

COMT, Extraversion, and Partisan Attachment

Christopher T. Dawes

University of California, San Diego

September 21, 2010

Abstract

A burgeoning literature focuses on the relationship between individual differences in personality traits and political behaviors (Gerber, Huber, Doherty, Dowling & Ha 2010, Mondak, Hibbing, Canache, Seligson & Anderson 2010, Gerber, Huber, Raso & Ha 2008, Gerber, Huber, Doherty & Dowling 2009, Mondak & Halperin 2008, Denny & Doyle 2008). Two recent papers found that extraversion is a strong predictor of whether an individual affiliates with a major political party as well as the strength of the affiliation (Gerber et al. 2008, Gerber et al. 2009). Extraversion (Bouchard & Loehlin 2001) and partisan attachment (Settle, Dawes & Fowler 2009, Hatemi, Hibbing, Alford, Martin & Eaves 2009) have been shown to be heritable and both have been linked to the neurotransmitter dopamine (Dawes & Fowler 2009, Munafo, Clark, Moore, Payne & Flint 2003, Carver & Miller 2006, Depue 1995). This paper tests the hypothesis that extraversion *mediates* a relationship between COMT and partisan attachment. COMT is a gene that regulates dopamine levels in the brain and that has previously been found to be associated with extraversion (Stein, Fallin, Schork & Gelernter 2005, Reuter & Hennig 2005). We find that individuals with a less efficient version of a well-studied variant of the COMT gene are significantly less likely to identify themselves as partisans than those with the more efficient allele. Further, extraversion partially mediates this association. This is the first such formal test of a pathway between genes, personality, and political behavior and suggests an empirical framework for future research.

Introduction

A burgeoning literature focuses on the relationship between individual differences in personality traits and political behaviors (Gerber et al. 2010, Mondak et al. 2010, Gerber et al. 2008, Gerber et al. 2009, Mondak & Halperin 2008, Denny & Doyle 2008). Two recent papers, Gerber et al. (2008) and Gerber et al. (2009) find that extraversion is a strong predictor of whether an individual affiliates with a major political party as well as the strength of that affiliation. In fact, Gerber et al. (2009) show, using a sample of more than 10,000 individuals, that the magnitude of the effect of extraversion is larger than education, age, income, and religious attendance.

Both personality traits and partisan attachment have a genetic basis. Behavior geneticists have long known that personality traits are heritable (Bouchard & McGue 2003) and an association has been established between variants of several individual genes and personality traits (Luo, Kranzler, Zuo, Zhang, Wang & Gelernter 2007, Luo, Kranzler, Zuo, Wang & Gelernter 2007, Luo, Zuo, Kranzler, Zhang, Wang & Gelernter 2008, Stein, Schork & Gelernter 2004, Stein et al. 2005, Reuter & Hennig 2005). Likewise, the strength of partisan attachment has been shown to be heritable (Settle, Dawes & Fowler 2009, Hatemi et al. 2009) and a variant of the D2 dopamine receptor gene has been found to be associated with partisan attachment (Dawes & Fowler 2009).

The next wave of research must test whether these distinct lines of research actually form two links in a causal chain. One possibility is that personality traits *mediate* the relationship between genes and political behavior. Research focussing on the link between personality traits and political behaviors suggest that since heritability of both personality traits and political behaviors are large, and the formation of personality traits predates political participation, it is likely to be the case

that genes influence personality which then affects political behavior (Gerber et al. 2009).¹ Another possibility is that the same gene or set of genes influences personality traits and political behaviors independently rather than sequentially. A test of these hypotheses requires a sample that includes individual-level genetic, personality, and political behavior information.

We examine a variant of COMT gene, Val158Met, that has been found to be associated with extraversion (Stein et al. 2005, Reuter & Hennig 2005) and test the hypothesis that extraversion mediates the relationship between Val158Met and partisan attachment. To preview our results, we find a significant association between the COMT gene and partisan attachment and are able to replicate this result based on an independent data set. Further, this association is partially mediated by the personality trait extraversion. We find that approximately 8% of the observed association with partisan attachment is via extraversion. This represents the first formal test of a pathway between genes and political behavior and suggests an empirical framework for future work. Given the fact that a single gene likely affects a complex behavior like partisan attachment through a number of pathways (Munafo 2006), finding significant evidence of mediation is promising for future research. Also, since complex behaviors are influenced by many genes (Plomin 2008), this approach suggests variants related to Val158Met should also be investigated.

Genetic Polymorphisms

Genes are distinct regions of human DNA that form the blueprint for molecules that regulate the development and function of the human body. DNA is made up of subunits called nucleotides. There are four such nucleotides: adenine (A), cytosine (C), thymine (T), and guanine (G), named

¹Heritability estimates for personality traits range from 41% to 61% (Bouchard & McGue 2003) and estimates for turnout (Fowler, Baker & Dawes 2008) and strength of partisan attachment (Settle, Dawes & Fowler 2009) are 53% and 46% respectively.

based on the nitrogenous base that they contain. Some genes come in different versions, known as *alleles*. A *polymorphism* exists when there is more than one type of allele (at a locus) that exists in the population. When individuals differ in terms of a single nucleotide pair, it is known as a single nucleotide polymorphism (SNP). For example, a portion of DNA from one individual may be CCTA and from another be C**T**TA. In this example, the SNP (in bold) has two alleles, C and T. An illustration of this is provided in the appendix (*Figure 3*).

Most genes specify the composition of proteins (Hartl 2000) which are the basic building blocks for bodily structure and function. Polymorphisms are important to study because they may *change* the protein being produced or *regulate* protein production by turning genes on and off.² Complex behaviors, including political behaviors, are likely *polygenic*, meaning they are influenced by multiple genes (Mackay 2001, Plomin 2008). Moreover, phenotypes are typically shaped by a multitude of environmental forces. As a result, an association study examining a single gene is an oversimplification and may only capture a relatively small proportion of the observed variation in political behavior.

Personality, Neurotransmission, and COMT

The prevailing model of personality, the so-called Five Factor Model or Big Five, holds that generally speaking, personality can be characterized by five dimensions: extraversion, agreeableness, conscientiousness, neuroticism, and openness to experience. *Extraversion* is marked by sociability including friendliness towards others and a desire to be in their company (McCrae & Costa 1992).

