

What is a ‘Gene’ and Why Does it Matter for Political Science?

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Abstract

A recent stream of influential research suggests that the inclusion of behavioral genetic models can further inform our understanding of political preferences and behaviors. But it has often remained unclear what these models mean, or how they might matter for the broader discourse in the political science literature. The initial wave of behavioral genetic research focused on foundational discovery, and has begun to outline the basic properties of genetic influence on political traits, while a second wave of research has begun to link genetic findings to broader aspects of political behaviors. In the introduction to this special issue, we explicate how genes operate, the most common forms of behavioral genetic analyses and their recent applications toward political behaviors. In so doing, we discuss what these findings mean for political science, and describe how best to interpret them. We note potential limitations of behavioral genetic approaches and remain cautious against the overextension of such models. The five articles which follow strive to move beyond discovery and focus more on the integration of behavioral genetic models with mainstream theories of political behavior to analyze problems of interest to political scientists.

Until recently, the majority of political science scholarship has adhered to the assumption that differences in behavior and preferences result entirely from environmental influences. Biological systems were understood to play little or no role in producing the infinitely divergent and conceptually sophisticated differences in political behavior which appear manifest in modern society. In this way, the body was viewed merely as the vehicle for the self-conscious perpetuation of political choice, rather than the navigator of the journey itself. Yet the culmination of behavioral research across the sciences suggest that our biological container remains central to how we interpret and react to the world around us, and may have an important role in forming political preference structures, and in guiding us into the very environments which influence our behavior. Thus, this special issue focuses on ground-breaking applications of genetics to enduring questions in political research.

Over the course of the last 30 years of research, the view that preferences are almost exclusively environmentally driven has eroded. A new understanding, resulting in large part from the clear recognition of the vast complexity and individual variance which so obviously characterizes all human behavior, has emerged (Eaves and Eysenck, 1974; Lumsden and Wilson, 1981; Martin et al., 1986). And, over the last 5 years in particular, it has become widely accepted that genetic factors contribute to individual differences in political and social behaviors (for a review see Hatemi, Dawes et al., 2011). Indeed, in this short period, scores of articles have explored genetics influences on political preference and behaviors. The majority of these publications have appeared in the disciplines' top journals, including the *American Journal of Political Science*, the *Journal of Politics*, *Political Analysis*, the *American Political Science Review*, *Foreign Policy Analysis*, *Political Psychology*, *Political Behavior*, and *Political Research Quarterly* among others (Alford, Funk and Hibbing, 2005; Dawes and Fowler, 2009;

Dawes, Loewen and Fowler, 2011; Fowler and Dawes, 2008; Fowler, Baker, and Dawes, 2008; Hatemi, Alford et al., 2009; Hatemi, Funk et al., 2009; Hatemi, Medland and Eaves, 2009; Hatemi, 2010; Hatemi et al., 2010; Hatemi, Gillespie et al., 2011; Hatemi and McDermott, 2011abc; McDermott and Hatemi, 2011; Medland and Hatemi, 2009; Sturgis et al., 2010; Verhulst et al., 2012). Studies have focused on attitudes, ideology, voter turnout, vote choice, personality and politics, reward systems, culture, aggression, group affiliation, gender, fear, trust, and violence among others. Additional articles written by political scientists have also appeared in journals published in the life sciences and interdisciplinary outlets (Boardman et al., 2011; Dawes et al., 2007; Eaves and Hatemi, 2008; Eaves et al., 2008; Fowler and Schreiber, 2008; Hatemi et al., 2007; Klemmensen et al., 2011; McDermott et al., 2009; Verhulst et al., 2010). Thus, the question is no longer whether genetics informs political preferences and behavior. Rather, questions now center on how to engage the broader political science community into this discussion. We propose this might best be accomplished by providing political scientists with the basic information on how to use genetics research most effectively, and how to apply findings from this research to help answer questions of import to the discipline.

The first wave of modern genetics research on political traits focused on the discovery of foundational elements, and outlined the basic properties of genetic influence on complex social and political preferences. This included quantifying the relative influence of genetic factors and identifying latent pathways involved in particular behaviors, such as shared genetic variance between personality and attitudes (e.g., Verhulst et al., 2012), or exploring various underlying mechanisms involved in emotion and cognition, and specifying the import of genetics on the psychological platform and architecture through which humans perceive and react to stimuli (Fowler and Schreiber, 2008). These avenues of discovery will undoubtedly continue, since this

field of inquiry is only in its infancy. A parallel line of research is now beginning, one we seek to both highlight and advance through this special issue, which focuses on application of genetics to political behavior, but does so embedded within the main theories and approaches central to the discipline.

Why should political scientists in general, or those working primarily in other areas be interested in these developments? Precisely because these developments hold critical implications for a wide array of models whose application may not appear obvious on the surface to those unfamiliar with their import. Indeed, despite the wave of recent research which examines the role of biological inheritance and environmental influence on the transmission of political behavior, the extant models and theoretical conceptualizations drawn from evolutionary theory and behavior genetics remain largely unknown to political scientists. Moreover, the recent “genetic” findings remain disconnected from the central theories of political behavior which continue to emphasize socialization and rational choice approaches. Rational models assume that preferences are given and exogenous and remain largely unconcerned with the ontological basis of preferences. Though not explicitly stated, or invoked in most of the social science literature (for an exception see Kinder and Kam, 2009), the logic of rational choice does allow for the influence of genetic sources through its “black box” approach to the source of preferences. Alternatively, behavioral models assume that preferences and actions result from processes of social conditioning. Simply put, rational and socialization approaches do not include sources of preferences that originate from internal mechanisms, or differences in motivation for human behavior absent revealed choices or social forces; nor do they address the nature of the human organism, its physiological needs or drives.

In this regard, traditional approaches have so far remained incomplete due to the lack of a concomitant theory describing the origins of preferences (Bueno de Mesquita and McDermott, 2004). This might be provided by evolutionary models which include genetic influences (Lumsden and Wilson, 2005). Thus, advancing the inclusion of biological mechanisms into models of human decision making and preference structures suggests that traditional and biological approaches might quite profitably be merged to establish more accurately predictive models of political preferences, precisely because genetic approaches can speak to one important aspect of behavior which rational choice models remain agnostic to, or take as given. In this way, genetics research may illuminate novel sources of preference formation (e.g., Hatemi, Gillespie et al., 2011). In other words, the approaches we describe below can be usefully tractioned by rational choice theorists, as well as by those who have studied processes of political socialization, to provide novel pathways to explain where preferences come from. Such a perspective may offer the foundation for more accurate and predictive models of behavior in the future.

