Bivariate Genetic Analyses of Stuttering and Nonfluency in a Large Sample of 5-Year-Old Twins

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Purpose: Behavioral genetic studies of speech fluency have focused on participants who present with clinical stuttering. Knowledge about genetic influences on the development and regulation of normal speech fluency is limited. The primary aims of this study were to identify the heritability of stuttering and high nonfluency and to assess the relative contribution of genetic and environmental factors to the correlation between these 2 fluency phenotypes.
Method: Information on 6 specific speech fluency behaviors was obtained by maternal report for over 10,500 5-year-old Dutch twin pairs.
Results: Genetic analyses revealed that both fluency phenotypes were moderately heritable, with heritability estimates of 42% and 45% for probable stuttering and high nonfluency, respectively. Shared environmental factors were also significant, explaining 44% of the individual differences in probable stuttering and 32% in nonfluency. For both phenotypes, the magnitude of the genetic and environmental influences did not differ between boys and girls. The overlap between the 2 traits was substantial (tetrachoric correlation was .72). A bivariate genetic analysis showed that this overlap was due to both overlapping genetic and environmental influences.
Conclusions: These findings provide a foundation to justify further studies in normal fluency control, a scientific area that has received little cross-disciplinary attention.

KEY WORDS: stuttering, nonfluency, heritability, twins

The word *fluency* is derived from the Latin for *flowing,* and speech that is recognized as highly fluent generally connotes this quality. Individuals whom we recognize as highly fluent speakers are characterized by "the ease and grace with which they produce long utterances without stopping" (Starkweather, 1987). Like other complex behaviors, speech fluency is a skill for which there is considerable individual variation. At one extreme is the clinical disorder known as *stuttering,* defined by the chronic and severe loss of ability to initiate and maintain smooth, forward-moving speech. At the other extreme is the speech produced by professional voice users (e.g., broadcasters, experienced lecturers, actors) that is often remarkably free of speech disruptions. Although it is now generally accepted that fluency is a complex skill reflecting an intricate coordination between extrinsic and intrinsic factors (Conture et al., 2006; DeNil, 1999; Smith & Kelly, 1997; Starkweather, Gottwald, & Halfond, 1990; Wall & Myers, 1984), the specific mechanisms that underlie the uniquely human ability to develop and maintain fluency under varying speaking conditions have not been well established.

Multifactorial Models of Fluency Development in Children

Most present models of fluency development have focused on identifying the complex set of factors that are responsible for the onset of stuttering in children, with few proposing specific mechanisms to explain individual differences in fluency performance across the continuum of ability. One of the first models to emphasize the multidimensional nature of stuttering at its onset was the demands and capacities (DC) model described by Starkweather et al. in 1990. In this model, whether or not a child developed a stuttering disorder was determined by a mismatch between that child's internal capacities in speech-motor, linguistic, cognitive, and emotional domains and the self-imposed internal or external (e.g., parental) demands placed on that child at developmentally sensitive points in time. Importantly, what was emphasized in the DC framework was not the presence of "deficits" in one or more of the intrinsic domains believed to underpin fluency, but rather the dynamic interaction between a given child's constitutional capabilities and the fluid extrinsic factors that he or she encountered.

More recent multifactorial models of stuttering have provided additional details about the factors believed to be necessary for fluency to develop. As with the DC model, these more contemporary models emphasize the centrality of the interaction between internal factors (e.g., genetic predisposition, neurophysiological processes, emotional regulation) and external factors (e.g., situational demands, speech models) in the precipitation and maintenance of stuttering. Smith (1999) and Smith and Kelly (1997) proposed a dynamic and nonlinear model of stuttering development that emphasized the interaction between organism variables (e.g., emotion, language, cognition) and "behavioral context" in shaping an individual's ability to stabilize speech-motor control. Similarly, DeNil (1999) has suggested that stuttering, like many complex human behaviors, occurs at three levels that influence and inform one another: a processing level that involves multiple neurophysiological events, an output level that contains observable behaviors (e.g., speech, motor performance), and a contextual (environmental) level that can modulate the expression of behaviors in different ways at different points in time. In much the same way as argued by Smith (1999), these levels are not conceptualized as linear or "top down." Instead, DeNil argues that external factors (e.g., stress) can exert an influence on an individual's central neurophysiological processes, which in turn may directly affect one or more observable behaviors (e.g., fluency, anxiety reactions).