Based on their functional roles, specific neurotransmitter systems are theorized to play a prominent

²An example of the former is sickle-cell anemia. A SNP in the beta-globin gene comes in two versions, A and T. The T allele codes for the amino acid valine rather than glutamate which leads to protein chains that form crystals under low oxygen concentration. This causes red blood cells to collapse into sickle shapes (Hartl 2000).

role in determining individual differences in personality traits (Revelle 2005, Depue 1995, Depue & Collins 1999).

Neurons are nerve cells that are responsible for sending, receiving, and processing information. In order for this information to be sent from one neuron to another, signals must cross a small gap called a synapse that exists between the axon of a sending neuron and dendrite of the target neuron. Neurotransmitters, released by the axon of the sending neuron cross the synaptic gap and bind with receptors on the dendrite of the postsynaptic (receiving) neuron, triggering changes in the postsynaptic neuron's metabolic activity. Neurotransmitters are reabsorbed into the presynaptic neuron via a transporter as part of a process called reuptake. Once the neurotransmitter is back inside the neuron it is degraded by enzymes so that its components can be reabsorbed into the cell. Reuptake is necessary to ensure proper neurotransmitter levels in the synapse.³ Scholars seeking to understand behavior focus on genes involved in neurotransmission. These genes influence transcription, RNA processing, and translation as well as receptor density and binding, reuptake, and degradation of neurotransmitters.

Dopamine is responsible for the control of emotion and positive reinforcement and therefore the dopamine system is believed to influence approach-oriented behaviors like extraversion (Munafo et al. 2003, Carver & Miller 2006, Depue 1995). The COMT gene codes for an enzyme called Catechol-O-Methyltransferase that degrades the neurotransmitter dopamine primarily in the prefrontal cortex (PFC), a region of the brain that is responsible for executive function like working memory. Val158Met is a functional SNP that results in a nucleotide substitution from G to A that changes the amino acid produced from valine to methionine. Like most SNPs Val158Met has two

³Reuptake inhibitors are prescribed to inhibit the reuptake process. For example, selective serotonin reuptake inhibitors (SSRIs) like the antidepressant Prozac prevent the reuptake of serotonin and therefore increase the level of serotonin in the synapse. This allows for increased receptor binding and signaling resulting in improved mood.

alleles: G (Val) and A (Met). The Val allele has been found to produce higher enzymatic activity: individuals with two Val alleles have been found to have 40% higher COMT enzyme activity in the brain of those with two Met alleles (Chen, Lipska, Hamlin, Ma, Matsumoto, Melhem, Kolachana, Hyde, Herman, Apud, Egan, Kleinman & Weinberger 2004). Therefore, the Met allele is associated with less effective breakdown of dopamine translating into higher levels of dopamine in the PFC relative to the Val allele.

A large body of empirical evidence has shown the Met allele to be associated with vulnerability to stress and anxiety (Goldman, Oroszi & Ducci 2005). The precise relationship between dopamine levels in the PFC and anxiety is not completely understood, however Bilder, Volavka, Lachman & Grace (2004) suggest that COMT's role in regulating the balance between the average level of dopamine maintained over long time horizons, tonic dopamine, and the amount of dopamine released in quick bursts, phasic dopamine, is crucial. The Met allele is known to increase tonic dopamine levels and reduces phasic levels in the PFC. Phasic release is in response to environmental stimuli and allows working memory to be updated with this new information. Therefore, muted phasic dopamine release results in suboptimal updating of working memory and thus the information stored in working memory may no longer reflect the present environment. If what is stored in working memory is based on stimuli originally perceived to be threatening, and thus prompting anxiety, this anxiety may persist even though a threat no longer does. The connect between anxiety and extraversion is that individuals suffering from anxiety had been shown to exhibit low extraversion (Bienvenu & Stein 2003).

Samples

This study employs two distinct samples. The first, referred to as the *primary sample*, consists of undergraduate psychology students at San Diego State University recruited between the fall of 1999 and the spring of 2007. As part of the study, subjects completed either the full NEO-Personality Inventory-Revised (NEO-PI-R) (McCrae & Costa 1992) or the shorter NEO Five Factor Inventory (NEO-FFI) (McCrae & Costa 2004). These are the two widely used measures of the Big Five personality traits. The second sample, referred to as the *replication sample*, is comprised of nuclear families including identical and non-identical twins, siblings, and their parents. A majority of these subjects were residing in the Southern California area at the time of their recruitment. Subjects in both studies volunteered, were paid for their participation, and gave written consent. Both studies were approved by the University of California, San Diego Institutional Review Board. In addition, both studies asked participants to report race/ethnicity information and genotyped a majority sample for the COMT Val158Met polymorphism.⁴

In order to determine whether or not subjects are attached to a party, they were matched with public voting records available through the California Secretary of State's office.⁵ California voting records identify whether registered voters wish to be affiliated with a political party. The matching process for the primary sample utilized available personal information including name, date of birth, phone number, and email address. The matching process for the replication sample included home address information. We were able to match 74% of the subjects from the primary sample and 75% from the replication sample, consistent with the fact that 75% of eligible

⁴See Stein, Schork & Gelernter (2004) and Zhang, Rao, Wessel, Kennedy, Rana, Taupenot, Lillie, Cockburn, Schork, Ziegler & O'Connor (2004) for a detailed description of the respective samples.

⁵Voter records are as of June 2009.

Californians were registered to vote as of the November 2008 election.⁶

In the primary and replication samples respectively, 511 and 622 subjects have genotypic information for Val158Met. The dependent variable in this study is whether a registered voter is affiliated with a major political party, defined as being registered as either a Democrat or a Republican.⁷ Summary statistics for the sample are presented in the appendix *Table 3*. The replication sample is older, on average, and therefore has a higher percentage of partisans. There are also more females in both of the samples. The distribution of Val158Met are comparable to one another as well as to other published studies.

