PSYCHOLOGICAL CONSEQUENCES OF GENETIC TESTING

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A Thesis Presented to

The Faculty of Humboldt State University

In Partial Fulfilment of the Requirements for the Degree

Master of Arts in Psychology: Academic Research

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May 2017

Abstract

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Direct-to-consumer genetic testing describes genetic testing which is done using online or mail in services, without the direct supervision of a counselor or physician. Individuals can order information about their ancestry, trait information, and even disease risk information. Online testing services have previously been prevented from offering certain types of genetic self-knowledge to consumers due to government regulation, however, there is little information available about how genetic self-knowledge may affect consumers. The present study evaluated whether simply believing oneself to be genetically disadvantaged could cause an individual to perform poorly on a working memory task.

University students participated in a two-part study which was advertised as investigating the impact of the COMT gene. COMT is a gene that regulates the production of COMT enzymes, which break down dopamine in the pre-frontal cortex, and in turn may impact certain cognitive abilities. During session one, participants were exposed to information about differences between two genetic groups: Met allele carriers, and Val allele carriers. Under deception, participants submitted a saliva sample. The saliva sample was disposed of, and participants were randomly assigned to be either Met

allele carriers or Val allele carriers. During session two, participants were informed of their genetic group. Val allele carriers were told that they possessed a genetic disadvantage, and Met allele carriers were told that they possessed an advantage. Participants took a computerized card sorting task designed to measure their working memory ability both before and after they received genetic information. Additionally, participants took a survey which measured to what extent they believed genetics could affect their abilities. I expected to find that Val allele carriers would perform significantly worse than Met allele carriers on the card sorting task. Additionally, I expected to find that genetic essentialism beliefs would impact card sorting scores. Genetic essentialism describes a belief where our genetics are very deterministic of our abilities and traits.

I found no evidence of a genetic stereotype threat. Val allele carriers did not decrease significantly in their performance between baseline and posttest. There was evidence for a stereotype lift effect, Met allele carriers performed slightly better after hearing they had the advantaged gene. Additionally, I found no evidence to support that genetic essentialism beliefs impacted card sorting scores.

Acknowledgements

I have no shortage of gratitude for the many people in my life who helped make this thesis a reality. Entering graduate school, it seemed as if my thesis would be the most substantial solo undertaking of my lifetime. I was wrong. My thesis required the help, attention, and patience of many people. In no particular order, and in too few words, I'd like to thank the following people:

Dr. Chris Aberson. I think it suffices to say that we've jived well together over these past four to five-ish years, and my gratitude to you extends well beyond this thesis. R on.

Dr. Ethan Gahtan. I have sincerely enjoyed working on this project with you, and I seem to recall it was your idea in the first place.

Dr. Amber Gaffney. Thank you for always being a sounding board for my one thousand and ten ideas, and of course always sharing yours.

Neha Arora, for doing so much of the groundwork for this research.

All my fellow lab mates who worked for free to help collect data: Mike, Ben, other Ben, Cat, Hannah, Lily-pad, Maria, Natasha, and Olivia.

My family, especially my dad, without whom I'd never finish anything I started.

My friends and coworkers, who were a great source of comic relief.

And in no way the least, Anthony, my partner, who smiled the whole way through a very exhausting two years.

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Psychological Consequences of Genetic Testing

Human behavior is the product of a complex interaction between genetics and environment, but neither sufficiently explains behavior (Goldman, 2010). An individual's genetics can tell us that they are predisposed to schizophrenia or other psychiatric diagnoses (Craddock, Owen, & O'Donovan, 2006). This information allows us to assess risk factors or tailor treatments. Because individuals increasingly have access to their own genetic information through personal genome services, such as 23andme.com, it is important to evaluate the consequences of genetic self-knowledge.

One widely researched gene, Catechol-O-methyltransferase (COMT) has attracted attention in the popular media. For example, a New York Times article explored how variations in this gene may "explain to a large degree" why some children perform better under stress in school than others (Bronson & Merryman, 2013). The article offers anecdotes of intelligent children who are sickened by stress, whereas their equally gifted siblings and classmates are unaffected by test anxiety. The explanation posited in the article is that perhaps a single nucleotide polymorphism in the COMT gene translates to dramatically different stress responses in the children.

The polymorphism in codon 158 of the COMT gene involves substitution of a valine (*val)* allele for the methionine (*met)* allele, resulting in more efficient breakdown of dopamine (Lachman et al., 1996). Val allele carriers consequently breakdown the neurotransmitter dopamine more quickly in the prefrontal cortex, leaving less dopamine

available for neurotransmission. Met allele carriers break down dopamine slower, leaving more dopamine available for neurotransmission. Many researchers believe this difference in dopamine transmission is responsible for emotional and cognitive differences. Since the popularity of COMT research has grown, Met allele carriers have been named "worriers" for their advantageous cognitive skills, and Val allele carriers have been named "warriors" for their emotional resilience (Zhu et al., 2004).

In my research, I will investigate whether knowledge of one's genetic group (Val or Met) impacts future behavior. Informing an individual that their cognitive ability or emotional resilience is genetically predetermined may have unforeseen consequences. With the advent of direct-to-consumer genetic testing (e.g., 23andme.com), it is important to consider the impact of genetic self-knowledge in this particular domain. Knowledge of hereditary or genetic predispositions to illness has had inconsistent effects on future behavior (Marteau & Weinman, 2006), but the impact of self-knowledge regarding COMT status has not been explored.

My study will evaluate how university students react to knowledge about their COMT status. Employing a stereotype threat model (Steele & Aronson, 1995), I will investigate whether individuals conform to expectancies about their abilities based on the Val "warrior" or Met "worrier" stereotypes. Additionally, I will investigate the role that genetic essentialism (Keller, 2005) plays in susceptibility to stereotype threat performance changes. Genetic essentialism describes a belief that our genetics determine our abilities and the type of person we are. Based on previous research about essentialism

and prejudice (Haslam, Bastian, Bain, & Kashima, 2006; Keller, 2005), it is possible that genetic essentialism beliefs may change the individual impact of genetic information.

Literature Review

Direct-to-Consumer Genetic Testing

Direct-to-consumer genetic testing allows individuals to order genetic information through a service rather than a medical provider. One popular example is the website 23andme.com. The genetic information included in the analysis provides consumers with information about their physical traits (i.e. male pattern baldness in adulthood), ancestry information, and disease risk. In 2013, 23andMe Inc. was ordered by the U.S. Food and Drug Administration (FDA) to immediately stop their service (Yim & Chung, 2014). The FDA warned that genetic disease risk information should only be accessible under the supervision of a clinician qualified to discuss the results. Genetic test results from 23andme.com now feature non-diagnostic disease risk information, such as genetic contributions to late onset Alzheimer's disease, and Parkinson's disease. .

Genetic risk information. It is possible that information about disease risk can have negative psychological consequences, and there is additional concern about the use of genetic testing for risk of psychological disorders (Rimes & Salkovskis, 1998). Genetic tests may improve pharmacological treatment for psychiatric disorders, but not all psychiatrists agree about risks associated with direct to consumer testing (Thompson, Hamilton & Hippman, 2015). Research about how genetic testing affects patient outcomes primarily involves discussing disease risk information in a clinical setting, such as discussing genetic markers for Huntington's disease, hereditary breast and ovarian cancer, and other illnesses (Broadstock, Michie, & Marteau, 2000).

Genetic self-knowledge about disease risk has variable effects on behavior depending on how many genes might factor into the illness, what role the environment plays, and whether or not the individual feels they can control the fate of their disease (Marteau & Weinman, 2005). Because the average consumer finds genetic information deterministic (Dar-Nimrod & Heine, 2011), personal genome services should consider the influence of genetic self knowledge on consumers.

Catechol-O-methyltransferase (COMT)

One single nucleotide polymorphism at codon 158 of the Catechol-O-methyltransferase (COMT) gene, Val158Met, alters the amino acid sequences of the COMT enzyme responsible for breaking down dopamine in the brain. Individuals who inherit the Met allele have considerably lower COMT enzymatic activity, and higher resting dopamine levels than Val allele carriers (Lachman et al., 1996). It has been suggested that the mechanism through which COMT variation affects cognitive performance is by modulating dopamine activity in the pre frontal cortex, differentially regulating executive function such as that required for working memory tasks (Aguilera et al., 2008; Egan et al., 2001). In the following sections, I will address how variation in the COMT gene affects dopamine transmission, and how changes in dopamine levels affect behavior.

COMT and dopamine. The relationship between available dopamine in the synapse and prefrontal cognition is complex and affected by whether one carries the Val or Met allele variant. It is unlikely to be a linear relationship such that more dopamine is better. Some researchers have suggested a curvilinear relationship between dopamine and

cognitive function, meaning that too much or too little may be detrimental (Craddock, Owen & O'Donovan, 2006). A similar idea has been applied to the relationship between dopamine and positive emotionality, where researchers describe a "Yin and Yang" effect of dopamine levels. Higher dopamine levels do not translate to positive emotionality indefinitely, despite the advantage of carrying the Val allele in this specific context (Felten, Montag, Markett, Walter, & Reuter, 2011). Still, it would seem that there are advantageous and disadvantageous qualities of both allele variants.

