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RESEARCH ARTICLE



Advancing the frontiers of genomic public administration: From genetics to administrative attitudes, behaviors, and practices

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Abstract

Biology's increasing applicability to the social sciences can inspire new approaches to public administration research and practice. Drawing on advances in behavioral genetics, genomic public administration may push its frontiers by examining the genetic foundations of administrative behaviors. While public administration scholars have pioneered the use of the twin design to assess the heritability of public sector employment and public service motivation, they may also use molecular genetics to explore how specific genes interact with environmental factors to shape administrative attitudes, traits, and behaviors. We highlight how relevant studies in management and political science may serve as models for similar explorations in public administration. We also outline four research agendas for genomic public administration. In addition to complementing traditional public administrative behaviors and practices, genomic public administration may enrich genetic inquiries by adding public sector applications.

Evidence for practice

- Genomic public administration seeks to enhance our understanding of how genetic factors and their interactions with socialization agents shape variations in administration-related attitudes and behaviors.
- Researchers seeking to analyze the genetic foundations of administrative attitudes and behaviors typically rely on methodologies such as twin/adoption design and molecular genetic approaches.
- Policymakers and public sector managers should understand how genetic makeup shapes the effects of organizational processes and management practices on individual attitudes and behaviors.
- Certain administrative traits and behaviors are less genetically determined and more malleable than others. Policymakers and public sector managers should direct resources toward shaping those psychological traits and behaviors.

INTRODUCTION

Behavioral genetics research has opened new frontiers in recent decades, revealing both genetic and environmental factors to be critical sources of heterogeneity in social traits and behaviors (Ebstein et al., 2010; Plomin et al., 2016; Polderman et al., 2015; Turkheimer, 2000). Biologically informed knowledge can push the conventional boundaries of public administration, which has historically focused on the social and cultural variables shaping administrative attitudes, behaviors, and practices (Christensen et al., 2021; Florczak, 2023; Frederickson et al., 2018). Without considering biological factors, existing socialization-oriented theories may fail to adequately explain attitudinal and behavioral differences among individuals. To what extent can attitudinal, behavioral, or institutional variations be attributed to social practices and norms rather than to individuals' innate genetic

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inclinations? Public administration scholars must address this question as the field can only advance through interdisciplinary perspectives and collaboration (Farmer, 2015; J. L. Hall & Paul Battaglio, 2018; McDonald III et al., 2022; Wright, 2011).

Biology and genetics are not entirely new in the field of public administration. Early public administration scholars noted the value of integrating biological insights into the field (Caldwell, 1980; Farmer, 2006; Gulick, 1986; Meyer-Emerick, 2007; Oldfield, 2003; White, 1991). Despite their calls for probing the biological "truth" of administration, mainstream public administration scholars were more ambivalent than their counterparts in other related social science disciplines, such as political science (Aarøe et al., 2021; Alford et al., 2005; Dawes et al., 2014; Fowler et al., 2008), economics (Barnea et al., 2010; Barth et al., 2020; Cesarini et al., 2009), and management (Patel et al., 2021; Z. Zhang et al., 2009), about including genetics in their research.

Fortunately, multiple empirical studies have been conducted in recent years on the genetic causes of administration-related traits and behaviors, suggesting that public administration has begun to acknowledge, if not fully appreciate, the need to account for genetics in theoretical advancement. In particular, Christensen et al. (2021) studied the genetic roots of job selection, whereas, in an exciting twist, Florczak et al. (2022) assessed the role of environmental and genetic factors in the development of public service motivation (PSM). Although these two twin-based studies estimated the effects of genetic variants on public administration traits to be small to null, both highlighted how genetic insights might help advance public administration theory and research. Moving beyond twin design, Tao et al. (2023) recently employed the molecular genetics approach to investigate the genetic overlap between psychological traits and public service employment selection, opening a new avenue for studying the genetic underpinnings of public administration behaviors.

The broad incorporation of genetic perspectives into the social sciences and the recent application of this knowledge in public administration inquiries may eventually open a new perspective on the study of public administration phenomena. In this regard, the subfield of genomic public administration (GenoPA) explores public administration attributes and behaviors through the lenses and methods of genetics in general and behavioral genetics in particular. Our study, however, does not strive to provide a comprehensive template for GenoPA. Instead, it offers a roadmap for understanding how the insights gained from genetics and public administration can enrich each other in the long term. By synthesizing the current behavioral genetics literature across various disciplines, this article culminates in a GenoPA framework. This framework sheds light on how genes influence administrative traits and behaviors. Additionally, we propose pertinent research directions for theoretical developments in public administration.

By examining the genetic roots of public administration attitudes and behaviors, genomic public administration may help resolve significant conundrums in many existing public administration theories that explicitly or implicitly assume that social and institutional factors alone determine public sector employees' value perceptions, behaviors, and work-related outcomes. It may also enrich current public administration theories with additional causal factors. For instance, public administration scholars have long debated whether the attractionselection (Pandey & Stazyk, 2008) or the adaptationsocialization hypothesis (Moynihan & Pandey, 2007) explains why some individuals prefer to work in the public sector. Emerging evidence on the heritability of sector choice-individuals self-selecting into specific job sectors-may help refine the existing attractionselection hypothesis (Christensen et al., 2021; Tao et al., 2023).

