Genome-Wide Analyses on Assortative Mating

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Background

Assortative Mating (AM): tendency of individuals to mate with a partner more similar (positive AM) or dissimilar (negative AM) on a specific trait than expected by chance. Has been reported in humans for various traits, such as life style traits (i.e. drinking, smoking, etc.), IQ and physical attributes such as obesity and height.

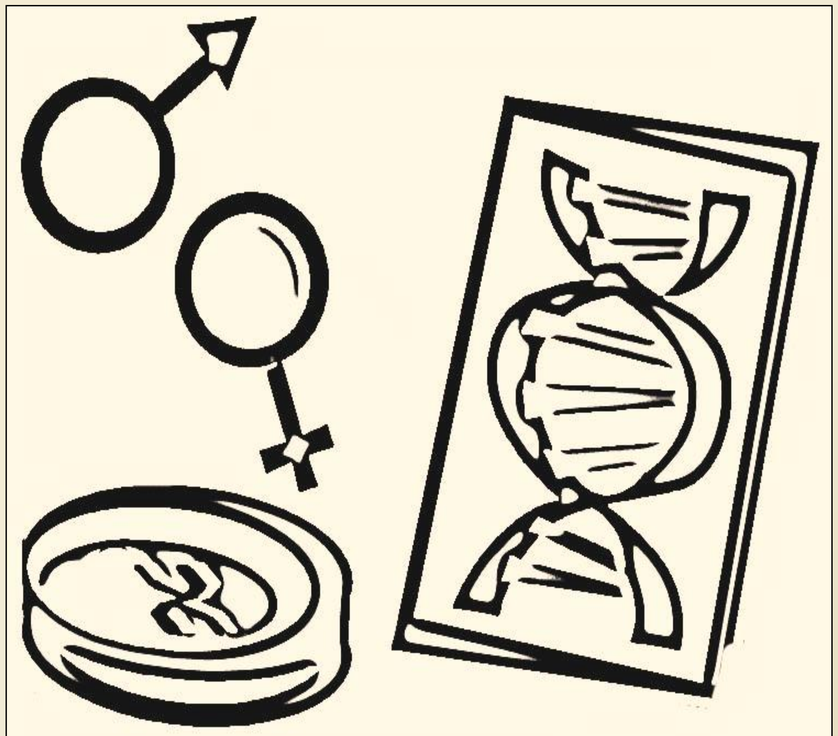
Social homogamy: AM occuring because the individuals live in similar social groups, therefore share demographic backgrounds and/or social experiences, creating greater proximity and/or exposure → not what we are looking for! This study corrects for social homogamy by regressing the measures on the 2 significant principal components (PCs) representing ancestry (= subpopulation), and then repeating the AM analysis on the residuals.

Methods

Datasets: Two datasets with about 500,000 SNPs from the entire genome. One dataset of 758 spouse pairs from QIMR, one dataset of 438 spouse pairs from the Framingham Heart Study (FHS).

Tests on groups of SNPs: The IBS-distance (a measure for genetic similarity) of the spouse pairs was compared to the IBS-distance of random male-female pairs from the same sample obtained by a permutation procedure. This was done on all SNPs simultaneously, on ~ 60 SNPs known to explain 5 % of the variance of height (positive AM expected: phenotypic spouse correlations of ~ .2 have been reported) and on SNPs from the MHC region (negative AM expected: offspring of two MHC-dissimilar parents are expected to be more heterozygous in the MHC region, which is expected to increase the resistance of the immune system to pathogens).

Test for AM on scores on height SNPs: Spouse correlations were calculated for height scores. Scores for height were calculated by multiplying the genotype scores of the ~60 height SNPs with their effect sizes and summing them.



Results: tests on groups of SNPs

	QIMR (N = 758)		FHS (N = 438)	
Correction:	No correction	2 PCs	No correction	2 PCs
All SNPs	***p* = .024**	*p* = .177	***p* = .001**	*p* = .343
Height SNPs	*p* = .255	*p* = .274	*p* = .939	*p* = .947
MHC SNPs	*p* = .643	*p* = .664	*p* = .071	*p* = .108

Results: scores on height SNPs

Dataset	Number of SNPs	Spouse correlation
QIMR	58	*r* = .037, *p* = .305
FHS	43	*r* = .036, *p* = .454
QIMR + FHS	39	*r* = .024, *p* = .415

Conclusions

There was significant AM only when considering all SNPs simultaneously without correcting for ancestry, suggesting AM based on membership of a subpopulation (= social homogamy). To detect AM in the other groups of SNPs (if present) we need larger sample sizes and/or more information about which genetic variants influence the phenotypes (= more SNPs and their effect sizes).

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