In order for these approaches to prove most useful for political science, it is necessary for scholars to begin from the same set of starting assumptions regarding the nature and meaning of genetic approaches, and an understanding of the history and limitations of behavioral genetic research. Therefore, in this introduction, we identify what a gene is, how genes operate, and how knowledge of the genome changes our understanding of environmental influence. We explicate how to interpret the findings of twin designs, association studies and genome-wide analyses, with an eye toward their application to problems in political behavior. In doing so, we discuss the general theory of genetic influence and the meaning of models built upon its foundations. In this way, we hope to provide a common ground for scholars moving forward to utilize these

approaches to systematically address enduring and pervasive challenges in understanding the nature of political choice.

What is a Gene, and What is Genetic Influence?

At some point, almost everyone has pondered the nature and limitations of our own biology. How does my eye actually see things? Why do I feel the way I do? How does my body fight infection? It can be overwhelming to consider how every single emotional or physical thought or action that we experience, even those we cannot see, such as the way our immune system reacts to the incursion of bacteria, the influence of a person's touch, a smile, or the feeling of warm sunlight on our face, is initiated by the combination of some stimulus and the concomitant expression of genes within our cells. This leads to the reciprocal action of other cells which result in signals that govern the expression of other genetic and neurobiological systems, which eventually inspire feeling, thought and behavior. Once we combine this fascinating interaction with the human ability to transcend our biology, to reason, to feel, to perceive, to question, to talk, to love, to empathize, and all other self-reflective dynamics which make us human, only then can we appreciate both the wonder and complexity of the human genome.

Pearson (2006) describes a gene as "locatable region of genomic sequence, corresponding to a unit of inheritance, which is associated with regulatory regions, transcribed regions and/or other functional sequence regions". While such a definition might be useful for a genetics audience, for many political scientists this constitutes a definition without meaning because the vast majority of political scientists have not been exposed to molecular biology, genetics, or functional genomics. Interdisciplinary research is often hindered by the lack of a common language or understanding. In this way, the lack of previous integration of genetics and social

science has unfortunately led to misunderstandings of what recent genetics models can tell us about complex human behavior. For example, a recent article in the popular media introduced a finding from a gene–environment exploration of liberalism, claiming with the article title that “Researchers find the Liberal Gene” (Kaplan, 2010), despite the fact the authors made no such claim in the actual journal article. Editors, academics, and the media unfortunately often make reference to the genes ‘for’ ‘x’. Of course, any credible scientist is well aware that it is essentially impossible for any single gene to be responsible for any complex social or political trait. Genes simply regulate the cellular environment and create proteins. The question of how, when and why they influence our behavior involves a complex marriage between genes and environments. The exact steps remain unknown even to the most experienced in the area, and thus conveying the methods and findings to those without a scientific background is incredibly difficult.

To begin with, only in the most extreme and unusual of circumstances does a single gene or gene mutation result in a specific behavior or phenotype; Huntington’s disease represents the prototypical example in this very rare category (Imarisio et al., 2008). The genetic effects on the propensity to exhibit any complex social trait will be indirect, and result from the aggregate interaction of thousands of genes in interaction with their local and exogenous environmental conditions (e.g., Hill et al., 2008). We will never find “the” gene for liberalism because it does not exist. The popular misunderstanding that complex social or political behavior can be explained by a single gene, or even a small number of genes, can unfortunately mislead unsuspecting audiences. This representation remains counterproductive because it implies a simplistic genetic underpinning of human behavior and mode of action of genes.

Rather, at the highest level, genes provide the information to generate different proteins, the main functional tools in the cell, which in turn instigate or restrict hormonal and other biological pathways in both state and trait circumstances. Many of these proteins act as regulators of genes, controlling when and where they are switched on, leading to a complex network of interacting genes. These biochemical pathways operate through a complex cognitive and emotive architecture, including critical aspects of development, such as in utero environments, in an infinitely variegated social world as individuals interact with other people and the environment.

The processes then becomes operationalized through a psychological architecture in a human organism that walks around, moves and experiences the world, resulting in outcomes we observe at the macro level as behaviors, preferences, attitudes and other recognizable measures. Figure 1 provides a visualization of some of the high level mechanisms of these interactive processes. The figure was originally intended to focus on mental capital across the life course, but is just as easily applicable to almost all complex traits, social, political, psychological or otherwise.

