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# Measuring racial essentialism in the genomic era: The genetic essentialism scale for race (GESR)

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## Abstract

Racial essentialism is the belief that races are biologically distinct groups with defining core "essences," a notion associated with increased social distance and racial bias. While there are different kinds of racial essentialism, understanding and measuring genetic essentialism – the belief that racial groups and their defining core essences are determined by genes – is increasingly important in the wake of the Human Genome Project and the genomic revolution that it spurred. Many have questioned whether such genomic advances will reinforce genetic essentialist beliefs about race, but scholarly research is limited by measures that do not specify the role of genes in these beliefs or allow for distinct theoretical sub-components. In this paper, we develop and validate the Genetic Essentialism Scale for Race (GESR) using a sequential transformative mixed methods approach. Data for analysis come from an original survey-based study with a sample of 1069 White native-born Americans. We employ both exploratory factor analysis and confirmatory analysis to derive and confirm a three-factor model of genetic essentialism (*category determinism*, *core determinism,* and *polygenism*). Due to the high correlation between these factors, we also test for a second-order measurement model with three first-order factors. After conducting additional reliability, validity, and construct validity testing, we propose the GESR— a second-order construct with three first-order dimensions— as a reliable measure of genetic essentialism. The GESR will allow researchers to determine the impact of new genetic developments like race-based medicines and genetic ancestry testing on genetic essentialist beliefs about race.

**Keywords** Genetic essentialism · Racial essentialism · Scale · Race · Racial conceptualization · Second-order factor model

## Introduction

Belief in racial essentialism – the concept of races as biologically distinct groups with defining, inherent qualities (Morning 2011; Tawa 2017) – has negative consequences for intergroup behavior ranging from an unwillingness to interact with other racial groups to racial bias, Apartheid, eugenics, and genocide (Cornell and Hartmann 1998; Williams and Eberhardt 2008; Heine et al. 2017; also see No et al. 2008). Understanding the social impact of essentialist beliefs is particularly important in the wake of the Human Genome Project given its ironic potential impacts on lay understandings of race. On the one hand, the project disconfirmed the existence of genetically distinct racial groups, showing that all individuals share 99.9% of DNA, both within and across presumed racial groups (Nelson 2016). On the other hand, it spurred a "genomic revolution" of research increasingly focused on the 0.1% of human genetic difference in search of racial differences in disease risk at the genetic level (Fullwiley 2007; Phelan et al. 2013). It also produced the mass industry of direct-to-consumer genetic ancestry testing, which often presents genetic ancestry as overlapping with common racial categories (Nelson 2016; Roth & Ivemark 2018). Many argue that such phenomena will increase popular belief in racial essentialism (Bliss 2012; Bolnick et al. 2007; Duster 2015; Fullwiley 2008; Panofsky and Bliss 2017; Phelan et al. 2013, 2014; Roberts 2011).

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The growing scholarly interest in these trends, and in lay beliefs in the relationship between race and genes more generally, requires a reliable measure of racial essentialism focusing on the role of genetics. There are several measures of essentialism at present, but none adequately captures the belief that inherent racial differences have fundamental genetic causes. Such a scale is needed for emerging scholarship seeking to test, for instance, whether the genomic revolution, genetic ancestry testing, or personalized medicine increases essentialist views about race. We expect these processes to be associated with genetic essentialism – the belief that essential racial differences are genetically determined – but they may not be associated with other forms of essentialism, and existing scales therefore may not adequately capture the relationship.

In this paper, we theoretically distinguish genetic essentialism from other forms of essentialism, and develop and validate the Genetic Essentialism Scale for Race (GESR). First, we employ an exploratory factor analysis to identify the factor structure, and then use confirmatory factor analysis to validate the factor structure. After examining the validity and reliability of the scale measure, we test for a second-order model to reflect the potential of genetic essentialism as an overarching construct (a higher-order latent variable that accounts for the first-order latent variables). A second-order model allows for factoring in the distinct contributions of first-order variables. We find that GESR is a second-order variable that subsumes three first-order variables, as the second-order model performs much better than first-order models with respect to model fit, reliability, and validity. By developing the GESR, we hope future researchers can use this novel measurement of genetic essentialism for race and that identifying its distinct dimensions will also assist theoretical understanding of the concept.

