statistically significant, we fitted two models in which we first constrained the variance of intercept, and then the variance of the slope to be equal for MZ and DZ twins. The model fitting results for this models and the comparison against the full model is shown in table 6.4. The likelihood ratio tests indicate that these equality constraints are tenable ($\chi^2(2)=0.80$,p.=0.670; and $\chi^2(2)=0.68$,p.=0.712), and we therefore concluded that MZ and DZ twins do not differ in the variance of

intercept or the variance of the slope. Given that there is no sufficient evidence to support the presence of sibling interaction effects, we concentrated on the analysis of non-additive genetic effects.

Table 6.4

Model fitting results from genetic modeling: Proportion of variance of intercept and slope explained by A, D and E

	Model Fitting Results[a]						
	$LL_{(ML)}$	AIC	BIC	C.T.[b]	χ^2	DF	p
Saturated model							
Model 1: Twin correlations (Saturated)	-33875.02	67832	68079				
Model 1a: Variance intercept equal across MZ and DZ	-33875.42	67828	68064	1	0.80	2	0.670
Model 1b: Variance slope equal across MZ and DZ	-33875.36	67828	68064	1	0.68	2	0.712
Model 1c: Variance of slope fixed to zero for males	-33990.96	67881	68069	1b	69.20	8[c]	<0.001
Model 1d: Variance of slope fixed to zero for females	-*33917.04*	67896	68083	1b	83.36	8[c]	<0.001
ADE model							
Model 2: Full ADE	-33883.60	67829	68016	1	17.16	10	0.071
Model 3: ADE♂=ADE♀	-33885.61	67817	67956	2	4	9	0.911
Model 4: D on slope = 0							
AE on slope	**-33886.16**	**67814**	**67941**	**3**	**1.12**	**2**	**0.571**
ADE on intercept							
Model 5: D on intercept = 0	-33889.60	67819	67939	4	6.88	2	0.032
Model 6: D on slope = 0							
C on slope free	-33885.34	67816	67955	4	1.63	2	0.442
ACE on slope							
ADE on intercept							

	Proportion of variance explained by ADE			
	Model 2		Model 4	CI (95%)[d]
	Males	Females		
A on the intercept	0.315	0.161	0.262	-0.009,0.534
D on the intercept	0.380	0.501	0.398	0.114,0.682
E on the intercept	0.306	0.338	0.340	0.282,0.397
A on the slope	0.686	0.671	0.850	0.634,1.067
D on the slope	0.311	0.170	0.000	-
E on the slope	0.003	0.159	0.150	-0.067,0.366

a. Models are nested to the previous: each subsequent model incorporates the constraints of the previous one. E.g., model 4 includes equality constraints on the parameters over males and females.

b. Compared to model

c. With the constraint of the variance to be zero, all the covariances that involve that variance are also fixed to zero.

d. Symmetric confidence intervals based on standard errors.

Model 1c and 1d were intended to test the significance of the variance of the first slope in males and females, given the low values compared to the variances of the intercept. The two models in which the variance of the first slope was constrained to zero fitted the data worse that the saturated model ($p<.001$), indicating that there is significant variation in the slope between 11 and 18 years old for males and females.

The second part of table 6.4 shows the results of the genetic analyses. Model 2, the full ADE model depicted in figure 2, shows the same AIC and a lower BIC than the saturated model, in which only the twin correlations were estimated. According to the likelihood ratio test, the ADE model explains the data as well as the saturated model, and thus provides a good explanation of the pattern of correlations. In model 3, A, D and E for both intercept and slope were constrained to be equal for males and females. This resulted in a decrease of the AIC and the BIC, and a non-significant chi square difference. Thus males and females do not differ in the amount of variance of the intercept and of the slope explained by genetic and environmental effects. In model 4, the non-additive genetic effects on the slope where fixed to zero, with a subsequent decrease in the AIC and the BIC. In terms of the likelihood ratio test, model 4 did not differ significantly from model 3 ($\chi^2(2)=1.12$, $p.=0.571$), and thus individual differences in the slope of aggression between 11 and 18 are not explained by non-additive genetic variance. In model 5, dominance genetic effects on the intercept were fixed to zero. This constraint resulted in an increase in the AIC, whereas the BIC remained the same compared to model 4. Model 5 provided a significantly worse fit ($p<0.05$) than model 4, indicating that the non-additive genetic effects on the intercept are significantly different from zero. Finally, given that D could be fixed to zero on the slope in model 4, and in concordance with the pattern of twin correlations on the slope for males and DOS, we estimated in model 6 an ACE model for the slope, The C factors were correlated 1 for MZ and DZ twin pairs. Model 6, with an ADE model on the intercept and an ACE model on the slope fitted the data as well as model 4, with an ADE model on the intercept and an AE model on the slope ($p=0.442$). Model 4 was selected as the best model, as it provides the most parsimonious explanation of the data, according the AIC and the BIC. According to model 4, 26% of the variance on the intercept is due to additive genetic effects, 40% to non-additive genetic effects, and 34% to the non-shared environment. Most of the variance on the slope between 11 and 18 years old was explained by additive genetic effects, with no non-additive genetic effects, and small effects of the non-shared environment. Note that this is the variance of the latent factors, considered as true variance, and therefore the E component does not comprise measurement error.

Point estimates and confidence intervals for the estimates of the final model 4 can be found in Table 6.5. In this table it can be observed that the path coefficients from A_i and D_i to the slope factor were non significantly different from zero. The path coefficient from E_i to the slope was significant ($p<0.05$), indicating that the low correlation between intercept and slope is entirely explained by the non shared environment.

Table 6.5.

Confidence Intervals of parameter estimates for final models constrained in table 6 4

	Lower 99%	Lower 95%	Point Estimate (%variance)	Upper 95%	Upper 99%
a_i	0.632	0.873	1.639	2.404	2.645
d_i	0.946	1.165	1.865	2.565	2.785
e_i	1.533	1.583	1.741	1.900	1.950
a_{is}	-0.511	-0.425	-0.149	0.126	0.212
d_{is}	0.000	0.000	0.000	0.000	0.000
e_{is}	-0.048	0.015	0.215	0.415	0.478
a_s	0.636	0.693	0.874	1.055	1.112
d_s	0.000	0.000	0.000	0.000	0.000
e_s	-0.407	-0.271	0.159	0.590	0.725
Mean intercept: males	6.53	6.59	6.81	7.02	7.09
females	6.90	6.95	7.13	7.60	7.36
Mean slope 1: males	-0.80	-0.75	-0.59	-0.43	-0.38
females	-0.52	-0.47	-0.35	-0.22	-0.18
Mean slope 2: males	-0.22	-0.21	-0.18	-0.15	-0.14
females	-0.22	-0.21	-0.19	-0.17	-0.16

DISCUSSION

In the present paper longitudinal changes on aggressive behavior between the ages of 11 and 40 were analyzed. Mean scores on aggressive behavior decrease during adolescence. These changes are steeper in males than they are in females, which is probably due to the higher prevalence of aggression in males in the early ages (Loeber et al., 1997). As shown by the results of the growth modeling, the end of adolescence, represented by the age 18, can be considered the beginning of the stabilization of aggressive behavior in the adult life, and thus marks an important developmental period. Aggression continues decreasing slowly to the age of 40, while sex differences fade.

The presence of individual differences in the rate of change until the age of 18 is consistent with previous studies that found different trajectories that helped to identify normative groups and groups with potential behavioral problems over time. Normal

adolescents either show consistent low levels of aggression, or decreasing levels in aggression during late adolescence (Moffit, 1993; Schaeffer et al., 2003).

Females showed larger mean levels of aggression at age 18 compared to males. This result has been observed in previous studies using self reports in young adults (Ferdinand et al., 1995; Pulkkinen et al., 1993), and might be related to the later onset of aggression in females (Loeber et al., 1997).

The genetic analyses focused on the variation at a specific age point, namely 18 years old, and the variation in the rate of change in aggression, as estimated by the growth curve model. This choice contrasts with the majority of studies on adult samples where it is common practice to work with heterogeneous samples with respect to age, and obtain a pooled estimate of heritability for the entire sample. Given that aggression is a variable especially sensitive to age differences, compared to other personality variables (Rebollo, Dolan, & Boomsma, 2006), we chose to estimate the sources of variance at a specific age, parallel to what is commonly done in children samples. The pattern of DZ correlations observed is consistent with the previous studies on adult samples (Coccaro et al., 1997; Rushton et al., 1986; Sluyter et al., 2000; Tellegen et al., 1988). The results of the genetic analysis showed that 26% of the variance on aggression at the age 18 is explained by additive genetic effects, 40% by non-additive genetic effects, and 34% by the non-shared environment. There were no sex differences in the amount of variance explained by A, D and E. These results differ from previous results in two aspects. The estimate of the non-shared environmental component is rather low, considering that it is expected to rise in adulthood (Rhee & Waldman, 2002). This result is probably due to the fact that in most studies the variance decomposed is that of the observed scores, and therefore the E component includes measurement error. In the present study it is the variance of the true score, as identified in the latent growth model, that is modeled, and therefore the E component is free from measurement error. Measurement error is comprised in the residual term (ε_i in equation 1).

The clear presence of non-additive genetic effects had only been detected in Coccaro et al.'s study (1997). The progression from shared environment in childhood to non-additive genetic effects in adulthood is a relatively new finding. We might speculate that the shared environmental effects in childhood reflect the progress of the learning process through which children acquire the social skills to express their anger or frustration in a socially acceptable way. At the age of 18, most children will have completed this learning process, and as a result, shared environmental effects tend to fade. Furthermore, in the transition to young adulthood, when the siblings leave their parents house, they no longer share influences stemming from the neighborhood, or

the school, i.e., influences that are known to moderate the expression of aggressive behavior, and are part of the shared environment during childhood (Loeber et al., 1997). Another likely explanation is that the C component, often found in children studies, might be due to a bias in parental ratings (Hudziak et al., 2003) that disappears when self ratings are used. Nevertheless, it should be noted that with the classic twin design, the presence of non-additive genetic effect does exclude the effects of the shared environment; such effects may be present, but overruled by the effects of non-additive genetic variance.

The emergence of dominance genetic effects may be due to changes in the prevalent ways through which aggression is expressed in adulthood. There is a developmental trend from adolescence to young adulthood, which entails a decrease in overt aggression (Achenbach, Howell, CcConaughy, & Stanger, 1995). Coccaro et al.'s (1997) study suggests that it is the emotional and indirect expression of aggression that is mostly influenced by non-additive genetic effects, and not its physical expression. This is consistent with previous evidence on Type A Behavior, and Anger (Rebollo & Boomsma, 2006a; Rebollo & Boomsma, 2006b; Sims et al., 1991), which comprise the emotional components of the Aggression-Hostility-Anger syndrome (Sluyter et al., 2000).

The importance of non-additive genetic effects in the explanation of individual differences in personality has been emphasized previously (Eaves, 1988; Loehlin, 1986; Lykken et al., 1992), and is gaining support with the addition of extended families designs to the classic twin design (Eaves & Carbonneau, 1998; Keller et al., 2005; Rebollo et al., 2006a; Rebollo et al., 2006b). High levels of non-additive genetic variation are indicative of the evolutionary origins of the variation in a given trait, indicating that it has not been neutral to selection (Eaves, 1988; Keller et al., 2005; Mather, 1966). This specific finding is not surprising in human traits like aggression, hostility, or anger, as these behaviors are related to the basic emotions of fear, frustration, and stress, which are also present in more primitive species (Gray, 1987).

Future studies should explore if different subtypes of aggression previously found with the CBCL are applicable to the YSR in young adults, i.e., relational aggression vs. direct aggression (Ligthart et al., 2005). This is especially relevant given that it is expected that relational-social aggression gains importance with adulthood (Achenbach et al., 1995; Ferdinand et al., 1995). It has been suggested that social aggression is more environmentally determined, whereas physical aggression is more genetically determined (Brendgen et al., 2005), but it is unlikely that this would apply in adult samples given the observed low DZ correlations in the present and previous studies. In this vein, Coccaro et al. (1997) in a sample of adults found zero DZ correlations and

non-additive genetic effects from 28-40% for verbal assault, indirect assault and irritability, whereas for direct assault the DZ correlations was slightly higher .16, and exclusively additive genetic effects were found.

The distinction between the emotional and the behavioral components of aggressive behavior in adult individuals, in combination with the statistical power that is conferred by extended family designs, will help to extend and clarify the results found in the present study. Advances in molecular genetics, and the study of the effects of specific genes (Manuck et al., 1999; Sluyter et al., 2000), and particularly the interaction between different genes (Reuter et al., 2005) are powerful tools to enhance our understanding of the precise ways through which non-additive genetic variation translates into phenotypic variation.