Population Stratification

A genetic association study indicates whether an allele is found more frequently than can be attributed to chance in a group exhibiting a particular trait than those without the trait. In our case, we seek to identify if the frequency of the Met allele is lower among those attached to a party than those not attached. A significant association can mean that the allele itself influences partisan attachment or that the observed association is a false positive signal due to what is known as *population stratification*. Population stratification occurs when groups have different allele frequencies due to their genetic ancestry. Political behavior in these groups may be affected by their environments, alleles other than the one of interest, or some unobserved factor. Once these two groups mix in a larger population, simply comparing the frequency of the Met allele to the the number of partisans would lead to a spurious association.

Unfortunately, subpopulations cannot be directly observed. However, there are several

⁶This information come from the California Secretary of State (<http://www.sos.ca.gov/elections/sov/historical-voter-reg/hist-voter-reg-and-part-general-elections-1910-2009.pdf>).

⁷We refer to this throughout the paper as partisan attachment.

techniques regularly utilized in the literature to attempt to ameliorate the problem of population stratification. A typical way to control for this problem is to include controls for the self-reported race of the subject. Another approach is the *structured association* method (Pritchard, Stephens & Donnelly 2000). Structured association is a clustering technique that assumes a sample is made up of a mixture of individuals drawn from K subpopulations where K is likely unknown. Subpopulations are identified based on allele frequencies of polymorphisms spread across the genome, grouping individuals who are genetically similar to one another. Individuals may be assigned to more than one subpopulation if their genetic information suggests that they are admixed. Tests of association can then be conditional on subpopulation assignment.

Results

To test for an association between the Val158Met SNP and partisan attachment in our primary sample we employed the simple regression:

$$\text{logit}(P[\textit{Partisanattachment}_i = 1]) = \tau + \beta_{\textit{Met}}\textit{Met}_i + \beta_{\textit{Age}}\textit{Age}_i + \beta_{\textit{Male}}\textit{Male} + \beta_Z Z_i \quad (1)$$

where i indexes the subject, \textit{Met} is the number of COMT Met alleles (0,1,or 2), \textit{Age} is age in 2009, and \textit{Male} is an indicator variable for whether the subject is male (1) or female (0). To guard against population stratification, we used subpopulation assignments based on the structured association method described in the previous section. Assignments to three population groups were derived from an analysis of 36 genetic markers using the software package STRUCTURE (Pritchard, Stephens & Donnelly 2000).⁸ STRUCTURE adopts a Bayesian cluster approach to find the optimal

⁸The marker panel includes D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S443, vWA, TPOX, D18S51, D5S818, FGA, amelogenin, D1S196, D1S2628, D2S162, D2S319, D5S407, D5S410,

number of clusters under the main modeling assumptions of Hardy-Weinberg equilibrium within populations and complete linkage equilibrium between loci within populations (Pritchard, Stephens & Donnelly 2000). The goal is to identify population groupings that are not in disequilibrium (Pritchard, Stephens & Donnelly 2000). A more detailed description of the ancestry-informative marker panel used here can be found in Yang, Zhao, Kranzler & Gelernter (2005). Z is a vector of the subpopulation assignments.

Since the replication sample is made up of nuclear families, and thus the observations are correlated, we estimate the logit model in *Equation 1* using general estimating equations (GEE) (Liang & Zeger 1986) with an exchangeable working correlation matrix. Alternatively, we specify the within-family correlation structure based on genetic theory rather than estimate it from the data. This approach yields nearly identical results as the exchangeable correlation matrix and therefore we relegate it to the appendix. Subpopulation assignments based on the structured association method are not available for the replication sample, therefore we control for the effects of the underlying population structure by including a vector of indicator variables (Z) for whether a subject self-reported as Black, Asian, Hispanic, Native American, Filipino, or Other (omitted category is White).

Table 1 presents the results for the test of association between the Val158Met SNP of the COMT gene and partisan attachment using our primary and replication samples. Both samples show the *Met* allele is significantly associated with partisan attachment ($p = 0.002$ and $p = 0.04$).⁹

The *Met* allele remained significant ($p = 0.002$) in the primary model with the addition of SES

D6S1610, D7S640, D7S657, D8S272, D8S1827, D9S175, D10S197, D10S1786, D11S935, D12S352, D14S68, D15S1002, D16S3017, D17S799, D22S274.

⁹The results are similar for the primary model when self-reported race is used instead of the subpopulation assignments. The parameter estimate on *Met* is -0.42 ($p = 0.004$).

	Primary Sample			Replication Sample		
	Coef	SE	P Value	Coef	SE	P Value
Intercept	0.39	0.88	0.66	0.49	0.34	0.15
Met	-0.43	0.14	0.00	-0.30	0.14	0.04
Age	0.03	0.03	0.42	0.03	0.01	0.00
Male	-0.28	0.21	0.18	-0.37	0.20	0.06
SP 1	0.25	0.29	0.40			
SP 2	-0.38	0.39	0.32			
Black				-0.05	0.43	0.91
Asian				-0.33	0.74	0.66
Hispanic				0.95	0.42	0.03
Native American				-1.14	1.11	0.30
Filipino				-1.06	0.91	0.25
Other				-1.08	1.14	0.34
<i>N</i>		510			622	
Wald Test of Model Fit (χ^2)		12.8			33.7	
Wald Test Degrees of Freedom		5			9	
Wald Test P value		0.00			0.00	

Table 1: Test of association between COMT Val158Met SNP and partisan attachment. The primary model is a simple logit and the replication model is a GEE logit with an exchangeable working correlation. The dichotomous dependent variable is *Partisan*, which is whether a registered voter is affiliated with the Democratic or Republican party. *Met* is the number of Met alleles (0, 1, or 2), *SP* is the subpopulation assignment, and *Black*, *Asian*, *Hispanic*, *Native American*, *Filipino*, and *Other* are self-reported race categories. Logit coefficients (Coef), standard errors (SE), and p-Values are presented.

measures.¹⁰ *Figure 1* presents the simulated first differences for the primary and replication sample. Holding the control variables at their means and changing the number of Met alleles from zero to one decreases the likelihood of partisan attachment by approximately 10 percentage points and from zero to two by approximately 20 percentage points. Both simulated first differences are significantly different from zero. The effect size for the replication sample is nearly half of those for the primary sample. Changing the number of Met alleles from zero to one decreases the likelihood of partisan attachment by approximately 4 percentage points and from zero to two by approximately

¹⁰The measures include family income and employment status at the time of participation in the original study. These results are not presented since they are nearly identical.