## Different Forms of Essentialism

Essentialist views about race need not be based on beliefs about genetic difference; indeed, essentialist beliefs existed well before people were aware of genes (Cornell and Hartmann 1998; also see Keller 2005, p.687–688 for origins of essentialist beliefs). Psychological essentialism, for instance, is a tendency to view certain categories of things as "natural kinds" with immutable, unique properties while others are not (e.g., a Black person cannot be changed into a White person, but a bed can be changed into a table), and to use the categories of "natural kinds" to infer attributes about each item within it (Phelan et al. 2013; Rothbart and Taylor 1992; Bastian and Haslam 2006; Dar-Nimrod and Heine 2011; Tawa 2017). By contrast, cultural essentialism is the belief that people's beliefs, attitudes, and achievements reflect a fixed, uniform essence determined by their culture. It associates racial categories with distinct, static cultural patterns such as lifestyles, practices and values that permanently shape the psychological characteristics of members of the group (Morning 2009; Soylu Yalcinkaya et al. 2017). Cultural essentialism has previously been associated with opposition to policy measures that have real-world consequences for racial minorities, such as affirmative action policies (Soylu Yalcinkaya et al. 2017). Other forms of essentialism may locate essential racial differences in the soul or the psyche (Morning 2011).

### Conceptualizations of Genetic Essentialism

Genetic essentialism views genes as the location of this fixed, uniform essence. With regard to race, it is the belief that racial groups and their defining core essences are determined by genes, and the tendency to infer a person's behaviors, characteristics, or traits from her or his perceived genetic makeup (Dar-Nimrod and Heine 2011; Rothbart and Taylor 1992). A genetic essentialist worldview is one in which genes define the essence of humans and determine the differences and commonalities between and within human groups (Phelan et al. 2013). Some argue that evidence from the human genome emphasizing genetic differences between racial groups should increase genetic essentialist views about race, while evidence suggesting that races are genetically similar should decrease those views (Bolnick 2008; Kimel et al. 2016; Phelan et al. 2014, 2013). Such considerations necessitate a scale identifying genetic essentialist beliefs about race that could be used in research on this topic.

As with other forms of essentialism (Tawa 2017, 2018), there is reason to believe that genetic essentialism is multidimensional. In particular, genes may be seen as determining the category one falls into – what we call "category determinism" – while a separate dimension captures the belief that genes create differences in essential traits or skills that are associated with those categories – what we call "core determinism." In an earlier qualitative study, we found that many genetic ancestry test consumers believed that genetics determined a person's racial category, but did not believe that there were essential differences in the abilities or traits of people in different racial groups (Roth 2013). These distinctions map onto the two primary components identified in other forms of essentialism between a "natural kind" factor that views social categories as discrete and immutable, and a "reification" factor that sees the differences between categories as meaningful and deeply informative as to the categories' underlying essences (Rothbart and Taylor 1992; Haslam et al. 2000).[1] There may

[1] Similarly, with regard to race, Byrd and Hughey (2015) differentiate between the concept that genes determine fixed, innate racial categories, and the belief that those racial categories have core essences that determine their character and behavior. They refer to these constructs as biological determinism and genetic essentialism, respectively, but argue that while distinct, these beliefs are frequently intertwined. We use different terminology to emphasize that these are both dimensions of genetic essentialism.

be other dimensions of genetic essentialist views of race as well.

Genetic essentialist beliefs are not applied only to race; they may also affect the way people think about gender, sexual orientation, mental illness, criminality, and obesity, for instance (Dar-Nimrod and Heine 2011). Indeed, some scales of genetic essentialism (e.g. Keller 2005) apply its logic simultaneously to a variety of these aspects of human life, behavior, and personality. Yet, genetic essentialist beliefs toward these different categories and characteristics may vary. Recent debates contrasting the concepts of transgenderism and transracialism (e.g. contrasting reactions to Caitlyn Jenner and Rachel Doležal) have shown much greater support for essentialist beliefs about race than about gender (Birmingham 2018; Brubaker 2016; Tuvel 2017). This indicates the need for a scale that measures genetic essentialist beliefs about race specifically, as one or two relevant items within a broader scale would fall short of accurately gauging such a complex construct and distinguishing its potential dimensions.