Chapter 7

GENERAL DISCUSSION

> *¨Sciences need systems for classifying their phenomena whether these are astronomical objects, units of matter, or species of animals. A science of astronomy that made no distinctions among planets, stars, and galaxies, a geology that regarded every rock as a unique structure, or a biology that could only distinguish two-legged from four-legged creatures, would not progress very far in understanding or prediction. (…) Disinterest in the classification of personality traits (if not total denial of the existence of behavioral consistencies) has led to faddish areas of study and endless generalizations about "personality", per se, rather than study of actual phenomena. Personality psychology has been more involved in search for a paradigm than in the development of a paradigm, the exception being the work of Eysenck (1985) and Gray (1987). One might say we are in an era of "paradigm conflict" (Zuckerman, 1991, p. 1).*

Marvin Zuckerman wrote this fifteen years ago. His own work in the subsequent years (Zuckerman, 1992; Zuckerman et al., 1996; Zuckerman et al., 1993; Zuckerman et al., 1991) was directed towards the development of a paradigm of personality, on the basis of Eysenck's and Gray's theories. In 1986, Cloninger developed his psychobiological theory of personality based on the results of twin and family studies. Cloninger's dimensions seemed to have a great deal in common with Gray's and Zuckerman's dimensions. The relationship between these and Eysenck's personality types was less clear (Zuckerman et al., 1996). Nowadays, the Five Factor Model (McCrae et al., 1997; Norman, 1963) has received a great deal of empirical support, largely based in the identification of the five factor structure across methods, gender, ages and cultures. It is in view of this support that the Five Factor Model is considered by some as a predominant paradigm (Bazana et al., 2004; McCrae et al., 1997). However, from a psychobiological perspective, the identification of basic dimensions of personality requires the satisfaction of several criteria (Eysenck, 1992a; Zuckerman, 1992), in addition to the reliable identification of dimensional factor structures across methods, genders, ages, and cultures. These include (1) the stability of the dimensions over time, (2) at least moderate heritabilities of the dimensions, (3) the identification of similar kinds of behavioral traits, which are indicative of the dimensions, in infrahuman species, (4) the identification of the dimensions with some significant biological markers, and (6) the identification of the neural substrate of the dimensions (Zuckerman, 1991; pp.4-5). Given these requirements, personality psychology is still far from the establishment of a commonly accepted paradigm, analogous to what is

found in other fields, such as, say, the study of cognitive abilities (Carrol, 1993). Apart from the two generally accepted traits, common to the majority of personality theories, namely Neuroticism (N), and Extraversion (E), little agreement and great variability exist with respect to the number and the nature of the basic dimensions of personality, which are considered necessary to explain individual differences in human behavioral tendencies.

This thesis uses a large sample of 17557 individuals, combined with a repeated measures design, to investigate the structure of personality, while taking into account intra and interindividual differences due to age. With this strategy we have tried to get closer to a latent representation of the variation in basic personality dimensions. The combination of a large sample, a wide variety of personality variables, and advanced statistical modeling has led to the identification of a potential third basic dimension of personality, along side Extroversion or Neuroticism. The importance of this dimension has been recognized before, although different labels have been used to denote it. For instance, personality theorists like Gray and Zuckerman have considered this dimension, denoting it Aggressive-Hostility (Zuckerman), and the Flight-Fight System (FFS; Gray). Medical psychologist and psychiatrist have discussed this dimension in terms of Type A Behavior Pattern (TABP; Friedman & Rosenman, 1974), and the "Agression-Hostility-Anger syndrome" (Sluyter et al., 2000). The theoretical and practical importance of this third dimension is great. For instance, it is worth noting that "presently, anger, hostility and aggressiveness collectively represent one of the most widely studied psychosocial risk factors for CHD (Coronary Heart Disease) and premature mortality, and most –but certainly not al- of the available studies support this association" (Smith, Glazer, Ruiz, & Gallo, 2004, p.1218).

Given the presence of substantial genetic variance with respect to TABP, anger, and aggression (see chapter 4 to 6 of the present thesis), and in view of Cloninger's definition of character [character is based on the conceptual organization of experience, i.e. verbal learning, the acquisition of learning sets, and abstract conceptualization that influences behavioral goals and expectancies. Environmental effects should be more important character development than for temperament (Cloninger et al., 1993)] , it is difficult at this point to identify our third factor with Cloninger's cooperativeness. The relationship between our third factor and the N dimension, suggested in chapter three, might be based on the fact that both entail some kind of negative emotionality. Both anxious and aggressive (or hostile) reactions may be responses to the same kind of stimuli, namely those related to fear, stress, or frustration. According to Gray (1987), the predominant reaction is governed by the conditioned versus unconditioned nature of the stimuli. Conditioned stimuli are sup-

posed to activate the Behavioral Inhibition System, whereas unconditioned stimuli would activate the FFS. However, Gray's distinction seems difficult to apply to human behavior, especially in modern societies, where few stimuli, to which we react, are indeed unconditioned. We might speculate that the predominant emotional and behavioral reaction to stimuli related to fear, stress, or frustration, as well as the consequences of those reactions for health and lifestyle, is determined by the personality of a given person, i.e., high or low trait levels on N, and the third factor that we will label Aggressive Emotionality (AE).

In this study we have attempted to satisfy some of the criteria that were established by Zuckerman (1991; 1992) and Eysenck (1992a) to identify Aggressive Emotionality as a basic dimension of personality. Zuckerman's first criterion is "reliable identification of dimension factor structures across methods, genders, ages and cultures" (Zuckerman, 1991; p.4). According to the results of chapter three, these variables –anger, aggression, TABP, rule breaking behavior- tends to cluster together, and are distinct from other factors. Similarly, Zuckerman's studies with several different instruments and variables showed consistent evidence for the emergence of AE as a coherent factor that is independent from Psychoticism, Impulsivity or Neuroticism (Zuckerman et al., 1996; Zuckerman et al., 1988; Zuckerman et al., 1993; Zuckerman et al., 1991). Aluja et al. (2004) provided empirical support the presence of the AE factor in the Spanish population. Further research is necessary to refine the exact description of this factor, and to replicate its structure with different instruments and across different cultures. Age variability was modeled and controlled for in chapter 3, but generational differences might still be present and are certainly a matter of study in the future. The factor model estimated in chapter three can be extended to study measurement invariance across gender and cohorts.

Zuckerman's second criterion is the "stability of measured dimensions in the same individuals over time" (Zuckerman, 1991; p.4). Chapter 3 provided support for the longitudinal stability of the components of the AE factor (with the exception of TABP, which was assessed only once). Anger, aggression, and rule breaking behavior are characterized by stability coefficients in a two years interval ranging from 0.382 to 0.616. For Aggression and Rbb, stability coefficients over a nine year interval are 0.424 and 0.301, respectively. Thus, anger, the variable closest to the emotional experience (as opposed to its behavioral manifestation), shows the highest stability. The results of the latent growth models of chapter three showed that Aggression and Rbb are the personality variables that are most affected by age differences. Chapter 6 shows that the great majority of changes in Aggression take place before individuals reach young adulthood. After the end of adolescence, aggressive behavior tends to

stabilize. Genetic analyses in chapter 5 showed that genetic factors explained 61% (47% in females) and unshared environmental effects explained 39% (53% in females) of the stability of anger. Additive genetic effects were very stable (genetic correlations 0.88-0.98), while dominance genetic effects (0.65) and the non-shared environment (0.48-0.51) were also considerably stable. In chapter 6, the genetic analysis of the growth curves showed that variability in the changes occurring in aggression during adolescence between 12 and 18 years old is due exclusively to additive genetic effects. It should be interesting to find out whether more indirect forms of aggression (than purely physical expressions of aggression) show a different pattern of stability. Further research is also necessary to study the intraindividual changes occurring on anger over a longer time interval. This will be possible after survey 7 of the Netherlands Twin Register, collected in 2005/06 which includes the anger inventory.

The age variability of the sample was handled differently in chapter 3 and chapter 6. The Mehta and West approach (2000) applied in chapter six is in principle preferred, as it is more flexible in terms of establishing the shape of the growth and testing alternative models. This approach could not be applied in chapter three, as the multivariate character of the data made the estimation impossible, due to an excessive number of integration points. According to Mehta and West (2000), both ways of modeling age differences are equivalent, when the growth is linear across age. Certain deviations from linearity along age are accounted for by the age covariate (chapter 3), when the effects of age on the slope are significantly different from zero. Thus, when the purpose of the study, as it was in chapter 6, is to model the shape of the growth along age as precisely as possible, the Mehta and West (2000) approach is more flexible. In chapter three, the purpose was to control for the effects of age and the longitudinal design, and that was efficiently done through the growth model with age as a covariate on intercept and slope.

Zuckerman's third criterion concerns the "identification of similar kinds of behavioral traits marking the factor in other species of animals" (Zuckerman, 1991; p.4). Although we did not address this issue in the present thesis, there is a large body of literature that focuses on aggression in primates, as a model for human aggression (Honess & Marin, 2006). Studies with primates are quite relevant to the study of humans, because of the importance of social behavior, and its close relationship with aggressive behavior. Research on aggressive behavior in mice, in contrast, has been more directed towards the study of the neurological and genetic causes of variation in aggression (D'Souza, Kel, & Sluyter, 2003; de Boer, van der Vegt, & Koolhaas, 2003; Feldker, de Kloet, Kruk, & Datson, 2003; Miczek, Maxson, Fish, & Faccidomo, 2001).

Zuckerman's fourth criterion requires "at least moderate heritability for the dimension" (Zuckerman, 1991; p.4). Figure 7.1 displays the results of the variance decomposition of TABP, anger, and aggression, as reported in chapters four, five, and six of this thesis. The estimates of broad heritability were consistently significant, and ranged from 34% for anger (in females) to 66% for aggression. The relatively larger estimate obtained for aggression is in part explained by the fact that the latent phenotype was modeled, which eliminates the measurement error from the unshared environmental component.

Consistent with the literature, the three phenotypes showed DZ correlations lower than half the MZ correlations. The DZ correlations were conspicuously low for anger and TABP, calling for alternative explanations in addition to the presence of additive genetic effects. These low DZ correlations could be explained by the presence of non-additive genetic effects on the three variables, except for anger in females. Competitive sibling interaction effects were rejected as a possible explanation for the low DZ correlations because they were found to be non-significant and non-consistent for both Anger and Type A Behavior.

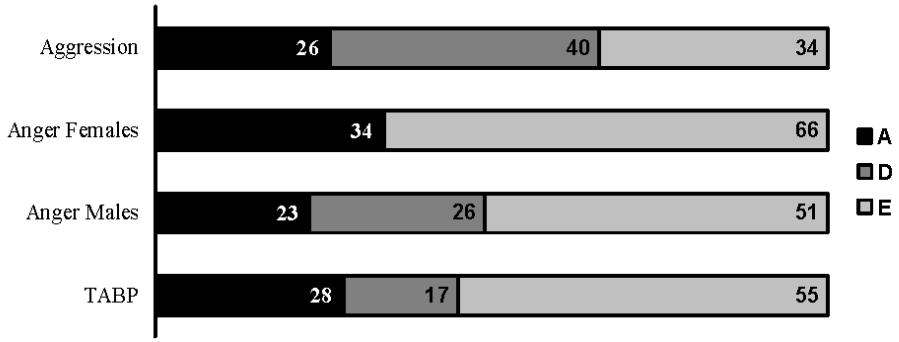

Figure 7.1

Decomposition of the variance of Aggression, Anger and TABP into A-Additive genetic effects, D-non-additive genetic effects and E-Non-shared environment, from chapters 4, 5 and 6.

Our results are consistent with recent pervasive evidence for non-additive genetic variation in personality dimensions obtained with extended families design (EFD) (Eaves et al., 1999; Eaves et al., 1998; Keller et al., 2005). As established repeatedly in twin studies dating back to the nineteen eighties, there is little influence of shared environmental effects on individual differences in adult personality (Plomin & Daniels, 1987). However, the role of additive and non-additive genetic effects has remained unresolved, because of the lack of power to detect genetic non-additivity in

the majority of classical twin studies (Coventry & Keller, 2005). Recently, the inclusion of family members of the twins, such as their parents, siblings, spouses, or children, has proven to be a very efficient way to increase the power to detect and distinguish a variety of effects, ranging from non-additive genetic effects to the effects of assortative mating, cultural transmission, or gene-environment correlations. Using an extended families design, the Eaves et al. (1998, 1999) and Keller et al. (2005) studies revealed strong evidence for non-additive genetic effects in Extroversion and Neuroticism (but not in Psychoticism), as well as in Cloninger's personality dimensions, harm avoidance, reward dependence and novelty seeking. Also in concordance with our results for AE, the authors did not find evidence of sibling interaction effects. Keller et al. (2005) discarded gene-by-age interaction as possible explanation of their results, as the DZ twin correlations and the sibling correlations were the same.

Although the presence of dominance genetic effects seems a fairly plausible explanation for the pattern of correlations found for aggression in chapter 6, the DZ correlations observed for anger and TABP are still too low to be explained exclusively by these effects. Another possible explanation proposed by Loehlin (1986) is the violation of the Equal Environments Assumption (EEA), according to which the MZ twin environments may be more similar than DZ twin environments, with a subsequent inflation of the MZ correlations with respect to the DZ correlations. The EEA has been tested repeatedly using a variety of methods. The results often indicate that MZ twins do actually tend to have more contact, and share more environmental factors, such as education, occupation, health behavior, and social support (Horwitz, Videon, Schmitz, & Davis, 2003; Lykken, McGue, Bouchard, & Tellegen, 1990; Posner, Baker, Heath, & Martin, 1996; Scarr & Carter-Saltzman, 1979). However, this greater similarity does not seem to result in bias in the estimates of heritability or shared environment. Carmelli et al. (1988) demonstrated how adjusting the heritability estimates for environmental covariates shared by siblings barely changed the results. Posner et al. (1996) and Lykken et al. (1990) investigated the relationship between frequency of contact and similarity, and its possible effects on the estimates of the variance components. Lykken et al. (1990) demonstrated that it is similarity between pairs of individuals that leads to an increase in contact, rather than the other way around. The results of Posner et al. (1996) suggested that, although the direction of causality between similarity and contact might be bidirectional, unless the sample is divided into high and low contact individuals, the parameter estimates of genetic models are not biased. In addition, and more generally, to the extent to which the direction of causation is similarity to contact for a given trait, no bias at all is expected. Finally, Eaves et al. (2003) demonstrated in a simulation study that the claim that differ-

ences in similarity in contact falsify the EEA are clearly unfounded, and that stratification studies may be simply pointing to the role of genetic factors in niche selection. Thus, violation of the EEA is not a likely explanation of the pattern of DZ correlations for anger and TABP.