Finally, Conture and colleagues (2006) have recently described an interactive model to explain the development of stuttering that they have called the communication–emotional (C-E) model. In this model, stuttering is described as having both proximal and distal causal contributors that are mediated by emotional reactivity and prefrontal regulatory processes. Specifically, in this model, underlying factors such as genetic predisposition and specific shared and unique environmental processes that undermine fluency are considered distal contributors to stuttering development. These distal factors are posited to interact with one another to cause difficulties in speech and language planning and possibly speech production (the proximal contributors). These proximal factors, in turn, are the direct contributors to stuttered speech. Conture et al. argue that there is a fundamental relationship between communication planning and production and emotional reactivity and regulation. In their view, the proximal speech and language disruptions are "filtered through" the child's disposition and emotional reactions, and these connections become strengthened with repeated experience.

Twin Studies of Stuttering

The theoretical models just described all share a common conviction that stuttering develops as a result of a complex interplay between nature and nurture. To establish the relative contribution of nature (i.e., genes) and nurture (environment) to the expression of complex problems such as stuttering, a twin study design is the methodology of choice (McGue & Bouchard, 1998). A handful of large international twin studies of stuttering have been performed since 1990, and each has contributed important information about the etiology of stuttering (Andrews, Morris Yates, Howie, & Martin, 1991; Dworzynski, Remington, Rijsdijk, Howell, & Plomin, 2007; Felsenfeld et al., 2000; Ooki, 2005). In all of these investigations, structural equation modeling revealed moderate to high heritability estimates for both child and adult samples. Additive genetic (a^2) estimates in the moderate range were reported for 4-year old children (a^2 = .65) who were participants in the Twins Early Development Study in the U.K. (Dworzynski et al., 2007), and high heritability estimates (a^2 = .83) were found for Japanese twin pairs with a mean age of 11.5 years (Ooki, 2005). Two studies of adult twins participating in the Australian Twin Project (Andrews et al., 1991; Felsenfeld et al., 2000) both obtained intermediate heritability estimates of .70.

If twin studies are sufficiently large, it is also possible to distinguish and quantify the effects of the shared environment (e.g., family background) and shared genes on the resemblance between relatives growing up in the same family. The extent to which children raised together do not resemble each other must be attributed to the unique environment (the individual events that shape a life) and, with the exception of identical twins, to nonshared genes. Shared environmental variables such as excessive parental concern about imperfect speech, a

competitive and "perfectionistic" parental style, a family drive for upward mobility, and rapid and linguistically complex maternal speaking styles have all been implicated in stuttering etiology at one time or another (Andrews & Harris, 1964; Gottwald, 1999; Guitar, 2006; Johnson, 1959). Interestingly, in the twin studies performed to date, the nongenetic effects that have reached significance have been attributed to the nonshared environment, with shared environmental effects being uniformly nonsignificant.

Purpose of the Present Study

None of the twin studies of fluency performed thus far has examined the heritability of speech fluency among speakers from a population-based sample or examined the overlap between stuttering and high nonfluency. Although knowledge about one extreme variant of fluency performance is important for purposes of clinical management, there is a considerable gap in researchers' knowledge about the genetic and environmental mechanisms that are responsible for determining fluency performance in speakers who are not fluency impaired. In the present study, we obtained parental survey results about speech fluency from a large population sample of 5-year old twins (N = 10,683 pairs) ascertained from the Netherlands Twin Register (NTR; Bartels et al., 2007; Boomsma et al., 2006). Parents were asked to evaluate their child's typical speech fluency by responding to six items, and these responses were used to define "probable stuttering" and "high nonfluency" at age 5. The primary objective of the present investigation was to estimate the heritability of both the probable stuttering and the high nonfluency phenotypes in this large cohort of children who were not sampled because of known problems with speech or fluency development. A second objective was to assess the relative contribution of genetic and environmental factors to the correlation between both speech fluency phenotypes.

Method

Participants

The data presented in this article were derived from a longitudinal study using the NTR, which is maintained by the Department of Biological Psychology at the VU University in Amsterdam (Bartels et al., 2007; Boomsma et al., 2006; Boomsma, Vink, et al., 2002). From 1987 onwards, the NTR has recruited families with twins a few weeks or months after birth. Currently, 40%–50% of all multiple births are registered by the NTR.

Surveys were mailed to parents of twins around the fifth birthday of the twins. After a procedure of mailing reminders to nonresponders—and, if resources were available, contacting persistent nonresponders by phone—a response rate of 66% was obtained. Families whose addresses were not available were included in the nonresponse group. In this study, questionnaires from 10,683 5-year-old twin pairs from birth cohorts 1989–1999 were available. A twin pair was excluded when one of the pair had a handicap or a disease that interferes with normal daily functioning (n = 256 pairs) or when the mother did not complete the screening items (n = 80). For the majority of participants (77.6%), the mother completed the ratings. Therefore, for convenience, ratings are hereafter referred to as maternal reports, although some ratings were actually completed in a few cases by fathers (4.5%), by both parents (17.7%), or by others (0.2%).