9 percentage points. Again, the simulated first differences are significantly different from zero. It is unclear whether the difference in effect size is due to sampling variability or some feature of the sample such as age.

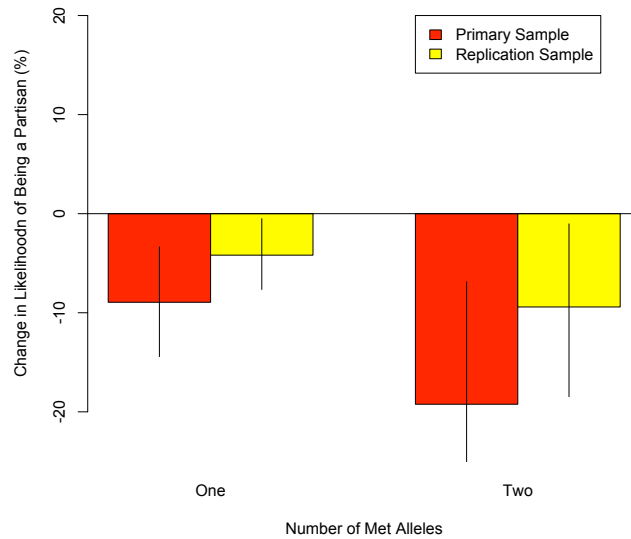


Figure 1: Changing the number of Met alleles yields significantly lower partisan attachment. First differences, based on simulations of *Table 1* parameters, are presented along with 95% confidence intervals. All other variables in the model are held at their means.

Mediation

We find a highly significant association between the Val158Met SNP and partisan attachment based on the primary sample and are able to replicate this finding in another distinct sample. The next step, suggested by the findings of Gerber et al. (2008) and Gerber et al. (2009) that extraversion is a strong predictor of partisan attachment, is to formally test whether the effect of this SNP is mediated by the personality trait extraversion. In other words, is the Met allele associated with

partisan attachment because carriers of this allele tend to be less extraverted and thus less likely to affiliate with social groups in general?

To formally test for mediation, we followed the steps laid out by Baron & Kenny (1986). A variable M mediates the relationship between an independent variable X , in our case the Val158Met SNP, and a dependent variable Y , in our case partisan attachment, if (1) X significantly predicts M and (2) M significantly predicts Y controlling for X (Baron & Kenny 1986). This relationship is illustrated in *Figure 2*.

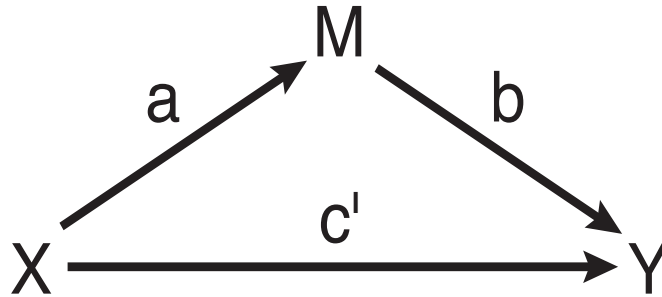


Figure 2: The mediation relationship described by Baron and Kenny (1986). Path c' is called the direct effect and the product of paths a and b is the indirect effect.

A test of whether extraversion mediates the association found between Val158Met and partisan attachment can be represented in the context of this analysis by the following two equations:¹¹

$$Extraversion_i = \beta_0 + \beta_{Met}Met_i + \beta_{Age}Age_i + \beta_{Male}Male_i \quad (2)$$

$$\text{logit}(P[Partisan_i = 1]) = \delta_0 + \delta_{Met}Met_i + \delta_{Extraversion}Extraversion_i + \beta_{Age}Age_i + \beta_{Male}Male_i \quad (3)$$

The indirect effect $ab = \beta_{Met}\delta_{Extraversion}$, the direct effect $c' = \delta_{Met}$, and the total effect is equal to

¹¹The vector of the subpopulation assignments (Z) has been suppressed for presentation purposes. Subpopulation assignments are included as controls in both models.

$ab + c'$. The size of the mediated effect in relation to the total effect can be calculated by $\frac{|ab|}{|ab|+|c'|}$.

The parameter estimates from equations (3) and (4) are presented in *Table 2*.

	<i>Extraversion</i> (3)			<i>Partisanship</i> (4)		
	Coef	SE	P Value	Coef	SE	P Value
Intercept	46.4	5.3	0.00	-0.56	1.02	0.58
Met	-1.96	0.74	0.01	-0.39	0.14	0.01
Extraversion				0.02	0.01	0.04
Age	0.10	0.28	0.71	0.03	0.03	0.42
Male	3.58	1.12	0.00	-0.36	0.22	0.10
SP 1	1.98	1.51	0.19	0.21	0.30	0.49
SP 2	1.39	2.04	0.50	-0.37	0.39	0.35
<i>N</i>		496			496	
Wald Test of Model Fit (χ^2)		20.1			15.4	
Wald Test Degrees of Freedom		5			6	
Wald Test P value		0.00			0.02	

Table 2: Test of association between COMT Val158Met SNP and both partisan attachment and extraversion. The partisan attachment model is a simple logit and the extraversion model is a linear regression. The dichotomous dependent variables are *Partisan*, which is whether a registered voter is affiliated with the Democratic or Republican party, *Met* is the number of Met alleles (0, 1, or 2), and *Extraversion*, which is the T-score of the NEO-FFI extraversion factor score. *SP* is the subpopulation assignment. Logit and linear coefficients (Coef), standard errors (SE), and p-values are presented.