Reed et al. (1991) found effects of placentation on twin similarity on TABP measures. Monochorionic pairs resembled each other more than dichorionic pairs. The authors interpreted these results as a special case of violation of the EEA. In any case, violations of the EEA that entail the existence of special MZ, more generally twin environments (as opposed to those of full siblings, half siblings, or even singletons), can nowadays be modeled explicitly in Extended Families Designs in combination with Structural Equation Modeling. Derks et al. (2006) explore the conditions under which the EEA can be tested. The authors found that violations of the EEA can lead to overestimation of the heritability and underestimation of the shared environmental influences. They analyzed data on spatial ability and aggression from the NTR, finding no detectable violation of the EEA.

Thus, if dominance genetic effects are not enough, and neither sibling interaction effects nor violations of the EEA are viable explanations, what is the explanation of the low DZ correlations? Eaves (1988; 1999) suggested that DZ and sibling correlations of zero or close to zero are too low to be explained exclusively by dominance genetic effects. However, the idea of large contributions of high-order interactions between large numbers of relatively infrequent alleles at different loci, that swamp additive genetic effects (e.g. emergenesis, Lykken et al., 1992), also seems unlikely, as there is little evidence in experimental organisms that heterozygous effects exceed additive deviations. However, the very low sibling correlations compared to those of MZ twins could be explained by interactions between pairs of loci ("digenic interactions"). These epistatic duplicate gene effects, or digenic interactions, are consistent with the hypothesis that links the presence of genetic non-additivity in personality traits with processes of strong directional or ambidirectional (stabilizing) selection, where the action and interaction of alleles is modified to optimize the expression of the trait by favoring one extreme of the population (directional), or an intermediate optimum (stabilizing), or to protect the expression of the trait against possible disadvantageous mutations (Fisher, 1958; Hay, 1980). Therefore, some authors hypothesize that basic personality traits may manifest phylogenetically early properties of the nervous system (Eaves et al., 1999).

The genetic analyses of anger and TABP in this thesis benefited from the inclusion of parental data, as such additional data increases of power to detect

genetic the variance component A. However, chapter 6, concerning the genetic analysis of aggression, did not include such additional data. A recent review on parameter bias in the classical twin design (CTD) compared to the estimates obtained using the CTD and the EFD. This review showed that, on average, the CTD provides upwardly biased estimates of A, and downwardly biased estimates of D (Coventry et al., 2005). However, the estimate of additive genetic effects on the aggression paper did not differ conspicuously from those for anger and TABP, and contrary to the expectations, the non-additive genetic component on aggression was the largest estimate compared to those obtained in the analyses of the other phenotypes. It may well be that the large sample size, the larger DZ correlations and the repeated measures design increased the power of the aggression study to detect genetic non-additivity.

Summing up, the evidence for genetic variability, be it additive or non-additive, in Aggressive Emotionality is pervasive in the three phenotypes studied in this thesis, i.e., in all three components of the Aggressive Emotionality dimension. This evidence is well in line with the results of previous studies on related phenotypes, and with evidence on basic personality dimensions such as Extroversion and Neuroticism.

The last of Zuckerman's criteria refers to "the identification of the dimension with significant biological markers, and the identification of the biological systems comprising the neural substrate for the dimension" (Zuckerman, 1991; p.4-5). Although, we did not address this criterion in this thesis, there are several lines of research that support the relationship of a polymorphic variation in the gene for monoamine oxidase-A (MAOA) and a polymorphism of the gene coding for tryptophan hydroxylase (TPH) with aggression and anger related traits (Jacob et al., 2005; Manuck et al., 1999; Manuck, Flory, Ferrell, Mann, & Muldoon, 2000). Additionally, the allele of the MAOA gene, which is associated with higher aggression scores, has also been associated with low central nervous system serotonergic responsivity (Manuck, Flory, Muldoon, & Ferrell, 2002).

In summary, the evidence presented in this thesis work contributes to the evidence from previous research related to anger, aggression, and type A Behavior. The result results suggest that there is sufficient support to consider Aggressive Emotionality a basic, psychobiological, dimension of personality, which exists at the same hierarchical level as Extroversion and Neuroticism.

FUTURE DIRECTIONS

The study of the nature of Aggressive Emotionality is an interesting line of research to continue, both for its basic theoretical interest, and for its possible practical implications for the individual and society.

On the basic theoretical level we need to develop a more detailed description of the Aggressive Emotionality dimension. There are various studies that can be conducted to this end. First, multivariate studies should be undertaken that involve these (anger, aggression and TABP) and other, related, measures in the study of common genetic and environmental sources of variance. If the dimension is robust and unitary, these variables should share a common causal background. Recent research has also pointed to the need to differentiate between different expressions of anger and aggression, e.g., anger in, anger out, physical aggression, and social aggression. Different expressions of aggressive emotionality may not only be caused by different factors, but may also have different consequences (Siegman, 1994a).

Further research should also address the identification of the specific genes and neural systems involved in the regulation of aggressive emotionality (Houston, 1994; Siegman et al., 1994) . Advances in this field may lead to treatment for people with high trait levels by the regulation or modification of relevant underlying endophenotypes. As mentioned above, recent research suggests that the focus, at least initially, should be on the genes that are involved in the MAOA system, and the central nervous system serotonergic responsivity, which is in turn related to responsivity to environmental stressors, particularly social stressors (McCaffery, Bleil, Pogue-Geile, Ferrell, & Manuck, 2003). Considering the results from the present study regarding the importance of the non-additive genetic variation to explain individual differences in AE, the research on gene finding may benefit from a focus on gene–by-gene interactions, instead of the additive effects of single genes (Reuter et al., 2005).

As argued in chapter one, no less important than the effect of specific genes, are the specific environmental effects. However, the nature of the environmental variance in behavioral genetic models is still unclear, at least in adult samples. It seems that shared environmental effects present during school years fade completely after adolescence. One possible explanation for this phenomenon would be that the C component is merely a manifestation of rater bias that characterize parental reports (Bartels et al., 2003). The increase in the magnitude of non-shared environment in adulthood (Rhee et al., 2002) might suggest that the effective environment in the adult years is not shared by the siblings who originate from the same family. This also implies that, regardless of the exact nature of the shared environmental effects, they are transitory. This calls for a redefinition, or at least a refinement, of the concept of environment in genetic analysis. As discussed in chapter 6, the majority of people embark upon adulthood around the age of 18. From that age, approximately, each person builds his or her own shared environment, or adult family environment, either alone or with a partner. The extended families design allows distinctions by defining different classes of envi-

ronmental effects, e.g., an environmental factor shared by the spouses, different from that shared by the twins and their parents (Keller et al., 2005). In order to establish whether the influences of shared and non-shared environments are actually temporary, or whether they have long lasting, or cumulative effects (Roberts et al., 2002) will emerge eventually from longitudinal studies. Overall, the research on environmental effects will benefit from the inclusion of measured environments and spousal data in twin studies, in order identify the effective factors in the non-shared environment black box.

Finally, merging theory and practice, the study of the interaction between genes and environment is a promising line of investigation. An ongoing research program on antisocial behavior has shown how, for example, response to the same environmental hazards varies with genotype (Caspi et al., 2002; Foley et al., 2004). Caspi et al. (2002) and Foley et al. (2004) found that the association between childhood maltreatment and subsequent antisocial behavior was a function of MAOA activity, which is the gene expression level associated with allelic variants of the polymorphism in the MAOA gene, i.e., the same polymorphism that has been associated with aggression and serotonergic responsivity (Jacob et al., 2005). Conversely, the effects of identical genotypes may be moderated by different environments. It is this second kind of interaction that may be relevant given therapeutic and preventive objectives. For example, for the purpose of prevention, children and adolescents with high levels of Aggressive Emotionality may benefit from the imposition of a specific life style that alleviates or helps to avoid specific behavioral and or health problems. In terms of treatment, adults, who suffer health problems that are associated with a certain personality type, may benefit from the adoption of certain behavioral strategies or life changes that can compensate, and help them to manage, their behavioral tendencies, leading to healthier life styles (e.g., a change of profession). In other words, we might want to learn how to avoid certain gene environment correlations that can buffer the outcome of a given genotype.

In a review on the relationship of anger, hostility, and aggression on the one hand, and coronary heart disease on the other, Smith et al. (2004) discussed recent research that suggests that hostile persons display heightened reactivity (e.g., blood pressure, heart rate, cortisol, etc.) to interpersonal stressors, but not to nonsocial stressors. If physiological reactivity is one of the links between AE and the increase in the risk of coronary heart disease, then people with high AE would be well advised to adopt a life style that avoids interpersonal stressors. Smith et al. (2004) also pointed out that hostility is associated with less social support, and less psychophysiological benefit stemming from social support. Hostile individuals not only show high reactivity to

stressors, but also behave in a way that results in more frequent and more pronounced exposure to those stressors. It is this kind of phenotype-environment correlation that should be avoided. However, it should be noted that Smith et al. (2004) discussed only correlational studies. These studies have the same limitations that characterize developmental studies, as discussed in chapter one. If a correlation is found between a phenotype like AE and an environmental factor, such as exposure to social stressors or low social support, the exact causal connection between the two remains to be elucidated. Some individuals might have a genetic proneness to high levels of AE, and have a tendency to be exposed to those environmental factors. On the other hand, some individuals may be characterized by a neutral genotype i.e., a genotype not prone to high AE, and display heightened aggressive emotions, as a consequence of the exposure to the environmental hazards (Middeldorp, Cath, Beem, Willemsen, & Boomsma, 2006). Similarly, some individuals with the AE prone genotype might have avoided risky environmental factors, and maintained adaptive average levels of AE. A number of research design have been developed within the field of behavioral genetics to disentangle the nature of the interaction between the environment and the genotype (Purcell, 2002; Purcell et al., 2002). These involve, inter alia, the use of twin and family samples combined with the measurements of the environment, where the latter feature in the model as modifiers of genetic effects. In addition, the measurement of both genotype and environment has been proposed to study the responses of different genotypes to the same environment, or the responses of the same genotype to different environment circumstances.

Summing up, Aggressive Emotionality can be viewed as a basic dimension of personality, which is factorially distinct from the other basic dimensions considered in this study. Variability in this dimension is influenced by non-additive genetic variation in adulthood, and the effective environmental factors are, in principle, not shared by the members of the same family. Those personality traits that form this dimension have been consistently related with several social phenomena, but especially with cardiovascular health problems. Behavior genetic studies of the proportion of variance explained by genes and environment constitute only a first step towards the understanding of the process through which genetic and environmental variation act and interact to give rise to variation in a specific phenotype (Kendler, 2005). A detailed understanding of this process may be instrumental in the prevention of the coronary heart disease and cardiovascular disease associated with high levels of Aggressive Emotionality.

SUMMARY

ENGLISH SUMMARY

When considered in the light of the aims and principles of psychobiology (Zuckerman, 1991), a commonly accepted paradigm, analogous to that which characterizes the study of cognitive abilities (Carroll, 1993), has yet to be established in personality psychology . Apart from the two generally accepted traits Neuroticism (N), and Extraversion (E), which are common to most personality theories, , little agreement and great variability exist with respect to the number and the nature of the basic dimensions of personality, which are considered necessary to explain individual differences in human behavioral tendencies.

The present thesis represents a contribution to the identification of the basic dimensions of personality from a psychobiological perspective (Eysenck, 1992a; Zuckerman, 1992). To this end, we made use of the personality data from the ongoing longitudinal study of the Netherlands Twin Register (Boomsma et al., 2002). Data from close to twenty thousand individuals from twin families were collected in six survey studies from 1991 to 2002. Because of the large sample size, the composition of the measured phenotypes, and the longitudinal design of the study, the present data form an invaluable resource for the study of the structure of personality and its sources of variance.

Chapter 1 provides an introduction to the field of Behavioral Genetics, the methods of twin and family studies, and the general findings concerning the genetic and environmental sources of individual differences in personality. Chapter 2 contains a simulation study that gauges the effects in terms of bias on standard errors and chi-square statistics of treating clustered data (due to dependency of family members) as if there were independent. In addition, chapter 2 assesses the efficiency of an estimator, which corrects for dependency. The results showed that when family-clustering is ignored in phenotypic analysis, i.e., by treating individual cases as independent, and using standard Maximum Likelihood estimation, there is a tendency for the chi-square statistic to be overestimated, and the standard errors of the parameters to be underestimated. This bias increases with greater family resemblance, due to heritability or shared environment. The source of family resemblance, i.e., heritability (h^2) and/or shared environment (c^2), interacts with the composition of the sample. In the absence of c^2, samples with twins, parents, and spouses are associated with the least bias, whereas in the presence of c^2, samples with only twins are associated with the least bias. In all conditions the bias remained below 15%. The use of the ‘complex option’ available in Mplus (clustering corrected Robust Maximum Likelihood estimation) reduces the bias to the levels observed when only independent cases are considered. Thus with the use of robust estimates the bias due to family dependency is practically

negligible in all conditions of dependency. In conclusion, chapter 2 shows that the bias due to dependency in family data does not form a serious obstacle to phenotypic data analysis. Therefore Robust Maximum Likelihood estimation was applied in subsequent chapters.

Chapter 3 provides an overview of the leading psychobiological theories of personality, namely the theories of Eysenck, Gray, Cloninger and Zukerman, and contains the results of an empirical study of the structure of personality. The aim of this study was to identify the nature of the third factor (or factors), beyond Extraversion and Neuroticism. Because this study was based on a longitudinal design, we could control age effects on inter- and intra-individual differences in personality. Using this approach, we extracted a third factor, which was defined by the variables Aggression, Anger, Type A Behavior, Extraversion, and Rule Breaking Behavior. This factor resembles Gray's Fight Flight System and Zuckerman's Aggressive-Hostility factor, and is labeled Aggressive Emotionality in this study. The remainder of this thesis addressed the genetics of three of the components of the Aggressive Emotionality factor, namely Type A Behavior, Anger, and Aggression. These studies provide the the first steps towards the study of the characteristics of this third factor, as a possible basic dimension of personality.