For 795 same-sex twin pairs, zygosity was based on blood group (n = 12) or DNA polymorphisms (n = 783). DNA and blood collection were done in families that took part in various experimental and laboratory studies being performed through the NTR (Boomsma et al., 2006), including studies that investigated the genetics of cognition, brain function and structure in children, attention-deficit/hyperactivity disorder, and the genetics of twinning. For the remaining same-sex twins, zygosity was based on questionnaire items dealing with similarity in physical characteristics (hair color, eye color, face color, facial appearance) and frequency of mistaking one twin for another by parents, relatives, and strangers (Goldsmith, 1991; Rietveld et al., 2000). The classification of zygosity was based on a predictive discriminant analysis, relating the questionnaire items to zygosity based on blood/DNA typing in a group of same-sex twin pairs (for a detailed description of the procedure, see Rietveld et al., 2000). Complete data on zygosity questions and on genetic markers of blood profiles were available for 768 twin pairs. According to this analysis, the zygosity was correctly classified by questionnaire in nearly 95% of the cases. If zygosity was missing, then the zygosity status was determined by items from questionnaires sent at other ages. For 33 twin pairs, zygosity could not be established, and these pairs were omitted from the genetic analyses.

Measures

Highly unstable fluency (hereafter, *high nonfluency* or just *nonfluency*) and probable stuttering classifications were based on maternal responses to six survey items. These items asked the parent to evaluate "how often" the following behaviors occurred during the child's typical conversational speech: (a) repeats a part of a sentence, (b) shows a slow repetition of words in a sentence, (c) shows a fast repetition of words in a sentence, (d) shows a fast part-word repetition, (e) blocks at the beginning of a word, and (f) shows a prolongation of a sound within a word. Each question was presented with a model or a verbal example by the interviewer and was rated using

a 5-point scale (1 = *never,* 2 = *rarely,* 3 = *sometimes,* 4 = *often,* and 5 = *very often*). Items 1–3 are nonfluency behaviors that are observed in varying degrees in typically developing children of this age (Ambrose & Yairi, 1999; Carlo & Watson, 2003; Yairi, 1972). In contrast, Items 4–6 correspond to the classic triad of core stuttering behaviors (part-word repetitions, blocks, and sound prolongations) that are traditionally used as diagnostic indicators of incipient stuttering in English (Ambrose & Yairi, 1999; Curlee, 2007; Pellowski & Conture, 2002) and in Dutch (Boey, Wuyts, Van de Heyning, De Bodt, & Heylen, 2007).

Children were classified as probable for stuttering if they were reported to display one or more of the three core behaviors (Items 4–6) "often" or "very often." Children who did not meet the criterion for probable stuttering were classified as nonaffected for stuttering. For this nonaffected group of children, mothers reported that the core behaviors (Items 4–6) occurred infrequently ("never," "rarely," or "sometimes"). Children were classified as highly nonfluent if they were reported to display at least two of the three nonfluent behaviors (Items 1–3) "often" or "very often." Children were considered to be nonaffected for high nonfluency if they did not meet this criterion; that is, if the mother reported that the core behaviors of nonfluency occurred infrequently ("never," "rarely," or "sometimes"). (See the Appendix.)

Overview of Genetic Analyses

The relative contribution of genetic and environmental factors to the variance in speech fluency and stuttering can be inferred with data from monozygotic (MZ) and dizygotic (DZ) twins. The twin method compares the resemblance for a certain trait in MZ twin pairs, who are genetically identical, with resemblance in DZ twin pairs, who share on average 50% of their segregating genes (Boomsma, Busjahn, & Peltonen, 2002; Plomin, DeFries, McClearn, & McGuffin, 2008). The classical twin method assumes that MZ and DZ twin pairs share their family environment to the same extent. If the MZ resemblance, often expressed as a correlation, is twice as large as the DZ resemblance, then the trait is influenced by genetic factors because the only difference between the zygosity groups is in genetic relatedness. If the DZ correlation is larger than half the MZ correlation, then the trait is also influenced by shared environmental factors. Shared environmental factors include experiences due to growing up in the same family (e.g., parental education style or socioeconomic status). Any true differences, apart from measurement error, between MZ twins are mainly attributable to their nonshared environment. However, there may also be genetic (e.g., copy number variation) or epigenetic differences between MZ twins (Bruder et al., 2008; Martin, Boomsma, & Machin, 1997).

