The Effect of Genetics on Risk Preferences and Household Financial Decisions

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ABSTRACT

This study investigates how genetics influence risk preferences and financial decisions. We hypothesize that genetic differences can result in heterogeneous financial outcomes through both their impact on risk tolerance and other human characteristics. We measure genetic differences using established polygenic scores and develop a measure of risk tolerance that is independent of certain demographic and genetic characteristics. Using the Health and Retirement Study, which includes a rich set of information on households including biomarkers and genetic data for a large portion of the sample, we test for the separate effects of risk preferences, demographics, and genetics on various household financial measures. We find that genetic factors that are correlated with risk tolerance also have significant direct effects beyond just their impact on risk tolerance. The polygenic score for Big Five personality trait "neuroticism" is found to be negatively related to our estimated measure of risk tolerance and positively related to risky financial decisions.

Introduction and Background

This study investigates how genetics influence risk preferences and financial decisions. It has long been recognized that, along with physical traits like hair color and height, some aspects of personality and behavior seem to be passed down from parent to child. While it is common to hear "you take after your father (or mother)" regarding personality traits, the question of whether these commonalities are the result of genetic influences (nature) or upbringing (nurture) continues to be a topic of research in psychology and economics.

In this study, we explore whether the genetic differences and risk tolerance differences between individuals have independent impacts on financial risk-taking behavior. In other words, do the genetic factors that are correlated with risk tolerance also impact financial risk taking in a direct manor or do they solely operate through their impact on risk tolerance? To answer these questions, we rely on previous genetic research and also build on research on risk attitiudes and preferences. In this section, we first provide some background on recent genetics research and measurement tools and then review the literature on measurement of risk preferences.

Background on Genetics Research in Economics

The first approach to studying genetic effects employed samples of twins. The classical twin study methodology does not involve any genetic testing, but rather makes use of the differing amounts of genetic similarity between identical and fraternal twins to determine the amount of variation in a given trait that can be explained by genetic versus environmental factors.[1] Researchers have analyzed the role of genetics in economic outcomes (Taubman, 1976; Björklund, Jäntii and Solon, 2005), and economic preferences and behaviors (Wallace, et al.,

[1] Sometimes other family members with different genetic or environmental similarities are included in these studies.

2007; Cesarini, et al., 2008, 2009, 2010; Cronqvist, et al., 2014, 2015). These studies have generally found evidence of both genetic and environmental factors influencing the economic variables analyzed. Cesarini, et al. (2009) found that 22-28% of the variation in altruistic behavior in an economic experiment was explained by genetics, as was 14-16% of the variation in experimentally elicited risk aversion parameters. Evidence of the heritability of a preference for fairness was found in Wallace, et al. (2007). In a study of the investment decisions of Swedish twins in response to a policy change allowing more choice in retirement fund allocations, Cesarini, et al. (2010) found a genetic component of about 25% of the variation in portfolio risk levels.

Although the twin study methodology is still commonly used, and it can be useful for measuring the percentage of variability explainable by additive genetic factors, its weaknesses include an inability explore which genetic variants impact behavioral and physical traits and the directions of these effects. In addition, twin studies cannot provide the data necessary to develop measures of individual predispositions for disease and behavioral characteristics.

Much of the early research based on actual genetic testing followed the candidate gene approach. This involves investigating a specific gene based on knowledge of its biological function to determine whether it is correlated with a disease or a physical or behavioral trait. The impact on financial risk taking of genes related to dopamine function was studied using the candidate gene approach by Kuhnen and Chiao (2009), Dreber et al. (2009), Zhong et al. (2009a, 2009b), Frydman et al. (2010), Carpenter et al. (2011), and Mata et al. (2012). All found evidence of correlation between the gene studied and financial risk taking, measured in various ways. But most complex behavioral traits, like those of interest to economists, are thought to involve an accumulation of small effects from many genes (Chabris, et al, 2015). The relatively small sample sizes for candidate gene studies led to questions about the lack of power and a corresponding risk of false positive results (Benjamin, 2012).[2] Concerns about the lack of replicability in behavioral genetics research as a whole led to new research protocols for candidate gene studies[3] and a greater reliance on the results of large-scale projects performed by consortia of research groups.

As DNA sequencing has become more efficient, the method of genome-wide association studies (GWAS) has been increasingly employed to elucidate the role of genetics in a variety of physical and behavioral traits and diseases. These studies scan large numbers of genetic variants for correlations with the trait or disease of interest. Genome-wide association studies are quite expensive, involving the sequencing of hundreds of thousands to millions of genetic variants from thousands of subjects. Sample sizes in some cases are now approaching, or even exceeding, a million subjects (Linnér, et al., 2019). The number of genetic variants found to be statistically significant predictors of various diseases and physical and behavioral traits has grown with sample size, even with the more stringent commonly used p-value threshold of $5x10^{-8}$ employed to correct for multiple hypothesis testing. For behavioral traits, many of the statistically significant genes play a role in brain development and function.