Figure 1: The Interaction of Biology and Environment Over the Life Course

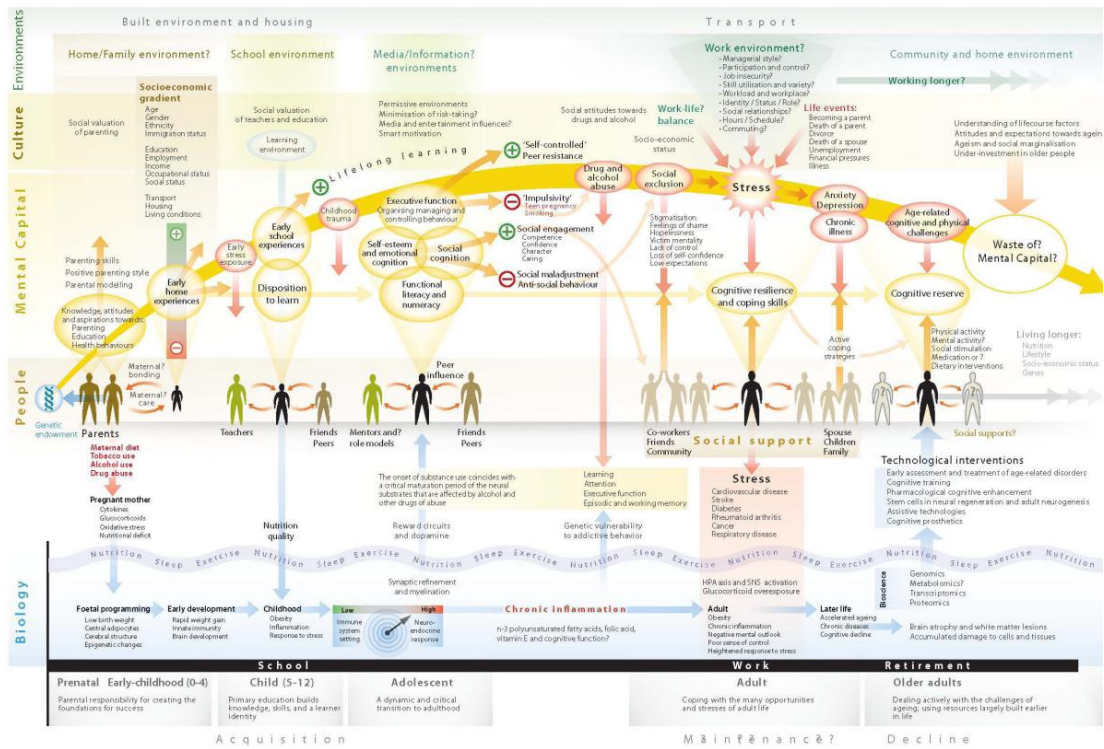


Figure 1 is striking in illuminating the numerous ways in which social and environmental factors intervene and interact with the human organism to affect outcomes of interest. Many of these forces interweave social and structural forces with internal tendencies into the complex intertwined process of development across the life course. Indeed, most of these factors are recursive and interactive, as well as developmentally informed. However, even such a superbly designed illustration that highlights the myriad biological, developmental, cognitive, psychological, dispositional, social, institutional, and idiosyncratic events one encounters through a lifetime struggles to capture the infinitesimal dynamic interactions of all human behavior. Indeed, arrows can be drawn between every mechanism; few processes in the development of complex human behaviors are linear. This is equally true regarding genetic influences because the genome itself remains dynamic. Often popular interpretations of genetic

influences lead the public to believe that a single gene, possibly in combination with a particular environmental cue, leads to a specific behavior. This may be in part because the statistical models prevalent in academic research often imply such a direct relationship (e.g., Caspi et al., 2003). However, scientists familiar with genetics understand that gene-environment relationships are much more complex, and that we remain limited by our statistical tools to adequately capture these complex dynamics. This level of sophistication is rarely communicated to the public or even to the social sciences. Much in the same way that social science research relies on regression models to predict behavior, and depends on the critical assumptions inherent in such models which assume that everything else not measured in the model stays constant, genetic analyses make similar assumptions regarding other parts of the genome. Yet the public at large, and the majority of the social sciences, who are mostly untrained in biology and genetics, do not necessarily espouse such a sophisticated view, and instead perceive a deterministic view of genetic influences which they absorb from the mass media. Therefore, it becomes critically important to explain in more detail the supremely complex pathway from DNA to protein regulation and ultimately behavior to social science audiences and the interested public.

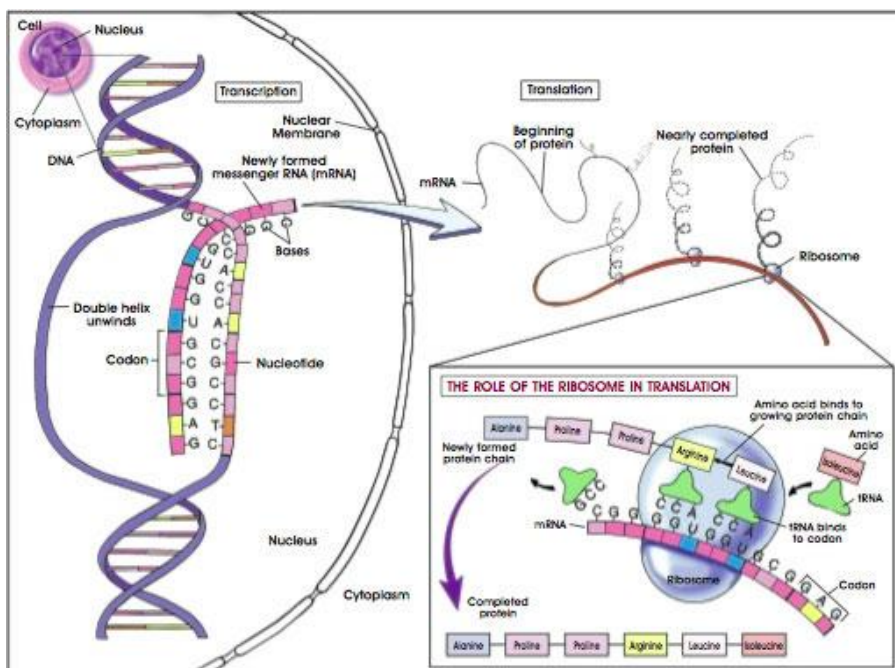
DNA, Genes, and Gene Expression: How do Genes Lead to Behavior?

Untangling the interaction between genes and behavior is among one of the most difficult tasks in science. The identification of the human genome over a decade ago dispelled any ideas of one-to-one mapping genes to behavior. Rather, humans have far fewer genes than imagined, and uncovering how genes shape individuals and their behaviors is a monumental task.

For the purpose of this review, and of importance to political scientists seeking to understand the genome, we define a gene as a segment of a DNA molecule that encodes one or

more proteins through three major steps: Transcription; Translation; and Protein Synthesis (for a brief history of gene mapping and some basic background on genetic analyses, see Web Appendix 1). Figure 2 is helpful for a visual representation of this process. The following descriptions will still remain at a higher level than those who work in molecular biology or genetics would find natural, but we wish to provide enough information to allow those untrained in biology the tools necessary to engage in this growing area of scholarly discourse.

Figure 2: Gene Transcription, Translation, and Protein Synthesis



Source: National Institutes of Health Report Regenerative Medicine (2006)

DNA specifies the synthesis of messenger RNA (called transcription) and the messenger RNA specifies the synthesis of polypeptides, which form proteins. Transcription is influenced by a host of genetic and environmental factors. The genetic portion of these transcription factors are known as the ‘promoter’. Promoters need not be in the gene whose transcription they control and, in fact, are often some distance from the site where transcription begins. Furthermore, enhancers, which increase transcription activity, and silencers that inhibit them, are also part of

the process outside of the gene. Promoters activate first, and are located physically prior to operator regions. These operator regions are controlled by regulatory proteins which, through a sequence of chemical signals, can start or stop the transcription process. These various DNA sequences, while not typically included in the public's understanding of what constitutes a gene, are similarly inherited along with the rest of the DNA. So not only are genes heritable, but the rules which govern them, such as transcription, also appear to be heritable.