For dichotomous variables, tetrachoric correlations, based on the liability threshold model (Falconer, 1989), can be estimated to index twin similarity. The threshold model assumes that a categorical variable has an underlying liability with a continuous and standard normal distribution. Thresholds divide the liability distribution into discrete categories (e.g., affected and unaffected). The thresholds are based on the prevalence of the trait in the population. It is assumed that many genes and environmental influences affect individual differences in liability, resulting in a normal distribution (Falconer, 1989; Neale, Boker, Xie, & Maes, 1999; Neale, Eaves, & Kendler, 1994). With structural equation modeling, genetic and environmental contributions to variance in liability are estimated and their significance tested (Neale et al., 1999). The modeling procedure starts with a model specifying additive genetic (A) factors, common environmental (C) factors shared by twins growing up in the same family, and unique environmental (E) factors (ACE full model). The significance of A, C, and E can be tested by omitting them from the model. A significant decrease in goodness of fit implies that the omission is not allowed and that the factor contributed significantly to the variance of the trait. Sex differences in genetic architecture can be tested by constraining the parameters that represent the influence of A, C, and E to be equal across sex. If the goodness of fit deteriorates significantly, then the omission is not allowed and the genetic and environmental contributions differ across sex.

To study whether the two fluency phenotypes, high nonfluency and stuttering, are influenced by the same genes and by the same environmental factors, a bivariate genetic model was fitted to the data. The bivariate analysis makes use of cross-twin–cross-trait correlations (i.e., stuttering in one twin is correlated with nonfluency in the co-twin) in MZ and DZ pairs. If the cross-trait–cross-twin correlation in MZ pairs is higher than in DZ pairs, then the association between the two phenotypes can be attributed to genetic factors. If the DZ correlation is larger than half the MZ correlation, then shared environmental factors play a role in the association. The proportion of overlapping genetic factors that contribute to both speech phenotypes is measured by the genetic correlation. If the genetic correlation is 1, then the same genes influence both phenotypes. A correlation of 0 indicates that each speech phenotype is affected by a different set of genes. The genetic correlation is independent of the heritability of each speech trait (e.g,. the correlation can be high, meaning that the two traits are influenced by the same genes, whereas the heritabilities can be low). The same is true for environmental correlations and influences. To estimate the proportion of the phenotypic correlation between stuttering and nonfluency due to overlapping genetic and environmental factors, the genetic and environmental correlations are weighted by

the square roots of the heritabilities and environmentalities, respectively, of the traits and divided by the phenotypic correlation.

In all genetic analyses of stuttering and nonfluency, traits were defined as dichotomous variables (0 = *unaffected,* 1 = *affected*). All twins were included in all univariate genetic analyses; that is, analyses of stuttering were done regardless of a child's score on nonfluency and vice versa. In the bivariate analyses, all data on both traits were analyzed. Genetic model-fitting analyses were carried out with Mx software (Neale et al., 1999), using raw-data maximum-likelihood estimation (Neale & Cardon, 1992). Mx jobs for the genetic analyses were obtained from the Mx library (Posthuma & Boomsma, 2005).

Results

Prevalence

For 20,445 twins, the data were complete for the fluency and stuttering items. A large percentage of children, approximately one third across zygosity groups, already exhibited highly stable fluency at age 5, with mothers reporting that all six of the questionnaire items about (non)fluency essentially "never occurred." The overall prevalence rate for probable stuttering was 4% (826/20,445), which is consistent with published estimates of the population prevalence of stuttering in children of this age (Guitar, 2006). The ratio of male:female affected children found in this study was 1.5:1, which is also consistent with past epidemiological research of young children who stutter (Yairi & Ambrose, 2005). The overall prevalence of the nonfluency phenotype was 4.3% (889/20,445), with a male:female ratio of 1.7:1. Because this is the first study to report population estimates of the prevalence of the nonfluency phenotype, there are no data against which these values can be compared.

To test whether prevalence rates differed by zygosity and sex, we performed separate likelihood-ratio tests using Mx (Neale et al., 1999). Results confirmed that the prevalence of both nonfluency and stuttering was significantly higher in boys than in girls: nonfluency, $\Delta\chi^2(1, N = 20{,}372) = 71.64, p < .001$; stuttering, $\Delta\chi^2 (1, N = 20{,}372) = 43.36, p < .01$. Therefore, in the subsequent model-fitting analyses, thresholds were allowed to differ between boys and girls. As can be seen from Table 1, the prevalence of nonfluency and stuttering did not differ between same-sex DZ and MZ twin pairs: nonfluency, $\Delta\chi^2 (2, N = 20{,}371) = 2.38, p = .30$; stuttering, $\Delta\chi^2 (2, N = 20{,}371) = 5.09, p = .08$.