Methodologically, typical genetic approaches such as twin/adoption design and molecular genetics may offer valuable tools for public administration scholars to mitigate the inherent limitations of observational research. While Florczak (2023) introduced and discussed the relevance of twin-based literature, further efforts are needed to synthesize the various approaches in behavioral genetics research. Along these lines, our paper summarizes and compares the advantages and disadvantages of both twin/adoption and molecular genetics designs. This comparative analysis will help scholars critically evaluate the usefulness of behavioral genetics in public administration research and embark on new endeavors that harness the potential of these approaches. By examining how certain genetic factors contribute to variations in individual attitudes and behaviors, estimation models that incorporate genetic determinants can help reduce omitted variable bias. Additionally, genetic data can help address concerns regarding reverse causality as genes precede socialization. However, caution is warranted when interpreting strong causal patterns; several threats must be addressed before drawing such conclusions, including genetic heterogeneity, gene-gene interactions, and population stratification (Cordell, 2009; Martin et al., 2017; McClellan & King, 2010). Fortunately, recent methodological developments in Mendelian randomization have helped to identify causal mechanisms using genes as instrumental variables (Lawlor et al., 2008).

Policymakers and public sector managers can capitalize on research findings in the context of genomic public administration. For example, research suggests that children genetically prone to developing antisocial behaviors benefit more from public prevention campaigns (Albert et al., 2015). This discovery enables policymakers to realize that the intended policy effects may not be equal for everyone, even within the same target group. In other words, individuals' innate characteristics matter. Additionally, genetic factors affect some but not all administration-related attributes (Christensen et al., 2021; Florczak et al., 2022; Tao et al., 2023). Certain administrative traits and behaviors may be more malleable than others. Knowledge about the presence or absence of genetic effects will enable public sector managers to devise more effective interventions and regulatory practices.

The remainder of this article begins by reviewing historical calls to use genetic knowledge in public administration research. We then develop a framework for genomic public administration based on the existing knowledge of genetics, psychology, and public administration. Next, we examine two typical methodologies used in genetically informed research. We subsequently draw lessons from political science and management studies on incorporating genetics into research. Finally, we propose four promising research directions for genomic public administration.

THE HISTORICAL AND RECENT DEVELOPMENTS OF GENOMIC PUBLIC ADMINISTRATION

Biology and genetics are not foreign to public administration. According to Caldwell (1980), "Biology and the new science of sociobiology now compel lawmakers, administrators, and judges to consider issues that were once beyond the pale of political response. Biological findings undermine assumptions long accepted in public law and policy" (p. 1). Similarly, Gulick (1986) suggested that the field of public administration must learn not only from economics and psychology but also from human biology. In a narrower subfield of public budgeting, Oldfield (2003) argued that genetic science might change a nation's demographic composition and influence public service spending priorities. Inspired by the application of the life sciences in political science, Meyer-Emerick (2007) discussed the potential of incorporating biological insights into public administration research, envisioning the reciprocal value of a public administration perspective on research in biological politics.

Despite the longstanding interest in biology and genetics within the field, the extant literature in genomic public administration has largely been abstract and speculative. Fortunately, some promising breakthroughs have recently been made that may disentangle the problems related to central public administration in a scientifically rigorous manner. The work of Christensen et al. (2021) is a prominent example. Using a twin design and samples from the United States, they identified a difference in sector choice between twin pairs, confirming the heritability of public service employment. Another example is an empirical study that focused on PSM based on a Danish twin sample by Florczak et al. (2022). They examined how genetic factors combine shared and unique environmental influences to shape PSM. Their findings suggest that environmental factors are more likely than genetic factors to shape the non-affective components of PSM.

These two empirical studies showcase the possibility of generating a nuanced understanding of the innate roots of administration-related attitudes and behaviors. Christensen et al. (2021) examined how innate characteristics and public sector work environments may induce individuals to seek public sector employment. Their findings provide a genetic explanation that differs from the dominant research paradigm, which emphasizes the socialization sources of public administration traits. Likewise, Florczak et al. (2022) revealed the origins of PSM that distinguish themselves from related "other-regarding" concepts. This finding significantly contributes to PSM research and can help scholars rethink its conceptual relationships with other prosocial constructs.

Despite these major contributions to understanding the genetic causes of public administration traits, several interesting avenues remain for future exploration. Although genes may have independent effects on social trait variation, it is also possible that the effects of one gene could be modified by other genes and the environment (Cordell, 2009; Manuck & McCaffery, 2014). Both studies described above investigated the roles played by genetic and environmental factors separately, leaving possible gene-environment interactions unexamined. Additionally, both studies reported a deficiency in the measurement instrument and a single sample, suggesting the need to employ more diverse samples and precise measures to establish external validity. Notably, these two studies used a typical twin design to estimate the heritability of administration-related traits or behaviors. This approach, nonetheless, can hardly trace specific genetic markers. In this regard, some newly developed genebased approaches promise to identify specific genetic markers associated with particular behavioral traits.

As pioneering research in genomic public administration, the two twin-based studies highlight the need to embrace alternative insights derived from molecular genetics. Such insights can help generate testable hypotheses regarding the intricate relationships between specific genes and administration-related behavioral traits. Coincidentally, the most recent study by Tao et al. (2023) demonstrated that genetic predictors of positive affect are significantly associated with individuals' selection for public service work, indicating the possibility of incorporating molecular genetic insights into public administration research. Further research is also merited into the fundamental question of how genetics interact with environmental factors to shape administrationrelated attitudes and behaviors. Thus, it is timely to advance the frontiers of genomic public administration by gauging how both genetics and environmental factors simultaneously shape individuals' attitudinal and behavioral patterns in administrative settings (Florczak, 2023). Drawing on the existing knowledge of behavioral genetics, the following section details how genetic factors may affect the development of administrative attributes and behaviors.

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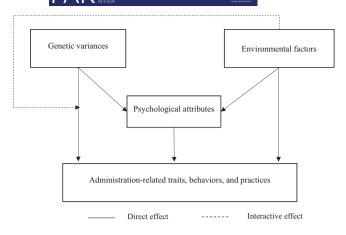


FIGURE 1 A framework for genomic public administration, adapted from Arvey and Bouchard (1994).