Moving from transcription to translation represents a second step in the long chain from genes to behavior. Translation is the process by which messenger RNA regulates the production of polypeptides (later proteins). The precise mechanisms involved in protein generation are not fully understood. The biological machinery that carries out translation consists of a large complex of many different proteins. Translation takes place outside the nucleus in the surrounding cytoplasm, unlike transcription, which takes place within the nucleus of cells. Thus, translation is also influenced by the environment of the cell and the cell membranes. Thus, a gene's role in protein regulation is hardly "fixed". For example, even if two people have a similar genotype, the function of that genotype could differ in numerous ways depending on the individual's transcription and translation processes, as affected by environmental stimulus. In this way, environments can set the degree to which genes operate and create the stage upon which genes are expressed. In addition, differences in the DNA sequence (genotypes) can also lead to changes in the protein sequence, which can affect the function of the protein. In some cases, such as in the case of rare genetic disorders, the loss of function caused by the changed sequence can be so devastating as to make the protein completely non-functional, which can have dire consequences for the carrier of that genetic variant. In most cases however, the change in protein function is more subtle and therefore has a much smaller effect. It is the cumulative

effect of thousands of genotype differences between any two people that helps create the variability in behavior seen in the population.

Finally only a proportion of the genes in any one cell are significantly ‘expressed’ (functionally activated) and expression varies by cell type. The mechanisms which regulate expression of specific genes in different tissues occur through numerous genetic and environmental pathways. One example, is methylation of DNA, which is an epigenetic signaling mechanism that cells use to switch genes into an "off" position and is a critical component in numerous biological processes, including embryonic development and X-chromosome inactivation (for a non-technical primer on methylation of DNA see Phillips, 2008). For example, if serotonin “genes” are methylated, they will be less active, thus resulting in differences in serotonin release and uptake, which may lead to individuals becoming more or less susceptible to depression (van IJzendoorn et al., 2010).

Some genes are expressed in all cells because they deal with general functions that are carried out in every cell in the body (e.g., protein synthesis). These genes are known as ‘housekeeping genes’. Other genes are expressed only in specific tissues or organs, or only during critical developmental phases (e.g., infancy, puberty, etc.), or as a result of environmental triggers (both within the organism and outside of it). In this way, while genes may be able to influence our behavior, one’s behavior also influences genetic expression. Gene expression can be temporarily or permanently altered by extra-cellular signals and environmental influences. Thus, the differential patterns of gene expression provide one way by which a single gene can have multiple effects on multiple traits, or explain how people with the same combination of genotype and observed environment can have remarkably different phenotypes.

DNA may be the platform on which the causal chain instigates, and there is no question that genotype matters. That is, some people have the potential for higher or lower promotion of a particular hormone based on their genotype, but hormonal release or uptake, the actual end result, can show enormous variance based on environmental contingency. Perhaps a macro analogy might prove helpful for understanding. While this example does not provide a perfect illustration, it can offer an accessible and intuitive reference. Imagine a car which represents the platform (genotype) and a driver as the one who controls the expression (environment, epigenetics). Further, consider there are many different types of vehicles, such as an off road vehicle or a stock racing car. Each one is optimal for different kinds of tasks and usage in different conditions and different drivers would operate the vehicles differently. Off road vehicles operate better than others through the mountains on tough terrain, while the stock car will prove superior in the Daytona 500. Yet, if a professional race car driver was operating the off road truck on the Daytona track, the truck might just prove superior to my great grandmother driving the stock car. Yet, the stock car would operate horribly on rocky terrain, regardless of the driver. Different variations (i.e., terrain) and different platforms (i.e., cars) with different drivers (environment) will produce different baselines of function and different interactions. Similarly, the human genome, and the environments we operate in, and are exposed and select into, display enormous variance as well. It is not necessarily that one genotype/car or environment/driver is privileged over another in general. Rather, different genes may provide advantage to different individuals depending on the environment and context in which they live. Some genes appear to support certain pathways toward general behaviors, such as oxytocin promotion and its influence on mating, while others advantage goals such as cellular division and aging. There is variance in the function of these genes, some more advantageous for certain

functions than others in differing circumstances. Yet, it is important to reiterate, that only in the rare exception, such as Huntington's disease, do individual genes completely regulate behavior (Imarisio et al., 2008). In this way, DNA provides the platform; it has some import in leading people into environments, and gene expression is affected and based on exposure to certain environments and one's own behavior. There are no genetic effects without expression. And expression effects are distinctive in that they involve heritable and environmental states that do and do not depend on the DNA sequence (for a more detailed explanation of all of the processes noted above, see Rutter, Moffitt and Caspi, 2006).

If we take into account the hundreds of thousands of genetic markers, and the various ways expression can take place in the aggregate in a living breathing organism who selects into various social and environmental experiences in real time, in part based on disposition (genetic, hormonal, psychological and cognitive), then the concept of a single genetic marker having substantial and direct influence on a complex social trait remains inconceivable. Does this realization mean that individual genes have no discernible effect? Should we abandon the enterprise of trying to understand the effect of genes on behavior? Certainly not; the same conceptual and theoretical challenges exist when focusing on the influence of culture, or the environment on behaviors of interest. For example, just as we cannot say a single gene, or polymorphism on a gene, motivates behavior, nor can we say a single conversation with your parents made you who you are today. Yet we use questions such as "do you talk about politics at home" as a measure to encompass parental socialization used to predict political interest. What we often refer to as culture, or parenting, actually incorporates a whole complex series of behaviors and thousands of social interactions which encompass emotional bonding, reinforcement, and daily interactions between parents and children in a cultural context

constantly modified by television, diet, peers, weather, life events, and societal events. Such factors cannot be completely captured with a single survey item, and yet they are often adequately characterized by such a question. Exploring the genome represents much the same challenge. The finding that a single genetic marker has some influence on a trait, may implicate a particular biological pathway consisting of hundreds or thousands of genetic and neurobiological mechanisms that result in hormonal release and cognitive and emotive changes, which in turn influence behavior. Thus, it is important to recognize that, like complex organisms in a moving social world, genes operate in an equally complex world within complex mechanisms that function in a living thinking person. In this way one can use the word “gene” in much the same way as one might use “culture”, or “parenting”. Thus, while it is not possible to find a single gene or a small group of genes “for” any given social or political behavior, a single gene might nonetheless have a significant influence on a given trait by representing the operational system helping to drive the pathways which influence the behavior of interest. In a similar manner, latent measures of the totality of genetic influence, such as those provided by studies of kinships, provide accurate and useful latent measures of genetic and environmental influence. Investigating the nature of these processes can help scholars develop novel hypotheses regarding the nature and manifestation of political preferences and behaviors, and begin to help explain why people faced with the same social stimulus have different reactions. In this way, we should care about the influence of genes not for what one genetic variant might account for, but rather because of what such findings signal about the relevant pathway by which particular behaviors emerge. If, given the complexity of genetic and environmental forces, a particular genetic marker still emerges as significantly related to some behavior, this suggests that a particular pathway (i.e., for example, the serotonergic pathway if looking at depression)

along a given channel may be indicted in the operation and manifestation of some systematic outcomes of interest.