Concordance

We examined twin similarity (probandwise concordance) for both the nonfluency and stuttering phenotypes for each zygosity group, which is summarized in Table 1. Probandwise concordance reflects the probability that a twin is affected, given that the co-twin is affected, and is calculated as [2 × (AA)]/ [(2 × (AA)) + (UA)]. The tetrachoric correlation (see the last column in Table 1) identifies the similarity in the underlying liability for nonfluency and stuttering. The higher MZ than DZ correlation

Table 1. Prevalence (in percentages), number of unaffected-unaffected (UU), unaffected-affected (UA), and affected-affected (AA) pairs; the probandwise concordance rate, and tetrachoric correlation for high nonfluency and probable stuttering by zygosity and sex.

Twin pairs	% affected	UU	AA	UA	A–	U–	Probandwise concordance	Tetrachoric correlation
				High nonfluency				
MZM	6.22	1,439	46	106	0	2	0.46	.76
DZM	5.12	1,620	21	141	0	12	0.23	.47
MZF	3.25	1,738	28	62	1	6	0.47	.81
DZF	3.41	1,531	16	79	0	5	0.29	.62
DZ-OS_mf	4.9 (m) 2.8 (f)	1,589	16	97	1	8	0.25	.57
DZ-OS_fm	2.7 (f) 6.3 (m)	1,508	16	116	0	6	0.22	.53
				Probable stuttering				
MZM	4.68	1,482	39	70	1	1	0.53	.84
DZM	4.92	1,640	31	111	3	9	0.36	.67
MZF	3.77	1,733	42	53	1	6	0.61	.90
DZF	3.44	1,533	19	74	0	5	0.34	.68
DZ-OS_mf	4.9 (m) 2.8 (f)	1,590	17	95	2	7	0.26	.60
DZ-OS_fm	2.1 (f) 5.1 (m)	1,537	16	87	0	6	0.27	.65

Note. A– = pairs with one twin affected and one missing; U– = pairs with one twin unaffected and one missing; MZ = monozygotic; M = male; DZ = dizygotic; F = female; DZ-OS_mf = opposite-sex twin pair with male (m) as first born and female (f) as second born; DZ-OS_fm = opposite-sex twin pair with female as first born and male as second born.

suggests that genetic factors are involved in both phenotypes. However, because the DZ correlations are relatively high, the importance of shared environmental factors at this age is also suggested.

The twin concordance rates for stuttering are comparable with those reported in three previous twin studies. Two of these earlier studies (Dworzynski et al., 2007; Ooki, 2005) obtained probandwise concordance rates using questionnaires completed by mothers of young twins, similar to the methods used in the present investigation. Dworzynski and colleagues (2007) obtained probandwise concordance of 0.32 and 0.12 for MZ and DZ twin pairs, respectively. The concordance rate in the study of Ooki (2005) was 0.52 and 0.12 for MZ and DZ twin pairs, respectively. The third study obtained an interview diagnosis of stuttering from twins who were aged 25–32 years and reported an MZ concordance rate of 0.62 and 0.26 for DZ twins (Felsenfeld et al., 2000). Although variability across studies in concordance rates can be seen, the interpretation of the findings across studies was consistent: All reported significantly higher MZ than DZ concordances for stuttering, with genetic effects interpreted as moderate.

Genetic Model Fitting

Univariate genetic analysis. The top portion of Table 2 summarizes the univariate genetic model-fitting results. The full model for nonfluency and stuttering included estimates for the influence of A, C, and E parameters. In the first model, parameters representing these influences were allowed to differ between boys and girls. When parameters were constrained to be equal in boys and girls, no significant drop in the fit of the model occurred for either nonfluency or stuttering. This suggests that there are no significant sex differences in genetic and environmental influences for probable stuttering and nonfluency. Dropping either the A or C parameters from the model, for both phenotypes, led to a significant deterioration in the fit. This means that both genetic and shared environmental factors are likely to play a role in the two speech phenotypes. The bottom portion of Table 2 gives the percentages of variance explained by A, C, and E in the liability to stuttering and nonfluency. For stuttering, the relative influence of additive genetic factors (a^2) was 42%, and the influence of shared environmental factors (c^2) was 44%. For nonfluency, the relative influences of A and C were 45% and 32%, respectively. The remainder of the variance (23% and 14%) was attributed to the unique environment.