A FRAMEWORK FOR GENOMIC PUBLIC ADMINISTRATION

Advances in molecular biology have revealed that genes are the building blocks of human traits, and nearly all human traits and behaviors are heritable (Turkheimer, 2000). A framework for genomic public administration focuses on how genetic variations shape administrationrelated attitudes and behaviors. Figure 1 depicts three pathways through which genetic factors may affect administration-related attitudes and behaviors: direct effects, gene–environment interactions, and mediation through psychological factors. Table 1 summarizes these pathways and examples.

The direct linkage between genes and individual traits and behaviors

While developing within social and institutional contexts, social behaviors are shaped by underlying feelings, emotions, and brain activities (Ebstein et al., 2010). For instance, humans use their sensory and emotional systems to detect and interpret social cues and react to social circumstances (Porges, 2007). Neuroscience research has revealed how and which biomarkers affect essential human functions. For example, arginine vaso-pressin and oxytocin are two fundamental neurotransmitters and hormones that sustain general cognitive function, brain activity, and the nervous system (Carter et al., 2008). Since some genes determine how key biomarkers develop, biological mechanisms link genes to human traits and behaviors.

For example, genetic variations in oxytocin and arginine vasopressin relate directly to human socioemotional processes such as autism, stress reactivity, and empathy (Rodrigues et al., 2009; R. Zhang et al., 2017), which in turn influence public employees' general decision-making ability, service motivation, and other psychological propensities. Nonetheless, because most administrationrelated behaviors and attitudes are socially conditioned, it is unlikely that any set of genes can fully explain all varieties of administration-related attitudes and behaviors. Instead, complex administrative behaviors are shaped by mechanisms involving gene–environment interactions and psychological mediation (see Table 1).

Gene-environment interaction effects

Genes interact with the environment to shape administrative attitudes and behaviors (Manuck & McCaffery, 2014). For example, the social control model explains how the social environment interacts with genes to shape behavior (Shanahan & Hofer, 2005). "Social control" refers to social norms, institutions, or sociohistorical environments that may limit an individual's development and choice of social attitudes and behaviors (Janowitz, 1975). When social control is low (e.g., owing to a lack of resources and socialization opportunities), individuals' social attitudes and behaviors conform closely to their genetic tendencies. Conversely, when social control is high, genes influence individuals' social attitudes and behaviors less.

Using data from the Southern Illinois Twins and Siblings Study, DiLalla et al. (2009) examined how parental and peer influences interact with genes to shape children's social behaviors. They found that children with high-risk genes exhibited less aggressive behaviors in a lowaggression environment, where their peers exhibited noncombative behaviors. In contrast, in a high-aggression environment where peers and parents are bellicose, children with a low genetic tendency toward aggression behave more aggressively. These findings suggest that social environments modify genetic effects on human behavior. Alternatively, the social context may magnify genetic influences. For instance, the genetic impact on children's verbal intelligence is more pronounced in families with higher educational levels (Rowe et al., 1999).

In addition to family socialization, religious socialization can moderate the genetic impact. Sasaki et al. (2013) examined how the dopamine receptor D4 (DRD4) gene interacts with religious socialization to shape prosocial behaviors. Specifically, participants with a low genetic tendency toward prosocial behaviors exhibited higher prosociality after being primed with religious influences. In other words, the synergistic effects between genes and the environment can better explain social behavior. The genetic perspective is compatible with social explanation models and promises to enhance the explanatory power of existing theories on administrative traits and behaviors.

Psychological factors as mediator

No specific gene alone is likely to entirely determine administrative attitudes and behaviors. Other factors,

TABLE 1 Three pathways through which genetic factors may affect administration-related attitudes and behaviors.

Pathways	Insights	Examples	Implications for the existing socialization-based paradigms
Direct effects	Genes can directly influence the development of human attitudes and behaviors	Arginine vasopressin and oxytocin are two fundamental neurotransmitters and hormones. Genetic variations in oxytocin and arginine vasopressin are directly related to different human socioemotional responses.	Individuals' social traits and behaviors are determined not only by socialization processes but also by natural factors. The parental influence could also be interpreted as genetic intergenerational transmission.
Gene–environment interaction effects	Environmental factors interact with genes to shape attitudes and behaviors	 The social control model explains how the social environment interacts with genes. In an environment where peers are friendly, children with a high genetic tendency toward aggression exhibit less aggressive behaviors. 	The effects of the environment on individuals' social traits and behaviors also depend in part on genes and vice versa.
Psychological factors as mediators	The effects of genes on attitudes and behaviors are mediated by psychological attributes	The Big Five personality model. Extraversion and openness to experience mediate the genetic influence on the likelihood of individuals becoming entrepreneurs.	New perspectives in understanding the biological and psychological underpinnings of social attitudes and traits.

METHODOLOGIES FOR DETECTING THE **INFLUENCE OF GENES**

such as psychological traits, may mediate the influence of these genes. Research in biological psychology suggests that nearly all personality traits are heritable, with genetic factors accounting for approximately 30%-50% of their variations (Plomin et al., 1990). A meta-analysis of more than 45 primary articles found that positive emotionality and constraint personality are the most highly heritable in this regard (Vukasović & Bratko, 2015). More than 50% of the variation in these two personality traits was attributable to genetic influences. Conscientiousness showed the lowest heritability at 31% of the five personality traits. The heritability of extraversion, openness, and agreeableness ranged from 35% to 37%. Neuroticism exhibited the highest heritability, with an average estimate of 41%.