In chapter 4 the genetic and environmental influences of Type A Behavior (TABP) were studied using an extended twin design (twins and their parents) in an attempt to identify the presence of non-additive genetic effects and sibling interaction effects. The results showed that 45% of the variance in TABP is due to genetic factors, (28% additive and 17% non-additive). The remaining 55% of the variance is attributable to environmental factors not shared by the members of the same family. Competitive sibling interaction effects were not significant, and there was no evidence of sex differences either in variances or means. Chapter 5 addressed the same issues as chapter 4 with respect to the trait anger, by incorporating a repeated measures design that increased the power to detect replicable effects. Results showed that the sources of variance differ across sexes. In males, 23% of the variance is due to additive genetic effects, and 26% to dominance genetic effects. In females, 34% of the variance is due to additive genetic effects, and no dominance effects are found. There was no consistent evidence to confirm the presence of competitive sibling interaction as an alternative explanation for the low correlations in DZ males. Finally, in chapter 6, we used the analysis of individual growth curves to study individual changes in aggression, and the genetics of aggression at age 18, in a sample of twins from 11 to 40 years old who participated in four survey studies between 1991 and 2000. The results showed that mean scores on aggressive behavior decrease during adolescence. By the

age 18, aggressive behavior stabilizes. The genetic analysis showed that most of the variance on the slope between 11 and 18 years old was explained by additive genetic effects. The results also showed that 26% of the variance on aggression at the age 18 is attributable to additive genetic effects (A), 40% to non-additive genetic effects (D), and 34% to the non-shared environment (E). There were no sex differences in the amount of variance explained by A, D and E.

In summary, this thesis, in conjunction with other evidence, shows that Aggressive Emotionality should be considered a basic dimension of personality, which is factorially distinct from the other basic dimensions considered in this study. Variability in this dimension is attributable to non-additive genetic factors in early adulthood. The personality traits that form this dimension have been consistently found to be related with several social phenomena such as delinquent behavior or alcohol dependence, as well as with cardiovascular health problems. Behavior genetic studies addressing the contribution of genetic and environmental factors of the phenotypic variance constitute only a first step towards the understanding of the process through which genetic and environmental factors act and interact to give rise to variation in a specific phenotype (Kendler, 2005). A more detailed understanding of this process will require both molecular genetic studies, and a more thorough study of specific environmental effects.

SAMENVATTING (DUTCH SUMMARY)

Dimensies in persoonlijkheid: een genetische benadering

Bezien in het licht van de doelstellingen en de principes van de biologische psychologie (Zuckerman, 1991), moet binnen de persoonlijkheidspsychologie een algemeen geaccepteerd paradigma, analoog aan dat wat het onderzoek naar cognitieve vaardigheden karakteriseert (Carroll, 1993), nog geformuleerd worden. Er zijn twee algemeen geaccepteerde persoonlijkheidsdimensies, namelijk Neuroticisme (N) en Extraversie (E), die worden gevonden in de meeste persoonlijkheidstheorieën. Daarnaast bestaat er weinig consensus en grote variabiliteit met betrekking tot het aantal en de aard van de basisdimensies van persoonlijkheid, die nodig zijn om individuele verschillen in menselijke gedragingen te verklaren.

Dit proefschrift is een bijdrage aan de identificatie van de basisdimensies van persoonlijkheid vanuit een psychobiologisch perspectief (Eysenck, 1992a; Zuckerman, 1992). Hiervoor is gebruik gemaakt van persoonlijkheidsdata uit het lopende longitudinale onderzoek van het Nederlands Tweelingen Register (Boomsma et al., 2002). Gegevens van bijna twintig duizend individuen uit tweeling families zijn

verzameld met zes vragenlijstmetingen tussen 1991 en 2002. Vanwege de grote steekproef, de samenstelling van de gemeten fenotypes en het longitudinale karakter van dit onderzoek vormen de data een waardevolle bron voor onderzoek naar de structuur van persoonlijkheid en oorzaken van verschillen in persoonlijkheid.

Hoofdstuk 1 geeft een inleiding in de gedragsgenetica, de methoden van tweelingen familieonderzoek en vat de algemene bevindingen betreffende de genetische en omgevingsinvloeden op individuele verschillen in persoonlijkheid samen.

Hoofdstuk 2 is een simulatie studie naar de mogelijke bias in de standaardfouten en de chi-kwadraat waarden wanneer geclusterde data (als gevolg van afhankelijkheid tussen familieleden) behandeld worden als onafhankelijk. Daarnaast wordt in hoofdstuk 2 de efficiëntie van een schatter onderzocht die corrigeert voor deze afhankelijkheid. De resultaten laten zien dat wanneer familie clustering wordt genegeerd in fenotypische analyses en wanneer Maximum Likelihood schattingen worden gebruikt, er een tendens is dat de chi-kwadraat waarde wordt overschat en de standaardfouten van de parameters worden onderschat. De bias neemt toe met familiegelijkenis, veroorzaakt door erfelijkheid of gedeelde omgeving. De oorzaak van familiegelijkenis – erfelijkheid (h^2) en/of gedeelde omgeving (c^2)- interacteert met de samenstelling van de steekproef. In de afwezigheid van c^2, laten steekproeven met tweelingen, ouders en partners de minste bias zien, terwijl in de aanwezigheid van c^2 steekproeven met alleen tweelingen de minste bias laten zien. In alle onderzochte condities bleef de bias onder de 15%. Het gebruik van de ‘complex’ optie in Mplus (cluster gecorrigeerde Robust Maximum Likelihood schatting) zorgt voor een afname in de bias naar niveaus vergelijkbaar met de situatie waarin alleen onafhankelijke data worden gebruikt. Met het gebruik van de robuuste schattingen wordt de bias als gevolg van familie afhankelijkheid dus praktisch verwaarloosbaar onder alle condities van afhankelijkheid. Op basis van hoofdstuk 2 kan geconcludeerd worden dat de bias door afhankelijkheid in familie data geen serieus obstakel vormt voor fenotypische data analyse. Daarom is de Mplus Robust Maximum Likelihood schatting toegepast in volgende hoofdstukken.

Hoofdstuk 3 begint met een bespreking van de leidende psychobiologische theorieën van persoonlijkheid, namelijk de theorieën van Eysenck, Gray, Cloninger en Zuckerman, en bevat de resultaten van een empirische studie naar de structuur van persoonlijkheid. Het doel van deze studie was om de aard van derde factor van persoonlijkheid te identificeren, naast Extraversie en Neuroticisme. Omdat dit onderzoek gebruik maakte van longitudinale data, was het nodig om te corrigeren voor leeftijdseffecten op inter- en intraindividuele verschillen in persoonlijkheid. Deze analyse heeft geleid tot de extractie van een derde factor, die bestaat uit de variabelen

Agressie, Boosheid, Type A gedrag, Extraversie en Norm overschrijdend gedrag. Deze factor lijkt op Gray's "Fight Flight" systeem en Zuckermans Agressieve Hostiliteitsfactor en wordt in deze studie Agressieve Emotionaliteit genoemd. De overige hoofdstukken in dit proefschrift gaan over de erfelijkheid van de drie componenten van de Agressieve Hostiliteitsfactor, namelijk Type A gedrag, Boosheid en Agressie. Deze studies vormen het begin van het onderzoek naar de kenmerken van deze derde factor als een mogelijke basisdimensie van persoonlijkheid.

In hoofdstuk 4 zijn de genetische en omgevingsinvloeden op Type A gedrag (TABP) onderzocht met behulp van een "extended twin design" (tweelingen en hun ouders) in een poging om de aanwezigheid van niet-additieve genetische effecten en sociale interactie tussen tweelingbroers en zusters te identificeren. De resultaten laten zien dat 45% van de variatie in TABP toe te schrijven is aan genetische factoren (28% is additief en 17% niet-additief). De overige 55% van de variatie is toe te schrijven aan omgevingsfactoren die niet gedeeld worden door leden van dezelfde familie. Competitieve interactie tussen tweelingen waren niet significant en er waren geen aanwijzingen voor sekse verschillen in varianties of gemiddelden.

Hoofdstuk 5 stelt dezelfde vragen als in hoofdstuk 4 met betrekking tot Boosheid. Door het gebruik van een herhaalde metingen design nam de statistische power om repliceerbare effecten te kunnen detecteren toe. De resultaten laten zien dat de oorzaken van individuele verschillen in Boosheid verschillend zijn voor de beide seksen. Bij mannen wordt 23% van de variatie verklaard door additieve genetische effecten en 26% door genetische dominantie effecten. Voor vrouwen wordt gevonden dat 34% van de variatie verklaard wordt door additieve genetische effecten en er worden geen genetische dominantie effecten gevonden. Er was geen sprake van competitieve interactie binnen tweelingparen.

Tot slot is in hoofdstuk 6 individuele groei curve analyse gebruikt om zowel de individuele veranderingen in agressie te bestuderen als de erfelijkheid van agressie op 18-jarige leeftijd. Agressie gegevens waren beschikbaar in een steekproef van tweelingen tussen de 11 en 40 jaar oud die in vier achtereenvolgende onderzoeken tussen 1991 en 2000 hebben meegedaan. De resultaten laten zien dat de gemiddelde scores op agressief gedrag afnemen tijdens de adolescentie. Op 18-jarige leeftijd stabiliseert agressief gedrag. De genetische analyse laat zien dat het merendeel van de variatie in de verandering van agressie tussen 11 en 18 jaar verklaard werd door additieve genetische factoren. De resultaten tonen ook dat 26% van de variantie in agressie op 18-jarige leeftijd verklaard wordt door additieve genetische factoren (A), 40% door niet-additieve genetische factoren (D) en 34% door niet-gedeelde omgeving

(E). Er waren geen sekse verschillen in de hoeveelheid verklaarde variatie door A, D en E.

Samengevat laten de resultaten van dit proefschrift, in combinatie met eerder onderzoek, zien dat Agressieve Emotionaliteit als een basisdimensie van persoonlijkheid moet worden gezien. Deze dimensie verschilt van andere basisdimensies die in dit proefschrift besproken zijn. Variabiliteit in deze dimensie wordt beïnvloed door niet-additieve genetische factoren in de jonge volwassenheid. De persoonlijkheidstrekken die deze dimensie vormen zijn herhaaldelijk gerelateerd aan zowel verschillende maatschappelijke verschijnselen zoals delinquent gedrag of alcoholverslaving, als ook aan bijvoorbeeld cardiovasculaire gezondheidsproblemen. Gedragsgenetische studies die de contributie van genetische en omgevingsfactoren op fenotypische variatie in kaart brengen vormen slechts een eerste stap naar het begrip van het proces hoe genetische en omgevingfactoren acteren en interacteren om vervolgens te leiden tot variatie in een bepaald fenotype (Kendler, 2005). Voor een meer gedetailleerd begrip van dit proces zijn zowel moleculaire genetische studies als een meer gedegen onderzoek naar specifieke omgevingsinvloeden noodzakelijk.

REFERENCES

Achenbach, T. M. (1990). *The Young Adult Self Report*. Burlington, VT: University of Vermont, Department of Psychiatry.

Achenbach, T. M. (1997). *Manual for the young adult self report and young adult behavior checklist*. Burlington, VT: University of Vermont, Department of psychiatry.

Achenbach, T. M., Howell, C. T., CcConaughy, S. H., & Stanger, C. (1995). Six-Year Predictors of Problems in a National Sample: III. Transitions to Young Adult Syndromes. *Journal of the American Academy of Child and Adolescent Psychiatry, 31,* 658-669.

Akaike, H. (1987). Factor-Analysis and Aic. *Psychometrika, 52,* 317-332.

Allik, J., Laidra, K., Realo, A., & Pullman, H. (2004). Personality development from 12 to 18 years of age: changes in mean levels and structure of traits. *European Journal of Personality, 18,* 445-462.

Aluja, A., Garcia, O., & Garcia, L. F. (2002). A comparative study of Zuckerman's three structural models for personality through the NEO-PI-R, ZKPQ-III-R, EPQ-RS and Goldberg's 50-bipolar adjectives. *Personality and Individual Differences, 33,* 713-725.

Aluja, A., Garcia, O., & Garcia, L. F. (2004). Replicability of the three, four and five Zuckerman's personality super-factors: exploratory and confirmatory factor analysis of the EPQ-RS, ZKPQ and NEO-PI-R. *Personality and Individual Differences, 36,* 1093-1108.

Appels, A. & Jenkins, C. D. (1985). *JAS: De Jenkins Activity Survey (Dutch adaptation of Jenkins activity survey*. New York: Swets & Zeitlinger b.v.

Appels, A., Jenkins, C. D., & Rosenman, R. H. (1982). Coronary prone behavior in the Netherlands: a cross-Cultural Validation Study. *Journal of Behavioral Medicine, 5,* 83-90.

Atchison, M. & Condon, J. (1993). Hostility and anger measures in coronary heart disease. *Australian & New Zeland Journal of Psychiatry, 27,* 436-442.

Azzelini, A. (1996). *Statistical inference based on the likelihood*. London: Chapman Hill.

Barbour, K. A., Eckhardt, C. I., Davison, G. C., & Kassinove, H. (1998). The experience and expression of anger in maritally violent and maritally discordant-nonviolent men. *Behavior Therapy, 29,* 173-191.

Bartels, M., Hudziak, J. J., van den Oord, E. J. C. G., van Beijsterveldt, C. E. M., Rietveld, M. J. H., & Boomsma, D. I. (2003). Co-occurrence of aggressive behavior and rule-breaking behavior at age 12: Multi-rater analyses. *Behavior Genetics, 33,* 607-621.

Bazana, P. G. & Stelmack, R. M. (2004). Stability of personality across the life span: a Meta-Analysis. In R.M.Stelmack (Ed.), *On the psychobiology of personality* (pp. 113-144). Elsevier.