COMT phenotypes. Variation in Met and Val COMT activity relates to cognitive and emotional differences. Met/Met carriers are stereotyped as "worriers", and Val/Val carriers "warriors" (Zhu et al., 2004). Val homozygotes, individuals who carry two copies of the Val allele, demonstrate an advantage in processing aversive stimuli, protection against pain susceptibility, and perform better on memory tasks under stress (Stein, Newman, Savitz & Ramesar, 2006). Carriers of the Met allele perform better than Val warriors on tasks such as verbal working memory (Aguilera et al., 2008) and problem solving (Malhotra et al., 2014). A study evaluating reading performance found that Met carrier children had better phonological awareness and spelling skills, but found no difference for overall reading comprehension (Landi et al.,2013). Another study found that carriers of the Met allele scored higher on a measure of impulsivity than Val carriers, so Met allele carriers are not necessarily always at an advantage (Soeiro-De-Souza, Stanford, Bio, Machado-Vieira & Moreno, 2013).

Not all COMT research concludes that cognitive differences exist between Val and Met allele carriers, including an extensive review of studies utilizing cognitive

measures to compare the groups (Barnett, Scoriels, & Munafò, 2008). Some authors find mixed results between measures that address the same construct (i.e. working memory). One study found that a significant cognitive difference only emerged between Val and Met carriers on one of four measures of working memory (Bruder et al., 2005). Consistent with previous research, the same authors found that Met allele carriers outperformed Val allele carriers on a computerized version of the Wisconsin Card Sorting Task (WCST).

The WCST will be used in the present study. Rather than further investigating true Val and Met carrier differences on this task, I will investigate whether or not group differences in future research may result from knowing one's carrier status and the strengths or weaknesses associated with either allele. Although COMT research generates mixed findings on cognitive differences between Val and Met carriers, studies which utilize the WCST have been consistent in their findings. In the present study, participants will be given mock genetic test results. If group differences on the WCST are demonstrated, there will be a plausible alternative explanation. The present study will investigate whether stereotype threat effects, as described below, may serve as an alternative explanation for COMT group differences.

Stereotype Threat Model

The stereotype threat model posits that individuals confronted with stereotypes about their group will underperform on a variety of outcomes compared to a non-stereotyped group (Steele & Aronson, 1995). Meta analytic approaches have found overall support for stereotype threat effects, and have also found evidence of several

moderators (Lamont, Swift & Abrams, 2015; Nguyen & Ryan, 2008). Stereotype threat effects are found across a variety of group memberships, though stereotypes related to race seem to produce larger effect sizes than stereotypes related to gender (Nguyen & Ryan, 2008). Similarly, the subtle presence of a stereotype produces larger effect sizes than situations where group differences are presented as factual information (e.g., cognition is shown to have declined with age; Lamont et al., 2015).

Pioneering research on stereotype threat found a significant main effect for number of correct verbal GRE questions answered, where Black students underperformed compared to White students. There was a significant interaction between race and test description, where Black participants in a condition described as diagnostic of ability performed worse than Black participants in a condition described as non-diagnostic and worse than White participants in the diagnostic condition (Study 2; Steele & Aronson, 1995). When researchers presented the test as non-evaluative of the participant's ability, the performance gap between White and Black participants closed.

Any person in a stigmatized group can experience stereotype threat effects (Steele & Aronson, 1995). Stereotype threat might be influenced by, but is distinctive from, other performance anxieties in testing situations. In addition to the test domain being relevant to the stereotype, (i.e. stereotypes exist that Black Americans have poor verbal skills) the test domain must also be relevant to the individual, (i.e. a student cares about their intelligence). In the Steele and Aronson (1995) study the stereotypes were never presented to the participants directly. The researchers believe the stereotypes were implied as the test was evaluative of verbal ability, and there were well known social

stereotypes about verbal ability and race. The researchers found evidence of stereotype activation using a word completion task (Study 3). Black participants in the diagnostic condition completed more stereotype related items than Black participants in the non-diagnostic condition.

Additionally, they discovered that simply asking participants to report their race before taking an evaluative test was enough to trigger poorer test performance. Black participants asked to report their race performed significantly worse than Black participants not asked to report their race. In sum, the authors provided evidence that stereotypes alone can have a negative impact on a stigmatized individual's academic performance, regardless of their true ability. Research following this original work has demonstrated that stereotype threat effects are not limited to race.

Stereotype threat in gender. Stereotype threat effects also exist in the gender domain. One study found that students matched for mathematics ability performed differently on mathematics GRE questions as a function of gender and testing condition. The study included both men and women in either a no gender difference condition, or a condition where participants were informed that men were better at math. Female participants who were told they were taking a test to confirm that men were better at math performed worse than female participants who were told there was no gender difference, and a significant sex by condition interaction was revealed. Men and women in the group told there were no gender differences performed equally well (Spencer, Steele, & Quinn, 1999).

Stereotype threat in non-marginalized groups. Stereotype threat effects have also been demonstrated in non-marginalized groups, such as Christians, where group identity is not as salient as gender or race. One study investigated stereotypes about Christians having low scientific competence (Rios, Cheng, Totton, & Shariff, 2015). When stereotypes about low scientific competence were made salient to Christian students in a high threat condition, they identified less with science compared to non-Christian students. Christians in the high threat condition also underperformed compared to non-Christians on a syllogism logical reasoning task when it was presented as a task of scientific ability. When a remote associations task was presented as a measure of intuitive thought (non-scientific), there were no significant group differences. Although the effect size for each of these studies is small, it is evident that non-marginalized groups can also be impacted by stereotype threat to some degree.

Stereotype threat effects have also been demonstrated in White men. One study primed White male students with information suggesting that Asians have superior mathematics skills and often outperform White students. Students in the stereotype threat condition solved less GRE mathematics questions correctly than students in the control condition. A follow up study with calculus students found that how much the participant identified with math mediated the stereotype threat effect. Calculus students who were highly identified with mathematics and primed with stereotype threat underperformed, but students under threat who were moderately identified with mathematics did not underperform compared to the control group (Aronson et al., 1999).

Stereotype threat and genetic groups. Whether or not stereotype effects might be found in genetic groups has not been researched. COMT allele status, unlike sex or race, is not a visible trait, nor a trait many individuals know about themselves. Stereotype threat effects have been found in individuals with minor head injury, a phenomenon the authors refer to as "diagnosis threat" (Suhr & Gunstad, 2002; 2005). If having a diagnosis for an illness may influence patients to change their future behavior in spite of their true abilities, it may be plausible that consumers who purchase personal genome services may view their genetic information as being deterministic of their abilities. My study will investigate whether being provided with genetic information about oneself can produce a stereotype threat effect in students.

Statement of the Problem

Stereotype threat effects are associated with poor performance on standardized tests and cognitive measures (Cadinu et al., 2002; Maas & Cadinu, 2003). Under pressure to perform well individuals in a stereotyped group tend to perform poorly, despite being equally competent as non-stereotyped individuals. Pioneering stereotype threat research primarily evaluated socially marginalized groups, such as women (Spencer, Steele, & Quinn, 1999) and Black students (Steele & Aronson, 1995). Typically non-marginalized groups such as White men (Aronson et al., 1999) and Christians (Rios et al., 2015), can underperform under stereotype threat conditions.

A stereotype threat study investigating self-knowledge of genetic group has not been conducted. Individuals can learn about their genetic makeup through direct-to-consumer genetic (DTC) testing services like 23andme.com, but the impact of information unrelated to disease risk (i.e. traits) has not been evaluated. Because disease risk information is included in the individual's personal genome report, the U.S. Food and Drug Administration had previously tried to sanction 23andMe Inc. from offering their service (Yim & Chung, 2014). The controversy over DTC genetic testing comes from the concern that genetic self knowledge, especially disease risk information, will be misinterpreted by consumers. Information about interpreting DTC genetic tests is readily available online, though the company 23andme.com recommends consumers consult a genetic counselor about their test results. It is possible that information about disease risk can have negative psychological consequences (Broadstock, Michie, & Marteau, 2000),

and there is additional concern about the use of genetic testing for risk of psychological disorders (Rimes & Salkovskis, 1998). The literature has not considered whether or not non-disease risk information included in the report can have a negative impact on the consumer.

Behavioral genetics research implicates a single nucleotide polymorphism in the COMT gene as a potential cause of cognitive differences between individuals, specifically that Met allele homozygotes have better working memory, verbal skills, and higher IQ than Val allele carriers (Aguilera et al., 2008; Barnett et al., 2009; Malhotra et al., 2014). COMT has been one of the most studied genes in psychiatry, especially because it is implicated in schizophrenia (Craddock et al., 2006), but much of the literature concerns Val and Met allele cognitive differences.

As research about the cognitive differences between healthy Val and Met allele carriers grows, the impact of knowing one's carrier status should be evaluated. Many individuals view genetics as fatalistic and immutable (Dar-Nimrod & Heine, 2011), and research has shown that genetic disease risk information has a different impact on patients than lifestyle or environmental risks (Marteau & Weinman, 2006). Considering the public's attitude toward genetic information, it is possible that personal genome service customers may self handicap if they discover they are carriers of the seemingly less beneficial COMT Val allele. Research has also found that individuals who have beliefs high in genetic essentialism have more prejudice attitudes (Keller, 2005), which may relate to any impact genetic information has on consumers.