[2] For example, Dreber et al. (2009), Kuhnen and Chiao (2009), Carpenter et al. (2011), Dreber et al. (2011), Frydman et al. (2011), and Kuhnen et al. (2013) had sample sizes between 60 and 175.
[3] See, for example, Hewitt (2012) and Johnston, et al. (2013).

Since complex traits are influenced by the small effects of many genetic variants, early hopes of finding individual genes with strong predictive power for diseases had to be reassessed. In recent years, polygenic risk scores have begun to show promise as a way of aggregating additive genetic influences to assess the predisposition for such diseases as type 2 diabetes and cardiovascular disease. In a recent study with direct clinical applications, researchers at Harvard Medical School, the Broad Institute, and Massachusetts General Hospital developed algorithms for polygenic risks scores for five major diseases: coronary artery disease, type 2 diabetes, inflammatory bowel disease and breast cancer (Khera, et al., 2018). These scores can identify a substantially larger fraction of at-risk individuals than any single gene test. Approximately 20% of the 409,258 participants studied had at least a 3-fold higher than average risk for one or more of the diseases.[4]

How are polygenic risk scores calculated and can they be used to predict behavioral traits and physical traits as well as diseases? The foundation for the development of a polygenic risk score is a genome-wide association study. The human genome is made up of two sets of twenty-three chromosomes, one from the mother and one from the father. The well-known double helix of DNA in each chromosome is made up of a string of units each characterize by one of four nucleotides, A, T, C or G. The order in which the nucleotides appear in the DNA represents a code that is ninety-nine percent identical across all individuals. Among the approximately three billion sites, there are several million sites where a nontrivial minority of the population has a nucleotide that is different than the commonly found one. These sites are called single nucleotide polymorphisms or SNPs (referred to as snips). The two possible nucleotides at a given SNP are referred to as the major and minor alleles.[5] Each SNP is found twice in an individual, on the maternal and paternal chromosomes. In a genome-wide association study, a subset of several hundred thousand to several million SNPs is chosen and it is determined which nucleotides appear at each SNP. The SNPs are coded with a 0, 1 or 2, the value being a count of the number of minor alleles. This data is collected for a large sample of individuals, along with data on a particular trait or disease and demographic data, often in multi-location studies.

The coefficient or beta for each SNP is determined using regression analysis, where the trait is the dependent variable and gender and age control variables are included along with up to ten principal components of the genotype matrix.[6] Polygenic risk scores can then be calculated for individual subjects in any sample that was not included in the original analysis. These scores are a weighted average of the SNP values where the weights are the associated betas.[7] Typically, the

[4] A website was created by the authors of the study to allow individuals to upload the results of genetic tests like 23andme and Ancestry.com for the purpose of calculating their polygenic risks scores using the methods developed in the paper. See "Clues to Your Health are Hidden at 6.6 Million Spots in Your DNA," New York Times, August 13, 2018, https://www.nytimes.com/2018/08/13/health/genetic-test-heart-disease.html?login=email&auth=login-email.

[5] Some SNPs have more than two possible alleles, but those are not commonly used in genome-wide association studies.

[6] The principal components control for population stratification and address the issue that some traits may be correlated with geographic or cultural ancestry.

[7] Because SNPs that are close to one another are not independently inherited, a phenomenon called linkage disequilibrium, several methods are used to determine which SNPs to include in the score. The polygenic risks scores in the Health and Retirement Study that are used in this paper use all available SNPs. An alternative method called LDPred uses a Bayesian approach to correct for linkage disequilibrium.

larger the sample used to derive the betas, the greater the percentage of the trait's variation that can be explained by the polygenic risk score, other things equal. If the summary statistics of a genome-wide association study are made public, polygenic risk scores can be calculated for any sample of individuals whose genetic data is available if they are not included in the original GWAS.

Polygenic risk scores have been calculated and tested for a number of behavioral and physical traits. The Health and Retirement Study includes polygenic risk scores based on summary SNP coefficients from a wide array of genome-wide associations studies. These include behavioral traits like neuroticism (Okbay, et al., 2016a), educational attainment (Okbay, et al., 2016b), autism (Anney, et al., 2017), smoking (Furberg, et al., 2010), and ADHD (Neale et al., 2010; Demontis, et al., 2017), as well as physical traits like body mass index (Locke, et al., 2015) and height (Wood, et al., 2014), and disease susceptibilities e.g. type 2 diabetes (Morris, et al., 2018) and coronary artery disease (Schunkert, et al, 2011). These polygenic scores can be used to study genetic influences on economic behaviors and outcomes.