These findings from biological research suggest that personality traits mediate the influence of genetics on social attitudes and behaviors. For example, Zhao et al. (2010) showed that the personality traits of extraversion and openness to experience are highly related to excitement-seeking, innovative behaviors and a tendency to be assertive and outgoing, which are lynchpins of entrepreneurship. Employing two independent samples from the UK and the United States, Shane et al. (2010) confirmed that genes influencing the development of extraversion and openness to experience also predicted an individual's likelihood of being an entrepreneur. This finding is one of the many examples of how personality traits mediate genetic effects on social behavior. Similarly, behavioral public administration (Grimmelikhuijsen et al., 2017) can explore how genetics, with personality traits as mediators, influence various administrative attitudes and behaviors.

Two common approaches are available for studying the influence of genes in behavioral genetics research. The first approach, by studying twins and adoptees, investigates the relative importance of genetic and environmental factors in shaping certain behaviors or traits. The second approach employs molecular genetics to identify specific genes that are associated with individual traits and behaviors. Both approaches seek to understand heritability and various interactive dynamics to explain why some individuals develop specific social behaviors (see Table 2 for a detailed comparison).

The twin/adoption design

The twin design can be considered a guasi-experiment to disentangle genetic and environmental influences (J. G. Hall, 2003; Medland & Hatemi, 2009). Twin studies reflect that monozygotic twins arise from one ovum fertilized by a single sperm, whereas dizygotic twins develop from two ova (J. G. Hall, 2003). Consequently, monozygotic twins are genetically identical, unlike their dizygotic counterparts who share approximately half the segregating genes (Medland & Hatemi, 2009). A typical twin design compares the phenotypic differences between monozygotic and dizygotic twin pairs. Genetic factors play a discernible role in the phenotype if significant variances exist. Conversely, the failure to detect significant differences indicates that variances in a certain phenotype

TABLE 2	Comparison between twin-based and molecular genetics studies.	
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	Twin-based design	Molecular genetics studies
Non-shared objective	Disentangle the relative importance of genetic and environmental factors in shaping traits and behaviors.	Identify the linkages between specific genes and certain traits and behaviors.
Shared objectives	Estimate the heritability of certain traits and behaviors. Explore the gene–environment interplay.	
Typical research questions and examples	 Can the formation of political attitudes be traced back to genetic and environmental causes? For the attitude of conservatism, genetic factors account for 43% of the variation, whereas the remaining 57% are attributed to the shared and non-shared environment (Alford et al., 2005). 	 Is the genetic variation in educational attainment and intelligence test performance associated with voter turnout? The polygenic scores of educational attainment and intelligence test performance can predict voter turnout, suggesting that education and intelligence are possible mediators through which genes determine voter turnout (Aarøe et al., 2021).

Source: Adapted from Friedman et al. (2021).

(e.g., social attitudes and behaviors) cannot be attributed to genetic factors.

Many twin studies have successfully demonstrated genetic predispositions to numerous social attitudes and behaviors, such as entrepreneurship (Shane et al., 2010), prosocial attitudes (Rushton, 2004), and personality traits (Jang et al., 1996). This method can help estimate the overall heritability of a specific phenotype while disentangling shared and unique environmental influences. It can also identify gene-environment interaction effects when coupled with various extended models and datasets (Purcell, 2002). Political scientists, for instance, have long used twin designs to study whether specific political attitudes and behaviors are heritable (Alford et al., 2005; Dawes et al., 2014; Fowler et al., 2008). Twin design, however, is susceptible to biased estimation due to certain restrictions, such as the equal environment assumption (Richardson & Norgate, 2005). For instance, monozygotic twins are more likely to be shaped to varying degrees by shared environmental influences, such as clothing and friends, than are dizygotic pairs. Consequently, the observed differences between monozygotic and dizygotic twin pairs may not be solely attributable to genetic factors but also to distinct environmental factors. Classical twin design is also limited in accurately estimating both shared environmental and nonadditive genetic influences as it tends to overestimate genetic influences while underestimating shared environmental effects.

Similarly, adoption studies reflect the reality that adoptive children share genes with their biological parents/ siblings but are raised by adoptive families (Scarr & Weinberg, 1983). We can discern the impacts of genes and environmental factors by comparing the similarities between adoptees and siblings or the phenotypes of adoptive children with those of both their biological and adoptive parents. If we assume that the phenotypes of adoptive children more closely resemble those of the adoptive parents/non-biological siblings than those of their biological parents/non-adoptive siblings, environmental factors, in that case, significantly influence the development of these phenotypes. Conversely, if we assume that adoptive children exhibit traits similar to those of their biological parents/non-adoptive siblings, genes are more likely than environmental factors to be the primary influencers of these phenotypes. Adoption design has been used to examine the genetic and environmental influences on various phenotypes, including voting (Cesarini et al., 2014), entrepreneurship (Lindquist et al., 2015), and vocational interests (Betsworth et al., 1994).

Apparently, adoption designs are more potent than twin studies in detecting shared environmental effects (Plomin et al., 2001) because adoptees share no segregating genetic information with their non-biological relatives. Hence, any similarities between adoptive children and non-biological relatives can be directly attributed to shared environmental effects. However, a critical methodological concern in adoption studies is the non-random placement of adoptive families (Scarr & Weinberg, 1983). Adoptive families tend to have a higher-than-average socioeconomic status, leading to a biased sample of adoptees and casting doubt on the generalizability of the research findings. Additionally, the constrained environment within which adoptive families operate may deflate the estimates of shared environmental factors (Stoolmiller, 1999).