The purpose of this research is to evaluate what impact COMT allele carrier status may have in college students. Employing a stereotype threat model, I will evaluate whether being labeled a Val carrier and being informed of the stereotypes about this group from the literature will lead to lower performance on a cognitive measure. Students will serve as the consumers and will be randomly assigned to be Val or Met carriers. All genetic testing and personal genome results will be falsified. This study may help elucidate potential consequences of DTC genetic testing. A potential benefit of this study is its implications to medical practice and genetic counseling. The experimental design of the study will allow us to more directly observe what impact being given genetic information has on an individual in a way that would not be feasible in clinical practice. It would be unethical to experimentally provide individuals with disease risk information under deception, but COMT allele carrier status may be a useful analogue.

Primary Research Hypotheses

Hypothesis One. Val allele carriers will perform significantly worse on the Berg Card Sorting Task (BCST) than the Met allele group after the stereotype threat is introduced.

Rationale. Stereotype threat research has demonstrated that an individual in a stereotyped group will underperform on a variety of cognitive measures compared to the non-stereotyped group individuals, especially when the stereotype is made immediately salient (Steele & Aronson, 1995; Spencer & Steele, 1999). Students will be randomly assigned to either be Val or Met allele carriers, and informed that research has found that Met allele carriers have superior cognitive processing. If the students believe their fake

genetic report, they may buy into their role as a Val or Met carrier. If stereotype threat effects can be found in this domain, then Val carriers should experience a deficit in performance compared to Met allele carriers.

Secondary Research Hypotheses

Hypothesis Two. Val carriers high in genetic essentialism beliefs will perform significantly worse on a cognitive test than Val carriers low in genetic essentialism beliefs.

Hypothesis Three. Genetic essentialism beliefs will be unrelated to performance for Met carriers.

Rationale. Genetic essentialism is a mindset where individuals perceive others as having immutable, natural, genetic or biological essences which explain their behavior and ideas. This mindset encourages one to understand other people as belonging to homogenous and discrete groups, therefore explaining their stereotyped behaviors as part of their innate nature (Haslam, Rothschild & Ernst, 2002). Research has found that prejudice and stereotyping are associated with genetic essentialism, and that increased prejudice beliefs can be experimentally primed in individuals who score high in genetic essentialism (Keller, 2005). I hypothesize an interaction effect between genetic essentialism and the stereotype threat condition, such that Val carriers highest in genetic essentialism beliefs will have the lowest scores of all the conditions. Genetic essentialism beliefs will be measured using the Beliefs in Genetic Determinism Scale (Keller, 2005). If genetic essentialism beliefs do interact with stereotype threat effects, then Met carriers should be unaffected as they are not the target group.

Method

This study utilized a between-subjects experimental design where the independent variable was genetic group, and the dependent variable was test performance. Test performance was measured both before and after the threat was introduced to obtain a baseline measure of ability. Beliefs in genetic essentialism were evaluated as a potential covariate of the effect of group on test performance. Participants were randomly assigned to either be a Val or Met carrier.

IRB Approval and Ethical Adherence

Institutional Review Board (IRB) approval for this experiment was renewed on November 18th 2016 under approval number IRB 15-097. I was granted an informed consent waiver as the initial informed consent was deceptive (Appendix A), and did not disclose the true purpose of the study to participants. Participants were asked for true informed consent (Appendix D) and permission to use their data in analyses after debriefing, at which time they had the option to withdraw their data. All participant information was kept as confidential as possible by identifying their surveys and results using a randomly generated ID number. Paper surveys and informed consent were stored in locked restricted access lab on campus. Each research assistant on my research team had completed the IRB Refresher Course for Human Subjects Research.

Participants

Participants were Humboldt State University Students (n = 49), who were predominantly female (70%) with a median age of 21 years old. Stereotype threat

research typically tests participants in groups, so participants were run in groups of up to six students. Effect sizes in stereotype threat research are highly variable, and depend on what the target of the threat is (i.e. race, gender, or age). Because of this variability, and the uniqueness of this study design, determining a target effect size for power analysis requires approximation. Studies which address "diagnosis threat" (Suhr & Gunstad, 2002; 2005) were most similar to this design, and used to approximate effect sizes. Power analysis in R using the package "pwr" revealed that to achieve a similar effect size (d = .40), a sample size of approximately 156 participants was required (78 per group; $\alpha =$ .05, power = .80). Data were collected until the end of April 2017, producing a total of (n = 25) for the Met group and (n = 24) for the Val group. Post hoc power analyses were done using the package "pwr" in R. To detect a mean differences of d = 0.29 between groups on posttest scores, I had power of .13 given my sample size. To detect mean differences of d = .07 between testing times for the Val group, I had a power of .06. To detect mean differences of d = 0.93 between testing times for the Met group, I had a power of .95.

Recruitment. Participants were recruited through the University's SONA Systems Psychology Research Pool. In addition to hanging recruitment posters around campus, I presented my research in selected courses to bolster participation. Participants were granted course credit for their voluntary participation. Participants were also entered into a raffle to win one of two Amazon gift cards.

Materials and Apparatus

The study took place in a reserved computer lab at Humboldt State University in the Behavioral and Social Sciences building. Signs were hung on the door of the room to limit interruption and distraction. Participants each had one computer and workspace.

Mock genetic tests. Participants were informed that prior to their research appointment they needed to submit a saliva sample to a reserved lab in the BSS at least 24 hours before the study will take place. To obtain mock genetic tests, participants were asked to collect their saliva onto a sterile cotton swab, which was then transferred to a test paper. All materials for the saliva sample were materials that could be utilized in a saliva based PCR analysis for genetic testing. After the participant left, the researcher disposed of their saliva sample into a biohazard bag. No genetic test was done with the saliva sample, but the deception was intended to seem genuine.

Genetic test results. Participants were provided with a mock genetic test result during the second research session prior to taking the card sorting task for the second time (Appendices B & C). The genetic test results were prepared prior to the session, and delivered in a sealed envelope with the participant's confidential ID number written on it. The genetic test result paper was generated from real test result templates.

Presentation and script. To ensure consistency between testing sessions, the research assistant conducting the second session was given a script and slide set to follow. Both research assistants that ran the second session practiced together for consistency. The research assistant used a PowerPoint presentation to educate participants about their genetic group, and group differences.

Assessment and Measures

P.E.B.L. I used the Psychology Experiment Building Language (PEBL; Mueller & Piper, 2014) program to administer a test of working memory, as well as a survey on genetic attitudes (Appendix F). PEBL is a free open source program which has been growing in popularity since it's creation in 2006. Researchers can create their own measures in PEBL, or modify existing ones using the coding language C++. Many of the measures included in the PEBL battery are free versions of trademarked pay for use cognitive batteries. To avoid copyright and trademark infringement, all PEBL batteries must use completely new stimuli, sounds, imagery and source code.

Wisconsin (Berg) Card Sorting Test (BCST).

The PEBL BCST is the most widely cognitive measure of the entire battery, and has been used in more than a dozen reports (Piper et al., 2015). The measure is taken on a computer. Participants are shown four stacks of cards, each stack contains a different number, color and shape. The object of the task is to sort a series of cards into the stacks following a sorting rule. Participants selected the pile they thought the card belonged to. After each pile selection, the participant was given automated feedback about whether they selected the right pile for the card. The rule for sorting changed as frequently as every ten cards, requiring cognitive flexibility to continue figuring out the sorting rule. The WCST produces many dependent measures, such as total correct responses and preservative error. A preservative error refers to when the participant uses the previous rule to sort the card, indicating that they have not learned the new rule. A lower score of

preservative errors means better performance on the task (Piper et al., 2012; Piper et al., 2015; Piper, Mueller, Talebzadeh, & Ki, 2016).

Beliefs in genetic essentialism. Genetic essentialism was measured using the Belief in Genetic Determinism (BGD) scale (Keller, 2005). The 18 items on the BGD had acceptable internal consistency for the study ($\alpha = .80$). Discriminant validity of this measure was previously demonstrated by low correlations with measures of self-efficacy ($r = .09$, $p > .05$), self-determination ($r = .04$, $p > .05$) and social-desirability ($r = .09$, $p > .05$). The scale has convergent correlations several scales which measured negative attitudes towards adoption ($r = .30$, $p < .01$), and both blatant ($r = .38$, $p < .001$) and subtle prejudice ($r = .30$, $p < .001$; Keller, 2005).

Debriefing questionnaire. Participants completed a debriefing questionnaire (Appendix D) immediately after being debriefed about the nature of the study. The debriefing questionnaire asks participants to indicate whether or not their believed the deception. This question serves as a manipulation check to use during the analysis and will be used in exploratory analyses for future research directions. Participants are also asked to indicate whether or not they thought their test result and genetic group accurately described them. Previous stereotype threat research has found that identifying with one's group can act as a moderator of stereotype threat effects, where individuals are not generally impacted by stereotype threat if they do not identify strongly with the stereotyped group (Maas & Cadinu, 2003). Because COMT allele status is not an established social identity, I have no specific hypothesis regarding group identification as a moderator in my study. Additionally, I asked participants how much they knew about

human genetics before coming into the study, and what percentage of human behavior they thought was due to genetic influence.