Understanding what a gene is, and how it critically informs behavior also requires a change in the way political scientists define and understand the environment. In a neurobiological view, the environment represents much more than simply the stimuli that the entire organism faces. Rather the environment refers to both internal cellular processes *and* the external forces operating on an individual. Specifically, the environment refers to many factors, including the cellular environment, in utero hormones and maternal stress during gestation, and all processes that manifest across the lifespan, including the environment one's parents were in when a person was conceived, the environment a person faces as both a child and an adult, diet, parenting, family environment, social and economic issues, emotional bonding and random life events. In short, the environment can refer to everything both inside and outside the body before and after an individual was born. And, the same environmental stimulus, such as cold weather, or trauma, can have multiple effects on both the internal mechanisms and the overall person's behavior. Thus, different stimuli can exert similar effects under particular conditions as well, both within the same person and across individuals. At times, the same stimulus can trigger entirely different genetic mechanisms that may or may not work together or in opposition to one another. In this way, the actual objective nature of a given stimuli is less important than the subjective way in which it is interpreted and assimilated in light of a person's history and unique physiology.

Moving From Theory to Application: Interpreting Empirical Findings

Given the description of the genome above, how do we think about the meaning of the empirical findings reported in the extant literature? What do the heritability findings in twin

studies, linkage signals or significant SNP's (Single Nucleotide Polymorphisms – a change in the sequence at one base-pair) identified by candidate gene or genome wide studies mean? How do political scientists interpret them?

The majority of genetics and politics studies have so far relied on models of heritability, or the extent to which genetic similarity contributes to individual differences in observed behavior. Classical twin designs (Medland and Hatemi, 2009), extended kinships (Eaves and Hatemi, 2008), adoption studies (Abrahamson, Baker and Caspi, 2002), or twins reared apart (Bouchard et al., 1990), are typically referred to as genetically informative samples. By using samples that collect data from two or more different kind of relatives, it becomes possible to statistically distinguish which part of the differences between individuals can be attributed to genetic similarity or environmental influences.

These designs and extensions have been used to explore the source of individual variance for a wide variety of politically relevant traits, such as ideology (Alford Funk and Hibbing, 2005; Eaves et al., 1999), political attitudes (Martin et al., 1986; Hatemi et al., 2010), partisan intensity and attachment (Hatemi, Alford et al., 2009), vote choice (Hatemi et al., 2007) and voter turnout (Fowler, Baker and Dawes, 2008). Most models restrict variance component estimates to additive genetic (A), shared or common (C), and unique environmental (E) influences. However, variance can be partitioned into genetic dominance (interactions of multiple alleles within a gene), parental influences, environments unique to being a twin, and sibling environments as well (Eaves et al., 1999).

Table 1, recreated from Eaves et al. (1999) is useful in explicating how to interpret variance component (heritability) estimates. In this population, individual differences in conservatism are accounted for to a large degree by genetic influences (>.6 and .4 in males and

females respectively). What does this mean exactly? First heritability estimates partition variance within a population, they do not explain the value of trait, but the difference of values on a trait within a population. That is, it is not that genes explain 40-60% of conservatism; rather, it is that between .4-.6 of the variance, or individual differences in conservatism within the population, are accounted for by the aggregate of genetic influences. That is, they explain how people differ. The estimates are simply an estimate of the population, not an estimate of the percentage within any given individual which is accounted for by genetic factors. They are not to be interpreted to mean that for every person in the population .4-.6 of their ideology is due to genes.

Table 1. Estimated contributions of principal sources of variation to differences in Conservatism

	Conservatism	
	Male	Female
Genetic		
Additive	35.5	19.8
Assortment	22.2	12.4
Dominance	6.7	12.5
Total Genetic	64.5	44.7
Environmental		
Maternal	1.5	0.1
Paternal	0	0
Sibling	0	5.2
Twin	0.1	4.2
Residual Unique Environment	40.1	36.6
Total Parental Environment	1.5	0.1
Total Shared Environment	1.6	10.6
Total Environment	41.7	47.2
G-E covariance	-6.2	8.1

Source: original table modified from Eaves et al. 1999

Second, all heritability estimates are population specific because the meaning of the measures, and the genetic and environment characteristics of the population, are often unique for every population. For example the term “strict punishment” means something entirely different in Indonesia (death sentence) than it does in Australia (life sentence in jail). Even between quite similar countries where the meaning of a term is the same, country specific effects exist. For example, support for the death penalty in the US is much higher than in Australia, but the amount of variance accounted for by genetic and environmental factors within those populations is quite similar (Eaves et al., 2011).

Indeed, the meanings of the measures across time and cultural contexts are critically important. Thus the exact same measures might elicit entirely different neurobiological, cognitive and emotive systems based on the meaning of those items in unique contexts. For example, the term abortion in modern day America elicits recognition of religion, morality, and group identity at the very least. In hunter-gather societies, abortion was more likely to mean sacrificing survival of a future child, ensuring resources available (i.e., survivability) for current children. Yet, the variance components estimates might be much the same, as we noted above, but it is very likely that the genetic variance would encompass entirely different genetic systems as the meaning of abortion is vastly different. This difference may exist in modern populations over a very short time span. For example, the term “liberal” has taken on a pejorative label of the far left; even those on the left tend not to define themselves as ‘liberal’; yet not a half century ago, despite political affiliation, the whole country was proud to be liberal and fighting for a liberal world. In this way, the meaning of the word changed dramatically over a short period of time.