In short, both twin and adoption designs serve as natural experiments to explore the relative contributions of genetic and environmental factors in shaping specific traits and behaviors. However, due to their distinct underlying assumptions, twin design excels in analyzing genetic influences, while adoption design is better suited for estimating shared environmental effects. Public administration scholars may employ twin design to investigate genetic variance in administration-related attitudes and behaviors; they may use adoption design, if data permit, to study shared family environmental effects with greater precision.

The molecular genetics approach

The second approach uses molecular genetic techniques to identify genetic variants. There are two ways to identify

molecular genetic impacts: candidate genes and genome-wide association studies (GWASs).

The candidate gene is a hypothesis-driven approach that typically relies on biological theory to connect specific genes to human traits and behaviors (Belsky & Israel, 2014). For example, oxytocin has biological functions that affect social cognition, affiliation, social memory, and emotional support (Carter et al., 2008). Based on this discovery, scientists have identified various oxytocin-related genes and determined how these candidate genes help predict empathy and prosocial behavior (Bakermans-Kranenburg & Van Ijzendoorn, 2014; Rodrigues et al., 2009).

As an early method in behavioral genetics research, the candidate gene approach has been extensively adopted to explore the association between genes and behaviors. The candidate gene approach excels in establishing a more focused association between specific genetic determinants and behaviors, providing initial validation for the proposed causality described in established biological theories. However, this approach has several limitations. Specifically, it relies heavily on advancements in the biological knowledge of biomarkers and genes. Although several candidate genes have well-theorized links to specific outcomes, most candidate genes remain poorly understood, restricting the ability of this approach to identify all genes that may influence behavior (Zhu & Zhao, 2007). Additionally, existing candidate gene studies have been criticized for their low replication rates, limiting our understanding of the biological mechanisms that drive candidate gene-behavior associations (Tabor et al., 2002). Because social behaviors and traits are complex and influenced by numerous genes and their interactions, the candidate gene approach is less useful than other methods.

In contrast to the candidate gene approach, the GWAS approach, also known as a "hypothesis-free tactic," does not rely on a priori hypotheses regarding the association between specific genes and social behaviors. Instead, this approach identifies genetic variants for particular traits and behaviors by examining hundreds of single nucleotide polymorphisms (SNPs) to measure the most common variations throughout the genome (Pearson & Manolio, 2008). It is assumed that genetic influences on observable traits (e.g., disease, behavior, or personality) are related to a limited number of allelic variants rather than millions of SNPs. After identifying a set of genes, researchers typically use a quantitative measure, the polygenic risk score (PRS), to calculate the aggregated effects of multiple genetic variants on human traits and behavior (Belsky & Israel, 2014). Scholars from neighboring disciplines, such as business management, political science, and psychology, have already applied the PRS approach to gauge the genetic roots of traits and behaviors such as entrepreneurship (Patel et al., 2021), job satisfaction (Rukh et al., 2020), and political participation (Aarøe et al., 2021).

GWAS is a powerful tool for identifying genetic variants associated with complex social behaviors and traits. PAR PUBL

It is advantageous for detecting the effects of multiple genes without pre-existing hypotheses; it can even identify as yet undiscovered genes and advance the understanding of potential biological mechanisms (Pearson & Manolio, 2008). Admittedly, the GWAS approach has its limitations. The most prominent drawback is its inability to capture rare genetic variants, leaving a large proportion of the heritability of many complex social traits unexplained (Wray et al., 2013). As a result, the explanatory power of the GWAS approach for heritability is typically lower than that of twin studies. Moreover, GWAS results are likely biased by population stratification, meaning that results from one population or ethnic group may not apply to others (Martin et al., 2017). Finally, the GWAS approach is limited by the requirement for large sample sizes to obtain sufficient statistical power because each gene has only a small effect on the polygenetic nature of complex social behaviors (Visscher et al., 2017).

Both candidate gene and GWAS approaches have unique advantages and limitations in GenoPA research. The candidate gene approach is more suitable when there is sufficient evidence of the underlying biological pathways as it can help answer questions about the underlying mechanisms (Wilkening et al., 2009). The GWAS approach, which can find genetic variants across the entire genome, has largely eclipsed the candidate gene approach due to the inherent methodological limitations and low replication rate associated with it (Duncan et al., 2019; Friedman et al., 2021). GWAS offers a powerful and promising tool for discovering new genes associated with public administration behaviors. Tao et al. (2023) exemplified this approach as they used GWAS to explore the genetic overlap between psychological attributes and public service employment selection.

In summary, when exploring potential aeneenvironment interactions, both twin/adoption studies and molecular genetics approaches can estimate the heritability of specific traits and behaviors. While twin/adoption design has been used longer than the recently developed molecular genetics approaches, the two are complementary rather than contradictory. Twin/adoption design remains a powerful method for connecting social trait and behavior variance to genetic and environmental factors. However, molecular genetics can pinpoint how specific genetic makeups contribute to attitudinal and behavioral variations, which may elude detection through twin/adoption design alone. Depending on the research question and available data, both twin/adoption studies and molecular genetics approaches are valid within the GenoPA framework. Public administration scholars must consider the advantages and limitations of each approach when crafting their research.

DEVELOPMENTS IN RELATED DISCIPLINES

Related disciplines, such as political science and management, have integrated genetic insights into their subfields. ASPA

In political science, the subfield of biopolitics has developed over nearly two decades. Similarly, management scholars have added genetics to their research agendas in recent years. Since public administration research draws insights from these two disciplines, it is worth observing how they incorporated genetics into their research.