Barth, Papageorge and Thom (2018) found that the genetically endowed abilities that lead to educational attainment, as measured by polygenic risk score, are more positively correlated with actual educational attainment for those from households with higher socioeconomic status than those from households with lower socioeconomic status, even though the distribution of the polygenic risk score is similar between socioeconomic groups. The educational attainment polygenic score is also positively related to labor income (Barth, Papageorge and Thom, 2018) and household wealth (Papageorge and Thom, 2018) even after controlling for the level of education completed. The relationship between household wealth and the genetic variants that predict educational attainment is in part mediated through the impact of genetics on financial decision-making. Those with lower educational attainment polygenic risk scores are more likely to have extreme assessments of stock market risks and are less likely to invest in the stock market.

A recent genome-wide association study with over 1 million subjects generated polygenic risk scores for self-reported risk tolerance. The trait was measured as the answer to one of two questions, the first given to subjects in the UK Biobank survey and the second asked of subjects in the 23andme cohort: (1) *"Would you describe yourself as someone who takes risks? Yes/No"* or (2) "*In general, people often face risks when making financial, career, or other life decisions. Overall, do you feel comfortable or uncomfortable taking risks?"* with 5 possible levels to choose from (Linnér, et al., 2019). Over six hundred genetic variants were found that were associated with self-reported risk tolerance, and the polygenic risk score was shown to be correlated with measures of risk tolerance elicited in surveys and with risky behavior.

Measurement of Risk Preferences. Risk preferences have been shown, both theoretically and empirically, to be related to individual risk taking and financial decisions. There are several methods for identifying risk preferences from survey data or in experimental settings. In the past, it was fairly common to infer risk preferences from individual portfolio choice (e.g. Bajtelsmit and Bernasek, 2001; Neelakantan, 2010), self-assessed risk attitudes (e.g. Bajtelsmit and Jianakoplos, 1998), or risky gamble choices in an experimental setting (e.g. Harrison, List,

and Towe, 2007). Financial advisors attempt to understand clients' risk profiles by assessing their answers to a series of questions.[8]

Several national surveys, most notably the Federal Reserve's Survey of Consumer Finances (SCF), have elicited investment risk attitudes by asking participants to answer the following question:

Which of the statements comes closest to the amount of financial risk that you and your (spouse/partner) are willing to take when you save or make investments?
1. take substantial financial risks expecting to earn substantial returns
2. take above average financial risks expecting to earn above average returns
3. take average financial risks expecting to earn average returns
4. not willing to take any financial risks

To economists, this question is not ideally designed to measure risk aversion because it cannot be used to identify a utility function and because respondents may differ in their understanding of the adjectives "substantial" "above average" and "average". Analysis of survey responses also calls the reliability into question in light of evidence that many respondents who say they are not willing to take any financial risks actually are holding stocks in their portfolios.

As an alternative to self-assessment of investment risk attitudes as above, the Health and Retirement Study (HRS)[9] elicits risk preferences through a series of "income gamble" questions developed by Barksy, Juster, Kimball, and Shapiro (1997). Respondents are asked to make a choice between a job with certain income and a job with risky income. The initial question asks:

Suppose that you are the only income earner in the family. Your doctor recommends that you move because of allergies, and you have to choose between two possible jobs. The first would guarantee your current total family income for life. The second is possibly better paying, but the income is also less certain. There is a 50-50 chance the second job would double your total lifetime income and a 50-50 chance that it would cut it by a third. Which job would you take—the first job or the second job?

Depending on the answer to this question, the respondent is given follow-up questions that vary the downside risk for the risky job, decreasing the risk if they did not select the risky job the first time, or increasing the risk if they did select the risky job. The complete selection of alternatives for downside risk include -10%, -20%, -33%, -50%, -75%. By observing the point at which respondents are willing to take the risk, each person is assigned to a risk tolerance category.[10]

[8] See Carr (2015) for an in-depth discussion of methods used for assessing client risk profiles.
[9] The Health and Retirement Study is a longitudinal biennial survey of individuals between the ages of 51 and 61 and their spouses. When the survey began in 1992, the primary respondents were ages 51 to 61. These households have been repeatedly surveyed every two years. Some other survey populations have been added to the historical data and additional households have been added to the HRS survey population over time such that the complete sample is now more than xxx unique households over 12 waves of the survey.
[10] The number of downside risk categories was increased from four to six in the 1994 survey. The frame of the question was changed in 1998 to remove the potential for status quo bias. In the initial surveys, respondents were asked to compare the risky job to their current job, but the question was rephrased in 1998 to presuppose that the person was required to switch jobs and thus was comparing a new safe job to a new risky job.

The advantage of this method of measuring risk tolerance, as compared to self-assessment, is that it is more objective. The disadvantage of the income gamble methodology is that it presumes that respondents understand probabilities sufficiently to make their selections.