Third, univariate estimates, such as those presented in Table 1, are used to describe the latent components of variance for a given trait or the relationship between traits. They are not immutable. Rather, much like regressing Y on X, once additional traits are introduced into the model, the estimates change. Broad based gene-environment interactions that separate the population out by a specific environmental characteristics (e.g., Boomsma et al., 1999), gene-environment covariation which models selection into environments based on one's genotype (e.g., Purcell, 2002), and multivariate models which simultaneously decompose variance of multiple items (e.g., Hatemi et al., 2007) are all extensions of basic heritability models. These extensions can be viewed in much the same way as interaction terms, multivariate regression, and path models in traditional political science explorations. The more items added, or the different types of models employed, the more one can explore the import of heritability in different contexts as well the nature of covariance between traits (e.g., environmental or genetic).

For political scientists, these methods have become potentially useful as ways to explore the extent to which differences in a given attitude or behavior might be influenced by genes, family environment or unique personal experience in varying contexts. Behavioral genetic models allow scholars to develop specific theories and models, supported by empirical data, to further explore the nature of underlying individual variance on a particular process or outcome, thus helping to illuminate sources of preference. Such models allow scholars to focus in and attempt to identify how causal traits are related through the sources of covariation. For example, recent literature has proposed that personality causes political attitudes through the biology of personality (Mondak et al., 2010). However, through behavior genetic models, this assumption was found to be invalid. Verhulst et al. (2010) found that the vast majority of covariation between personality and political attitudes resided at a genetic level, and in a follow up study

(2012), and further explicated in this special issue, found that the relationship was not causal, but rather pleiotropic. In summary, variance decomposition models provide important leverage in identifying latent pathways of transmission for social and political attitudes. They can also help highlight the general architecture of potential sources of influence on political traits along both genetic and environmental dimensions.

Gene Mapping: Association and Linkage Studies

Heritability estimates provide a sense of relative importance regarding general environmental and genetic influences and offer critical information on the latent causal pathways. Molecular DNA, however, is required to identify the specific neurobiological systems that underlie the genetic variance from heritability estimates. Improvements in molecular genotyping technology in conjunction with the development of robust statistical tests for analyzing high-throughput genetic data have led to a shift in focus in behavior genetics from quantifying the overall genetic component of traits to identifying the specific DNA variants that underlie variation in behavior in the population.

So far, two basic approaches for identifying specific genetic markers related to political traits have been undertaken. The first and more empirically rigorous method scans the entire genome for a genetic marker or chromosomal region that is significantly related to the trait of interest. The advantage of genome-wide approaches is that it assumes no prior knowledge of the underlying biology of the trait of interest. Instead, every region of the genome is tested for association with the trait with strict statistical significance thresholds applied to account for multiple testing of all genes. In this way, one can gain new insights into the biological pathways that influence the trait. This approach has been utilized to great effect over the past 5 years, and more than 1,000 genetic variants have been identified that influence common complex traits (for

a review, see Hirschorn, 2009). So far, however, only one genome wide study on political preferences has been published. Hatemi, Gillespie et al. (2011), relying on genome-wide linkage of a sample of over 13,000 Australians, found several genomic regions related to Liberalism–Conservatism.

The second approach, exploits *a priori* information which suggests that a certain genetic marker might be expected to be associated with a specific trait. This candidate marker approach is more common than genome-wide approaches due to lower costs and greater data availability, and offers a more natural match for more theoretically driven explorations in the social sciences because such models often begin by identifying a tangible genetic marker (as opposed to a latent genetic component), and uses previous knowledge about the genomic pathway.

Table 2. Association Between MAOA, 5HTT, and Voter Turnout (Fowler and Dawes 2008)

	OR	SE
High MAOA	1.28	0.12
Long 5HTT	1.04	0.15
Long*Attend	1.51	0.2
Attend	1.28	0.18
Black	1.54	0.18
Hispanic	0.93	0.2
Asian	0.91	0.25
Nat Am	0.96	0.43
Age	1.06	0.04
Male	1.09	0.12
Partisan	3.66	0.12
Income	1.02	0.02
Cognitive	1.01	0
College	2.34	0.13
Intercept	0.02	0.8

OR are the odds ratios. SE are the standard errors.

Table 2 provides an illustrative example of how association studies might inform political behavior, and also how such studies might be misunderstood. For example, Fowler and Dawes (2009) reported that MAOA (monoamine oxidase) is associated with voter turnout. The variant

on this gene was chosen based on the theory that pro-social behaviors, such as voting, share a similar foundation to cooperation and anti-social behavior, both of which had previously been found to be associated with MAOA (Garpenstrand et al., 2002; Mertins et al., 2011). If interpreted in a typical social science fashion, most political scientists would view the odds ratios in the table as direct predictors of turnout. As a result, they might conclude exactly what the paper title suggests: that “Two genes predict voter turnout”, despite the authors warnings that, “It is important to emphasize that there is likely no single ‘voting gene’— the results presented here suggest that at least two genes do matter and there is some (likely large) set of genes whose expression, in combination with environmental factors, influence political participation.” While it is necessary for authors to design their presentation of results in a manner that is accessible for a broader audience, unfortunately, any statistical method designed for, or even hinting at, causality or prediction can be confusing to the uneducated consumer. The authors of the current paper are no exception; for example Hatemi, Gillespie et al. (2011) stated “We consider DBH a potential candidate gene for political orientations”, even though they clearly state there is no single gene for anything (also see Hatemi, 2010). Among geneticists, these processes are well understood, but among those not familiar with the implied caveats of causality regarding genetic markers, results can easily be misinterpreted.

The regulation of the release and uptake of MAO and Dopamine, the proposed pathways suggested to influence voting behavior noted above, is certainly a function of the genotype; that is, certain genotypes appear to have a role in the greater or lesser release or uptake of hormones, but the regulation of these hormones are a function of gene expression. In this way, the interpretation of the results above suggests that individuals with a certain genotype are correlated with higher turnout. However, it is critical to note that most candidate markers account for a

very small amount of the variance, and most results fail to withstand efforts at replication or meta-analysis (e.g., see Risch et al., 2009).

The results from association studies, genome wide or candidate gene, are important, but for much more than the obvious identification of a single polymorphism. Through the tortuous road from DNA to behavior, including neurobiological processes, upbringing, life experiences, and so forth, discovering that a dopamine receptor has some significant relationship to turnout, or that NMDA is related to left right orientations, represent noteworthy findings. If replicated over time, the findings beg the question of what are the actual mechanisms by which dopamine is related to partisan behavior? Is it through anxiety, stress, cooperation, cognition, community, novelty, all of the above, or some other mechanism or function? Identifying the environmental triggers which regulate dopamine uptake and release become supremely important. Thus, candidate genes or genome-wide studies which identify specific markers remain critical to understanding the way in which environmental triggers regulate genetic expression.