Beck, A. T., Ward, C. H., Mendelson, M. J., Mock, J., & Erbaugh, J. (1961). An Inventory for Measuring Depression. *Archives of General Psychiatry, 4,* 561-571.

Benjamin, J., Li, L., Patterson, C., Greenberg, B. D., Murphy, D. L., & Hamer, D. H. (1996). Pupulation and familial association between the D4 dopamine receptor gene and measures of novelty seeking. *Nature Genetics, 12,* 81-84.

Bishop, G. D. & Quah, S. H. (1998). Reliability and validity of measures of anger/hostility in Singapore: Cook & Medley Ho Scale, STAXI, and BUSS-Durkee Hostility Inventory. *Personality and Individual Differences, 24,* 867-878.

Bollen, K. A. (1989). *Structural equations with latent variables*. NY: Willey.

Boomsma, D. I. (1998). Twin registers in Europe: an overview. *Twin Research, 1,* 34-51.

Boomsma, D. I., de Geus, E. J. C., van Baal, C. M., & Koopmans, J. R. (1999). A religous upbringing reduces the influence of genetic factors on disinhibition: evidence for interaction between genotype and environment on personality. *Twin Research, 2,* 115-125.

Boomsma, D. I., Vink, J. M., Van Beijsterveldt, T. C., de Geus.E.J.C., Beem, L., Mulder, E. J. et al. (2002). Netherlands twin register: a focus on longitudinal research. *Twin Research, 5,* 401-406.

Bortner, R. W., Rosenman, R. H., & Friedman, M. (1970). Familial similarity in pattern A behavior. *Journal of Chronical Disease, 23,* 39-43.

Bouchard, T. J. & Loehlin, J. (2001). Genes, evolution, and Personality. *Behavior Genetics, 31,* 243-273.

Bouchard, T. J. & McGue, M. (2003). Genetic and environmental influences on human psychological Differences. *Journal of Neurobiology, 54,* 4-45.

Bouchard, T. J. J. (1997). The genetics of Personality. In K.Blum & E. P. Noble (Eds.), *Handbook of psychiatric genetics* (pp. 273-296). Boca Ratón, F.L.: CRC Press.

Brendgen, M., Dionne, G., Girard, A., Boivin, M., Vitaro, F., & Perusse, D. (2005). Examining genetic and environmental effects on social aggression: A study of 6-year-old twins. *Child Development, 76,* 930-946.

Brown, A. S., Schaefer, C. A., Wyatt, R. J., Begg, M. D., Goetz, R., Bresnahan, M. A. et al. (2002). Paternal age and risk of schizophrenia in adult offspring. *American Journal of Psychiatry, 159,* 1528-1533.

Busjahn, A. (2002). Twin registers across the globe: What's out there in 2002? *Twin Research, 5,* V-VI.

Carmelli, D., Rosenman, R., Chesney, M., Fabsitz, R., Lee, M., & Borhani, N. (1988). Genetic heritability and shared environmental influences of type A measures in the NHLBI twin study. *American Journal of Epidemiology, 127,* 1041-1052.

Carrol, J. B. (1993). *Human Cognitive abilities. A survey of factor analytic studies*. New York: Cambridge University Press.

Caspi, A., McClay, J., Moffit, T., Mill, J., Martin, J., Craig, I. W. et al. (2002). Role of Genotype in the Cycle of Violence in Maltreated Children. *Science, 297,* 851-854.

Caspi, A. & Roberts, B. (2001). Personality Development Across the life course: The Argument for Change and Continuity. *Psychological Inquiry, 12,* 49-112.

Caspi, A., Sugden, K., Moffitt, T. E., Taylor, A., Craig, I. W., Harrington, H. et al. (2003). Influence of life stress on depression: Moderation by a polymorphism in the 5-HTT gene. *Science, 301,* 386-389.

Cattel, R. B. (1957). *Personality and motivation structure and measurement.* NY: Harcourt, Brace & World.

Chang, P. P., Ford, D. E., Meoni, L. A., Wang, N. Y., & Klag, M. J. (2002). Anger in young men and subsequent premature cardiovascular disease - The precursors study. *Archives of Internal Medicine, 162,* 901-906.

Church, A. T. & Burke, P. J. (1994). Exploratory and Confirmatory Tests of the Big 5 and Tellegens 3-Dimensional and 4-Dimensional Models. *Journal of Personality and Social Psychology, 66,* 93-114.

Cloninger, C. R. (1986). A unified biosocial theory of personality and its role in the development of anxiety states. *Psychiatric Developments, 3,* 167-226.

Cloninger, C. R., Svrakic, D. M., & Przybeck, T. R. (1993). A psychobiological model of temperament and character. *Archives of General Psychiatry, 50,* 975-990.

Coccaro, E. F., Bergeman, C., Kavoussi, R. J., & Seroczynsky, A. D. (1997). Heritability of Aggression and Irritability: A twin study of the Buss-Durkee Agression Scales in adult male subjetcs. *Biological Psychiatry, 41,* 273-284.

Costa, P. T. & McCrae, R. (1995). Primary Traits of Eysenck P-E-N System - 3-Factor and 5-Factor Solutions. *Journal of Personality and Social Psychology, 69,* 308-317.

Coventry, W. L. & Keller, M. C. (2005). Estimating the extent of parameter bias in the classical twin design: A comparison of parameter estimates from extended twin-family and classical twin designs. *Twin Research and Human Genetics, 8,* 214-223.

Crane, R. S. (1981). The role of anger, hostility and aggression in essential hypertension (Doctoral dissertation, University of South Florida, 1981). *Dissertation Abstracts Interantional, 42,* 2982B.

D'Souza, U. M., Kel, A., & Sluyter, F. (2003). From transcriptional regulation to aggressive behavior. *Behavior Genetics, 33,* 549-562.

Dalton, J. E., Blain, G. H., & Bezier, B. (1998). State-Trait Anger Expression Inventory scores of male sexual offenders. *International Journal of Offender Therapy & Comparative Criminology, 42,* 141-148.

de Boer, S. F., van der Vegt, B. J., & Koolhaas, J. M. (2003). Individual variation in aggression of feral rodent strains: A standard for the genetics of aggression and violence? *Behavior Genetics, 33,* 485-501.

De Moja, C. A. & Spielberger, C. D. (1997). Anger and drug addiction. *Psychological Reports, 81,* 152-154.

Dembroski, T. M., MacDougall, J. M., Costa, P. T., & Grandits, G. A. (1989). Componenetsof hostility as predictors of sudden death and myocardial infartion in the Multiple Risk Factor Intervention Trial. *Psychosomatic Medicine, 51,* 514-522.

Derks, E. M., Dolan, C. V., & Boomsma, D. I. (2006). A test of the Equal Environment Assumption (EEA) in multivariate twin studies. *Twin Research and Human Genetics (In Press).*

Diaz, A. & Pickering, A. D. (1993). The Relationship Between Gray and Eysenck Personality Spaces. *Personality and Individual Differences, 15,* 297-305.

DiLalla, L. F. (2002). Behavior genetics of aggression in children: Review anf future directions. *Developmental Review, 22,* 593-622.

Dolan, C. V., Molenaar, P. C. M., & Boomsma, D. I. (1992). Decomposition of Multivariate phenotypic means in multigroup genetic covariance structure analysis. *Behavior Genetics, 22,* 319-335.

Draycott, S. G. & Kline, P. (1995). The Big-3 Or the Big-5 - the Epq-R Vs the Neo-Pi - A Research Note, Replication and Elaboration. *Personality and Individual Differences, 18,* 801-804.

Duffy, D. L., Manicavasagar, V., O'Connell, D., Silove, D., Tennant, C., & Langelludecke, P. (1994). Type A Personality in Australian Twins. *Behavior Genetics, 24,* 469-475.

Eaker, E. D., Sullivan, L. M., Kelly-Hayes, M., D'Agostino, R. B., & Benjamin, E. J. (2004). Anger and hostility predict the development of atrial fibrillation in men in the Framingham Offspring Study. *Circulation, 109,* 1267-1271.

Eaves, L. J. (1976). A model for sibling effects in man. *Heredity, 36,* 205-214.

Eaves, L. J. (1988). Dominance Alone Is Not Enough. *Behavior Genetics, 18,* 27-33.

Eaves, L. J. & Carbonneau, R. (1998). Recovering components of variance from differential ratings of behavior and environment in pairs of relatives. *Developmental Psychology, 34,* 125-129.

Eaves, L. J., Eysenck, H. J., & Martin, N. G. (1989). *Genes, culture and personality*. New York: Academic Press.

Eaves, L. J., Foley, D., & Silberg, D. (2003). Has the equal environments assumption been tested in twin studies? *Twin Research, 6,* 486-489.

Eaves, L. J., Heath, A., Martin, N. G., Maes, H. H. M., Neale, M., Kendler, K. S. et al. (1999). Comparing the biological and cultural inheritance of personality and social attitudes in the Virginia 30000 study of twins and their relatives. *Twin Research, 2,* 62-80.

Eaves, L. J., Heath, A., Neale, M. C., Hewitt, J. K., & Martin, N. G. (1998). Sex differences and non-additivity in the effects of genes on personality. *Twin Research, 1,* 131-137.

Ebstein, R. P., Benjamin, J., & Belmaker, R. H. (2002). Behavioral genetics, genoimcs and personality. In R.Plomin, J. DeFries, I. W. Craig, & P. McGuffin (Eds.), *Behavior Genetics in the Postgenomic Era* (pp. 365-388). Washington, D.C.: American Psychological Association.

Eckhardt, C. I., Norlander, B., & Deffenbacher, J. (2004). The assessment of anger and hostility: a critical review. *Aggression and Violent Behavior, 9,* 17-43.

Edwards, K. L., Austin, M. A., Newman, B., Mayer, E., & Selby, J. V. (1994). Multivariate-Analysis of the Insulin-Resistance Syndrome (Irs) in Women. *Circulation, 89,* 934.

Eley, T. C., Bolton, D., O'Connor, T. G., Perrin, S., Smith, P., & Plomin, R. (2003). A twin study of anxiety-related behaviours in pre-school children. *Journal of Child Psychology and Psychiatry, 44,* 945-960.

Engebretson, T. O. & Matthews, K. A. (1989). Relations between anger expression and cardiovascular reactivity: Reconciling inconsistent findings through a

matching hypothesis. *Journal of Personality and Social Psychology, 57,* 513-521.

Eysenck, H. J. (1982). *Personality, genetics and behavior*. New York: Praeger Publishers.

Eysenck, H. J. (1991). Dimensions of personality: 16, 5 or 3? -Criteria for a taxonomic paradigm. *Personality and Individual Differences, 12,* 773-790.

Eysenck, H. J. (1992a). Four ways five factors are not basic. *Personality and Individual Differences, 13,* 667-673.

Eysenck, H. J. (1992b). The definition and measurement of psychoticism. *Personality and Individual Differences, 13,* 757-786.

Eysenck, H. J. (1997). Personality and experimental psychology: The unification of psychology and the possibility of a paradigm. *Journal of Personality and Social Psychology, 73,* 1224-1237.

Eysenck, H. J. & Eysenck, M. W. (1985). *Personality and Individual differences. A natural science approach*. New York: Plenum Press.

Eysenck, H. J. & Fulker, D. W. (1983). The components of Type A behavior and its genetic determinants. *Personality and Individual Differences, 4,* 499-505.

Falconer, D. S. (1989). *Introduction to quantitative genetics*. (3rd ed.) Harlow: Longman: Cientifical & Technical.

Fassino, S., Daga, G. A., & Piero, A. (2001). Anger and personality in eating disorders. *Journal of Psychosomatic Research, 51,* 757-764.

Feij, J. A., Dekker, P. H., Koopmans, J. R., & Boomsma, D. I. (1997). Nieuwe Normen en Stabiliteitsgegevens voor Spanningsbehoeftelijst (SBL). *Nederlands Tijdschrift voor de psychologie, 52,* 131-134.

Feij, J. A. & Van Zuilen, R. W. (1984). *Handleiding bij de sSpanningsbehoeftelijst (SBL)*. Lisse: Swets and Zeitlinger.

Feldker, D. E. M., de Kloet, E. R., Kruk, M. R., & Datson, N. A. (2003). Large-scale gene expression profiling of discrete brain regions: Potential, limitations, and application in genetics of aggressive behavior. *Behavior Genetics, 33,* 537-548.

Ferdinand, R. F., Verhulst, F. C., & Wiznitzer, M. (1995). Continuity and Change of Self-Reported Problem Behaviors from Adolescence Into Young Adulthood. *Journal of the American Academy of Child and Adolescent Psychiatry, 34,* 680-690.

Finkel, D. & McGue, M. (1997). Sex differences and nonadditivity in heritability of Multidimiensional Personality Questionnaire Scales. *Journal of Personality and Social Psychology, 72,* 929-938.

Finkel, D., Pedersen, N., Plomin, R., & McClearn, G. (1998). Longitudinal and corss-sectional twin data on cognitive abilities in adulthood: the swedich adoption/twin study of aging. *Developmental Psychology, 34,* 1400-1413.

Fisher, R. A. (1958). *The genetical theory of natural selection*. (2nd revised ed.) New York: Dover Publications Inc.

Foley, D., Eaves, L. J., Wormley, B., Silberg, J. L., Maes, H. H. M., Kuhn, J. et al. (2004). Childhood adversity, Monoamine Osicase A genotype and risk for conduct disorder. *Archives of General Psychiatry, 61,* 738-744.

Friedman, M. & Rosenman, R. (1974). *Type A Behavior and your heart*. New York: Knopf.

Garcia, O., Aluja, A., & Garcia, L. F. (2004). Psychometric properties of Goldberg's 50 personality markers for the big five model - A study in the Spanish language. *European Journal of Psychological Assessment, 20,* 310-319.