## Existing Racial Essentialism Scales

Despite the theoretical distinctions between genetic essentialism and other forms of essentialism, existing scales of racial essentialism do not distinguish adequately between them. Several studies use the 4-item Racial Essentialism Scale, deriving from an unpublished manuscript by No and Hong (see Chao et al. 2013), which includes one item referring to biology as the cause of racial differences in traits and abilities, but the three remaining items do not specify the nature or location of essential racial differences.[2] Williams and Eberhardt's (2008) Race Conceptions Scale measures the extent to which race is biologically based, although only 2 of the 22 items specify that race is determined by biology or DNA; because the scale adds measures together, it is possible for someone to have a high score without viewing race as genetic or biological. More importantly, the Race Conceptions Scale does not capture a central aspect of racial essentialism: the belief that specific abilities, traits, or behaviors are linked to race; for instance, the authors deliberately did not include items such as "Blacks are inherently less intelligent than Whites." Items in the scale could be used to capture the idea that racial categorization is biologically determined (i.e. category determinism), but not the concept that races have defining, inherent qualities (i.e. core determinism). Phelan and colleagues' 6-item measure of belief in essential racial differences similarly includes only one item that specifies genetics as a cause of racial difference (Phelan et al. 2014; Phelan et al. 2013).[3] Both of the latter two scales also focus on differences between Blacks and Whites in several items; our goal was to develop a scale that could be more broadly applied in studies focusing on other or multiple racial groups and in different national contexts.

Although not focusing on genetic essentialism per se, Tawa's (2017) Beliefs About Race Scale (BARS) is an improvement on earlier racial essentialism scales because of its exploration of the multidimensionality of the concept. However, it is not ideal for research on the impact of the genomic revolution and its new technologies because it does not specify the location or cause of essential racial differences; while some items and dimensions focus on biology, others are ambiguous and could also be consistent with cultural essentialism. Tawa (2017, 2018) identifies four dimensions of essentialist beliefs about race: (1) "Speciation," the belief that racial groups are distinct natural kinds such as distinct subspecies or species. This includes the belief that different races have different evolutionary origins rather than all descending from the same ancestors (e.g. each having their own Adam and Eve or ancestral parents). (2) "Genotypic essentialism" is the belief that racial groups have shared genetic predispositions to anatomical characteristics like bone or muscular structures, which may lead both to different group-level behavioral tendencies (e.g. running faster) and classification (e.g. racial identification during an autopsy). (3) "Phenotypic essentialism" denotes belief that racial groups have distinct phenotypic characteristics like skin color and hair texture, but that racial differences are only "skin deep" and do not indicate deeper essences or characteristics. And (4) "Behavioral essentialism" is a belief that races are distinct groups with shared cultural or behavioral tendencies, such as being soft spoken or a tendency to gesticulate.

The BARS does not distinguish between different forms of essentialism. Its "behavioral essentialism" dimension, for instance, does not specify the cause of shared behavioral tendencies, and could be explained by either cultural essentialism or genetic essentialist beliefs. This might underestimate the effects of genomic research and technology on essentialist beliefs because a lack of change in cultural essentialism dampens changes that do occur in genetic essentialism. Furthermore, we suspect that the "genotypic essentialism" dimension, which focuses on racial groups having shared genetic predispositions to anatomical characteristics that may be associated with performance, may subsume distinct

[2] The item referring to biology states "To a large extent, a person's race biologically determines his or her abilities." The others include: "Although a person can adapt to different cultures, it is hard if not impossible to change the disposition of a person's race."; "How a person is like (e.g., his or her abilities, traits) is deeply ingrained in his or her race. It cannot be changed much."; and "A person's race is something very basic about them and it can't be changed much." (Chao et al. 2013).

[3] A second item states "Different racial groups are all basically alike 'under the skin'" (reverse scored) which is ambiguous; people could interpret it as referring to genetics, but others may see it as consistent with psychological essentialism or belief that essential differences are located in the soul.

dimensions of genetic essentialism around classification and behavioral tendencies, what we call "category determinism" and "core determinism" respectively. While a distinct scale of genetic essentialist beliefs about race is needed, Tawa's research indicates the value of examining distinct dimensions in such a scale.