Although the risk tolerance category measured by the income gamble questions has been shown to be significantly positively related to risky behaviors (such as smoking, drinking, borrowing, failing to have insurance, starting new businesses and risky asset holding), it has significant measurement error[11] (Anderson and Mellor, 2009). Individuals who answer the question over several waves do not always give the same responses. For this reason, it is necessary to use answers to these questions over multiple waves of the survey. For example, to address the measurement error issue, Kimball, Sahm, and Shapiro (2009) use an imputation method across several waves of the survey. They argue that this method produces a risk preference parameter that is superior to those used from single survey responses. Although the adjusted measure has been used to explain some financial decisions, such as investment in risky assets, little research has addressed other risk-related financial decisions. As an alternative, Beauchamp, Cesarini, and Johannesson (2017) regress demographic factors on the income gamble risk tolerance category over multiple waves of the survey. As will be described in more detail in the empirical section below, their risk tolerance measure is the average of the estimated residuals from these regressions.

Sociodemographic Factors Affecting Risk Preferences. Many studies have investigated the effects of individual sociodemographic characteristics (e.g. age, gender, income, and education) on financial outcomes. Although many studies have made conclusions about the effects of these variables, it is difficult to know whether the results are due to the characteristic itself or through its impact on an unspecified variable such as risk tolerance. There are also problems associated with interactions between different sociodemographic variables. Identifying the independent effects of these variables becomes even more complex when we attempt to estimate the impact of other genetic factors. Generally, the literature has shown that age and education are both positively associated with higher risk tolerance, higher savings and better credit decisions (Xiao, Chen, and Sun, 2015; Allgood and Walstad, 2013) and women tend to be more risk averse in their financial decisions (e.g. Bajtelsmit and Jianakoplos, 1998; van Rooij, Lusardi, and Alessie, 2011; Almenberg and Dreber, 2015).

Our research contributes to this body of literature by looking at the role that genetic variants affecting the Big Five personality trait of neuroticism have on individuals' risk tolerances and financial decision making. We control for the effects of the educational attainment polygenic score and extend the work of Papageorge and Thom (2018) by testing for its effect on additional measures of financial risk taking. We show that the neuroticism polygenic score is positively related to our measure of risk tolerance, which is calculated according to the method used in Linnér, et al. (2019). We then remove the effects of the neuroticism and educational attainment polygenic scores from the risk tolerance measure by creating a new measure from the residual of a regression of the polygenic scores and other control variables on the risk tolerances elicited over several survey waves. We explore whether the polygenic scores and the average residual risk tolerance have independent impacts on financial risk-taking behavior. In other words, do the

[11] For example, Anderson and Mellor document that participant responses over several waves of the HRS survey are often inconsistent.

genetic factors that are correlated with risk tolerance also impact financial risk taking in a direct manor or do they solely operate through their impact on risk tolerance? We find that the neuroticism polygenic risk score is negatively related to the percentage of total wealth invested in risky assets and to whether an individual invests in the stock market, controlling for residual risk tolerance. Like Papageorge and Thom, we find that the educational attainment polygenic risk score is positively related to whether an individual owns stocks, but also find that it is positively related to the percentage of total wealth invested in risky assets.

Data and Methodology

The data used for this study are from multiple waves of the Health and Retirement Survey, a biennial survey that was first fielded in 1992 with a nationally representative sample of individuals between ages 51 and 61 and their spouses.[12] With the addition of new cohorts, the sample now includes more than 20,000 individuals as well as data on previous participants who have since died. In addition to rich demographic and financial information on HRS households, the data includes DNA information and biomarkers obtained through Enhanced Face-to-Face interviews between 2006 and 2012. The total number with genetic information in the survey is now more than 15,000. Based on GWAS, polygenic scores for the HRS sample pool have been created for a variety of scientifically established phenotypes, with more being added as they are confirmed through analysis of larger genome-wide databases.[13] Although we use several waves of the survey to obtain the genetic data and risk tolerance measures, household financial data is from the 2014 wave of the HRS survey.

Descriptive statistics and data definitions are provided in Table 1.

Table 1 Summary Statistics

Variable	N	Mean	Std Dev	Minimum	Maximum
Female	37,495	0.562	0.496	0	1
Education Years	37,368	12.054	3.458	0	17
Birth Year	37,494	1,937	15	1,890	1,995
Single	18,744	0.380	0.485	0	1
Total Income	18,747	69,401	145,515	0	11,000,000
Net value of house	18,747	125,414	232,100	-3,860,000	12,200,000
Nonhousing wealth	18,747	316,930	2,073,152	-1,454,500	245,000,000
Nonhousing financial wealth	18,747	140,793	1,608,137	-1,499,500	202,000,000
Wealth (n/inc 2nd home)	18,747	442,344	2,139,111	-2,751,000	246,000,000
Total wealth (inc 2nd home)	18,747	467,634	2,551,348	-2,729,000	308,000,000

[12] For more information on the Health and Retirement Survey, see hrs.isr.umich.edu/about.
[13] Add note for source of PGS scores.