Gillespie, N. A., Cloninger, C. R., Heath, A. C., & Martin, N. G. (2003). The genetic and environmental relationship between Cloninger's dimensions of temperament and character. *Personality and Individual Differences, 35,* 1931-1946.

Gray, J. A. (1987). *The psychology of fear and stress*. (2nd Edition ed.) Cambridge: Cambridge University Press.

Harris, J. R. (1995). Where is the child's environment? A group socialization theory of development. *Psychological Review, 102,* 458-489.

Harris, J. R. (1998). *The Nurture Assumption*. New York: Free Press.

Hay, D. A. (1980). Genetics in the Analysis of Behavior. *Neuroscience and Biobehavioral Reviews, 4,* 489-508.

Heath, A. C., Cloninger, C. R., & Martin, N. G. (1994). Testing a model for the genetic structure of personality: a comparison of the personality systems of Cloninger and Eysenck. *Journal of Personality and Social Psychology, 66,* 762-775.

Heath, A. C., Eaves, L. J., & Martin, N. G. (1989). The Genetic-Structure of Personality .3. Multivariate Genetic Item Analysis of the Epq Scales. *Personality and Individual Differences, 10,* 877-888.

Heath, A. C., Jardine, R., Eaves, L. J., & Martin, N. G. (1988). The Genetic-Structure of Personality .1. Phenotypic Factor Structure of the Epq in An Australian Sample. *Personality and Individual Differences, 9,* 59-67.

Herbst, J. H., Zonderman, A. B., Mccrae, R. R., & Costa, P. T. (2000). Do the dimensions of the temperament and character inventory map a simple genetic

architecture? Evidence from molecular genetics and factor analysis. *American Journal of Psychiatry, 157,* 1285-1290.

Hertzog, C. & Nesselroade, J. R. (2003). Assessing psychological change in adulthood: An overview of methodological issues. *Psychology and Aging, 18,* 639-657.

Honess, P. E. & Marin, C. M. (2006). Behavioural and physiological aspects of stress and aggression in nonhuman primates. *Neuroscience and Biobehavioral Reviews, 30,* 390-412.

Horwitz, A. V., Videon, T. M., Schmitz, M. F., & Davis, D. (2003). Rethinking twins and environments: possible social sources for assumed genetic influences in twin similarity. *Journal of Health and Social Behavior, 44,* 111-129.

Houston, B. K. (1994). Anger, Hostility and psychophysiiological reactivity. In A.W.Siegman & T. W. Smith (Eds.), *Anger, Hostility and the Heart* (pp. 97-116). NJ: IEA.

Hox, J. J. & Maas, C. J. (2001). The accuracy of multilevel structural equation modeling with pseudobalanced groups and small samples. *Structural Equation Modeling, 8,* 157-174.

Hudziak, J. J., van Beijsterveldt, C. E. M., Bartels, M., Rietveld, M. J. H., Rettew, D. C., Derks, E. M. et al. (2003). Individual differences in aggression: Genetic analyses by age, gender, and informant in 3-, 7-, and 10-year-old Dutch twins. *Behavior Genetics, 33,* 575-589.

Ihaka, R. & Gentleman, R. (1996). R: a language for data analysis and graphics. *Journal of Computational and Graphical Statistics, 5,* 299-314.

Jacob, C. P., Muller, J., Schmidt, M., Hohenberger, K., Gutknecht, L., Reif, A. et al. (2005). Cluster B personality disorders are associated with allelic variation of monoamine oxidase a activity. *Neuropsychopharmacology, 30,* 1711-1718.

Jonnal, A. H., Gardner, C. O., Prescott, C. A., & Kendler, K. S. (2000). Obsessive and compulsive symptoms in a general population sample of female twins. *American Journal of Medical Genetics, 96,* 791-796.

Joreskog, K. (1993). Testing structural equation models. In K.A.Bollen & S. J. Long (Eds.), *Testing Structural equation models* (pp. 294-317). Sage Publications.

Jöreskog, K. (1993). Testing Structural Equation Models. In K.A.Bollen & S. J. Long (Eds.), *Testing Structural Equation Models* (pp. 294-317). Sage Publications.

Julkunen, J., Salonen, J. T., Kaplan, G. A., & Chesney, M. A. (1994). HOstility and the progression of carotid artheroscherosis. *Psychosomatic Medicine, 56,* 519-525.

Kawachi, I., Sparrow, D., Kubzansky, L. D., Spiro, A., Vokonas, P. S., & Weiss, S. T. (1998). Prospective study of a self-report type a scale and risk of coronary heart disease - Test of the MMPI-2 type a scale. *Circulation, 98,* 405-412.

Kawachi, I., Sparrow, D., Spiro, A., Vokonas, P., & Weiss, S. T. (1996). A prospective study of anger and coronary heart disease - The normative aging study. *Circulation, 94,* 2090-2095.

Keller, M. C., Coventry, W. L., Heath, A. C., & Martin, N. G. (2005). Widespread evidence for non-additive genetic variation in Cloninger's and Eysenck's personality dimensions using a twin plus sibling design. *Behavior Genetics, 35,* 707-721.

Kendler, K. S. (2005). Psychiatric genetics: A methodologic critique. *American Journal of Psychiatry, 162,* 3-11.

Kirk, K. M., Hickie, I. B., & Martin, N. G. (1999). Fatigue as related to anxiety and depression in a community-based sample of twins aged over 50. *Social Psychiatry and Psychiatric Epidemiology, 34,* 85-90.

Kokko, K. & Pulkkinen, L. (2005). Stability of aggressive behavior from childhood to middle age in women and men. *Aggressive Behavior, 31,* 485-497.

Koopmans, J. R., Slutske, W. S., Heath, A., Neale, M. C., & Boomsma, D. I. (1999). The genetics of smoking initiation and quantity smoked in Dutch adolescents and young adult twins. *Behavior Genetics, 29,* 383-393.

Koskenvuo, M., Kaprio, J., Langinvainio, H., Romo, M., & Sarna, S. (1980). Coronary-Prone Behavior in Adult Like-Sexed Twins - An Epidemiological-Study. *Acta Geneticae Medicae et Gemellologiae, 29,* 70.

Laplante, B. & Hebert, B. P. (2001). An introduction to the use of linear models with correlated data. *Canadian Studies in Population, 28,* 287-311.

Lasko, N. B., Gurvits, T. V., Kuhne, A. A., Orr, S. P., & Pittman, R. K. (1994). Aggression and its correlates in Vietnam veterans with and without chronic posttraumatic stress disorder. *Comprenhensive Psychiatry, 35,* 373-381.

Lesch, K. P. (2002). Neuroticism and Serotonin: A developmental Genetic Perspective. In R.Plomin, J. DeFries, I. W. Craig, & P. McGuffin (Eds.), *Behavior Genetics in the Postgenomic Era* (pp. 389-423). Washington, D.C.: American Psychological Association.

Lesch, K. P., Gross, J., Franzek, E., Wolozin, B. L., Riederer, P., & Murphy, D. L. (1995). Primary Structure of the Serotonin Transporter in Unipolar Depression and Bipolar Disorder. *Biological Psychiatry, 37,* 215-223.

Ligthart, L., Bartels, M., Hoekstra, R. A., Hudziak, J. J., & Boomsma, D. I. (2005). Genetic contributions to subtypes of aggression. *Twin Research and Human Genetics, 8,* 483-491.

Linden, W., Stossel, C., & Maurice, J. (1996). Psychosocial interventions for patients with coronary artery disease - A meta-analysis. *Archives of Internal Medicine, 156,* 745-752.

Loeber, R. & Hay, D. (1997). Key issues in the development of aggression and violence from childhood to early adulthood. *Annual Review of Psychology, 48,* 371-410.

Loehlin, J. (1986). Heredity, Environment, and the Thurstone Temperament Schedule. *Behavior Genetics, 16,* 61-73.

Loehlin, J. (1992). *Genes, evironment and personality development*. Newbury Park: Sage.

Loehlin, J. (2004). *Latent variable models*. (4 ed.) Mahwah, New Jersey: Lawrence Erlbaum Associates.

Loehlin, J. & Nichols, R. C. (1976). *Heredity, Environment, and Personality*. (1 ed.) Austin and London: University of Texas Press.

Losoya, S. H., Callor, S., Rowe, D., & Golsmith, H. H. (1997). Origins of familial similarity in parenting: a study of twins and adoptive siblings. *Developmental Psychology, 33,* 1012-1023.

Lykken, D., McGue, M., Bouchard, T. J., & Tellegen, A. (1990). Does contact lead to similarity or similarity to contact? *Behavior Genetics, 20,* 547-561.

Lykken, D., McGue, M., Tellegen, A., & Bouchard, T. (1992). Emergenesis: genetic traits that may not rin in families. *American Psychologist, 47,* 1565-1577.

Maccoby, E. E. (2000). Parenting and its effects on children: On reading and misreading behavior genetics. *Annual Review of Psychology, 51,* 1-27.

Maccoby, E. E. & Martin, J. A. (1983). Socialization in the context of the family: Parent-child interaction. In P.H.Mussen & E. M. Hetherington (Eds.), *Handbook of child psychology: vol.4. Socialization, personality, and social development* (pp. 1-101). New York: Wiley.

Manuck, S. B., Flory, J. D., Ferrell, R. E., Dent, K. M., Mann, J. J., & Muldoon, M. F. (1999). Aggression and anger-related traits associated with a polymorphism of the tryptophan hydroxylase gene. *Biological Psychiatry, 45,* 603-614.

Manuck, S. B., Flory, J. D., Ferrell, R. E., Mann, J. J., & Muldoon, M. F. (2000). A regulatory polymorphism of the monoamine oxidase-A gene may be associated with variability in aggression, impulsivity, and central nervous system serotonergic responsivity. *Psychiatry Research, 95,* 9-23.

Manuck, S. B., Flory, J. D., Muldoon, M. F., & Ferrell, R. E. (2002). Central nervous system serotonergic responsivity and aggressive disposition in men. *Physiology and Behavior, 77,* 705-709.

Markon, K. E. & Krueger, R. F. (2004). An empirical comparison of information-theoretic selection criteria for multivariate behavior genetic models. *Behavior Genetics, 34,* 593-610.

Markovitz, J. H., Matthews, K. A., Wing, R. R., Kuller, L. H., & Meilahn, E. M. (1991). Psychological, biological, and health behavior predictors of blood pressure changes in middle-aged women. *Journal of Hypertension, 9,* 399-406.

Martin, N. G. (2002). Special issue: Twin registers as a Global Resource for Genetic Research. *Twin Research, 5*.

Mather, K. (1966). Variability and Selection. *Proceedings of the Royal Society Series B-Biological Sciences, 164,* 328-340.

Matthews, G. & Gilliland, K. (1999). The personality theories of H.J.Eysenck and J.A. Gray: a comparative review. *Personality and Individual Differences, 26,* 583-626.

Matthews, K. A. (1988). Coronary heart disease and Type A Behaviors: Update on and alternative to the Both-Kewley and Friedman (1987) Quantitative Review. *Psychological Bulletin, 104,* 373-380.

Matthews, K. A. & Jennings, J. R. (1984). Cardiovascular responses of boys exhibiting the type A behavior pattern. *Psychosomatic Medicine, 46,* 484-497.

Matthews, K. A. & Krantz, D. S. (1976). Resemblances of twins and their parents in pattern A behavior. *Psychosomatic Medicine, 38,* 140-144.

McArdle, J. J. (1988). Dynamic but structural equation modeling of repeated measures data. In J.R.Nesselroade & R. B. Cattel (Eds.), *Handbook of multivariate experimental psychology. Perspectives on individual differences* (2nd ed., pp. 561-614). NY, US: Plenum Press.

McCaffery, J. M., Bleil, M., Pogue-Geile, M. F., Ferrell, R. E., & Manuck, S. B. (2003). Allelic variation in the serotonin transporter gene-linked polymorphic region (5-HTTLPR) and cardiovascular reactivity in young adult male and female twins of European-American descent. *Psychosomatic Medicine, 65,* 721-728.

McCrae, R. & Costa, P. (1997). Personality trait structure as a human universal. *American Psychologist, 52,* 509-516.

McCrae, R. & Terracciano, A. (2005). Universal features of personality traits from the observer's perspective: data from 50 cultures. *Journal of Personality and Social Psychology, 88,* 547-561.

McGue, M. (2002). Genetics and personality. In D.L.Rimoin, J. M. Connor, R. E. Pyeritz, & B. R. Korf (Eds.), *Emery and Rimoins's principles and practice of medical genetics* (pp. 2791-2800). London: Churchill Livingston.

McGue, M., Bacon, S., & Lykken, D. (1993). Personality stability and change in early adulthood: a behavioral genetic analysis. *Developmental Psychology, 29,* 96-109.

Mehta, P. D. & West, S. G. (2000). Putting the individual back into individual growth curves. *Psychological Methods, 5,* 23-43.

Meininger, J. C., Hayman, L. L., Coates, P. M., & Gallagher, P. (1988). Genetics or Environment? Type A behavior and cardiovascular risk factors in twin children. *Nursing Research, 37,* 341-346.

Mendes de Leon, C. F. (1992). Anger and impatience/irritability in patients of low socioeconomic status with acute coronary heart disease. *Journal of Behavioral Medicine, 15,* 273-284.

Miczek, K. A., Maxson, S. C., Fish, E. W., & Faccidomo, S. (2001). Aggressive behavioral phenotypes in mice. *Behavioural Brain Research, 125,* 167-181.