In summary, heritability studies identify the latent pathways, and partition individual variance within a population into elements of genes and environments. Genomic studies identify genetic markers which represent the overall process by which genes may influence downstream behavior through changes in the function of proteins or the activation or expression of specific neurocognitive mechanisms or particular hormones. In this way, finding that a specific SNP is related to behavior in a single study is not simply valuable because of the specific gene it implicates. Rather, individual genetic markers provide a guide for where to undertake further explorations regarding the larger biological pathway.

What Does the Future Hold?

While heritability, candidate gene and genome-wide association studies have been tremendously exciting and brought many discoveries, they are only initial steps in the quest to understand how genes influence behavior. Many more variants remain to be discovered and there is much more to learn about the biology of complex phenotypes. There are several immediate avenues of investigation that are currently underway. One way by which many believe more genetic variants underlying complex behavioral traits will be discovered is by expanding the range of variants tested for association. The current generation of genome-wide association studies (GWAS) have only examined genetic variants that are common in the population (>5% frequency). This has been a prescient strategy given that the amount of variance explained in the population by a given genetic variant is proportional to its frequency. However, this assumes that common and rare genetic variants will have similar effect sizes on the phenotype. This assumption may not hold and rare variants may in fact have a larger effect on the phenotype than common ones. Evolutionary arguments suggest that variants with major effects on phenotypes that are detrimental will be selected against, and will therefore be driven to lower frequency in the population. The next phase in the GWAS era is therefore to test a wider range of variants, specifically those in the 1%-5% frequency range, for association with complex traits. This endeavor will be greatly aided by the results from the 1,000 Genomes Project, a publicly funded project to sequence 1,000 genomes from worldwide populations (www.1000genomes.org). The project has already identified a large number of new variants, many of which are rare and have not been well covered by the existing genotyping chips used for GWAS. Testing a wider range of variants will no doubt identify more SNPs, some of which may contribute more to the overall heritability of the trait than the common SNPs already identified.

The heritability of a complex trait may however be due to variants that are even rarer than those listed above. One case where rarer variants have been demonstrated to influence complex traits is that of copy number variants (CNVs). Since 2004 it has been known that in any individual, large regions of the genome – on the order of tens to hundreds of thousands of DNA base pairs - can be duplicated, deleted or rearranged. Large insertions or deletions of DNA, while rare, may have larger effects on phenotypes than SNPs. Associations between CNVs and complex traits have only just begun, but have already produced important findings, particularly around autism (Weiss et al., 2008) and schizophrenia (Stefansson et al., 2008).

The discovery of CNVs and SNPs with very low frequencies (<1%) will be driven by next-generation sequencing. Up to now, sequencing of DNA has been extremely cumbersome, due to the sheer amount of information carried in each individual's genome (approximately 3 billion base pairs). Collecting this information has been very expensive and thus restricted to only a handful of individuals prior to the 1,000 Genomes Project. The cost of sequencing is decreasing at a fast pace and studies analyzing sequence data from large cohorts are not far away from being feasible. Analysis of sequencing data is likely to prove challenging due to the sheer volume of data. The fact that a variant is rare means it will be found in very few individuals even in large cohorts and therefore statistical evidence of association will likely be unconvincing. In order to get around this problem and to narrow the focus of sequencing studies, regions that have been already found using GWAS will be targeted for sequencing. Other methods such as counting the number of rare variants in a particular regions and an approach that focuses only on individuals at the extreme end of the distribution for the trait have been suggested as strategies for increasing the power of association studies with sequencing data. Next-generation

sequencing is an exciting new technology that will dramatically increase the resolution at which we view human genetic variation and will give insight to the genetic architecture of behavior.

While many are understandably keen to begin to test whether rare variants or CNVs may contribute to a substantial portion of the variance for complex political and social traits, there is still much to be discovered about the loci that have already been found. The true causal variants have likely not been mapped in most cases as the association signals from GWAS may be variants that are not the truly causal variant, but are correlated with the true variant. The effect sizes of the causal variant may be larger than the detected variant. More thorough investigation of other regions of the genome identified in GWAS may also find rare variants of large effect, or further common variants of modest effect. Functional biological studies will also be important to elucidate the mode of action of the genes in the cell and the biological pathways in which they are found, potentially revealing other genes.

GWAS with larger sample sizes that have more power to detect associations will identify more loci and given that previous studies have been underpowered, they may identify variants of similar effect sizes that were missed previously. Large meta-analyses involving many thousands of individuals are identifying more loci than have been found in individual GWAS (e.g. Lango et al., 2010). However, in cases where very large sample sizes have already been analyzed and only variants of small effect have been found, increases in sample size will identify variants with smaller influences on the trait (Goldstein et al., 2009). This is important because there is growing evidence that complex traits are affected by a very large number of genetic variants each of very small effect (Yang et al., 2011), as originally suspected by Fisher (1918). The very small effect sizes mean that many of these loci do not reach the genome-wide significance threshold in GWAS studies. This was neatly demonstrated recently by two papers on the

genetics of height, a model human quantitative phenotype for genetic analysis due to its ease of accurate measurement and its high heritability (80%). The first paper was a meta-analysis of GWAS of height that included more than 180,000 individuals. This was the largest sample size ever in a GWAS and the study identified 180 loci that were significantly associated with height (Lango et al., 2010). While these loci tended to cluster into biological pathways such as control of skeletal growth, the combined effect of all of these loci explained only 10% of the total phenotypic variance of height. This still leaves a large amount of unexplained heritability. A novel analysis method developed by Yang and colleagues using a much smaller dataset showed that in fact the majority of the heritability of height is actually being currently tagged in GWA studies, but the effect sizes of the individual variants are so small that they do not reach the stringent significance thresholds (5×10^{-8}) imposed because of multiple testing. They propose that the rest of the unexplained genetic factors are due to rarer variants not covered by current genotyping chips. The implications of this study are that complex traits are likely to be affected by thousands of genetic variants and that extremely large sample sizes are required to explain the heritability of complex traits. This finding has been borne out in studies of behavioral phenotypes such as personality where studies that had sample sizes that previously would have been considered to be large have failed to detect any variants at the genome-wide significance level (De Moor et al., 2010). Clearly, even larger sample sizes will be needed to understand the genetic architecture of behavior.