Winsorized total wealth	18,747	407,831	736,846	-56,000	4,675,000
Has_Stocks	37,495	0.601	0.490	0.000	1.000
Credit Card Debt/Income	37,495	3.319	333.980	0.000	43,750.000
Total Debt/Total Wealth	17,456	9	338	-127	35,714
RiskTol	20,281	-0.003	0.950	-1.666	2.662
RiskTolx	10,132	-0.004	0.920	-1.260	2.674
KSS rtol	11,616	0.206	0.068	0.087	0.732
KSS log_rtol	11,616	-1.841	0.302	-2.625	-0.475
PGS Neuroticism	12,090	0.000	1.000	-3.709	3.573
PGS Education	12,090	0.000	1.000	-3.688	3.810
Respondent Self employed	6,868	0.214	0.410	0.000	1.000
Respondent Ever Smoker	18,642	0.557	0.497	0.000	1.000

Measurement of the Risk Tolerance Phenotype

We first replicate the Beauchamp et al. (2017) estimation of the income gamble risk preference phenotype using the HRS income gamble questions described in the previous section.[14] For waves in which there were 6 choices, we convert to the 4-point scale, and we also reverse code such that a higher score corresponds to higher risk tolerance. Following the Beauchamp methodology, to reduce measurement error and to remove the effects of age and gender from this measure, we compute the residuals for each wave *w* of the survey with an OLS regression of the form:

$$y_{w,i} = \boldsymbol{X}_i\beta_i + \epsilon_{w,i},$$
$$\hat{\epsilon}_{w,i} = y_{w,i} - \boldsymbol{X}_i\hat{\beta}_w \qquad \text{[Equation 1]}$$

where $y_{w,i}$ is the income gamble risk tolerance in wave *w* for individual *i* and $\mathbf{X_i}$ is a vector of control variables for individual *i: BirthYear, BirthYearSquared, BirthYearCubed, Gender (1=Male)*, and interaction terms between the gender and the birth year variables. $\hat{\epsilon}_{w,i}$ is the estimated residual for each wave *w* regression.[15]

The risk tolerance phenotype $RiskTol_i$ is calculated for each survey participant as the average residual from the previous regressions over all available waves, $\hat{\epsilon}_i = \overline{\hat{\epsilon}_{w,i}}$. This results in a sample of xxx individuals for whom we have this risk tolerance phenotype, consistent with

[14] Kimball et al. (2009) use a maximum likelihood estimation method as an alternative method of reducing measurement error over the multiple waves of the survey. As a robustness check, we also run our regressions using the Kimball risk tolerance measures and find similar results. We opt to use the Beauchamp (2017) methodology for easier comparison to their genetic results.

[15] To ensure that gender and age effects are removed from their measure, Beauchamp et al add another step, regressing the averaged residual on the same gender and age control variables a second time and then using the residuals from that regression for their risk tolerance phenotype. In the second regressions, age and gender are not significant, confirming that the first residual methodology effectively removed the gender and age effects from the risk tolerance variable. We also replicate this result but, given that the two residual measures of risk tolerance are highly correlated and that use of the second version of the residual measure does not change the results, we opt to use the original averaged residual in our analysis.

Beauchamp, et al. (2017). The advantage of this measure over other risk tolerance measures (such as the Kimball, Sahm and Shapiro (KSS) measure or using direct results from the income gamble questions) is that it is independent of gender and age effects. This allows us to include gender and age as controls in later regressions where gender and age may be controlling for factors other than risk tolerance.

The Effect of Genetic Factors on Risk Tolerance

To determine whether genetic variation influences this measure of risk tolerance, again following to the Beauchamp methodology, we estimate Equation 2:

$$RiskTol_i = \boldsymbol{X_i}\,\boldsymbol{\beta_i} + \boldsymbol{PGS_i}\boldsymbol{\Theta_i} + \mathcal{E}_i \qquad \text{[Equation 2]}$$

where $\mathbf{X_i}$ is a vector of time-invariant control variables for individual i as above, and PGS_i is a vector of polygenic scores and their principal components.[16] Equation 2 is estimated using OLS regression with household fixed effects. The results of this regression are reported in Table 2. Because the *RiskTol* has been constructed to be independent of the $\mathbf{X}_i$ vector variables (Age, Gender, and their interactions), these are no longer significant factors and we can isolate the effects of genetic factors on this measure of risk tolerance. We therefore control for genetic factors using the polygenic scores for Educational Attainment and Neuroticism (*PGS Education* and *PGS Neuroticism*) and their principal component. These PGS have previously been linked to risky decision-making. The sample is all individuals who have answered the income gamble questions and have provided the necessary genetic information (n = 8,573). Both PGS scores are highly significant (PGS Education $p < .001$ and PGS Neuroticism $p < .05$). *Education Yrs* is also a significant control variable, indicating that this measure of risk tolerance is higher for the more-educated people in the sample.