Middeldorp, C. M., Cath, D. C., Beem, A. L., Willemsen, G., & Boomsma, D. I. (2006). The interplay of life events and anxious depression, neuroticism and extraversion. *Unpublished work.*

Middeldorp, C. M., de Geus, E. J. C., Beem, A. L., Lakenberg, N., Hottenga, J. J., Slagboom, P. E. et al. (2006). Family based association analyses of the serotonin transporter gene polymorphism and neuroticism, anxiety, or depression. *Unpublished work.*

Moffit, T. (1993). Adolescent-limited and life-course-persistent antisocial behavior. A developmental taxonomy. *Psychological Review, 100,* 674-701.

Molenaar, P. C. M., Boomsma, D. I., & Dolan, C. V. (1993). A third source of developmental differences. *Behavior Genetics, 23,* 519-524.

Muthén, B. O. & Satorra, A. (1995). Complex sample data in structural equation modeling. *Sociological Methodology 1995, Vol 25, 25,* 267-316.

Muthén, L. K. & Muthén, B. O. (2005). *Mplus User's guide*. (Third ed.) Los Angeles, CA: Muthén & Muthén.

Neale, M., Boker, S. M., Xie, G., & Maes, H. H. M. (2003). *Mx: Statistical Modeling*. (6 ed.) VCU Box 900126, Richmond, VA 23298: Department of Psychiatry.

Neale, M. & Cardon, L. (1992). *Methodology for genetic studies of twins and families*. NATO.

Nesselroade, J. R. (2001). Intraindividual variability in development within and between individuals. *European Psychologist, 6,* 187-193.

Norman, W. T. (1963). Toward and adequate taxonomy of personality attributes: Replicated factor structure. *Journal of Abnormal and Social Psychology, 66,* 574-583.

Nothmann, J. (1999). The nature of anger in individuals with borderline personality disorder characteristics. *Dissertation Abstracts Interantional: Section B: The Sciences & Engineering, 60,* 0838.

Nunes, E. V., Frank, K. A., & Kornfeld, D. S. (1987). Psychologic Treatment for the Type-A Behavior Pattern and for Coronary Heart-Disease - A Metaanalysis of the Literature. *Psychosomatic Medicine, 49,* 159-173.

Obrist, P. A. (1976). The cardiovascular-behavioral interaction as it appears today. *Psychophisiology, 13,* 95-107.

Palmero, F., Diez, J. L., & Asensio, A. B. (2001). Type A behavior Pattern today: Relevance of the JAS-S factor to predict heart rate reactivity- Jenkin's Activity Survey. *Behavioral Medicine, 27,* 28-36.

Pastor, D. (1981). The quality of mother-infant attachment and its relationship to toddlers' initial sociability with peers. *Developmental Psychology, 17,* 326-335.

Pedersen, N., Lichtenstein, P., Plomin, R., DeFaire, U., McClearn, G. E., & Matthews, K. A. (1989). Genetic and environmental influences for Type A-like measures and related traits: A study of twins reared apart and twins reared together. *Psychosomatic Medicine, 51,* 428-440.

Peters, M. R. (1998). Anger as a predictor of aggressive behavior in an adolescent inpatient setting. *Dissertation Abstracts Interantional: Section B: The Sciences & Engineering, 59,* 0883.

Pickering, A. D. (2004). The neuropsychology of impulsive antisocial sensation seeking personality traits: from dopamine to hippocampal function. In R.M.Stelmack (Ed.), *On the Psychobiology of Personality* (pp. 543-476). Oxford, UK: Elsvier.

Plomin, R. (1990). *Nature and Nurture: an introduction to human behavioral genetics*. Pacific Grove, California: Brooks/Cole.

Plomin, R. & Bergeman, C. (1991). The nature of nurture: genetic influence on "environmental"measures. *Behavioral and Brain Sciences, 14,* 373-427.

Plomin, R., Chipuer, H., & Neiderhiser, J. M. (1994). Behavioral genetic evidence for the importance of nonshared environment. In E.M.Hetherington, D. Reiss, & R. Plomin (Eds.), *Separate social worlds of siblings: The impact of nonshared environment on development (* (pp. 1-31). Hillsdale, NJ: Erlbaum.

Plomin, R. & Daniels, D. (1987). Why are children in the same family so different from each other? *Behavioral and Brain Sciences, 10,* 1-16.

Plomin, R., DeFries, J., McClearn, G., & McGuffin, P. (2001). *Behavioral Genetics*. NY: Worth Publishers.

Posner, S. F., Baker, L., Heath, A., & Martin, N. G. (1996). Social contact,s ocial attitudes and twin similarity. *Behavior Genetics, 26,* 123-133.

Posthuma, D. & Boomsma, D. I. (2000). A note on the statistical power in extended twin designs. *Behavior Genetics, 30,* 147-158.

Pulkkinen, L. & Pitkanen, T. (1993). Continuities in Aggressive-Behavior from Childhood to Adulthood. *Aggressive Behavior, 19,* 249-263.

Purcell, S. (2002). Variance Components Models for Gene-Environment Interaction in twin analysis. *Twin Research, 5,* 554-571.

Purcell, S. & Sham, P. (2002). Variance components models for Gene-Environment interaction in quantitative trait locus linkage analysis. *Twin Research, 5,* 572-576.

Rahe, R. H., Hervig, L., & Rosenman, R. (1978). Heritability of Type A behavior. *Psychosomatic Medicine, 40,* 478-486.

Raykov, T. (1998). On the use of confirmatory factor analysis in personality research. *Personality and Individual Differences, 24,* 291-293.

Raynor, D. A., Pogue-Geile, M. F., Kamarck, T. W., McCaffery, J. M., & Manuck, S. B. (2002). Covariation of psychological characteristics associated with cardiovascular disease: Genetic and Environmental Influences. *Psychosomatic Medicine, 64,* 191-203.

Rebollo, I. & Boomsma, D. I. (2006a). Genetic and environmental influences on Type A Behavior Pattern: Evidence from twins and their parents in the Netherlands Twin Register. *Psychosomatic Medicine (In Press).*

Rebollo, I. & Boomsma, D. I. (2006b). Genetic analysis of anger: sex differences and competitive sibling interaction. *Behavior Genetics (In Press).*

Rebollo, I., de Moor, M. H., Dolan, C. V., & Boomsma, D. I. (2006). Phenotypic Factor Analysis of Family Data: Correction of the Bias due to Dependency. *Twin Research and Human Genetics (In Press).*

Rebollo, I., Dolan, C. V., & Boomsma, D. I. (2006). Basic dimensions of personality revisited on a sample of 17557 individuals from the Netherlands Twin Register: The third factor in psychobiological theories. *Unpublished work*.

Reed, T., Carmelli, D., & Rosenman, R. H. (1991). Effects of placentation on selected Type A behaviors in adult males in the National Heart, Lung and Bood Institute (NHLBI) Twin Study. *Behavior Genetics, 21,* 9-19.

Reiss, D., Neiderhiser, J. M., Hetherington, E. M., & Plomin, R. (2000). *The relationship code: deciphering genetic and social influences on adolescent development*. Cambridge, Massachusetts and London, England: Harvard University Press.

Reuter, M., Schmitz, A., Corr, P., & Hennig, J. (2005). Molecular genetics support Gray's personality theory: the interaction of COMT and DRD2 polymorphisms predicts the behaviorural approach system. *International Journal of Psychopharmacology, 8,* 1-12.

Rhee, S. H. & Waldman, I. D. (2002). Genetic and environmental influences on antisocial behavior: A meta-analysis of twin and adoption studies. *Psychological Bulletin, 128,* 490-529.

Rietveld, M., Posthuma, D., Dolan, C. V., & Boomsma, D. I. (2003). ADHD: Sibling Interaction or Dominance: An evaluation of Statistical power. *Behavior Genetics, 33,* 247-255.

Roberts, B. & Caspi, A. (2002). The cumulative continuity model of personality development. In Staudinger & Lindenberg (Ed.), *Understanding human development* (Kluwer academic publishers.

Roberts, B. & DelVecchio, W. F. (2000). The rank-order consistency of personality from childhood to old age: A quantitative review of longitudinal studies. *Psychological Bulletin, 126,* 3-25.

Robins, R. W., Fraley, R. C., Roberts, B. W., & Trzesniewski, K. H. (2001). A longitudinal study of personality change in young adulthood. *Journal of Personality, 69,* 617-640.

Rosenman, R., Friedman, M., & Strelau, J. (1964). A predictive study of coronary heart disease: The Western Collaborative Group Study. *Journal of the American Medical Association, 189,* 15-22.

Rowe, D. (1994). *The limits of family influence: genes experience and behavior*. NY: The Guilford Press.

Rowe, D. (1997). A Place at the Policy table?Behavior genetics and estimates of family environmental effects on IQ. *Intelligence, 24,* 133-158.

Rozanski, A., Blumenthal, J. A., & Kaplan, J. (1999). Impact of psychological factors on the pathogenesis of cardiovascular disease and implications for therapy. *Circulation, 99,* 2192-2217.

Rushton, J. P., Fulker, D. W., Neale, M. C., Nias, D. K. B., & Eysenck, H. J. (1986). Altruism and Aggression - the Heritability of Individual-Differences. *Journal of Personality and Social Psychology, 50,* 1192-1198.

Saggino, A. (2000). The Big Three or the Big Five? A replication study. *Personality and Individual Differences, 28,* 879-886.

Scarr, S. (1992). Developmental theories for the 1990s: Development and Individual Differences. *Child Development, 63,* 1-19.

Scarr, S. & Carter-Saltzman, L. (1979). Twin method: Defence of a critical assumption. *Behavior Genetics, 9,* 527-542.

Schaeffer, C. M., Petras, H., Ialongo, N., Poduska, J., & Kellam, S. (2003). Modeling Growth in Boys' Aggressive Behavior Across Elementary School: Links to Later Criminal Involvement, Conduct Disorder, and Antisocial Personality Disorder. *Developmental Psychology, 39,* 1020-1035.

Schafer, J. L. & Graham, J. W. (2002). Missing data: Our view of the state of the art. *Psychological Methods, 7,* 147-177.

Schneider, R. H., Egan, B. M., Johnson, E. H., Drobny, H., & Julius, S. (1996). Anger and anxiety in borderline hypertension. *Psychosomatic Medicine, 48,* 242-248.

Schwarz, G. (1978). Estimating the dimension of a model. *The Annals of Statistics, 6,* 461-464.

Shah, S. U., White, A., White, S., & Littler, W. A. (2004). Heart and mind: (1) relationship between cardiovascular and psychiatric conditions. *Postgraduate Medical Journal, 80,* 683-689.

Siegman, A. W. (1994a). Cardiovascular consecuences of expressing and repressing anger. In A.W.Siegman & T. W. Smith (Eds.), *Anger, Hostility and the Heart* (pp. 173-198). NJ: IEA.

Siegman, A. W. (1994b). Consequences of expressing and repressing anger. In A.W.Siegman & T. W. Smith (Eds.), *Anger, hostility and the heart* (pp. 173-198). Hillside, NJ: Erlbaum.

Siegman, A. W. (1994c). From Type A to Hostility to Anger: Reflections on the HIstory of Coronary-Prone Behavior. In A.W.Siegman & T. W. Smith (Eds.), *Anger, Hostility and the Heart* (pp. 1-22). NJ: IEA.

Siegman, A. W. & Dembroski, T. M. (1989). *In search of coronary prone behavior: Beyond Type A*. Hillside: NJ: LEA.

Siegman, A. W. & Smith, T. W. (1994). *Anger, Hostility and the Heart*. N.J. Lawrence Erlbaum Associates, Publishers.

Sims, J., Boomsma, D. I., Carroll, D., & Hewitt, J. K. (1991). Genetics of type A behavior in two European coutries: Evidence for sibling interaction. *Behavior Genetics, 21,* 513-528.

Slaton, B. J., Kern, R. M., & Curlette, W. L. (2000). Personality profiles of inmates. *Journal of Individual Psychology, 56,* 88-109.

Sloan, R. P., Bagiella, E., Shapiro, P. A., Kuhl, J. P., Chernikhova, D., Berg, J. et al. (2001). Hostility, gender, and cardiac autonomic control. *Psychosomatic Medicine, 63,* 434-440.

Sluyter, F., Keijser, J. N., Boomsma, D. I., van Doornen, L. J. P., Van der Oord, E. J., & Snieder, H. (2000). Genetics of testosterone and the aggression-hostility-anger (AHA) syhdrome: a study of middle -aged male twins. *Twin Research, 3,* 266-276.

Smith, T. W., Glazer, K., Ruiz, J. M., & Gallo, L. C. (2004). Hostility, anger, aggressiveness, and coronary heart disease: An interpersonal perspective on personality, emotion, and health. *Journal of Personality, 72,* 1217-1270.

Spielberger, C. D., Gorsuch, R. L., & Lushene, R. E. (1970). *STAI manual for the State-Trait Anxiety Inventory*. Palo Alto, CA: Consulting Psychologists Press.

Spielberger, C. D., Jacobs, G., Russell, J. S., & Crane, R. S. (1983). Assessment of anger: The state-trait anger scale. In J.N.Butcher & C. D. Spielberger (Eds.), *Advances in Personality Assessment, vol. 2* (Hillside, NJ: Erlbaum.

Stallings, M. C., Hewitt, J. K., Cloninger, C. R., Heath, A. C., & Eaves, L. J. (1996). Genetic and environmental structure of the Tridimensional Personality Questionnaire: three or four temperament dimensions? *Journal of Personality and Social Psychology, 70,* 127-140.

Steiger, J. H. (1990). Structural Model Evaluation and Modification - An Interval Estimation Approach. *Multivariate Behavioral Research, 25,* 173-180.

Stoel, R. D. & van den Wittenboer, G. (2003). Time dependence of growth parameters in latent growth curve models with time invariant covariates. *Methods of Psychological Research-Online, 19,* 21-41.

Stubbe, J. H., Posthuma, D., Boomsma, D. I., & de Geus, E. J. C. (2005). Heritability of life satisfaction in adults: a twin-family study. *Psychological Medicine, 35,* 1581-1588.