The results in *Table 2* are consistent with both criteria laid out by Baron & Kenny (1986). The Met allele significantly predicts extraversion ($p = 0.01$) in *Model 3* and extraversion is significant ($p = 0.04$) in a model of partisan attachment (*Model 4*) even when the Met allele is included. The Met allele remains significant in *Model 4* suggesting partial mediation. However, these results are only suggestive. To formally test for mediation, ab must be estimated. Since ab is not necessarily normally distributed (Bollen & Stine 1990, Lockwood & MacKinnon 1998, Mackinnon, Lockwood, Hoffman & West 2002, Shrout & Bolger 2002), the approach most researchers take is to bootstrap the estimated indirect effect and construct confidence intervals based on the bootstrapped values (Bollen & Stine 1990, Shrout & Bolger 2002). If ab is bounded away from zero the indirect effect

can be considered significant.

To estimate the indirect effect as well as the proportion of the total effect that is mediated by extraversion, we used the R package *mediation* (Imai, Keele, Tingley & Yamamoto 2009). We employed the Baron & Kenny (1986) parametric approach with quasi-Bayesian bootstrap to produce confidence intervals based on 1000 simulations.¹² We found a significant mediated effect and 8% (95 % CI 5%, 22%) of the effect of the Met allele on partisan attachment is via the personality trait extraversion.¹³ The test of mediation was only performed on the primary sample because the replication sample lacks measures of personality traits.

Discussion

We show that an extensively studied gene that is responsible for the degradation of the neurotransmitter dopamine is associated with partisan attachment. More specifically, the less active Met allele of the COMT Val158Met SNP is associated with a significantly lower probability among registered voters of being attached with a major party. Further, this association was replicated in a different sample of California voters. The first differences for individuals who have one and two Met alleles compared to none are 10% and 20% respectively. The predicted probability of being a partisan when having 0, 1, and 2 Met alleles is 74%, 64%, and 54% respectively. First differences for the replication sample were about half the size of the primary sample.

Based on previous research, we hypothesize that having the Met allele leads to being less extraverted which in turn makes one less likely to be a partisan. We do find a significant indirect

¹²A nonparametric bootstrap produces similar results.

¹³The results are nearly identical when family income and employment status, both asked at the time of participation in the original study, are included in the model of partisan attachment. The proportion mediated is 8% (95 % CI 5%, 21%).

effect, however our results are suggestive of partial mediation. Approximately 8% of the observed association with partisan attachment is via extraversion. This result provides the first empirical support for a casual relationship between genes, personality, and political behavior. However, the fact that a vast majority of the association is not mediated by extraversion is also consistent with pleiotropy meaning that Val158Met primarily influences both extraversion and partisan attachment independently rather than sequentially.

These results are novel in three important ways. Our main contribution is to conduct the first formal test of the conjecture that genes affect partisan attachment via their influence on the personality trait extraversion. This mediation hypothesis is plausible given that approximately half of the variation in both partisan attachment (Settle, Dawes & Fowler 2009) and extraversion (Bouchard & McGue 2003) can be attributed to genetic factors in general. More specifically, Stein et al. (2005) and Reuter & Hennig (2005) suggest the link between Val158Met and extraversion and Gerber et al. (2008) and Gerber et al. (2009) provide the link between extraversion and partisan attachment.

Another contribution is our presentation of the analytical framework necessary to explore the complex pathways that underly an association between a candidate genetic polymorphism and a behavior (Munafo 2006). Since individual genes tend to influence many different traits at the same time and complex behaviors are influenced by many genes, it is necessary to investigate each of the proposed theoretical pathways. The next wave of work in the area of genopolitics must attempt to better understand the causal links between genes and political behaviors. Mediation analysis is invaluable for uncovering those links and will ultimately allow us to develop and improve theories of political behavior.

A related contribution is our demonstration that proportion mediated by extraversion is relatively modest. This suggests, especially given the fact the Met allele remains significant in *Model4*, that the Val158Met SNP operates via additional pathways. Knowing that there are likely several mediators between specific genetic variants and political behaviors, each playing a relatively small role, is useful to set our expectations for future research. There is a consensus that approach behaviors in response to stimuli associated to reward are related to differential activity in dopamine neurotransmission (Revelle 2005, Munafò et al. 2003). Approach behaviors include extraversion, impulsivity, novelty seeking, and positive affectivity (Revelle 2005). Here we have focussed on extraversion because of its clear link to partisanship, however it may be the case that these related behaviors are also mediators and should thus be studied further.

Our results, combined with the findings reported by Dawes & Fowler (2009), strongly suggests that the dopamine system is a good place to look for additional genetic variants associated with partisan attachment. The authors of that study found that a polymorphism of the D2 dopamine receptor gene linked to lower density of dopamine receptors, and thus weaker dopamine signaling in the brain, to be significantly associated with a lower likelihood of partisan attachment. Since many genes influence a complex behavior like partisan attachment, it is likely that other systems play a role as well. A genome-wide association study represents an unconstrained search testing hundreds of thousands of variants across the entire human genome. Genetic variants identified by this process hold the power of illuminating presently unknown causal pathways based on the functions they perform. A genome-wide study of partisan attachment is currently underway.

This study has a few limitations. First, it is possible that the estimate of the association between the Val158Met SNP and partisanship mediated by extraversion is biased downward because

a self report measure of extraversion such as the NEO may not be sensitive enough to capture genetic variation especially given our relatively small sample size (Ebstein 2006). Second, our dependent variable is technically party registration rather than party identification. However, our party registration variable is identical to the one used by (Gerber et al. 2008) in their analysis of Connecticut voters that produced results very similar to a standard measure of strength of party identification (Gerber et al. 2009). Finally, genetic analyses are vulnerable to producing a spurious association due to population stratification. We were able to replicate our association result but did not have the necessary data to test for mediation in our replication sample. Therefore, even though we controlled for population stratification by including subpopulation assignments based on 36 ancestry-informative genetic markers, we urge caution in interpreting our mediation results until they can be replicated in another sample. Also, the fact that the effect of the Val158Met SNP was much larger in the primary sample means that additional replications are necessary to establish the true magnitude of this relationship. It is also possible that since our replication sample is significantly older on average that the effect of this SNP varies by age.