The primary objective of our study is to create a scale that would be broadly applicable to understanding the impact of a wide range of genomic innovations and technologies on genetic essentialist beliefs about race, and to identify the distinct dimensions of these beliefs and their underlying factor structure. Indeed, our exploratory factor analysis reveals three distinct dimensions that make up a broader, second-order measure of genetic essentialism: 1) category determinism – the belief that races are discrete, immutable categories determined by one's genes; 2) core determinism – the belief that genes cause racial groups to have distinct and innate essences associated with different skills, traits, or abilities; and 3) polygenism – the belief that races have evolved from different origins, rather than sharing common ancestral roots.[4]

## Methods

### Study Sample and Data Collection

The data for the exploratory factor analysis come from the pre-test survey of a randomized controlled trial with native-born White Americans. Through random digit dialing, participants were recruited for an experimental study designed to measure the impact of genetic ancestry testing on racial essentialism and other outcomes. We focused on native-born, non-Hispanic White Americans because our informal communications with several testing company representatives indicated that they were the largest consumer group of genetic ancestry tests (see also Roth & Lyon 2018). We also view this choice as appropriate given that the dominant group in a society is most able to act on essentialist views to enact discrimination, segregation, or otherwise turn racial bias into a pervasive social problem (Byrd and Ray 2015; Morton et al. 2009; Soylu Yalcinkaya et al. 2017). Stratified random sampling was used to recruit a sample that reflected the distribution of non-Hispanic Whites on gender, age, region, and educational attainment in the United States. Eligible individuals were born in the U.S., identified as non-Hispanic White, aged 19 years or older, had no prior experience taking genetic ancestry tests, and were willing to take a genetic ancestry test.

By using stratified random sampling based on characteristics of the entire native-born non-Hispanic White population, our sample mirrors that population on gender, age, region, and educational attainment. However, because the population of interest for this experimental study was native-born Whites who were willing to take genetic ancestry tests and had not previously taken any, it is not statistically representative of the larger population of all native-born non-Hispanic Whites. There is no nationally representative data on these two eligibility criteria regarding test-taking. Nonetheless, our large, nationwide sample is an improvement on the smaller convenience samples that are often used for scale development (e.g., Keller 2005; Tawa 2017).

Of the 4191 participants contacted, 1716 participants met the eligibility criteria. In total, 1069 participants consented to the study and completed the pre-test survey (October 2014 – February 2015).[5] This study received ethics approval from The University of British Columbia.

### Essentialism Measures

Participants were asked a series of 15 questions designed to measure beliefs about the relationship between genes and race, including essentialist beliefs (see Table 1 "Statements" column for full set of survey items). Eight items were drawn from a survey conducted by Outram et al. (2018), while the other seven scale items were developed from previous qualitative work and in response to a need for clear measures of essentialist beliefs about race that were related to genetics. Roth conducted a qualitative study with 115 people who had previously taken genetic ancestry tests, and asked participants open-ended questions about their conceptions of race and the relationship between race and genes (see Roth & Ivemark 2018). In many of those interviews, respondents expressed belief that genes determine a person's racial category, but do not have implications for their skills, abilities, or traits. New scale items were developed to capture themes emerging from those responses that were not captured by the existing scale items.

For all items, response options included a five-point Likert scale, ranging from "Strongly Disagree" to "Strongly Agree" with a "Don't Know" option. We originally included a "Don't Know" response choice because we thought there may have been respondents who did not feel they knew about this subject and would have left the question blank otherwise. We

[4] We use the term "polygenism" rather than speciation as this belief may not go as far as to believe that races are different human species. Nonetheless, there is considerable overlap between our dimension of polygenism and Tawa's (2017) dimension of speciation. We use this terminology because it reflects a long-established belief system that has been well documented (Jackson and Weidman 2005). However, it should not be confused with the term "polygenetic," a description of traits that result from a number of genes.

[5] See Online Supplement for further details of the study design. Because our development and analysis of the GESR uses the pre-test data only, and does not distinguish the Treatment and Control groups, the experimental nature of the original study is incidental to the analysis in this paper.