Sweda, M. G., Sines, J. O., Lauer, R. M., & Clarke, W. R. (1986). Familial aggregation of Type A behavior. *Journal of Behavioral Medicine, 9,* 23-32.

Tambs, K., Sundet, J. M., Eaves, L. J., & Berg, K. (1992). Genetic and environmental effects on type A scores in monozygotic twin families. *Behavior Genetics, 22,* 499-513.

Tellegen, A., Lykken, D., Bouchard, T., Wilcox, K., Segal, N., & Rich, S. (1988). Personality similarity in twins reared apart an together. *Journal of Personality and Social Psychology, 54,* 1031-1039.

Tomita, T., Aoyama, H., Kitamura, T., Sekiguchi, C., Murai, T., & Matsuda, T. (2000). Factor structure of psychobiological seven-factor model of personality: a model-revision. *Personality and Individual Differences, 29,* 709-727.

Tozzi, F., Aggen, S. H., Neale, B. M., Anderson, C. B., Mazzeo, S. E., Neale, M. C. et al. (2004). The structure of perfectionism: A twin study. *Behavior Genetics, 34,* 483-494.

Tschannen, T. A., Duckro, P. N., Margolis, R. B., & Tomazic, T. J. (1992). The relationship of anger, depression, and perceived disability among headache patients. *Headache, 32,* 501-503.

Turkheimer, E. & Waldron, M. (2000). Nonshared environment: A theoretical, methodological and quantitative review. *Psychological Bulletin, 126,* 78-108.

van Beijsterveldt, C. E. M., Bartels, M., Hudziak, J. J., & Boomsma, D. I. (2003). Causes of stability of aggression from early childhood to adolescence: A longitudinal genetic analysis in Dutch twins. *Behavior Genetics, 33,* 591-605.

Van den Oord, E. J., Boomsma, D. I., & Verhulst, F. C. (1994). A study of problem behaviors in 10-15 year old biologically related and unrelated international adoptees. *Behavior Genetics, 24,* 193-205.

van der Ploeg, H. M., Defares, P. B., & Spielberger, C. D. (1982). *In handleiding bij de Zelf-Analyse Vragenlijst Lisse*. Swets & Zeitlinger.

van der Sluis, S., Posthuma, D., Dolan, C. V., de Geus, E. J. C., Colom, R., & Boomsma, D. I. (2005). Sex differences on the dutch WAIS-IIIR. *Intelligence.*

van Prooijen, J. W. & van der Kloot, W. A. (2001). Confirmatory analysis of exploratively obtained factor structures. *Educational and Psychological Measurement, 61,* 777-792.

Verhulst, F. C. (1997). *Handleiding voor de Youth Self-Report.* Rotterdam: Afdeing Kinder- en Jeugdpsychiatrie, Sophia Kinderziekenhuis/Academisch Ziekenhuis Roterdam/ Erasmus Universiteit Rotterdam.

Vierikko, E., Pulkkinen, L., Kaprio, J., Viken, R., & Rose, R. (2003). Sex differences in genetic and environmental effects on aggression. *Aggressive Behavior, 29,* 55-68.

Vink, J. M., Willemsen, G., Stubbe, J. H., Middeldorp, C. M., Ligthart, R. S. L., Baas, K. et al. (2004). Estimating non-response bias in family studies: application to mental health and lifestyle. *European Journal of Personality, 19,* 623-630.

Wade, T. D., Wilkinson, J., & Ben Tovim, D. (2003). The genetic epidemiology of body attitudes, the attitudinal component of body image in women. *Psychological Medicine, 33,* 1395-1405.

Wilde, G. J. S. (1970). *Neurotische labiliteit gemeten volgens de vragenlijstmethode (The questionnaire method as a means of measureing neurotic instability)*. Amsterdam: Van Rossen.

Willemsen, G., Posthuma, D., & Boomsma, D. I. (2005). Environmental factors determine where the Dutch live: results form the Netherlands Twin Register. *Twin Research and Human Genetics, 8,* 312-317.

Williams, J. E., Paton, C. C., Siegler, I. C., Eigenbrodt, M. L., Nieto, F. J., & Tyroler, H. A. (2000). Anger proneness predicts coronary heart disease risk - Prospective analysis from the Atherosclerosis Risk in Communities (ARIC) study. *Circulation, 101,* 2034-2039.

Yan, L. J. L., Liu, K., Matthews, K. A., Daviglus, M. L., Ferguson, T. F., & Kiefe, C. I. (2003). Psychosocial factors and risk of hypertension - The Coronary Artery Risk Development in Young Adults (CARDIA) study. *Jama-Journal of the American Medical Association, 290,* 2138-2148.

Zuckerman, M. (1971). Dimensions of Sensations Seeking. *Journal Consulting Clinical Psychology, 36,* 45-52.

Zuckerman, M. (1991). *Psychobiology of personality*. NY: Cambridge University Press.

Zuckerman, M. (1992). What is a basic factor and which factors are basic? *Personality and Individual Differences, 13,* 675-682.

Zuckerman, M. & Cloninger, C. R. (1996). Relationships between Cloninger's, Zuckerman's, and Eysenck's dimensions of personality. *Personality and Individual Differences, 21,* 283-285.

Zuckerman, M., Kuhlman, D. M., & Camac, C. (1988). What Lies Beyond e and N - Factor-Analyses of Scales Believed to Measure Basic Dimensions of Personality. *Journal of Personality and Social Psychology, 54,* 96-107.

Zuckerman, M., Kuhlman, D. M., Joireman, J., Teta, P., & Kraft, M. (1993). A Comparison of 3 Structural Models for Personality - the Big 3, the Big 5, and the Alternative 5. *Journal of Personality and Social Psychology, 65,* 757-768.

Zuckerman, M., Kuhlman, D. M., Thornquist, M., & Kiers, H. (1991). 5 (Or 3) Robust Questionnaire Scale Factors of Personality Without Culture. *Personality and Individual Differences, 12,* 929-941.

Zyzanski, S. J., Wezesniewski, K., & Jenkins, C. D. (1979). Cross cultural validation of the coronary prone behavior pattern. *Social Science Medicine, 13A,* 405-412.

LIST OF PUBLICATIONS

PUBLISHED PAPERS

Colom, R., Abad, F.J., **Rebollo, I**., & Chun Shih, P. (2005). Memory span and general intelligence: a latent variable approach. *Intelligence*, 33, 623-642.

García-Moriyón, F., **Rebollo, I.** & Colom, R. (2005) Evaluating Philosophy for children: a meta-analysis. *Thinking: The Journal of Philosophy for Children, 17(4)*, 14-22.

Colom, R.; Escorial, S. & **Rebollo, I.** (2004). Sex differences on progressive matrices are influenced by spatial abilities. *Personality and Individual Differences*, 37, 1289-1293.

Colom, R.; **Rebollo, I**.; Palacios, A.; Espinosa, M.J. & Kyllonen, P. (2004). Working memory is (almost) perfectly predicted by *g*. *Intelligence, 32*, 277-296.

Abad, F.J, Colom, R., **Rebollo, I.** & Escorial, S. (2004) Sex Differencial item functioning in the Raven advanced progressive matrices: evidence for bias. *Personality and Individual Differences, 36, 1459-1470.*

Ruiz, M. A., Rejas, J., Soto, J., Pardo, A. & **Rebollo, I**. (2003). Adaptation and validation of the Health Utilities Index Mark 3 into Spanish and correction norms for Spanish population. *Medicina Clínica*, 120, 89-96.

Escorial, S.; Juan-Espinosa, M.; García, L. F.; **Rebollo, I.** y Colom, R. (2003): Does g variance change in adulthood?. Testing the age dedifferentiation hypothesis across sex . *Personality and Individual Differences, 34, 1525-32*

Colom, R., Flores-Mendoza, C. & **Rebollo, I.** (2003): Working memory and intelligence. *Personality and Individual Differences, 34, 33-39.*

Escorial, S. , García, L.F., Juan-Espinosa, M., **Rebollo I.** & Colom, R. (2003). Ability level differentiation in adult males and females. *Psicothema, 15, 172-175.*

Escorial, S., **Rebollo, I**., García, L.F, Colom, R., Abad, F.J, Juan-Espinosa, M (2003). Abilities that explain the intelligence decline: Evidence from the WAIS-III. *Psicothema, 15, 19-22*

Juan-Espinosa, M., García, L.F., **Rebollo, I**., Colom, R., y Abad, F.J. (2002) Age dedifferentiation hypothesis: Evidence from the WAIS-III. *Intelligence.30, 395-408*

Rebollo, I.; Herrero, O & Colom, R.: (2002) Personality in imprisoned and non-imprisoned people: evidence from the EPQ-R. *Psicothema,14,3, 540-543*

PAPERS IN PRESS

Boomsma, D.I., **Rebollo, I**., Derks, E.M., van Bijsterveldt, T.CEM., Althoff, R.R., Rettew, D.C., Hudziak, J.J.. (In Press) Longitudinal stability of CBCL-Juvenile Bipolar Disorder Phenotype: a study of Dutch twins. *Biological Psychiatry*..

Muthén, B., Asparouhov, T. & **Rebollo, I.** (In Press). Advances in behavioural genetics modelling using Mplus: Applications of factor mixture modelling to twin data. *Twin Research and Human Genetics.*

Rebollo, I., de Moor, M.H., Dolan, C.V. & Boomsma, D.I. (In Press). Phenotypic factor analysis of family data: correction of the bias due to dependency. *Twin Research and Human Genetics*.

Rebollo, I. & Boomsma, D.I. (In Press). Genetic and Environmental influences on Type A Behavior Pattern: Evidende from twins and their parents on the NTR. *Psychosomatic medicine*, In press.

Rebollo, I., Boomsma, D.I. (In Press). Genetic Analysis of Anger: Genetic Dominance or competitive sibling interaction. *Behavior Genetics.[Published online ahed of press]*

Colom, R., **Rebollo, I**., & Chun Shih, P. (In Press) Complex span tasks, simple span tasks, and cognitive abilities: A re-analysis of key studies. *Memory & Cognition.*

BOOK CHAPTERS

Rebollo, I. & Rich Harris, J. (In press). Genes, ambientes e personalidade. In Colom, R. & Flores-Mendoza, C. *Introdução à Psicologia das Diferenças Individuais*. Porto Alegre: ArtMed (pp. 293-315.) [Genes, Environment and Personality. In Colom, R. & Flores-Mendoza, C. *Introduction to the Psychology of Individual Differences.*]

ACKNOWLEDGEMENTS

First I want to thank Dorret Boomsma, for giving me the opportunity to visit the NTR first, and to realize what my professional whish was, i.e. investigating personality from a Behavior Genetics approach. Her supervision has been an excellent combination of direction instruction, and wise advice, but always providing me the space to make my own choices and develop my own style. From her I have learnt to be more practical, more pragmatic and more efficient; to pay attention to the possible applications and future directions of our work; and the value of the knowledge of the literature, not only the latest but also the classics. Conor Dolan's co-supervision has been invaluable. Without him this thesis would have not been finished. I want to thank him for his always precise methodological advice, his willingness and openness to discuss, and his direct style of asking questions and making suggestions. In Spanish we would say that "he doesn't have hairs on his tongue!". Collaborating with him is very stimulating. With Conor I have learnt to think very carefully what I write and the methodological decisions that I make, and to make sure that I understand and have a clear explanation for all of them.

I want to thank Judith Koopmans, Mirailla van den Berg, Jaqueline Vink, and Janine Stubbe for the great effort of data collection in surveys 1 till 6, and Gonneke Willemsen for the data management. I also would like to thank Natasha Stroo for the efficient work that she does as a secretary. And of course, I want to thank the generous collaboration of the unbelievable number of twins and their families without whom this research would never be possible.

I want to thank all my colleagues from the biological psychology department for the nice atmosphere that they have been for me. Especially, Caroline van Baal, who gave me a warm welcome, and introduced me to the department and to the Dutch culture in general. Danielle Posthuma for her trust in me and her support. Stephanie van den Berg for our great discussions that grow from her skepticism, and are always a good source of inspiration. Marleen de Moor and Janine Stubbe have been my roommates these years, and I am very thankful for their friendship, their openness and understanding of our cultural and personal differences, and their constant willingness to help, listen and give advice professional and personal.

From Spain, Manuel de Juan Espinosa introduced me to the world of science and individual differences. Roberto Colom was my supervisor during my first years. Both of them transmitted me their passion for knowledge and scientific research. From Roberto I learnt to think in scientific terms, to think about the answers before I ask questions, to criticize constructively, and to work in group. I learnt the value of a good theory, and the great importance of statistical methods. More importantly, he motivated me to pursue my interest in Judith Harris' theory and Behavior Genetics going

abroad. I also want to thank Miguel Ruiz and Antonio Pardo for their invaluable contribution to my knowledge and skills in statistical methods. I want to have a especial mention for my great friend and colleague Paco Abad. I have no enough words to express what I have learnt from him, and how much his friendship has meant to me all this years.

I thank, and dedicate this thesis to Judith Harris. Her work and our discussions have been an inspiration for me. I admire her critical thinking and her ability to merge evidence from different fields of research, and to find the best and the worst in all of them. I shouldn't forget to thank Thomas Bouchard for receiving me in his department at Minnesota for three months in my first year, before I barely knew anything about twin research. He had the smart idea to direct me to the NTR in Amsterdam.

Personally, I want to thank Cristina, for our beautiful friendship that made me feel home from the beginning and, of course, for her fantastic contribution to the design of this book! I also want to remember Rebeca, for being there for me all these years, even in the distance. Of course, I thank my love Ünal, for his love, his support and his patience during this last year. Finally, I don't forget the love of my friends and family in Spain. I especially thank my mother for teaching me from my school years the great value in life of having a career that you love and enjoy. That is a priceless lesson that I will never forget.

Irene
Abril 2006