Finally, how does this work change the way we view partisan attachment? Our study underscores previous work demonstrating that individual differences in the propensity to form a partisan attachment can be traced back to differences in genetic endowments (Settle, Dawes & Fowler 2009, Dawes & Fowler 2009). The prevailing narrative of partisan attachment states that as political issues become more salient due to close associations with social groups and integration into the community, it results in the formation or strengthening of partisan ties (Campbell, Converse, Miller & Stokes 1960). This assertion, combined with empirical evidence, suggests that genes may have a downstream effect on partisan attachment via more basic predispositions towards social

interactions. The Big Five trait extraversion is believed to represent this predisposition. While we find limited support for this proposed causal pathway, we believe this is the type of theorizing that will help fill in the gap between genes and political behaviors, ultimately leading to a better understanding of these behaviors.

Appendix

Sample Statistics

	Primary	Replication
Val / Val	0.32	0.25
Val / Met	0.50	0.49
Met / Met	0.18	0.26
Partisan	0.64	0.79
Age (mean)	24.21	49.50
Age (sd)	3.17	17.50
Male	0.26	0.31
Black	0.03	0.07
Asian	0.05	0.03
Hispanic	0.19	0.11
Native American	0.00	0.00
Filipino	0.08	0.01
White	0.57	0.77
Other	0.07	0.00
<i>N</i>	510	622
<i>N</i> with Extraversion	496	n/a

Table 3: Sample frequencies, means, and standard deviations.

Single Nucleotide Polymorphism

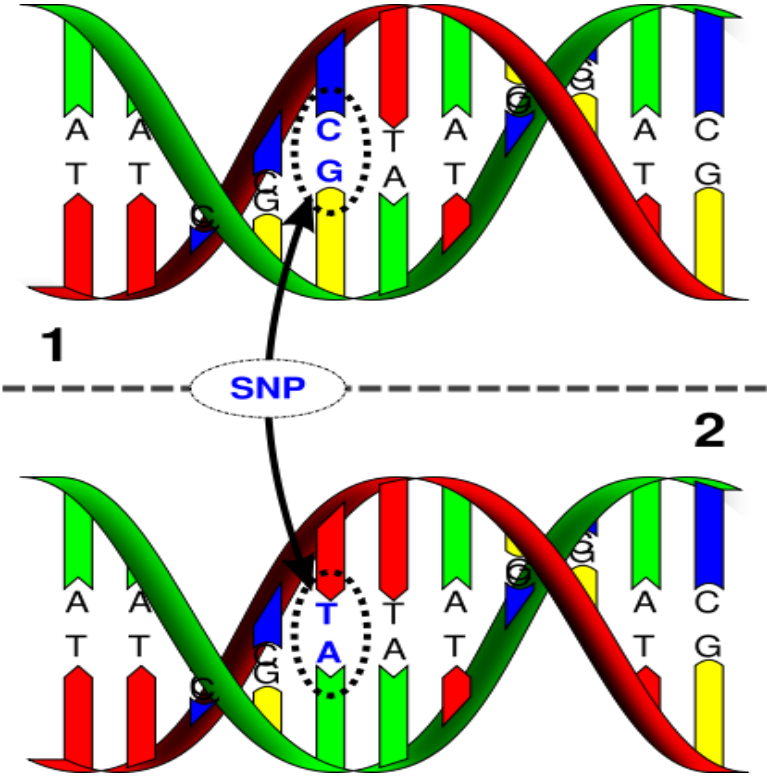


Figure 3: Single Nucleotide Polymorphism

Correlation Structure Based on the ACE Model

We can explicitly model the correlation for each pair of individuals (i and i') within a family as:

$$\rho_{i,i'} = R_{i,i'}a^2 + \gamma_{i,i'}c^2 \quad (4)$$

where R is the degree of genetic relatedness, equalling 1 for monozygotic twin pairs and 0.5 for both dizygotic twin and parent-child pairs, and γ is the degree to which pairs share a common environment, assumed to be equal to 1 for siblings and 0 for parent-child pairs. The three parameters a^2 , c^2 , e^2 are estimated within a univariate ACE model.

The ACE model assumes that the variance in observed behavior can be partitioned into additive genetic factors (A), and environmental factors which are shared or common to co-twins (C), and unshared environmental (E). Common environment includes the family environment in which both twins were raised, as well as any other factor to which both twins were equally exposed. In contrast, the unshared environment includes idiosyncratic influences that are experienced individually. The role of genes and environment are not measured directly but their influence is inferred through their effects on the covariances of twin siblings (Neale & Cardon 1992) described by the model¹⁴:

$$y_{ij} = aA_{ij} + cC_{ij} + eE_{ij} \quad (5)$$

where A is the additive genetic component, C is common environment component, and E is the unique environment component. All three components are assumed to be mutually independent

¹⁴All variables are assumed to be standardized to have mean zero and unit variance.

and are each distributed as a standard normal. For an a given twin pair in family j :

$$\text{cov}(y_{1j}, y_{2j}) = a^2 \text{cov}(A_{1j}, A_{2j}) + c^2 \text{cov}(C_{1j}, C_{2j}) + e^2 \text{cov}(E_{1j}, E_{2j}) \quad (6)$$

Since MZ twins share all of their genes while DZ share 50% on average, $\text{cov}(A_{1j}, A_{2j}) = 1$ for MZ twins and $\text{cov}(A_{1j}, A_{2j}) = 0.5$ for DZ twins. Since unique environment is by definition unique to each twin, $\text{cov}(E_{1j}, E_{2j}) = 0$. Finally, since both twins in a pair face the same common environment, $\text{cov}(C_{1j}, C_{2j}) = 1$. This leaves us with:

$$\text{cov}(y_{1j}, y_{2j})_{MZ} = a^2 + c^2 \quad (7)$$

$$\text{cov}(y_{1j}, y_{2j})_{DZ} = 0.5a^2 + c^2 \quad (8)$$

Since A, C, and E are assumed to be independent, the variance for all twins is:

$$\text{var}(y_{ij}) = a^2 + c^2 + e^2 \quad (9)$$

where a^2 is the proportion of the total variation attributable to genetic factors, c^2 is the proportion attributable to common environmental factors, and e^2 the proportion attributable to unique environmental factors.