Table 2 The Effect of Genetics on Risk Tolerance

Dependent variable is *RiskTol*, the average residual from OLS regressions of age, gender, and interaction terms on respondents answers to the HRS income gamble questions over multiple waves of the survey, estimated as in Beauchamp et al. (2017).

Variable	Coefficient	Std. Error	t	P>|t|
Constant	184.09	214.60	0.86	0.391
Female	-239.87	268.39	-0.89	0.371
Birth Year	0.0000	(omitted)		
Birth Year ^{2}	-0.0001	0.0002	-0.87	0.386
Birth Year ^{3}	0.0000	0.0000	0.87	0.384
Birth Yr X Female	0.0000	(omitted)		
Birth Yr ^{2} X Female	0.0002	0.0002	0.9	0.37
Birth Yr ^{3} X Female	0.0000	0.0000	-0.9	0.37

[16] Principal component analysis is commonly used for analysis of genetic data because it allows researchers to reduce the dimensions to the few principal components that explain main patterns.

Education Yrs	0.0263	0.0041	6.45***	0.000
PGS Neuroticism	0.0255	0.0121	2.11**	0.035
PGS Education	0.0403	0.0105	3.84***	0.000
Principle Components (Not Shown)				
* Significant at the .1 level , ** Significant at the .05 level, *** Significant at the .01 level.				
R-square	0.010			
Adj. R-square	0.009			
N	8,573			

Measuring Risk Tolerance Independent of Genetic Factors

Intuitively, it makes sense that genetic factors play a role in individual risk tolerance. The results from estimations of Equations 1 and 2 show that demographics and genetics are separate factors in risk tolerance measured through responses to the HRS income gamble questions. Ideally, however, we would like to isolate the impact of genetics on financial outcomes while controlling for other individual characteristics, including risk tolerance. To create a risk tolerance phenotype that is also independent of the PGS scores in our analysis, we extend the Beauchamp methodology by estimating Equation 3.

$$y_{w,i} = \boldsymbol{X}_i\beta_i + \boldsymbol{PGS}_i\Theta_i + \eta_{w,i} \qquad \text{[Equation 3]}$$

where $y_{w,i}$ is income gamble risk tolerance category in wave *w* for individual *i* and $\mathbf{X_i}$ is a vector of control variables for individual *i*, and $\mathbf{PGS}_i$ is a vector of polygenic scores and principal components. Similar to the process used to estimated *RiskTol* above, $\hat{\eta}_{w,i}$ is the estimated residual for each wave *w* regression. We define $RiskTolX_i$ as the average residual η_i from these regressions over all available waves: $\overline{\hat{\eta}_{w,i}}$. *RiskTolX* therefore represents a risk tolerance phenotype independent of the effects of age, gender, and the two polygenic scores.

The results of these regressions by wave are provided in **Table 3**. Although the specific results from the individual regressions are not the objective of this step in the procedure, we do note that the polygenic score for educational attainment has a consistent positive effect on the individual responses to the income gamble questions. Some of the controls in each of these regressions were omitted by STATA due to multicollinearity.

Table 3 Summary of t-statistics from Residual Regressions used to create *RiskTolX* average residuals

Dependent Variable: Income Gamble Risk Category						
	Wave 1	Wave 4	Wave 5	Wave 6	Wave 7	Wave 8
Female	-2.16	0.27	0.41	(omitted)	(omitted)	(omitted)
Birth Year	(omitted)	(omitted)	(omitted)	(omitted)	(omitted)	(omitted)

Birth Year^2	-1.1	1.52	-0.77	1.16	-0.3	-0.9
Birth Year^3	1.11	-1.51	0.78	-1.16	0.3	0.91
Birth Year X Female	(omitted)	(omitted)	(omitted)	(omitted)	(omitted)	(omitted)
Birth Year^2 X Female	2.15	-0.27	-0.4	-0.51	-0.23	0.99
Birth Year^3 X Female	-2.15	0.28	0.4	0.5	0.22	-1.01
PGS Neuroticism	2.41	0.04	0.28	-0.71	1.73	0.55
PGS Education	2.98	1.68	2.32	2.52	3.7	3.66
PC1_5A	-0.43	0.41	1.04	0.83	0.78	1.75
PC1_5B	-0.45	-0.83	-0.74	0.07	-0.29	2.12
PC1_5C	-1.2	-0.27	0.17	0.97	-1.2	-1
PC1_5D	-2.43	1.47	-1.53	-0.51	-1.6	0.51
PC1_5E	-0.89	-0.28	2.24	-0.59	-0.76	-0.03
PC6_10A	0	1.14	-1.47	-1.38	0.31	-0.42
PC6_10B	-0.98	-0.68	0.54	-1.37	0.71	1.11
PC6_10C	-0.15	-0.22	0.11	0.46	-0.6	0.87
PC6_10D	-0.75	-0.54	-0.68	-0.41	-0.23	0.23
PC6_10E	-1	0.57	-0.64	-1.15	-0.29	-0.86
Constant	1.09	-1.52	0.77	-1.16	0.31	0.89