Procedure

Saliva collection and analysis. Participants were instructed to report to a reserved room to submit a saliva sample no less than 24 hours before their second study time. Participants consented to the saliva sample using the deceptive informed consent (Appendix A). The research assistant instructed the participant to collect their saliva onto a sterile swab. The researcher then applied the saliva to the test paper in plain view within the participant. When activated by saliva, the test paper turns a different color. The researcher then disposed of the swab into a sterile biohazard bin and dismissed the participant.

Introduction and waived informed consent. Participants reported to their second testing session as early as 24 hours after their saliva sample was given. Sessions were run in groups of up to six students. Each participant was provided a computer station to work at in a quiet, reserved room. The researcher was guided through the second session by a slide set and script. The researcher greeted the participants, explained the agenda of the study, and review the deceptive informed consent (Appendix A), reminding participants that they are free to stop participating at any time without consequence.

Baseline testing.

Participants completed the computerized Berg Carding Sorting Task (BCST) using PEBL to collect a baseline measure. At this point, participants had not received

their test results or the presentation about genetic differences, so no "threat" had been introduced. Participants were told that this testing session was only to ensure that the program was working properly.

Genetic test results. Participants were instructed to open their genetic test result. The researcher explained how to interpret the test results, instruct the participants to pay most attention to the "allele type" Participants who tested negative for the "G108A mutation" were Val/Val carriers (Appendix C). Participants who tested positive for the "G108A mutation" were Met/Met carriers (Appendix B). The genetic test result also contained a short description of the enzymatic activity of each allele, and re-iterates that Met allele carriers have an advantage due to increased dopamine levels available for synaptic signaling in the pre-frontal cortex. Participants were informed that those who tested "undetermined" for the mutation are likely heterozygotes (Val/Met), but this is only to ensure the deception is authentic. No participant was assigned to this condition.

Genetic differences presentation. After the participants read their results and asked clarifying questions, the researcher began the presentation on genetic differences. Over a few slides, the researcher gave a brief scripted presentation on COMT research, and how the participant's genetics should affect their behavior. Participants were told that COMT is the single most researched gene in behavioral genetics and psychology. They were also told that a very robust body of research shows that Met allele carriers have an advantage over Val allele carriers when it comes to executive functioning tasks such as the card sorting task. Certain aspects of the literature were emphasized in this presentation, such as that the differences are genetic and lifelong; this emphasis is based

on research which has found that the public tends to find genetic dispositions as deterministic and immutable (Dar-Nimrod & Heine, 2011).

BCST. Participants were next given the computerized BCST for the second time. They were told that this was the true testing session which will be used to evaluate the likely differences between their genetic groups. At the completion of the BCST, the computerized Belief in Genetic Determinism Scale (Appendix F) automatically started.

Belief in genetic determinism scale. Participants were given a computerized version of the Belief in Genetic Determinism scale (Keller, 2005). The scale was built into the PEBL software. At the completion of the scale, the researcher moved onto the debriefing process.

Debriefing and exit questionnaire. The researcher read the true consent for the study (Appendix D). The participants were told that deception was used in the study, and explained that the true purpose of the study was to test if simply *believing* genetic differences might change their abilities could cause a deficit in performance. Participants were provided with contact information for the supervising faculty, the IRB, and the Counseling and Psychological Services (CAPS) on campus as per ethical guidelines. The research assistant then answered any questions the participants had and explained that no harm was intended through the deception. Participants were then given the true informed consent (Appendix D) and exit questionnaire (Appendix E). The true informed consent gives them the opportunity to withdraw their data if they choose. The exit questionnaire asks participants if they believed the deception, among other exploratory questions and demographic information.

Data Collection

Each participant's data is identified by their confidential and random ID number. Results from the BCST and survey were automatically outputted into a .csv formatted file in a specified directory on the computer by the PEBL program. The researcher retrieved each participant's results off the computer using a flash drive after the participant consented to have their data used in the study.

Management of Risks and Benefits

Participants were thoroughly debriefed after the completion of the study, which included contact information for faculty supervisors and the IRB if they wished to report any misconduct. Participants were also encouraged to contact me via email personally if they had further questions about the study. No participant reported adverse reactions to the deception of the study.

Data Analysis

To evaluate group differences on the post threat Berg Card Sorting Task (Hypothesis One), a mixed model repeated measure ANOVA was performed comparing pre-test and post-test within group, and posttest between group. To evaluate the secondary Hypotheses (Two & Three), ANCOVA was performed to evaluated the post-test differences between Met and Val carriers, using Belief in Genetic Essentialism scores as a covariate.

Toward the end of the study, I discovered from a participant that one of the RA's for the study had been following the saliva collecting protocol incorrectly. Because the RA disposed of the saliva sample directly in front of some of their participants, several of

those participants did not believe the deception from the beginning of the study. Below, I present results for all participants, and then a separate set of results for only those participants who believed the deception.

Results

Data screening

Data were screened for accuracy and overall normality. The belief in genetic determinism scores were normally distributed and had no extreme scores. Preservative error scores for both baseline and posttest were non-normally distributed. Logarithmic transformations were used to correct skew and kurtosis issues. Belief in genetic determinism scores were centered to prevent multicollinearity issues in analysis as a continuous by categorical interaction will be presented.

Hypothesis One

Hypothesis One predicted that Val allele carriers will perform significantly worse on the Berg Card Sorting Task (BCST) than the Met allele group after the stereotype threat is introduced. Below I present the results of a mixed model repeated measures ANOVA, which evaluated change in scores from baseline to posttest both within and between groups. Analyses are presented for both complete data, and data which only retains participants who believed the deception.

Complete data. Mean preservative error rate was compared between Met and Val groups using a mixed design ANOVA. Note that a lower score on preservative error indicates better performance on the task, and learning the changing sorting rules more

quickly. Contrary to my prediction from Hypothesis One Met (M = 21.36, SD=10.51, n = 25) and Val (M = 18.80 , SD = 8.32 , n = 24) scores did not differ significantly on post threat scores (see Table 1). There was no significant main effect for group or time, and no significant interaction between the two. Val allele carriers experienced a non-significant increase in preservative errors, and Met allele carriers experienced a non-significant decrease in preservative errors (see Figure 1).

Table 1 Mixed Model ANOVA: Group, Time, Interaction

	F	*p*	Gen η^2
Group	.05	.83	.00
Time	1.73	.20	.00
Group x Time	3.07	.09	.02

Note: Gen η^2 is a generalized eta-squared effect size. Degrees of freedom for all F tests are 1,46.

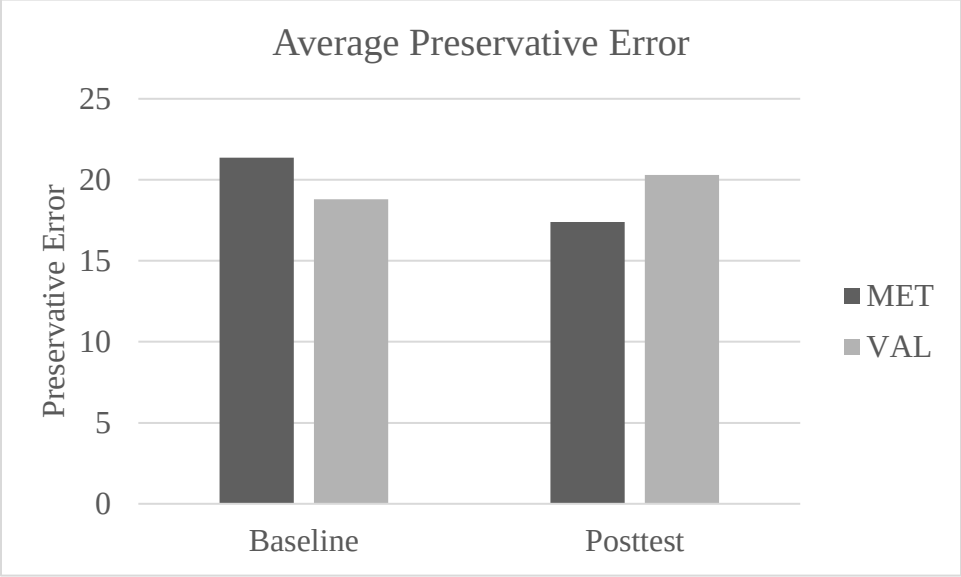

Figure 1Average Preservative Error at Baseline and Posttest

Note: Higher scores indicate poorer performance.