Political science

Political scientists in the field of biopolitics have attempted to examine how genes influence political behavior. Traditionally, political science explains voting behavior through demographic, attitudinal, behavioral, and institutional factors while ignoring possible genetic influences on an individual's tendency to participate in politics. Fowler et al. (2008) pioneered a new perspective by examining how genes relate to political participation. Using a twin design and two independent data sources, they demonstrated that genetic factors account for significant variations in voting behavior. Similarly, parental voting behaviors affect children's political participation not only because of family socialization but also because of genetic transmission. Accordingly, family socialization may moderate the relationship between genes and political participation. Other possible moderators include educational attainment, intelligence (Aarøe et al., 2021), and personality (Dawes et al., 2014).

Another example concerns the genetic roots of political ideologies. Using the twin dataset from the United States and Australia, Alford et al. (2005) found that genetic factors accounted for variations in political attitudes, suggesting that genetic influences on political attitudes might outweigh family socialization effects. They further indicated that genetic factors help explain why patterns of ideological division persist across space and time. For example, the proportion of conservatives in the present-day United States is similar to that in previous eras, implying that genes have shaped ideological divisions despite environmental changes.

In sum, political scientists have been more receptive to learning about the genetic roots of political attitudes and behaviors. Their articles appeared not only in leading journals in the discipline, such as *American Political Science Review* and *American Journal of Political Science*, but also in science journals, such as *Nature Human Behavior* (Aarøe et al., 2021; Dawes et al., 2014; Fowler et al., 2008). There is much scope for public administration scholars to better understand administrative attitudes and behaviors with the help of genetic insights.

Management

Management scholars, particularly those specializing in entrepreneurship, leadership, and work-related outcomes,

have recently incorporated genetics into their research. For example, some have used genetic insights to understand why some people start businesses or become entrepreneurs. Shane et al. (2010) argued that genetic predictors of the Big Five personality attributes affect the likelihood of becoming an entrepreneur. Relying on a twin design and data from the UK, they confirmed that the genetic predictors of extraversion and openness to experience correlated with individuals' entrepreneurial inclinations. This finding contributes to the existing person-job fit framework by suggesting that genes help sort individuals into different occupations. More recently, Patel et al. (2021) have used the molecular genetics method and constructed a PRS of subjective well-being to predict individuals' selfemployment status. Their findings suggest that the PRS of subjective well-being helps explain individuals' choice to pursue self-employment, providing further evidence for the heritability of entrepreneurship.

Using personality traits as potential mediators, scholars have also found that leadership- and work-related outcomes are heritable. For instance, Arvey et al. (2006) found that about 30% of the variance in leadership role occupancy is attributed to genetic factors, supporting the "trait" theory of leadership. Regarding work-related outcomes, job satisfaction was associated with genetic influences. For example, using the twin method and German samples, Hahn et al. (2016) found a high genetic overlap between the Big Five personality traits and job satisfaction. At the molecular level, Song et al. (2011) found two specific genes—dopamine DRD4 and serotonin 5-HTTLPR—to be associated with job satisfaction.

By incorporating genetics into their research, management scholars deepened their understanding of the natural roots of individual differences in entrepreneurship, leadership, and work-related outcomes. Public administration scholars can take a page from the book on cuttingedge management studies as these two fields share many similarities, especially since the advent of the new public management movement.

AGENDAS FOR GENOMIC PUBLIC ADMINISTRATION

Genomic public administration can be characterized as an interdisciplinary analysis of public administration attributes and behaviors through a lens and methods rooted in genetics. The ultimate goal was to enhance our understanding of how genetic factors and their interactions with various socialization agents shape variations in administration-related attitudes, behaviors, and practices. Typical twin/adoption design and molecular genetic methods can help identify the effects of genetic influence and its underlying causal paths. Concurrently, specific domain knowledge and perspectives from public administration and public organization settings can also provide fresh insights into genetics and other related disciplines.

TABLE 3 Agendas outlined for genomic public administration research.

- 1. What administrative traits and behaviors are heritable?
 - a. How robust is the existing genetic evidence regarding PSM and public service employment choice?
 - b. Besides PSM and public sector employment choice, do other administrative traits and behaviors contain heritable components?
- 2. Is there any genetic overlap between psychological factors and administrative traits and behaviors?
 - a. What personality attributes are possible mediators?
 - b. Do emotions and affections play a role?
- 3. To what extent do socialization processes in public organizations moderate the genetic effects on individual traits and behaviors?
 - a. Do bureaucratic structures and arrangements function as
 - moderating socialization contexts in their own right? b. What socialization practices matter in the public sector?
 - b. What socialization practices matter in the public sector
- 4. What insights can policymakers and public sector managers pragmatically draw from genomic public administration?
 - a. How may policymakers and public sector managers consider the genetic basis of human behavior?
 - b. What does genomic public administration research imply about the design of public policy and management practices?

Abbreviation: PSM, public service motivation.

We present the following four research questions for advancing the frontiers of genomic public administration (see Table 3 for a summary):

- 1. What administrative traits and behaviors are heritable?
- 2. Is there any genetic overlap between psychological factors and administrative traits and behaviors?
- 3. To what extent do socialization processes in public organizations moderate the genetic effects on individual traits and behaviors?
- 4. What can policymakers and public sector managers learn pragmatically from genomic public administration?