The Effect of Genetics on Financial Decisions and Wellbeing

To evaluate the effects of risk tolerance and genetics on financial decisions and outcomes, we next estimate several models of financial wellbeing measures as a function of risk tolerance and other individual characteristics. These regressions take the functional form:

$$\text{FinancialWellbeingMeasure}_i = RiskTolX_i + \boldsymbol{X_i \beta_i} + \boldsymbol{PGS_i \theta_i} + \mathcal{E}_i$$

The previous literature has found risk tolerance to impact a variety of decisions, such as portfolio allocation, home-ownership, business ownership, debt ratios, and others.[17] As discussed earlier, these studies have tended to use self-assessed risk tolerance or survey measures such as the income gamble questions employed here. One of our contributions is to decompose the risk tolerance effects into components that are due to genetic variation ("nature") and components that are due to other individual characteristics ("nurture"). The coefficients on the PGS variables measure the nature effect and the coefficient on $RiskTolX_i$ measures the effect of risk tolerance that is not due to age, gender or either of the PGSs. For the regressions in which we are measuring household outcomes with ratios, we winsorize total wealth at the 1% level and limit the sample to those who have positive wealth. This also ends up removing a few extreme outliers that have been noted by the Rand economists who created the combined multiwave dataset.

[17] Cites TBA

Table 4 summarizes the results from this analysis.

Table 4 Effect of Risk Tolerance and Genetics on Household Decisions

which the dependent variable is a household variable hypothesized to be related to risk tolerance. The dependent variable for each regression is identified in the header row. *RiskTolX* is the average residual from OLS regressions of control variables on risk tolerance measured from the HRS income gamble questions over multiple waves of the survey. Controls include polygenic scores for Educational Attainment and Neuroticism, their principal components, and demographic variables. The model

	Model 1		Model 2		Model 3		Model 4		Model 5		Model 6	
Variable	Risky Assets to Total Wealth		Respondent Has Stock Investments		Debt to Total Income		Total Debt to Total Assets		Respondent Was Ever a Smoker		Respondent is Self Employed	
RiskTolX	-0.0008		0.0046	**	0.0144		0.3083		0.0217	***	0.0646	***
	(0.0023)		(0.0021)		(0.0128)		(0.2185)		(0.0067)		(0.0111)	
Education Years	0.0061	***	0.0065	***	0.0056		-0.0099		-0.0172	***	-0.0003	
	(0.0011)		(0.0010)		(0.0061)		(0.1048)		(0.0027)		(0.0049)	
Gender	0.0025		0.0075	***	0.0105		0.4258		-0.1798	***	-0.1015	***
	(0.0031)		(0.0029)		(0.0176)		(0.3002)		(0.0118)		(0.0207)	
Birth Year	-0.0001		-0.0011	***	0.0029		-0.0270		0.0025	***	-0.0119	***
	(0.0004)		(0.0004)		(0.0028)		(0.0478)		(0.0008)		(0.0014)	
Single	-0.0327	***	-0.0396	***	-0.0756		8.9528	***	0.0450	***	0.0058	
	(0.0102)		(0.0102)		(0.0974)		(1.6838)		(0.0138)		(0.0251)	
Total Income	0.0000	***	0.0000	***	0.0000		0.0000		0.0000	***	0.0000	***
	(0.0000)		(.0000)		(0.0000)		(0.0000)		(0.0000)		(0.0000)	
Nonhous FinWlth	0.0000	***	0.0000	***	0.0000	**	0.0000		0.0000		0.0000	*
	(0.0000)		(0.0000)		(0.0000)		(0.0000)		(0.0000)		(0.0000)	
PGS Neuroticism	-0.0048	**	-0.0038	*	-0.0145		0.3137		0.0119		0.0046	
	(0.0024)		(0.0023)		(0.0136)		(0.2318)		(0.0073)		(0.0123)	
PGS Education	0.0053	**	0.0083	***	0.0016		0.1268		-0.0213	***	-0.0155	
	(0.0021)		(0.0020)		(0.0119)		(0.2029)		(0.0064)		(0.0109)	
Constant	0.3197		2.2901	**	1.3318		58.03		-3.9277	***	23.5406	***
	(0.8227)		(0.7848)		(8.6832)		(92.748)		(1.4649)		(2.7808)	
Principle Components not shown												
R square	0.06		0.11		0.00		0.00		0.05		0.10	
HH Fixed Effects	Yes		Yes		Yes		Yes		Yes		Yes	
Number of Observ	6,658		6,733		6,733		6,604		6,706		1,324	
Number of Groups	4,847		4,910		4,910		4,801		4,898		1,034	
* Significant at the .1 level , ** Significant at the .05 level, ***												