Believers only. Data were also analyzed retaining only participants who believed that they had been genetically tested. For Hypothesis one, I used the mixed design repeated measures ANOVA evaluating preservative errors on the card sorting task from test time and group. There was no significant main effect for group on preservative error, however, there was a significant main effect for time, and a significant interaction between time and group (see Table 2). To specify the main effects, I conducted paired t-tests for each group comparing their baseline and posttest score. For Met allele carriers, there was significant improvement from baseline *(M* = 21.94, *SD* = 10.33, *n* = 17) to posttest (*M* = 15.64, *SD* = 6.42, *n* = 17) scores, *t*(16) = 3.86, *p* = .001, *d* = 0.93. For Val allele carriers, there was no significant difference between baseline (*M* = 18.66, *SD* = 8.89, *n* = 18) and posttest (*M* = 19.5, *SD* = 10.56, *n* = 18) scores, *t*(17) = 0.32, *p* = .75, *d* = 0.07.

Table 2 Mixed Model ANOVA: Group, Time, Interaction for believers only

	F	*p*	Gen η^2
Group	.01	.91	.00
Time	6.51	.02	.03
Group x Time	5.87	.02	.03

Note: Gen η^2 is a generalized eta-squared effect size. Degrees of freedom for all *F* tests are 1,32.

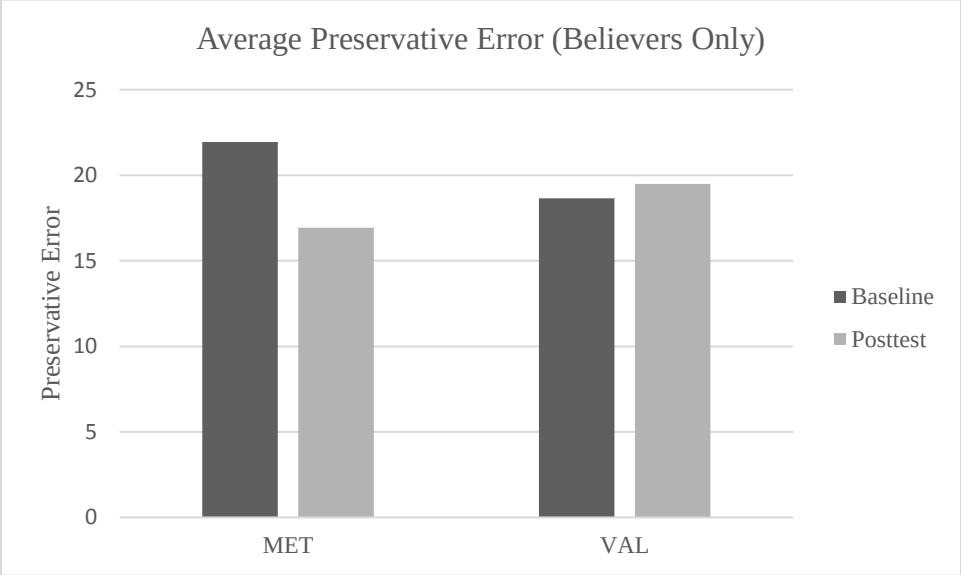

Figure 2Average Preservative Error for Believers Only

Note: Higher scores indicate poorer performance.

Hypotheses Two and Three

Hypothesis Two predicted that Val allele carriers higher in belief in genetic determinism would have lower performance on the card sorting task. Hypothesis Three predicted that this effect would be unrelated to Met allele performance. The sections below present analyses of complete data and analyses of those participants who believed the manipulation.

Complete data. To check that assumptions for ANCOVA were met, I tested for homogeneity of covariance to ensure that there was no significant interaction between the IV (group) and the covariate (belief in genetic determinism). The assumptions for ANCOVA were not met (see Table 3). Graphic simple slopes showing the relationship between preservative error and belief in genetic determinism between the two groups is also presented (Figure 3). It should be noted that genetic essentialism beliefs did not differ significantly between Met (M = 3.29, SD = 0.47) and Val (M = 3.33, SD = 0.55), $t(45) = 0.28$, $p = .77$, $d = 0.08$, so I do not believe that random assignment into either group affected BGD scores.

Table 3 ANOVA for Preservative Error by Group, Time, BGD & Interactions

	F	*p*	η^2
Group	.91	.34	.00
Time	2.21	.14	.00
BGD	3.02	.09	.00
Group x Time	2.11	.15	.02
Group x BGD	6.13	.02	.09
Time x BGD	.00	.96	.00
Group x Time x BGD	.18	.67	.00

Note: Belief in Genetic Determinism is abbreviated as BGD.

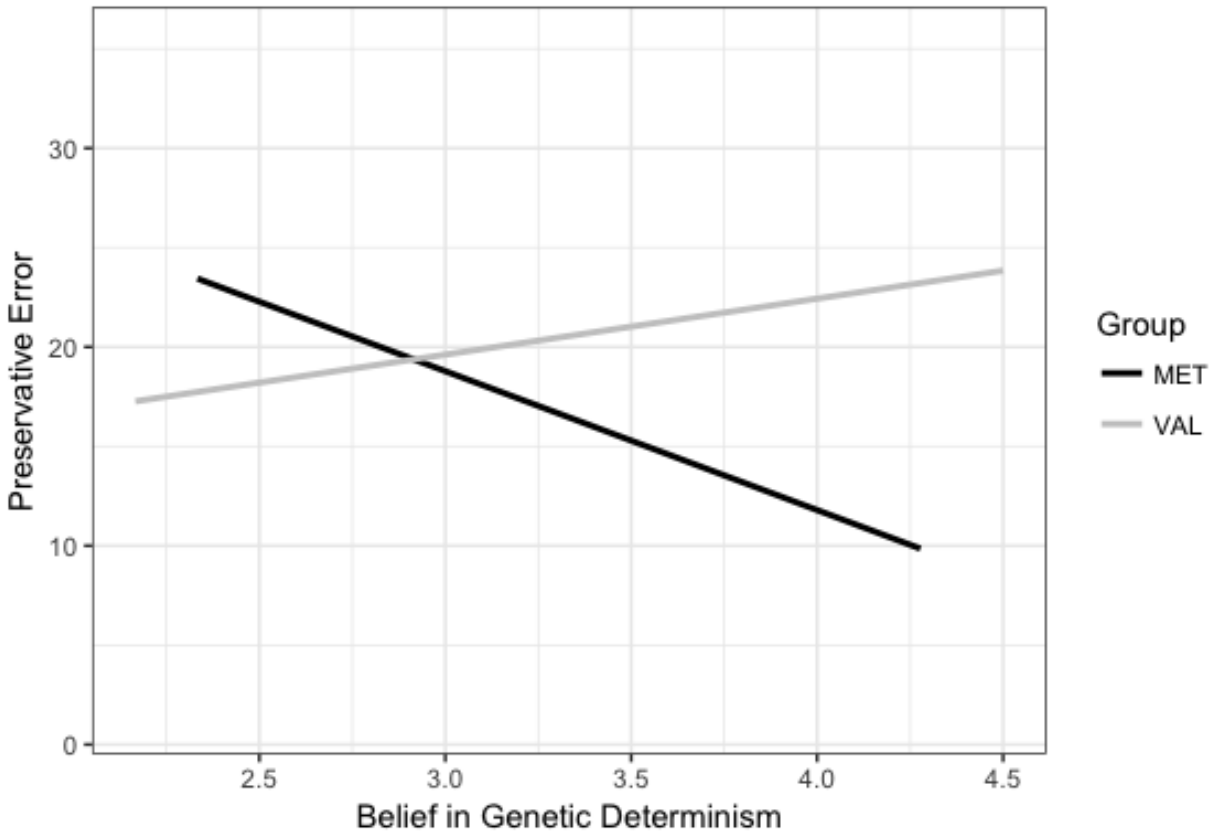

Figure 3. Preservative Error, Belief in Genetic Determinism, and Group

Note: Preservative error scores refer to posttest only. Higher scores on Preservative Error indicate poorer performance. Higher scores on Belief in Genetic Determinism mean higher genetic essentialism beliefs.

Believers only. The relationship between preservative error and belief in genetic determinism was also evaluated only for participants who believed the deception. Assumptions for ANCOVA were not met for this analysis. As before, a significant interaction between the IV (group) and the covariate (belief in genetic essentialism) emerged. The interaction model is presented in Table 4, as is a graphic representation of simple slopes (see Figure 4). I conducted separate linear models for both the Met and Val groups, predicting preservative error from time, belief in genetic determinism, and their interaction. For the Met group, test taking time significantly predicted preservative error, $F(1,30) = 4.76$, $p = .037$, $sr^2 = .13$, but belief in genetic determinism, $F(1,30) = 3.01$, $p = .09$, $sr^2 = .07$, and the interaction, $F(1,30) = .49$, $p = .48$, $sr^2 = .01$, were not significant. For the Val group, test taking time did not significantly predict preservative error, $F(1,32) = .07$, $p = .79$, $sr^2 = .01$, but belief in genetic determinism did, $F(1,32) = 4.25$, $p = .04$, $sr^2 = .11$. The interaction between test taking time and beliefs in genetic determinism was not significant for the Val group, $F(1,32) = .64$, $p = .43$, $sr^2 = .02$.

Table 4 ANOVA for Preservative Error by Group, Time, BGD & Interactions (Believers only)

	F	*p*	η^2
Group	.91	.34	.00
Time	2.21	.14	.00
BGD	3.02	.09	.00
Group x Time	2.11	.15	.02
Group x BGD	6.13	.02	.09
Time x BGD	.00	.96	.00
Group x Time x BGD	.18	.67	.00

Note: Belief in Genetic Determinism is abbreviated as BGD.