The heritability of administrative traits and behaviors

Decades of behavioral genetics studies have confirmed that nearly all individual traits and behaviors contain heritable components (Ebstein et al., 2010; Plomin et al., 2016; Polderman et al., 2015; Turkheimer, 2000). Therefore, a promising avenue for advancing genomic public administration is to ask what administrative traits and behaviors are heritable. Several recent studies have answered this question by examining the heritability of public sector employment (Christensen et al., 2021; Tao et al., 2023) and PSM (Florczak et al., 2022). Twin/adoption research has repeatedly confirmed that affection, such as empathy, is approximately 41.3%–50.6% heritable (Abramson et al., 2020). Considering the conceptual overlap between empathy and PSM, a relevant question is whether the affective component of PSM is genetically conditioned. In addition to the twin-based design, molecular biology studies have concluded that oxytocin-related genes shape the development of emotional and affective attributes (Rodrigues et al., 2009; R. Zhang et al., 2017). Future research should use molecular genetic methods to test whether oxytocin-related genes influence PSM levels. Identifying the overall biological mechanisms underlying one's affection can illuminate how individuals develop altruism and a broader orientation toward both others and society. If genetic variables shape PSM, the argument about the impact of the socialization process on PSM may be biased. Such potential bias helps explain the failure of some experimental interventions to activate individuals' PSM without controlling for possible genetic variation (Christensen & Wright, 2018).

While extant analyses have pondered the nuanced origins of individuals' PSM and public sector choices, more consequential research is needed in such areas of public administration as leadership, collective action, discriminatory attitudes and behaviors, and various work-related outcomes. Below, we use collective action as an example.

A large body of research within the field of public administration concerns the causes, notably the institutional roots, of collective action (Ostrom, 2010; Robertson & Tang, 1995). That said, beyond institutional explanations, Tybur and Griskevicius (2013) recommended an evolutionary psychology approach to understanding the development of collective action in administrative settings. From this perspective, collective action is conditioned not only socially and culturally but also by natural selection. Evolutionary biology demonstrates that the processes of evolution favor cooperation, especially in situations of kinship and reciprocal relationships (Oliver, 2018; Rand & Nowak, 2013; Trivers, 1971; West et al., 2007). This evolutionary perspective can be bolstered by genetic evidence of heritable differences across cooperative behaviors (Cesarini et al., 2008) and the saliency of "cooperative genes" (Manfredini et al., 2018; Walter et al., 2011). In summary, the heritability of cooperative behavior implies that collective action is premised on heritable drivers at the individual level.

Moreover, studying the genetic roots of collective action not only helps us understand the origins of collaboration but also has implications for organizational and institutional design. For example, if cooperation is intrinsic to human nature, are people innately inclined toward establishing and functioning groups or institutions of varying sizes, scopes, and forms? Scholars may connect mezzo- and macro-level public administration theories with their possible biological roots.

Genetic overlap between psychological factors and administrative traits and behaviors

Another promising frontier in genomic public administration is exploring the psychological mediators between genetic roots and administrative traits and behaviors. As mentioned previously, behavioral genetics research in psychology, political science, and management has confirmed the role of psychological attributes as mediators between genes, social traits, and behaviors. Two psychological attributes, personality traits and emotions, are particularly relevant to public administration.

Personality traits are relatively stable and fundamental to human behavior. Public administration scholars have long been concentrated on exploring the relevance of personality traits, such as PSM (Van Witteloostuijn et al., 2017), with decision-making (Filiz & Paul Battaglio Jr, 2017), administrative burdens (Aarøe et al., 2021), job satisfaction, and organizational citizenship behaviors (Cooper et al., 2013). Political scientists such as Dawes et al. (2014) have uncovered a genetic overlap between personality traits and political behavior. Florczak et al. (2020) found that high-level bureaucrats and politicians share similar personality traits. Hence, certain administrative behaviors can reasonably be expected to overlap with these personality traits from a genetic standpoint. Because all personality traits, including the Big Five and Eysenck's (1970) personality models, have genetic roots (Vukasović & Bratko, 2015), future research may seek to detect whether the genes associated with personality development can also predict administrative traits and behaviors.

Emotion is another psychological attribute with heritable components (Cloninger & Garcia, 2015). Psychologists have found that positive and negative emotions influence human judgment, motivation, and behavior (Angie et al., 2011; Baumeister et al., 2007; Bradley & Lang, 2007; Diener & Emmons, 1984). While fundamental to most human functions, emotional management is particularly essential for public employees because most civil service work requires emotional skills and intelligence (Guy et al., 2014). However, despite the copious literature on emotional labor, public administration scholars have yet to thoroughly examine emotion. Nørgaard (2018) called for more research on the roles of emotions and affection in public administration settings, especially regarding bureaucratic behaviors and citizens' interactions with governments. Hence, we envision emotions and affection as vital, albeit underexploited, theoretical constructs connecting genetics and administration-related behaviors.

Furthermore, exploring the psychological mediating mechanisms between genes and administration-related behaviors helps overcome the main weaknesses of existing twin-based studies. For instance, a recent study in public administration provided direct evidence that genetic factors influence an individual's choice of a public sector career (Christensen et al., 2021). However, it is not enough to merely prove that genes somehow affect public sector career selection without knowing which specific genes matter and through what mechanisms. No genes have been directly linked to career choice, so a more meaningful avenue is to detect the mediators that

connect genetic expression with public sector employment. Using the person-environment fit framework (Kristof, 1996), Tao et al. (2023) confirmed that genes of positive affect can influence an individual's public service employment selection, whereas genetic predictors of neuroticism do not. However, since most psychological traits and personality attributes affecting an individual's self-selection for public service work contain heritable components (Costa et al., 1984; Emmerling & Cherniss, 2003; Schermer et al., 2015), scholars should explore whether the other five personality traits and general psychological attributes can mediate the influence of genes on public sector intentions. Such research could illuminate the complex interplay between genetics and environmental factors in shaping public sector employment decisions.

Socialization processes in public organizations moderating genetic effects on individual traits and behaviors

Another promising frontier for genomic public administration research is gene–environment interactions. Genetically informed research typically focuses on the moderating genetic influences of family socialization, school socialization, religious socialization, and individual lifestyles on behavior (Shanahan & Hofer, 2005). However, few studies have focused on the moderating effects of public organizations in the context of socialization.