The variance-covariance matrix for MZ and DZ twin pairs respectively is then:

$$\mathbf{\Omega}_{MZ} = \begin{bmatrix} a^2 + c^2 + e^2 & a^2 + c^2 \\ a^2 + c^2 & a^2 + c^2 + e^2 \end{bmatrix} \quad (10)$$

$$\Omega_{\mathbf{DZ}} = \begin{bmatrix} a^2 + c^2 + e^2 & 0.5a^2 + c^2 \\ 0.5a^2 + c^2 & a^2 + c^2 + e^2 \end{bmatrix} \quad (11)$$

Since the partisanship is binary, we estimate a threshold model that assumes a continuous latent distribution underlying a given trait for which we observe thresholds demarcating categories.

The estimates based on our data are $a^2 = 0.52$ (0.26, 0.78), $c^2 = 0.00$ (0.00, 0.02), and $e^2 = 0.48$ (0.22, 0.74).¹⁵ Plugging the estimates into *Equation 4* yields a correlation between monozygotic twins of 0.52 and a correlation between non-monozygotic siblings, as well as between parents and their children, of 0.26. The GEE model is estimated using a “fixed” working correlation structure where the correlation between individuals is either 0.56 or 0.26 depending on the genetic relatedness between pairs.¹⁶ The results are presented in *Table 4*.

¹⁵These estimates are very similar to those reported for strength of partisan attachment by Settle, Dawes & Fowler (2009)

¹⁶Using only the parameter estimate for a^2 does not account for the uncertainty associated with the estimate. Therefore, we drew 1000 estimates of a^2 from a $N \sim (0.521, 0.133)$, constructed the correlation matrix given each estimate, and ran the GEE regression. The mean p-value associated with the parameter estimates for the Met allele (β_{Met}) from this process was 0.05.

	Primary Sample			Replication Sample with Fixed Correlation		
	Coef	SE	P Value	Coef	SE	P Value
Intercept	0.39	0.88	0.66	0.41	0.35	0.23
Met	-0.43	0.14	0.00	-0.29	0.15	0.05
Age	0.03	0.03	0.42	0.03	0.01	0.00
Male	-0.28	0.21	0.18	-0.39	0.20	0.05
SP 1	0.25	0.29	0.40			
SP 2	-0.38	0.39	0.32			
Black				-0.09	0.43	0.83
Asian				-0.40	0.77	0.60
Hispanic				0.97	0.43	0.02
Native American				-1.14	1.88	0.58
Filipino				0.01	0.20	0.98
Other				-1.14	1.11	0.30
<i>N</i>		510			622	
Wald Test of Model Fit (χ^2)		12.8			36.8	
Wald Test Degrees of Freedom		5			9	
Wald Test P value		0.00			0.03	

Table 4: Test of association between COMT Val158Met SNP and partisan attachment. The primary model is a simple logit and the replication model is a GEE logit with a “fixed” working correlation based on *Equation 2*. The dichotomous dependent variable is *Partisan*, which is whether a registered voter is affiliated with the Democratic or Republican party. *Met* is the number of Met alleles (0, 1, or 2), *SP* is the subpopulation assignment, and *Black*, *Asian*, *Hispanic*, *Native American*, *Filipino*, and *Other* are self-reported race categories. Logit coefficients (Coef), standard errors (SE), and p-Values are presented.

References

- Baron, R. & D. Kenny. 1986. "The Moderator-Mediator Variable Distinction in Social Psychology Research: Conceptual, Strategic, and Statistical Considerations." *Journal of Personality and Social Psychology* 51:1173–1182.
- Bienvenu, O. & M. Stein. 2003. "Personality and Anxiety Disorders: A Review." *Journal of Nervous Mental Disorders* 17:154–161.
- Bilder, R., J. Volavka, J. Lachman & A. Grace. 2004. "The Catechol-O-Methyltransferase Polymorphism: Relations to the Tonic-Phasic Dopamine Hypothesis and Neuropsychiatric Phenotypes." *Neuropsychopharmacology* 29:1943–1961.
- Bollen, K. & R. Stine. 1990. "Direct and Indirect Effects: Classical and Bootstrap Estimates of Variability." *Sociological Methodology* 20:115–140.
- Bouchard, T. & J. Loehlin. 2001. "Genes, Evolution, and Personality." *Behavior Genetics* 31:243–273.
- Bouchard, T. & M. McGue. 2003. "Genetic and Environmental Influences on Human Psychological Differences." *Journal of Neurobiology* 54(1):4–45.
- Campbell, A., P. Converse, W. Miller & D. Stokes. 1960. *The American Voter*. University of Chicago Press.
- Carver, C. & C. Miller. 2006. "Relations of Serotonin Function to Personality: Current Views and a Key Methodological Issue." *Psychiatry Research* 144(1):1–15.

- Chen, J., B. Lipska, N. Hamlin, Q. Ma, M. Matsumoto, S. Melhem, B. Kolachana, T. Hyde, M. Herman, J. Apud, M. Egan, J. Kleinman & D. Weinberger. 2004. "Functional Analysis of Genetic Variation in Catechol-O-Methyltransferase (COMT): Effects on mRNA, Protein, and Enzyme Activity in Postmortem Human Brain." *American Journal of Human Genetics* 75(5):807–821.
- Dawes, C. & J. Fowler. 2009. "Partisanship, Voting, and the Dopamine D2 Receptor Gene." *Journal of Politics* TBD.
- Denny, K. & O. Doyle. 2008. "Political Interest, Cognitive Ability and Personality: Determinants of Voter Turnout in Britain." *British Journal of Political Science* 38:291–310.
- Depue, R. 1995. "Neurobiological Factors in Personality and Depression." *European Journal of Personality* 9:413–439.
- Depue, R. & P. Collins. 1999. "Neurobiology of the Structure of Personality: Dopamine, Facilitation of Incentive Motivation, and Extraversion." *Behavioral and Brain Sciences* 22:491–569.
- Ebstein, R. 2006. "The Molecular Genetic Architecture of Human Personality: Beyond Self-Report Questionnaires." *Molecular Psychiatry* 11:427–445.
- Fowler, James H., Laura A. Baker & Christopher T. Dawes. 2008. "Genetic Variation in Political Behavior." *American Political Science Review* 102(2):233–248.
- Gerber, A., G. Huber, C. Raso & Shang Ha. 2008. "Personality and Political Behavior." Unpublished Manuscript.