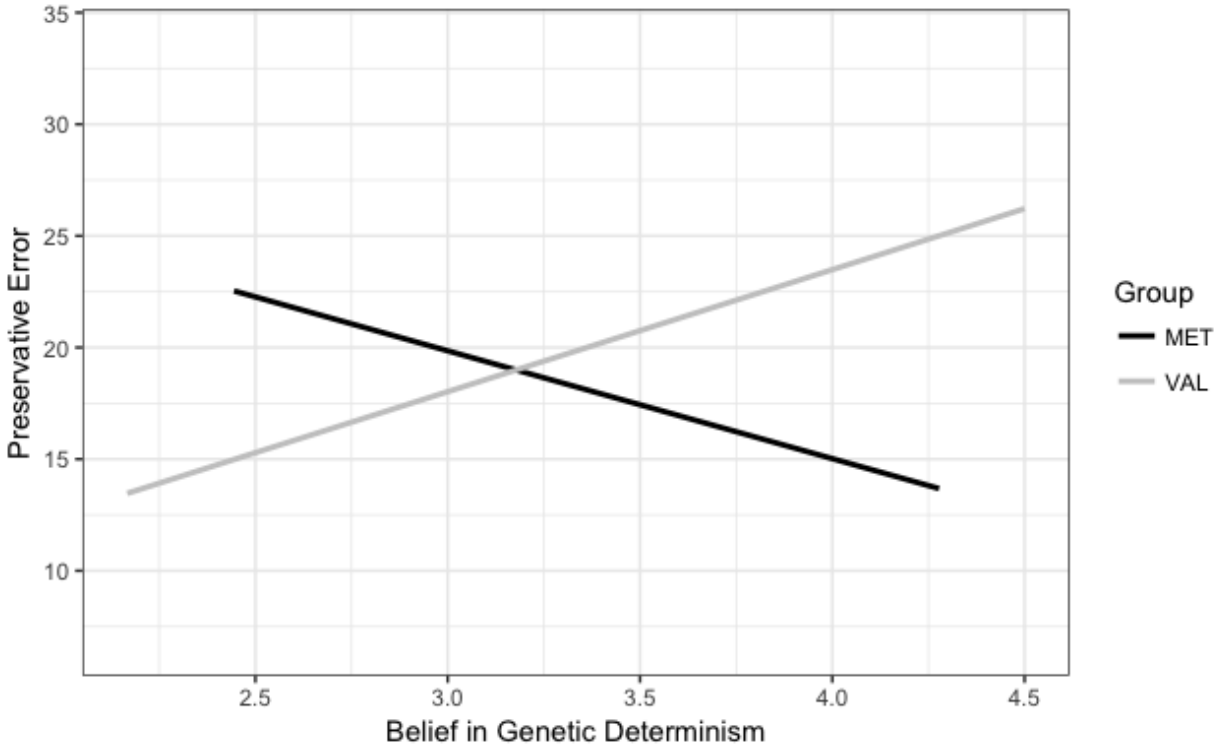

Figure 4The Relationship Between Preservative Error and Belief in Genetic Determinism by Group (Believers Only)

Note: Preservative error scores refer to posttest only. Higher scores on Preservative Error indicate poorer performance. Higher scores on Belief in Genetic Determinism mean higher genetic essentialism beliefs.

Discussion

In this study, I examined whether stereotypes about genetic groups threatened participant ability during an executive functioning task. Stereotype threat effects exist across race (Steele & Aronson, 1995), sex (Spencer et al., 1999), age (Lamont et al., 2015), and even with clinical diagnoses (Suhr & Gunstad, 2005). When individuals are informed that they naturally possess a deficiency, their behavior tends to align, regardless of their true ability. Previous research established genuine differences in ability between COMT gene variant groups on various tasks, such as working memory (Malhotra et al., 2014). Met allele carriers produce less COMT, and thus have more dopamine available for synaptic signaling in the pre-frontal cortex (Lachman et al., 1996). As COMT research grows, it may continue to implicate disadvantages in possessing certain genetics. This study was intended to evaluate if self-knowledge of a natural disadvantage at the genetic level influences test taking.

Participants were deceived into believing that they were members of a genetic group that was either deficient at executive functioning tasks (Val), or successful at executive functioning tasks (Met). Although a majority of participants believed that they had been genetically tested, there was no evidence for a genetic stereotype threat. I did discover some evidence for a lift effect for the advantaged group in the study (Met). Endorsement of genetic essentialism beliefs (i.e. some races are naturally more intelligent), did not impact my results. Overall, Met allele carriers improved on the card-sorting task, Val allele carriers did not.

Genetic Stereotype Threat Results

My study did not find evidence for a genetic stereotype threat. Although Val allele carriers saw a small increase in preservative error during posttest, the difference from baseline was non-significant. Met allele carriers who believed the deception saw a significant decrease in preservative error from baseline to posttest. It is possible that the Met allele carriers felt compelled to align their effort to the expectation that they should succeed at the card sorting task. Stereotype lift describes an increase in performance when an outgroup is described as inferior (Walton & Cohen, 2003). Although I did not have a specific hypothesis about stereotype lift, it is interesting to consider the potential symmetry of lift and threat occurring in tandem throughout the study.

One challenge to this study may be that the group assignments were based solely on genetics, and were not already socially defined outside of the experiment. An individual's sex, for example, is largely determined at the genetic level. Chromosomal sex is followed by the development of secondary sex characteristics, by which individuals are identified as male or female during typical development. Individuals are typically assigned a sex at birth which matches these characteristics, and develop a social gender throughout their lifespan. Many stereotypes addressing sex or gender are, in part, based on the idea that women have genetic inferiorities to men. It would be inaccurate to say that the cause of these stereotypes is genetic discrimination, however, because there is more to the identity of "female" than two X chromosomes. COMT allele status, however, is not a socially defined group. Stereotype threat research at its core emphasizes

that what drives underperformance is the fear of confirming existing stereotypes about our group's innate inabilities on some task (Spencer, Logel, & Davies, 2016).

It is also important to consider whether participants identified with their group during the study. Stereotype threat research generally finds that individuals who identify more strongly with their group are more likely to succumb to poor performance under threat (i.e. Spencer et al., 1999). I did not ask participants whether they identified with their group in a structured way. After receiving their test results, participants were prompted to consider whether they agreed with their test result. Then, participants responded to an open-ended question about their reaction to their test results on the exit questionnaire. Participants most often commented on the perceived accuracy of their results, how surprised they were by their results, or their level of test taking anxiety.

The relevance of the threatened domain is also an important factor in stereotype threat effects (Aronson et al., 1999). For example, the stereotype that women are poor at math would affect a female calculus student more than a female psychology student (Spencer et al., 1999). Val participants in this study learned that they should have inferior executive functioning skills, a trait which could be detrimental to student success. Part of the study's deception involved showing participants a real article from the NY Times which explores cognitive differences between COMT allele types. The article specifically addresses test taking ability, and test taking anxiety. These specific COMT research findings are what define the "Warrior / Worrier" paradigm. The researchers emphasized these differences repeatedly during the study. Although I expected the deficiencies in working memory to be most salient to the participants, they overwhelmingly commented

on test taking anxiety during the exit survey. It is possible that participants did not find working memory as relevant a domain as test anxiety. Further, several participants commented on both memory and anxiety.

Genetic Essentialism Results

Assessing genetic essentialism beliefs was of interest because essentialist thinking relates to prejudice beliefs. I expected that higher essentialism beliefs would increase participant's feelings of threat by genetic disadvantage. If participants believed that their ability was largely heritable, and therefor immutable, their behavior should align to stereotypes about their group more easily. This is consistent with research on the implicit theory of intelligence. This work found that people who believe intelligence is fixed and cannot change tend to endorse more stereotypes and are more likely to underperform when in a stereotype threat situation (Froehlich, Martiny, Deaux, Goetz, & Mok, 2016). Similarly, students who do not believe intelligence can change tend to progress less in school over time compared to students who believe intelligence can change (Blackwell, Trzesniewski, & Dweck, 2007).

Genetic essentialism beliefs did not impact participants results overall, although there was some evidence that for the threatened group (Val) higher genetic essentialism beliefs predicted marginally higher preservative error. Research that finds an association between essentialism and prejudice relates to stereotypes about outgroups (Haslam et al., 2002; Haslam et al. 2006; Keller, 2005). This work does not explore whether participants endorse stereotypes about their own group. A relationship between genetic essentialism

and experiencing stereotype threat effects, then, may not be an applicable application of this research.

I expected to find that genetic essentialism beliefs would impact stereotype threat effects because of their association with prejudice beliefs and stereotyping. Social essentialism, however, may have been a worthwhile component of essentialist beliefs to evaluate. Social essentialism, which attributes immutable qualities to groups based on their social upbringing (rather than genetics), is also associated with prejudice beliefs and stereotyping. Social essentialism beliefs and genetic essentialism beliefs are independent of each other, but share correlates with prejudice and stereotyping tendencies (Rangel & Keller, 2011). This study only evaluated the degree to which participants endorsed genetic essentialism. It is possible that participants would have been more inclined to endorse social essentialist beliefs, and therefor were not threatened by a genetic component to their ability.