**Table 1** Variables, statements, and uniqueness scores of the 15 items in a three-factor solution

| Variable | Statements | Uniqueness |
|---|---|---|
| 1. Athlete | Certain races may be better athletes than others because of genetics. | 0.717 |
| 2. Smart | Certain races may be smarter than others because of genetics. | 0.500 |
| 3. Pure | There used to be "pure" races in the past. | 0.590 |
| 4. PopDivide | The human population is divided into biological races. | 0.569 |
| 5. GeneticsTells | No matter what a person looks like, genetics can tell what race they really are. | 0.706 |
| 6. Classify | DNA technology will help us develop better racial classifications based on genetics. | 0.673 |
| 7. RaceInvent [R] | Races are groups that societies invent. | 0.645 |
| 8. AllAfrican [R] | Everyone's ancestors originally came from Africa. | 0.658 |
| 9. AllShare [R] | People of all races share most of the same genes. | 0.624 |
| 10. Disease | There are some diseases that only members of certain races can get. | 0.663 |
| 11. DocDisease | Knowing a person's race can help a doctor know what diseases that person is likely to get. | 0.670 |
| 12. SameTraits [R] | People from different races can have the same physical traits or features. | 0.806 |
| 13. Insignif [R] | There are genetic differences among races, but they are biologically insignificant. | 0.687 |
| 14. Physical [R] | The only genetic differences among races relate to their physical appearance. | 0.824 |
| 15. NoPure [R] | There are no "pure" races because the groups are so intermixed. | 0.819 |

| | Factor 1 | Factor 2 | Factor 3 |
|---|---|---|---|
| EIGENVALUES | 3.197 | 1.022 | 0.631 |
| Explained Variance | 0.699 | 0.224 | 0.138 |

Notes: Estimation Method: Principal Factor Method. Rotation Method: Promax Oblique Rotation. [R] = Reverse coded. Scale Reliability Coefficient = 0.734. $N = 525$

recoded the responses of "Don't Know" as "missing" (See Table S1 for distribution of missing values). To identify the nature of missingness, we conducted Little's Missing Completely at Random (MCAR) test, and assessed for covariate-dependent missingness (CDM) — an extension of the MCAR test when covariates are present. The MCAR test provides evidence that the missing data in the fifteen variables of interest are missing completely at random, with and without covariates such as age, gender, and education.[6] We then replaced missing values on each item with the median value for that item to be able to use the sample in its full size (See Harrell 2015, Chapter 3). To further validate the accuracy of the sample, we also ran the models used with the subsample where we have complete data (where all cases with missing responses are dropped) (See Table S2 for comparison of the two samples vis-à-vis major demographic variables). Yet, as the sample size of this subsample is rather low, we rely on the results of the full sample where missing values are replaced with the median-values. We include the analysis of our three-factor model with nine indicators using the subsample with no missing data in the Online Supplement.

## Results

### Exploratory Factor Analysis

We randomly split the data in half, and using the first random half we conducted exploratory factor analysis (unrestricted measurement model) along with principal component analysis to find out the number of latent variables (factors) that can explain the relations among this set of indicators on genetic essentialism. We first ran the Kaiser–Meyer–Olkin (KMO) test to assess the sampling adequacy for each variable in the model, and the resulting KMO score was .769, indicating that sampling is adequate (values above .6 are considered adequate) (Cerny and Kaiser 1977; Kaiser 1974). Finally, the Bartlett's test of sphericity resulted in very high chi-square value (1093.811, $df = 105$) with $p$ value less than 0.001, showing that correlation matrix is suitable for factor analysis. These results confirm that the sample was adequate and the variables are interrelated enough to conduct an exploratory factor analysis.

All 15 items are categorical with an ordinal four-point Likert scale, thus we use a polychoric correlation matrix, which assumes these variables reflect underlying continuous variables.[7] To determine relevant items and which factors to

[6] The $p$ value is 0.31 for the test without the covariates, and close to 1 for CDM, so we fail to reject the null hypothesis that the variables are missing completely at random.