Other methods for analyzing genetic data in the context of complex traits are being developed and have shown some promise. Many of these involve analyzing the data in clusters, such as gene-based tests that simultaneously test all variants in a specific gene (Liu et al., 2010). If the individual effects are small, the cumulative effects of all the variants in the gene may have

significant influence on the phenotype. Similar methods that involve testing genes that encode biological molecules known to act in specific pathways and that interact with each other have also been developed and have shown evidence that multiple variants across different genes in these pathways combine to produce the observable variation.

Finally, the study of gene expression, which we discussed earlier, may be the most exciting, but remains in its infancy. Which genes are switched on and off is dependent upon the cell type and environment, and the level of expression of particular genes in specific cell types is known to show substantial variation between people. Many of the variants discovered in GWAS have been shown to affect the level of activity of other genes (Cookson et al., 2009). For example, one of the most commonly studied genetic variants in behavior genetics is the serotonin receptor “long and short” variant. The long allele has been shown to increase the amount of the serotonin receptor in the cell and has in turn been suggestively associated with personality traits. However, there are likely to be many more variants that influence the expression of other neurotransmitters that affect political behaviors in humans. Indeed, many of the variants identified in GWAS studies have been demonstrated to have an effect on the expression of both the gene in which they’re located and also on other genes (Nicolae et al., 2010). New technologies allow the analysis of the expression of all genes in a given cell type. Studies are now being performed that can analyze changes in gene expression after the introduction of an environmental stimulus. As an example, one study looked at changes in gene expression after treatment with caffeine, and identified specific biological pathways that are switched on after caffeine consumption (Amin et al., 2011). As the technology improves, much more thorough experiments will be performed, and there is great potential to examine the effect of social environmental influences on gene expression.

Integrating Genetics and Political Science: Moving Beyond Discovery

In this introduction, we have tried to describe the complex forms of investigation which have governed the study of the influence of genes on politics in a manner that provides the minimal amount of information necessary to understand the meaning and limitations of such research. We have also given some glimpse as to future of gene mapping. We in no way offer a comprehensive understanding of the genome and epigenome. From early work focused around the discovery of basic mechanisms to more specific applications of such findings to political phenomena of interest, we have focused on several of the larger methods which now infiltrate the political science literature. Certainly, the incorporation of genetic models can help open doors to developing more powerful, sophisticated and accurate models of political choice which reflect both biological and environmental imperatives.

Scores of articles have described the sources of variance on the core traits that consume our field, such as ideology, vote choice, party identification, partisan intensity, civic duty, efficacy, political participation, attitudes, trust and many other variables (for a review see Hatemi, Dawes et al., 2011). What has so far remained absent in this area is the synthesis of behavioral genetic theory and findings into the extant behavioral and rational choice theories of political preferences. We recognize that a handful of studies have begun to look at specific genetic markers, however this research remains in its' infancy. Thus this issue is focused on twin and kinship studies and we expect future special issues will be dedicated to molecular designs. Therefore, in the remainder of this issue, we seek to begin this investigatory process by offering several articles which expand the meaning and utility of genetic influences on political processes of interest. Specifically, these works integrate behavior genetic findings and approaches into the core theories of political behavior in order to help guide future inquiry and investigation into the

intersection of biology and politics. In this way, we hope to show that such research does not exist within the confines of a particular methodological enclave, but rather offers powerful leverage to uncover the causal processes that lay at the center of our discipline's most central questions and concerns.

We begin with Verhulst and Estabrook who introduce a genetic and environmental direction of causation model to examine the nature of attitude formation. This paper sits at the heart of one of the enduring challenges in all of social science, the nature of causal inference. Verhulst and Estabrook introduce a model that shows how twin and family data can be used to assess the direction of causal flow between related traits. They focus on the relationship between attitudes and personality, as it has become a topic of renewed interest (Verhulst et al., 2012; Gerber et al., 2010). However, such models are incredibly important for addressing numerous long standing questions in the field.

The next article, by Hatemi, McDermott and Eaves explores how to use genetic and environmental variance to explicate the multilevel structure of political ideology. Ideology remains at the core of political belief structures, but despite decades of research inquiring into its ontological basis, how and why the public simultaneously maintains consistent right-left beliefs in some areas, while displaying remarkable volatility and seemingly irrational preference sets in other areas, has so far remained unexplained. Hatemi, Eaves and McDermott conduct an exploratory factor analysis on the latent genetic and environmental sources of variance on attitudes and find that political ideology not only has a multidimensional structure (e.g., foreign policy, economic and social) but that attitudes group together differently at genetic and environmental levels. The genetic factor structures of attitudes form around evolutionarily themes of procreation and defense, while the social environmental factor structure forms around

elite discourse. Their use of twin data offers one mechanism to bridge the gap between rational, psychological and evolutionary models of ideology.

The majority of research in political science has focused on environmental stimuli to account for behavioral and attitudinal differences; and so far the majority of research which has included partially genetic approaches has focused on discrete elements of genes and environment. What remains absent are models which focus on the interaction of genes and environment in institutional contexts with a specific application to public policy. Boardman et al. provides an illuminating example of gene-environment interplay through an analysis of the relationship between education, public health and public policy. In this contribution, he investigates the role of institutions in affecting the genetic basis for weight in a nationally representative sample of adolescents. By analyzing the gene by environment interactions which influence body weight, Boardman et al. show how schools and other institutions can work to intervene more effectively to help control the national obesity epidemic.

Spatial and rational approaches remain at the core of models of voting behavior and yet the preferences which define such theories have remained exogenous. Fazekas and Littvay begin to address this lacuna by combining spatial theory with behavioral genetic methods in order to explain individual differences in decision making strategies and to identify the basis of genetic variance in party identification and directional voting.

Finally, if genetic influences do provide some predictive value in identifying individual differences in political traits within a population, how do such influences integrate with cultural differences in accounting for human variation? Klemmensen et al. begin to address this question by comparing genetic and environmental sources of variation on political participation and efficacy between Denmark and the United States. They find that despite vast differences in

Western culture and age cohorts, the results across samples are remarkably similar. Thus, culture and country shape important mean differences between the two populations, but the source of individual differences within each population remains the same.

Together, these papers begin to answer the major questions this special issue is designed to answer: where are we now; where can we go with the use of genetic analysis; and why and how do genes matter for understanding complex and important political behaviors.

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