Bivariate genetic analysis. Results of the bivariate analyses suggest that there is considerable overlap between the stuttering and nonfluency phenotypes; the tetrachoric correlation between stuttering and nonfluency was high (correlation coefficient of .72). Moreover, in our sample, 342 children (25% of the "fluency-affected" participants) were reported to exhibit both stuttering and high nonfluency. This finding of a moderate amount of within-subject co-expression provides additional evidence for the presence of overlap between these two phenotypes.

In order to determine the extent to which the same genes and environmental factors were responsible for

Table 2. Univariate genetic model fitting results for high nonfluency and probable stuttering using liability threshold model and parameter estimates and 95% confidence intervals from the best-fitting univariate model for high nonfluency and stuttering at age 5.

Model	High nonfluency			Probable stuttering		
	χ^2	*df*		χ^2	*df*	
	Univariate results					
Full ACE	6793.77	20,373		6235.897	20,373	
Tests	$\Delta\chi^2$	Δdf	*p*	$\Delta\chi^2$	Δdf	*p*
No sex differences	2.72	2	.26	1.53	2	.47
No shared environment (drop C)	14.85	1	<.01	34.88	1	<.01
No genetic effects (drop A)	22.14	1	<.01	39.91	1	<.01
	Parameter estimates					
Speech fluency	a^2		c^2		e^2	
High nonfluency	45% (31%–68%)		32% (13%–44%)		23% (17%–28%)	
Probable stuttering	42% (27%–57%)		44% (30%–57%)		14% (11%–18%)	

Note. Univariate results represent test of sex differences in genetic architecture and of additive genetic and shared environmental effects. ACE = additive genetic, common environmental, and unique environmental model; a^2 = percentage of total variance explained by additive genetic effects; c^2 = variance explained by shared environmental effects; e^2= variance explained by unique environmental effects.

this association, we first calculated the cross-trait–cross-twin correlations (e.g., the correlation between stuttering in Twin 1 with nonfluency in Twin 2) in MZ and DZ pairs. The cross-trait–cross-twin correlation for the MZ twins was .56 and for DZ twins was .38, suggesting contributions of both genetic (because the cross-correlation is higher in MZ pairs) and environmental (because the MZ cross-correlation is smaller than twice the DZ cross-correlation) factors. Subsequent tests in which bivariate genetic procedures were used revealed that the same genes contributed to nonfluency and probable stuttering. Constraining the genetic correlation at zero resulted in a deterioration of the fit of the model (see the top portion of Table 3). The same held true for the C and E correlations (see the top portion of Table 3). The estimates of the genetic and environmental correlations between both phenotypes are provided in the bottom portion of Table 3. All correlations are high (.64–.81), indicating that same etiological factors influence both traits.

To estimate what proportion of the correlation between the two fluency phenotypes was due to genetic factors, the genetic correlation was weighted by the square roots of the heritabilities of the traits (i.e., the contribution of genetic factors to the phenotypic correlation is $\sqrt{.45} \times .75 \times \sqrt{.42} = .33$, which is 46% (.33/.72) of the phenotypic correlation). In like manner, the contributions due to the shared environmental correlation (33%) and the unique environmental correlation (21%) were obtained.

Discussion

The primary objective of the present study was to use structural equation modeling to estimate the heritability of both "probable stuttering" and "high nonfluency" in a very large sample of 5-year-old Dutch twins. Results of the genetic model-fitting analyses revealed that both fluency phenotypes were moderately heritable and that there was a significant contribution of shared environment. The phenotypic correlation between the two speech phenotypes was high (.72). Results of the bivariate genetic analysis revealed that this correlation was due to both overlapping genetic and environmental factors. These findings provide corroborative support for recent models of stuttering development that have emphasized the importance of complex interactions between genetic and nongenetic factors in the development of stuttering (Conture et al., 2006; DeNil, 1999; Smith & Kelly, 1997; Starkweather et al., 1990).

Table 3. Bivariate genetic model fitting results for high nonfluency and probable stuttering using liability threshold model and genetic and environmental correlations between high nonfluency and probable stuttering.

Model	Test		
	$\Delta\chi^2$	Δdf	*p*
Bivariate results			
No genetic correlation	28.73	1	< .01
No common environmental correlation	9.49	1	< .01
No unique environmental correlation	93.33	1	< .01
Genetic and environmental correlations			
	r_G	r_C	r_E
Correlation	.75	.64	.81

Note. Bivariate results represent tests of genetic and environmental correlations. r_G = genetic correlation; r_C = shared environmental correlation; r_E = unique environmental correlation.