For example, the existing gene-environment interaction literature suggests that religiosity moderates the relationship between genes and prosocial behaviors (Sasaki et al., 2013). This is because religious socialization provides a prosocial environment that suppresses personal impulses and encourages self-control. How can a public organization similarly influence an individual's social behavior? For example, the "public" setting of a government organization creates an environment for fostering service motivation and behaviors among its employees (Ward, 2014). In other words, the public nature of the government may moderate the effects of genetic orientation on prosocial behaviors. After several years of experience in the military, welfare, and social service programs, individuals with a high genetic predisposition to antisocial behaviors may begin to exhibit more robust prosocial behaviors. This strand of research may open a practical way to respond to a recent scholarly call to explore the "bright side" of public administration and build a triumphant story of government (Douglas et al., 2021).

In addition to exploring the role of institutions in counteracting genetic propensities, scholars may explore socialization practices in human resource management in the public sector. For instance, studies have found that positive social support decreases the likelihood of depression, even in individuals with high genetic risks (Arnau-Soler et al., 2019; Kaufman et al., 2004). This finding implies that public management practices, such as organizational support, fair workload assignments, and transformational leadership styles, can moderate the relationship between genetic orientation and workrelated outcomes.

Policymakers and public sector managers learning from genomic public administration

How can policymakers and public sector managers consider the genetic basis of human behavior? The existing literature on behavioral genetics generally agrees that our acknowledgment of genetic effects does not imply advocacy for genome selection. However, knowledge of genetic effects can help direct policy and administrative measures toward shaping psychological traits and behaviors that are less genetically determined and, hence, more socially and institutionally malleable.

When launching policy programs, public sector managers may draw on insights into how psychological processes mediate the relationships between genetic propensities and individual traits and behaviors. When designing broader political, social, and administrative reforms, political and policy leaders may also benefit from knowledge of how genetics influences individuals' choices regarding their own social and institutional environments. Such knowledge may help them assess the limitations and viable options for reform.

Under certain circumstances, socialization can mitigate or enhance genetic impacts, meaning that the effects of policy and management measures will also likely vary across individuals and populations, given their different genetic inclinations. Research on these dynamics invites a thought-provoking question for public administration practice: How can genomic public administration research inform public policy and management design that is robust across varying groups and settings? In the medical field, current precision practices have led to the creation of various intervention programs aimed at designing the most effective environmental manipulation strategies while considering genetic factors. Furthermore, the Precision Public Health Initiative is intended to provide more effective interventions for diverse population groups and seeks to transform medical practices (Khoury et al., 2016). Recent evidence has also demonstrated the growing potential of human genomic research in disease prevention for high-risk populations, infectious disease outbreaks, and practical guidelines for health systems (Roberts et al., 2021). Although many challenges remain, advances in precision public health have undoubtedly provided valuable insights for healthcare policymakers and managers. More broadly speaking, gene-based knowledge has shown promise in informing the design of various policy interventions to benefit different population groups.

CONCLUSION

In recent years, progress has been made in biologically informed social science research, advancing our understanding of the genetic roots of various social attitudes and behaviors. As an interdisciplinary field, public administration can embrace this trend by applying biological and genetic insights to advance current administrative theories and leveraging pertinent findings to extend the pragmatic scope of biology and other related disciplines.

In pursuing GenoPA wisdom, public administration scholars inevitably face several challenges. To begin with, although many secondary genetic datasets are available, certain tradeoffs must be considered. For example, while genetically informed samples are extensive and have potential for advancing genetics-based immense research, they are primarily developed by health scientists focusing on health-related variables. Many variables meaningful to public administration may not be available in these datasets. Hence, public administration scholars must rely on simplified or constrained measures when using genetically informed samples. Recent gene-based public administration studies conducted by Christensen et al. (2021), Florczak et al. (2022), and Tao et al. (2023) have demonstrated the limitations of relying on simplified measures in genetically informed datasets. Public administration scholars must thus understand that using these large genetic datasets may diminish theoretical power and measurement validity to a certain extent.

Moreover, despite the potential benefits of constructing first-hand genetic datasets for public administration research, several significant barriers hinder their development. One of the primary challenges is the polygenic nature of social traits, which suggests that multiple genes may explain the heritability of public administration behaviors, each having minor effects. Therefore, large-scale samples are required to detect these effects, necessitating considerably larger sample sizes than those used in typical survey studies. Unfortunately, substantial external funding is necessary to establish large-scale genetic datasets, creating a significant financial barrier for public administration.

In addition, scholars must consider both practical and ethical constraints when collecting genetic data. Unlike traditional survey studies, the collection of genetic information tends to be more invasive and often requires blood or saliva collection. Scholars must adequately address participants' privacy, abilities, and ethical concerns while complying with the regulations and ethical guidelines of the relevant research ethics committees.

That being said, the opportunities are still abundant. Standard methods for conducting genetic research have been well established and validated. Scholars already have access to large nationwide datasets containing both genetic data and social behavior variables, such as the UK Biobank, the Chinese Longitudinal Healthy Longevity Survey (CHLSL), and the US Health and Retirement Study

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(HRS). Moreover, the advent of low-cost genome tests has allowed public administration scholars to collect firsthand genetic data from saliva.

Therefore, we urge more scholars of public administration to engage in this line of research. Universities can delve into the ins and outs of genomic public administration by offering interdisciplinary courses and training programs. We hope this article serves as a point of departure and inspires like-minded peers to advance the frontiers of genomic public administration.

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DATA AVAILABILITY STATEMENT

The data used or mentioned to support the opinions expressed in this article are available upon reasonable request.

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