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Polygenic prediction within and between families from a 3-million-person GWAS of educational attainment

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ABSTRACT: Educational attainment (EA) is an important dimension of socioeconomic status that features prominently in research by social scientists, epidemiologists, and other medical researchers. We conduct a GWAS of EA in a sample of 3,037,499 individuals and identify 3,952 approximately uncorrelated genome-wide-significant SNPs. We also conduct a GWAS of the X chromosome (*N* = 2,713,033) and the first large-scale GWAS of dominance variance of EA on the autosomes (*N* = 2,574,253). Our X-chromosome GWAS identifies 57 approximately uncorrelated genome-wide-significant SNPs. Our dominance GWAS identifies no genome-wide-significant SNPs; moreover, with high confidence, we can rule out the existence of any common SNPs whose dominance effects explain more than a negligible fraction of the variance in EA. We report evidence of directional dominance for EA. We also investigate the scope and sources of the predictive power of a genome-wide polygenic predictor, or polygenic index (PGI), of EA. The PGI explains 12-16% of the variation in EA and adds non-trivial predictive power for 10 diseases we examine, even after controlling for disease-specific PGIs. Using a combined sample of ~53,000 individuals with genotyped siblings and ~3,500 individuals with both parents genotyped, we examine the predictive power of the EA PGI controlling for parental EA PGIs. The PGI's associations with EA and other phenotypes falls by roughly half when controlling for parental PGIs. Finally, we use the EA and other PGIs to study assortative mating and find that the correlation between spouses' EA PGIs is far too large to be consistent with phenotypic assortment alone.

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