The present study is the first to obtain heritability estimates for a fluency phenotype other than stuttering by examining children from a general population sample whose speech reportedly contained multiple whole-word and phrase repetitions but did not contain frequent core stuttering behaviors. Results of our genetic model-fitting analyses for high nonfluency suggested that both common environmental influences shared by children growing up in the same family (c^2) and genetic (a^2) influences were important in explaining familial resemblance (a^2 = 45%, c^2 = 32%) and were similar for boys and girls. Thus, although further work is needed to confirm these findings, it appears that how fluent or nonfluent we become as typical speakers may be at least moderately influenced by our genes.

For children in our sample with probable stuttering, both the additive genetic parameter (a^2) and the shared environment parameter (c^2) were significant and were comparable for both boys and girls (parameter estimates were 42% and 44% for a^2 and c^2, respectively). This heritability estimate is lower than in previous twin studies of this phenotype, which have ranged from 83% for Japanese twins aged 10–15 years (Ooki, 2005) to 65% for 4-year-old twins in the U.K. (Dworzynski et al., 2007). The parameter estimate reflecting the proportion of variance attributable to the shared environment in the present study was significantly larger than the c^2 parameters reported in earlier twin studies, all of which were nonsignificant.

There are several possible explanations for these differences. Unlike previous studies, the words *stuttering* or *stammering* were not included in any of our questionnaire items, and mothers were never directly asked whether they believed their child stuttered. As such, the present study is not directly testing the heritability of a clinically diagnosed fluency disorder but is instead examining the heritability of maternal reports of the presence of specific speech behaviors that are typical red flags for stuttering. Therefore, it is possible that the lower

heritability estimates we obtained for probable stuttering may be at least partly attributable to the fact that this is a population-based sample with a broad range of unstable fluency phenotypes. A similar effect was reported by DeThorne, Petrill, Hayiou-Thomas, and Plomin (2005) for mild versus severe expressive vocabulary deficits in 4-year-old twins. For their nonspecific expressive vocabulary impairment group, for example, these investigators found that "the heritabilities ranged from .24 for the least severe condition to .48 for the most severe condition" (p. 800) and concluded that "heritability appeared to increase and the relevance of environmental factors appeared to decrease as the severity of the proband groups' impairment increased" (p. 798). Because our participants represented a range of unstable fluency phenotypes that were likely to have been milder in severity than is the case for clinically referred samples, it is possible that our data reflect this same sampling phenomenon.

Another explanation for the lower heritability estimates found here is that our sample of 5-year-old children may have included many participants who will ultimately recover from stuttering (and perhaps high nonfluency) as they mature. It has been well established that spontaneous recovery from stuttering is a phenomenon that occurs for between 50% and 80% of young children who stutter, for reasons that are still unclear (Yairi & Ambrose, 2005) but may have a partially genetic basis (Ambrose, Cox, & Yairi, 1997). As part of their twin study, Dworzynski and colleagues (2007) followed their young twins who stuttered longitudinally; as expected, some of the twins who stuttered at age 4 recovered, and some persisted in stuttering. The authors' results suggested that both outcomes were moderately and approximately equally heritable, with heritability estimates of .60 and .67 for the recovered and persistent phenotypes, respectively. It is still unknown whether the same genes and/or environmental factors contribute to the probability of recovery versus persistence. Because we will follow the twins who participated in this project longitudinally, and have included questions about stuttering in the surveys they will complete when aged 14 and 16 years, we may ultimately be able to contribute data that can address these questions.

The proportion of variance attributable to the shared environment in the present study was relatively high (32% for nonfluency and 44% for stuttering) in comparison to previous research. One straightforward possibility for this finding is purely methodological and has to do with our large sample size. In order to detect significant contributions of the shared environment in the classical twin study, sample sizes need to be very large when the trait is dichotomous, as was the case here (Posthuma & Boomsma, 2000). Because the sample size in this study was larger (>10,000 twin pairs) than in previous twin studies, ours may be the first study to have had sufficient power to detect a significant contribution of the shared environment for the stuttering phenotype.

Is there Overlap between High Nonfluency and Stuttering?