- Gerber, A., G. Huber, D. Doherty & C. Dowling. 2009. "Reassessing the Effects of Personality on Political Attitudes and Behaviors: Aggregate Relationships and Subgroup Differences." SSRN working paper <http://ssrn.com/abstract=1412839>.
- Gerber, A., G. Huber, D. Doherty, C. Dowling & S. Ha. 2010. "Personality and Political Attitudes: Relationships Across Issue Domains and Political Contexts." *American Political Science Review* 104(1):111–133.
- Goldman, D., G. Oroszi & F. Ducci. 2005. "The Genetics of Addictions: Uncovering the Genes." *Nature Reviews* 6:521–532.
- Hartl, D. 2000. *A Primer on Population Genetics*. Sinauer Associates.
- Hatemi, Peter K., John Hibbing, John Alford, Nicholas Martin & Lindon Eaves. 2009. "Is There a Party in Your Genes." *Political Research Quarterly* 62(3):584–600.
- Imai, K., L. Keele, D. Tingley & T. Yamamoto. 2009. "Causal Mediation Analysis in R." Tech. rep., Department of Politics, Princeton University.
- Liang, K. & S. Zeger. 1986. "Longitudinal Data Analysis Using Generalized Linear Models." *Biometrika* 73:13–22.
- Lockwood, C. & D. MacKinnon. 1998. "Bootstrapping the Standard Error of the Mediating Effect." *Proceedings of the 23rd Annual Meeting of the SAS Users Group* pp. 997–1002.
- Luo, X., H. Kranzler, L. Zuo, H. Zhang, S. Wang & J. Gelernter. 2007. "CHRM2 Variation Predisposes to Personality Traits of Agreeableness and Conscientiousness." *Human Molecular Genetics* 16(13):1557–1568.

- Luo, X., H. Kranzler, L. Zuo, S. Wang & J. Gelernter. 2007. "Personality Traits of Agreeableness and Extraversion are Associated with ADH4." *Biological Psychiatry* 61(5):599–608.
- Luo, X., L. Zuo, H. Kranzler, H. Zhang, S. Wang & J. Gelernter. 2008. "Multiple OPR Genes Influence Personality Traits in Substance Dependent and Health Subjects in Two American Populations." *American Journal of Medical Genetics Part B* 147B:1028–1039.
- Mackay, T. 2001. "The genetic architecture of quantitative traits." *Annual Review of Genetics* 35:303–339.
- Mackinnon, D., C. Lockwood, J. Hoffman & J. West. 2002. "A Comparison of Methods to Test Mediation and Other Intervening Variable Effects." *Psychological Methods* 7:83–104.
- McCrae, R. & P. Costa. 1992. "An Introduction to the Five-Factor Model and its Implications." *Journal of Personality* 60:175–215.
- McCrae, R. & P. Costa. 2004. "A Contemplated Revision of the NEO Five-Factor Inventory." *Personality and Individual Differences* 36(3):587–596.
- Mondak, J. & K. Halperin. 2008. "A Framework for the Study of Personality and Political Behaviour." *British Journal of Political Science* 38:335–362.
- Mondak, J., M. Hibbing, D. Canache, M. Seligson & M. Anderson. 2010. "Personality and Civic Engagement: An Integrative Framework for the Study of Trait Effects on Political Behavior." *American Political Science Review* 104(1):85–110.
- Munafo, M. 2006. "Candidate Gene Studies in the 21st Century: Meta-Analysis, Mediation, Moderation." *Genes, Brain and Behavior* 5(Suppl. 1):3–8.

- Munafo, M., T. Clark, L. Moore, E. Payne & J. Flint. 2003. "Genetic Polymorphisms and Personality in Health Adults: A Systematic Review and Meta-Analysis." *Molecular Psychiatry* 8:471–484.
- Neale, M. & L. Cardon. 1992. *Methodology for Genetic Studies of Twins and Families*. Dordrecht, The Netherlands: Kluwer.
- Plomin, R. 2008. *Behavioral genetics*. Worth Publishers.
- Pritchard, J., M. Stephens & P. Donnelly. 2000. "Influence of Population Structure Using Multilocus Genotype Data." *Genetics* 155:945–959.
- Reuter, M. & J. Hennig. 2005. "Association of the Functional Catechol-O-Methyltransferase Val158Met Polymorphism with the Personality Trait of Extraversion." *NeuroReport* 16(10):1135–1138.
- Revelle, W. 2005. "Personality Processes." *Annual Review of Psychology* 46:295–328.
- Settle, Jaime E., Christopher T. Dawes & James H. Fowler. 2009. "The Heritability of Partisan Attachment." *Political Research Quarterly* 62(3):601–613.
- Shrout, P. & N. Bolger. 2002. "Mediation in Experimental and Nonexperimental Studies: New Procedures and Recommendations." *Psychological Methods* 7(4):422–445.
- Stein, M., M. Fallin, N. Schork & J. Gelernter. 2005. "COMT Polymorphisms and Anxiety-Related Personality Traits." *Neuropsychopharmacology* 30:2092–2102.
- Stein, M., N. Schork & J. Gelernter. 2004. "A Polymorphism of the Beta One Adrenergic Receptor is Associated with Low Extraversion." *Biological Psychiatry* 56:217–224.

Yang, B., H. Zhao, H. Kranzler & J. Gelernter. 2005. "Practical Population Group Assignment with Selected Informative Markers: Characteristics and Properties of Bayesian Clustering via Structure." *Genetic Epidemiology* 28:302–312.

Zhang, L., F. Rao, J. Wessel, B. Kennedy, B. Rana, L. Taupenot, E. Lillie, M. Cockburn, N. Schork, M. Ziegler & D. O'Connor. 2004. "Functional Allelic Heterogeneity and Pleiotropy of a Repeat Polymorphism in Tyrosine Hydroxylase: Prediction of Catecholamines and Response to Stress in Twins." *Physiol Genomics* 19:277–291.