It is interesting to see that genetics play a significant role for the ratio of risky assets to total wealth, but *RiskTolX* is not. As a robustness check, we also ran this regression with the original *RiskTol* variable and two versions of the Kimball risk tolerance measure (rtol and log_rtol) with similar results. In each case, the risk tolerance variable was not significant and the PGS scores were (marginal significance for PGS Neuroticism and strong for PGS Education. Contrary to our expectations, we found no significant relationship between the two debt ratios (Total credit card debt to Total income and Total Debt to Total Wealth) and either risk tolerance or the polygenic scores. In contrast, the choice to hold stock investments (defined as stocks, mutual funds and investment trusts) is significantly positively related to both risk tolerance and the PGS for Education. Neuroticism has a negative effect on the risk of the portfolio and also on stock ownership.

As a further test of the independent effects of genetics and other factors, Table 4 also includes two measures of personal risk-taking, smoking and small business ownership. Our prior hypotheses were that individuals may have genetic predispositions to these types of risk-taking, but that there are other sociodemographic factors that may influence such decisions. Previous research has linked various measures of risk attitudes to both of these decisions. The dependent variable for the smoking regression is a dummy variable equal to 1 if the respondent has ever been a smoker.[18] Both *RiskTolX* and *PGS Education* are significant factors in whether a person has ever been a smoker. The dependent variable for the small business regression is a dummy variable equal to 1 if the respondent is self employed.[19] Here we find that neither PGS is significant, but that *RiskTolX* is a highly significant factor. In addition to the models shown in Table 4, we have also considered several other measures of household finances.

Conclusions

In this paper, we contribute to the literature by developing a novel measure of risk tolerance that is independent of age, gender and certain genetic factors. This allows us to better explain heterogeneity in financial decisions based on individual differences in risk tolerance, and to decompose that effect into factors that are due to genetic differences versus other factors. Our study focuses on the role that genetic variants affecting the Big Five personality trait of neuroticism have on individuals' risk tolerances and financial decision making. We control for the effects of the educational attainment polygenic score and extend the work of Papageorge and Thom (2018) by testing for its effect on additional measures of financial risk taking. We show that the neuroticism polygenic score is positively related to our measure of risk tolerance. We then remove the effects of the neuroticism and educational attainment polygenic scores from the risk tolerance measure by creating a new measure from the residual of a regression of the polygenic scores and other control variables on the risk tolerances elicited over several survey waves. We explore whether the polygenic scores and the average residual risk tolerance have independent impacts on financial risk-taking behavior. In other words, do the genetic factors that are correlated with risk tolerance also impact financial risk taking in a direct manor or do they solely operate through their impact on risk tolerance? We find that the neuroticism polygenic risk score is negatively related to the percentage of total wealth invested in risky assets and to

[18] In an unreported regression, we also use a dummy variable equal to 1 if the respondent is currently a smoker. The results from that regression are extremely similar to those reported here.
[19] In an unreported regression, we also use a dummy variable equal to 1 if the respondent's spouse is self employed.

whether an individual invests in the stock market, controlling for residual risk tolerance. Like Papageorge and Thom, we find that the educational attainment polygenic risk score is positively related to whether an individual owns stocks, but also find that it is positively related to the percentage of total wealth invested in risky assets.

We find that 1) the polygenic scores for neuroticism and educational attainment are both factors determining individual risk tolerance; 2) when risk tolerance is measured independent of these polygenic scores, it is still a significant factor determining stock ownership, self-employment, and smoking; 3) the polygenic score for educational attainment is consistently a significant factor in many financial decisions; and 4) inclusion of polygenic scores in models of financial decision-making improves predictive power and betters our understanding of differences based on gender, income, wealth, and other individual characteristics.

Future research is needed to further explore these relationships and to consider other financial outcomes that may be explained by genetic factors. Because genetic research is in its infancy, these results do not have clear practical implications. However, the future may be quite different. Currently, geneticists are investigating the effects of many gene combinations and it may someday be possible to be tested for propensities related to financial decisions. As with risk questionnaire methodologies currently in use by financial advisors, knowing your "type" and using that knowledge to make constructive changes in behavior are two very different things.

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