Several authors (Dollaghan, 2004; Meehl, 1992, 1995; Smith, 1999) have suggested that there may be an underlying diathesis for many complex problem behaviors, including stuttering, that can best be modeled using quasi-continuous liability distributions that incorporate clinical thresholds. Although not articulated in these terms, Bloodstein's (1970) classic continuity hypothesis essentially made the same argument for the relationship between high nonfluency and stuttering by asserting that stuttering, as a clinical disorder, was "largely a more extreme degree of certain forms of normal disfluency" (p. 30). With the present data set, we cannot directly test the continuity hypothesis, nor can we determine whether or not an underlying fluency distribution exists with stuttering occupying a position at one end. However, by using bivariate genetic analyses, we were able to examine the degree of etiological overlap between probable stuttering and high nonfluency in an unselected sample of children in the present study. Our results suggest that the degree of overlap is substantial, although not complete (i.e., the genetic and environmental correlations were less than 1). This indicates that the same set of factors that may have increased susceptibility for the expression of stuttering core behaviors in our sample also increased susceptibility for the expression of the other nonfluent speech behaviors we identified (frequent word and phrase repetitions). Moreover, because the correlations we obtained were less than 1, our findings also make clear that, despite substantial overlap, there exist both genetic and environmental influences unique to these two phenotypes.

The present findings provide support for an earlier study by Felsenfeld, Kubarych, Aggen, Martin, and Neale (2005) in which the authors used a different analytical approach to examine the distributional properties of speech fluency in a population sample. In that study, responses to a 23-item speech fluency questionnaire were obtained from 589 adult speakers (people who stutter and controls) who were participants in the Australian Twin Study of Stuttering. From these data, a latent fluency distribution was created, and the likelihood of the observed response patterns relative to this distribution was tested under a variety of normality assumptions. Similar to the present findings, the results of that investigation also provided evidence for an underlying quasi-continuous speech fluency distribution for both males and females, with clinically diagnosed stuttering reflecting performance at the extreme low end.

Clinical Implications

The present results emphasize the dynamic nature of speech fluency in young children. At present, we do not know whether children who exhibit chronically unstable fluency, but who do not produce frequent core behaviors of stuttering, are at an increased risk for other problem behaviors and whether these children behave similarly to children with clinically diagnosed stuttering on various speech and nonspeech tasks. Children who stutter and those who are highly nonfluent have typically been viewed as categorically different, and there have been few recent efforts directed at examining areas of potential behavioral similarity. It is possible that, by learning more about highly nonfluent children, we can identify potential risk factors in this understudied group and may develop assessment and possibly intervention methods that may assist children who stutter.

Limitations of the Present Study

In interpreting the results of this study, it is important to emphasize that this was not a study of clinically diagnosed fluency disorders. Identification of participants as probable for stuttering and as highly nonfluent was based exclusively on parental (primarily maternal) responses to six questionnaire items. It is possible that, for an unknown number of cases, the fluency ratings we obtained were inaccurate (because raters did not correctly interpret the questions) or were biased. If a large number of raters in our sample had a tendency to either overestimate or underestimate nonfluent behaviors in both their children, this may have increased both MZ and DZ twin similarity, which would have, in turn, inflated our shared environmental estimate. Although parent ratings have been shown to be effective in identifying children who present with structural language deficits (Bishop, Laws, Adams, & Norbury, 2006), the questionnaire items pertaining to fluency that were used here were not validated against other diagnostic measures or clinical reports in this large population study. Future studies using this sample will include mechanisms beyond parental report to validate these classifications.

Future Studies

Several areas of inquiry are suggested by the findings of this study. One important area is to continue examining children who are highly nonfluent, using more direct assessment and measurement methods. In addition, an important challenge for future research will be to establish the extent to which the specific factors that increase liability for the clinical disorder of stuttering are the same as those influencing the rest of the fluency distribution. Ideally, this could be done using a prospective design that directly and repeatedly examines the development of speech fluency in children who span the fluency spectrum (from probable stutterers to those with precocious fluency). In addition to providing additional insight about the existence of overlap between stuttering and normal-range individual differences in fluency control, a prospective study could answer important questions about the relationship between fluency and other subject variables and the within-subject stability of this trait over time.

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Appendix. Criteria for probable stuttering and high nonfluency.

Probable stuttering	
Description	Children are reported to display one or more of the three "core" behaviors of beginning stuttering.
Selection criteria	Mother reports that at least one of the following core stuttering behaviors occurs "often" or "very often": 1. Rapidly repeats part of a word (e.g., "muh-muh-muh-may I go?") 2. Blocks at the beginning of a word (e.g., "I … . .go to school.") 3. Prolongs a sound within a word (e.g., "I go to sssssssschool.")
High nonfluency	
Description	Children are reported to exhibit fluency that is chronically unstable. These children's speech would be described as sounding disorganized, fragmented, and marked by the unnecessary repetition of words and phrases.
Selection criteria	Mother reports that at least two of the following occur "often" or "very often": 1. Repeats a part of a sentence (e.g., "And then he … and then he came home") 2. Slowly repeats a word in a sentence (e.g., "I … I … I go to school.") 3. Rapidly repeats a word in a sentence (e.g., "III go to school.")

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