Limitations

The largest limitation to this study is sample size. Forty-nine participants is a fraction of the proposed sample size, leaving the design underpowered. Several participants were processed using an incorrect protocol and thus immediately did not believe the deception of the study. With an already small sample size, dropping those cases may have dramatically reduced the ability to detect effects.

It is also important to note that although the company 23andme.com was a focal point of this paper, their at home test does not specifically offer COMT allele results. Clever consumers can interpret the genome provided by the company to find this

information for themselves. Still, COMT can serve as a useful analogue to any other situation in which an individual is confronted with potentially threatening information about their abilities. The 23andme.com home kit does offer information about susceptibility to Alzheimer's disease, for example.

Future Directions

Although the present study failed to find evidence for genetic stereotype threat effects, there are other avenues of investigation for future studies. There was evidence of a small stereotype lift effect for the non-threatened group. Similarly, it is possible that the Val group's failure to improve on the card sorting task did represent stereotype threat effects to some degree. Another study evaluating practice effects without threat could test this possibility. It is also possible that there may positive consequences of providing individuals with encouraging genetic feedback. Additionally, several moderators of stereotype threat found in the literature were not assessed in this study. Locus of control may be of relevance to a study evaluating genetic stereotype threat effects. Individuals with an internal locus of control tend to be most vulnerable to stereotype threat effects (Cadinu, Maass, Lombardo, & Frigerio, 2006). If participants feel their genetic makeup hinders their ability outside of their control, perhaps that knowledge provides consolation for deficits, rather than threat.

Future research could also evaluate whether participants identify with their genetic group during the study. Identifying strongly with their social group should make participants more susceptible to stereotype threat effects (Schmader, 2002). Similarly, it is important that the threatened domain be relevant to the participant. I believe that my

study provided participants with a task which measured a skill students should wish to excel at, however, I did not assess whether participants valued their working memory ability.

Finally, pioneering stereotype threat research (i.e. Steele & Aronson, 1995; Spencer, Steele, & Quinn, 1999) proposed that fear of confirming stereotypes induces anxiety, which then impacts test taking performance. The current study did not evaluate participant's anxiety level at any point during the study, thus it is unclear if the genetic threat induced anxiety levels sufficient to detect stereotype threat effects (Aronson et al., 1999).

There is opportunity to further evaluate the role of essentialist beliefs in genetic stereotype threat. Essentialist beliefs do have prejudice and stereotyping correlates however, sometimes less essentialist beliefs predict more prejudice (Haslam, Rothschild, & Ernst, 2002). The present work did not evaluate if participants who did not endorse genetic essentialism may value other essentialist beliefs, such as social determinism (Rangel & Keller, 2011). It is possible participants low in genetic essentialism may have some resilience to genetic stereotypes, but hold prejudices about groups based upon social construction.

Conclusion

The inspiration for this study is in response to a body of research that found legitimate behavioral differences between COMT allele groups, but also to research that found we invest a lot of trust in the deterministic nature of our genetic makeup. Fictional dramatizations, such as the movie *Gattaca,* have imagined a future where an individual's fate is decided at birth using advanced genetics. In this film, there are "valid" humans who were genetically engineered to be their best, and "invalid" humans of natural birth. From these distinctions followed a rigid cast system, where invalids were socially inferior. Whereas it is difficult to imagine that this could ever become our future, psychologists have been trying to identify a genetic cause of superior intelligence since the early 1900s.

In 2008, the Genetic Information Nondiscrimination Act (GINA) was passed in the U.S. to prevent employers and health insurance companies from discriminating against individuals due to genetic susceptibility to disease. GINA legislation addresses the historical injustice of sterilization laws, which mandated the sterilization of persons presumed to have mental deficits. GINA rests on the premise that these sterilization laws, and relate discriminations, were unjustly targeted at stigmatized societal groups. Although the focal point of this legislation is healthcare, the language of GINA openly acknowledges previously misunderstood and abused concepts like heritability of traits such as intelligence in the past. Going forward, it may become invaluable to elucidate exactly how the average consumer understands and uses genetic information.

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Appendix A

Consent to Participate in Research: GENETIC DIFFERENCES IN EXECUTIVE FUNCTION

Thank you for participating in this research study! Please read this consent form carefully. Your signature is required for participation. If you are under the age of 18 you should not participate.

Study Title: Genetic Differences in Executive Function
Primary Investigator: Jack Allen, M.A. Candidate, Neha Arora, B.A. Biology
Faculty supervisors: Christopher Aberson (Prof. Psychology), Dr. Ethan Gahtan (Prof. Psychology & Biology)
Various undergraduate and graduate research assistants.

Participation is voluntary. You have the right to stop participating at any time.

Purpose of the Study: This study will test whether different COMT genes are associated with different cognitive abilities. *Background:* all people have the same set of genes but there are different versions of each gene. People differ in which versions of a gene they have. The COMT gene influence dopamine levels in the brain. One version of the COMT gene, called the "warrior" gene, has been linked to better stress coping, and the other version, called the "worrier" gene has been linked to higher verbal intelligence. To study this link, we will ask you to do several computer-based cognitive tasks and to have your COMT genes tested through a saliva sample.

Study activities: Session 1 will last 15 minutes and includes (1) informed consent and (2) a saliva sample. **There is no guarantee that your saliva sample will produce a usable result.** Session 2, which is completed on a different day, will last approximately 75 minutes and will include (1) a computer task (2) a survey (3) a short lecture. Session 2 will include a break for snacks and rest.

Possible Risks: There is a risk of fatigue from the length of session 2 of the study, but we will make every effort to provide rest and snacks to keep you comfortable. Some participants may experience emotion discomfort in learning about their own genotype, however, we can direct you to counseling services if you should require them. Because there is no guarantee that your saliva sample will produce a usable result, it is possible that you will not know your genotype during the study. If you change your mind and do not wish to participate in session 2 of the study because of any of these risks, you can withdraw at any time.

Possible Benefits: Credit in a psychology course if you registered using the Psychology Research Participation pool. Participants may enroll in a raffle to win prizes, such as an Amazon gift card of a value of up to $100.

Confidentiality: You will be assigned a code number which will be used instead of your name on your study records. Only the consent form will show your name and that will be kept securely with access only by the experimenters. No identifying information will be present on any survey or task you do. Results of the study will be presented as group results only, never as an individual's results.

If you have questions: The investigators will answer any questions you have about this research and provide you with a summary of results when they're available if you ask. Question should be sent to

Jack Allen Phone: 805-490-3778 . Email: Jack.Allen@humboldt.edu

Dr. Chris Aberson: 707-826-3755. Email: Christopher.Aberson@humboldt.edu

If you have any concerns with this study or questions about your rights as a participant, contact the Institutional Review Board for the Protection of Human Subjects at irb@humboldt.edu or (707) 826-5165

Your signature below indicates that you voluntarily agree to participate in this study.

Your signature below indicates that you voluntarily agree to participate in this study. Your signature also provides your consent to voluntarily participate in session 2 of the study, should you choose to do so. **You may withdraw from either session of the study at any time without consequence.**

_____	_____	_____
Print Name	Signature of Participant	Date

Appendix B

BSS 122, Neuroscience Lab
Humboldt State University

Laboratory Report

Account Number: 334251

Name: Unspecified
Gender: Unspecified

Reference Number: CHANGE THIS

Researcher(s)
Human Genetics Lab Humboldt State

Date Collected: CHANGE THIS
Date Received: Unspecified
Date Reported: Unspecified

COMT Genotype Test Result

Test	Result	Allele Type
G108A mutation	Positive	Met / Met

The sample is homozygous and positive for G108A mutation
This genotype

- indicates slow enzyme activity and higher resting dopamine levels
- is associated with degrading dopamine from synaptic cleft at slower rate
- is homozygous across 25% of the population
- is associated with more efficient prefrontal cortex activity across a variety of domains

CLIA# 45D0710715

COMT Background Information

COMT (catechol-O-methyltransferase) is an enzyme that is involved in catabolism of monoamines, like dopamine and noradrenaline. COMT has two protein isoforms, S-COMT and MB-COMT, with the soluble cytosolic (S-COMT) isoform predominating. S-COMT has a greater role in degrading dopamine localized to prefrontal cortex.

Certain single nucleotide polymorphisms have been categorized that alter the function of COMT enzyme. These are the G108A and G158A mutations (which is a change from guanine to adenine at the position 108 and 158 within the gene). These mutations result in valine-to-methoinine (Met/Met) substitution in COMT enzyme making the enzymatic activity 40% slower compared to COMT enzyme with valine (Val/Val). Slower enzymatic breakdown means more available dopamine for synaptic signaling. Robust research findings implicate this allele variant of the COMT gene as having higher executive functioning and more efficient prefrontal cortex activity.

This enzyme is primarily associated with degradation of monoamines and thereby maintenance of optimal dopamine levels. Neither fast acting nor the slow acting homozygosity is efficient however the Val/Met heterozygous mutation is optimal.

Testing Limitations

The precise effect of COMT activity on PFC function is likely to be dependent on where on the inverted-U curve the individual in question lies in any given environmental or genetic context. This is likely governed by multiple factors, including the nature of the measure being examined, state factors, for example the relative amount of stress that the individual is under, which is known to affect PFC dopamine levels and trait factors, such as the complex genetic background on which the COMT genotype is expressed.

Appendix C

BSS 122, Neuroscience Lab
Humboldt State University

Laboratory Report

Account Number: 334251

Name: Unspecified
Gender: Unspecified

Reference Number: CHANGE THIS

Researcher's Name
Human Genetics Lab Humboldt State

Date Collected: CHANGE THIS
Date Received: Unspecified
Date Reported: Unspecified

COMT Genotype Test Result

Test	Result	Allele Type
G108A mutation	Negative	Val/Val

The sample is homozygous and negative for G108A mutation
This genotype

- indicates fast enzyme activity
- is associated with degrading dopamine from synaptic cleft at faster rate
- is homozygous across 25% of the population
- is associated with less efficient prefrontal cortex activity across a variety of domains

CLIA# 45D0710715

COMT Background Information

COMT (catechol-O-methyltransferase) is an enzyme that is involved in catabolism of monoamines, like dopamine and noradrenaline. COMT has two protein isoforms, S-COMT and MB-COMT, with the soluble cytosolic (S-COMT) isoform predominating. S-COMT has a greater role in degrading dopamine localized to prefrontal cortex.

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This enzyme is primarily associated with degradation of monoamines and thereby maintenance of optimal dopamine levels. Neither fast acting nor the slow acting homozygosity is efficient however the Val/Met heterozygous mutation is optimal.

Testing Limitations

The precise effect of COMT activity on PFC function is likely to be dependent on where on the inverted-U curve the individual in question lies in any given environmental or genetic context. This is likely governed by multiple factors, including the nature of the measure being examined, state factors, for example the relative amount of stress that the individual is under, which is known to affect PFC dopamine levels and trait factors, such as the complex genetic background on which the COMT genotype is expressed.

Appendix D

Debriefing and Consent to Use your Data from this Study: GENETIC DIFFERENCES…

Debriefing. The study you just participated in was done for a different reason than we originally gave you. Now that the study is over, we want to explain the real purpose of the experiment and exactly how we attempted to deceive you.

Deceptions. (1) No genetic tests were actually done. You were randomly assigned to the warrior (Val/Val) or worrier (Met/Met) group. We disposed of your saliva sample and never did anything with it. (2) The study was not done to test the relationship between genes and behavior.

Real study purpose. This study was designed to see if *simply believing* that your genetics influences you in certain ways causes you to act in those ways. In psychology this is called a "stereotype threat effect." We believe studying this kind of stereotype threat is important because genetic information is becoming more available to people, and that there are psychological risks to learning about your genetic makeup. We greatly appreciate your participation and hope we have explained why we believe this study is important and why we tried to deceive you in these ways.

Re-consent. Since the original consent form was deceptive we are asking you to consent again to the use of your data now that you are fully informed about the study. You can decline to have your data used without penalty, but your data are valuable and we hope you will consent to let us use them by signing this form.

Real study title: Psychological Consequences of Genetic Testing
Principal Investigator: Jack Allen, M.A. Candidate
Faculty supervisors: Christopher Aberson (Prof. Psychology), Dr. Ethan Gahtan (Prof. Psychology & Biology)

Confidentiality: Your data will be kept confidential by never using your name in connection with results and never presenting individual results (only group averages). Only the consent forms contain your name, and these will be stored securely by the investigators and destroyed after 3 years.

Possible risks. Your participation has ended, but if you are upset by the deception or any aspect of this study please use the contact information below to voice your concerns.

Possible Benefits: Credit in a psychology course if you registered using the Psychology Research Participation pool. Participants may also enter in a raffle to win prizes, such as an Amazon gift card of up to $100 in value.

If you have questions: The investigators will answer any questions you have about this research and provide you with a summary of results when they're available if you ask. Question should be sent to

- Jack Allen Phone: 805-490-3778 . Email: jack.allen@humboldt.edu
- Dr. Chris Aberson: 707-826-3755. Email: Christopher.aberson@humboldt.edu
- If you have any concerns with this study or questions about your rights as a participant, contact the Institutional Review Board for the Protection of Human Subjects at irb@humboldt.edu or (707) 826-5165
- Your signature below indicates that you voluntarily agree to participate in this study.

Consent: May we use your data? Please sign below if you agree to the use of your data in this study.

_____ _____ _____

Signature of Participant Print Name Date

We believe this research may have valuable implications in the field of psychology and genetics. To obtain realistic study results, future sessions will still use deception. Revealing the nature of this study to participants who have not yet participated will have negative consequences for the integrity of this study's research design. ***Please do not discuss this study, or the nature of its deception, with other students or faculty – whether they will participate or not****. A lot of hard work has gone into this study, and we thank you in advance for your help!*

Appendix E

Exit Questionnaire – Genetic Stereotype Threat Study

The following short survey is to give us feedback about this study, and your interest in human genetics. Please circle your answers

Before the true purpose of the experiment was explained to you, did you…

Believe your test result was real ?

1. YES 2. NO

Believe that we had actually genetically tested you?

1. YES 2. NO

How *believable* did you find your genetic test results?

1	**2**	**3**	**4**	**5**
Completely Unbelievable	**Somewhat Unbelievable**	**Neutral**	**Somewhat Believable**	**Completely Believable**

How *accurate* did you find your genetic test results?

1	**2**	**3**	**4**	**5**
Completely Inaccurate	**Somewhat Inaccurate**	**Neutral**	**Somewhat Accurate**	**Completely Accurate**

How *informative* did you find your genetic test results?

1	**2**	**3**	**4**	**5**

Completely Uninformative	Somewhat Uninformative	Neutral	Somewhat Informative	Completely Informative

Please describe in your own words what reaction you had to receiving your test results

Before you volunteered to participate in this study, had you ever been genetically tested before?

1. YES **2. NO**

If you answered yes, please tell us *why* in your own words:

If you answered yes, how was the test done? For example, through a mail in service such as 23andme.com or through a doctor's office:

Before you volunteered to participate in this study, how much did you *know* about human genetics? Circle all that apply.

1. I knew nothing about human genetics
2. I knew a little about human genetics

3. I had taken a class about human genetics	4. I've done research about human genetics
5. I know a lot about human genetics	6. I've learned about human genetics through popular media, such as TV shows, podcasts, movies etc.

In the future, would you be interested in having a real genetic test tell you which genotype or variant of the COMT gene you have?

1. YES **2. NO** **3. UNDECIDED**

Did you understand why the researchers found it necessary to deceive you into believing your genetic test result was real?

1. YES **2. NO** **3. UNDECIDED**

Please estimate about what percent (out of 100%) of *human behavior* do you think is explained by one's genetics:

_____ %

Is there anything else you'd like us to know about your participation in this study?

Is psychology your major? **1. YES** **2. NO**

What is your age in years? _____

What is your class standing?

1. Freshperson
2. Sophomore
3. Junior
4. Senior
5. Graduate student

What gender do you identify with?

1. Female
2. Male
3. Prefer not to disclose
4. I'd like to tell you how I identify in my own words: _____

Appendix F

Belief in Genetic Determinism Scale (Keller, 2005)

Item
1. I think the chief reason why parents and children are so alike in behaviour and character is that they possess a shared genetic inheritance.
2. In my opinion, alcoholism is caused primarily by genetic factors.
3. I think that differences between men and women in behaviour and personality are largely determined by genetic predisposition.
4. I believe that children inherit many of their personal traits from their parents.
5. In my view, the development of homosexuality in a person can be attributed to genetic causes.
6. I am convinced that very few behavioural traits of humans can be traced back to their genes. (R)
7. I believe that many talents that individuals possess can be attributed to genetic causes.
8. I think that the upbringing by parents and the social environment have far greater significance for the development of abilities and personal traits than genetic predispositions. (R)
9. I believe that many differences between humans of different skin color can be attributed to differences in genetic predispositions.

10. I think that genetic predispositions have little influence on a person's personality characteristics. (R)
11. I my view, many forms of human behaviour are biologically determined and can therefore be seen as instinctual.
12. The fate of each person lies in his or her genes.
13. I am of the opinion that intelligence is a trait that is strongly determined by genetic predispositions.
14. I believe that genetic predispositions have no influence whatsoever on the development of intellectual abilities. (R)
15. I am convinced that the analysis of the genetic predispositions of an embryo allows good predictions as to which characteristic and abilities the child will develop.
16. I think the genetic differences between Asians and Europeans are an important cause for the differences in abilities between individuals from these groups.
17. I think that twins, because of the identical genetic predispositions, will be very similar in their behaviour even if they were adopted and raised in different families.
18. I believe that an analysis of my genetic predispositions will allow a trained scientist to predict many of my abilities and traits without having any personal knowledge of me.

Note. R = reverse scored.

Response scale ranging from (1) *not at all true* to (7) *completely true*