[7] Polychoric correlation coefficients are maximum likelihood estimates of the product-moment correlation among the underlying normally distributed variables.

retain, we use a multi-stage approach. In the first stage, we ran the analysis on all 15 items. Table 1 shows the uniqueness scores of all 15 items on a three-factor model.[8] Using iterative analysis and our judgment for theoretical value of the items, we omitted complex items (cross-loading on multiple factors), items with high uniqueness scores (usually higher than .70) and item loadings that were too weak or did not make theoretical sense, which left us with 9 items (see Table 2 for the distribution of these 9 items).[9]

To determine the number of factors, we used principal component analysis, scree plots, and parallel analysis as well as theoretical reasoning (Costello and Osborne 2005). First, we ran a principal component analysis, and results indicated at least two components (eigenvalues 3.14 and 1.23) and a potential third component with an eigenvalue of 1.09 (see Table 3 and Table S3). Given the very high eigenvalue for the first factor, we carefully entertained the possibility of unidimensionality. Yet at least five of the items had very high uniqueness scores (AllShare—0.808, GeneticsTells—0.804, RaceInvent—0.790, AllAfrican—0.783, and Classify—0.748). We explored unidimensionality with and without the RaceInvent variable, which is a bit more complex as explained below, and in both scenarios it is clear that a one-factor solution is not feasible due to many items with high uniqueness scores (see Table 4 and Table S4). The principal component analysis already showed us that there are multiple components gauged by our list of variables. These cues led us to explore multidimensionality while continuing to consider the possibility of a unidimensional solution.

Next, we ran an unrestricted factor analysis, using principal axis factoring as the estimation method, and examined the screeplot as well as the parallel analysis results. The screeplot depicts the point at which the declining slope of eigenvalues appears to level off at either Factor 2 or Factor 4 (see Fig. 1), again indicating multiple underlying factors. Parallel analysis suggests retaining up to 4 factors (Fig. 1), but more than three factors did not seem sensible. A fourth factor would decrease the number of items per factor to less than 3, which is often not recommended (Hair et al. 2010; MacCallum et al. 1999; Raubenheimer 2004). More importantly, the fourth factor did not make theoretical sense whereas we were able to meaningfully interpret each of the factors in the 3-factor solution (Worthington and Whittaker 2006).

Finally, we looked at the Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) scores of different factor models for model comparisons to ensure there is more than one factor (Akaike 1987; Schwarz 1978). Lower scores of AIC and BIC indicate a better model. Both criteria suggested that a unidimensional (one-factor) model is the weakest and the three-factor model is the strongest model in terms of relative fit to the data and quality (see Table 5 and Table S5).

A three-factor model also fit our theoretical expectations much better than a one-factor model. As discussed above, we believe that Tawa's "genotypic essentialism" and "speciation" subscales, both of which seem to encapsulate aspects of genetic essentialism, imply that there is more than one dimension to genetic essentialism. Theoretically, believing that a race's intelligence or talents stem from its genetic composition and believing that humankind does not all emerge from the same origin do not have to go hand in hand; these could be distinct dimensions of a broader concept of genetic essentialism. And as mentioned above, our prior findings from qualitative interviews provided an additional foundation for our theoretical expectation that there are different components to the concept of genetic essentialism.

Based on the factor loadings, scree plots, parallel analysis results, and theoretical expectations, a three-factor model provided the best fit. We named these factors as follows: core determinism (Athlete, Smart, and Pure), category determinism (PopDivide, GeneticsTells, and Classify,) and polygenism (RaceInvent[R], AllAfrican[R], and AllShare[R]) for Factors 1, 2 and 3 respectively (see Table 6 and Table S6 for factor loadings).

The item RaceInvent appears volatile as it loads onto polygenism in the main analysis using the sample where the missing values are replaced with median values (Table 6), but onto category determinism using the subsample with no missing values (Table S6). RaceInvent measures the degree of agreement with the statement "races are groups societies invent," which could underlie both category determinism and polygenism. We initially decided to keep it in the analysis for two reasons: 1) attitudes towards race as a social construct vs. a biological trait are very informative to gauge the broader construct of genetic essentialism—our main goal in the paper; 2) we wanted to ensure there are at least three items per factor. Yet, the complex nature of the variable and its high uniqueness score (.738) renders it less robust. We checked the factor structure and loadings by omitting RaceInvent, and the remaining 8 items have the same factor structure in a three-factor solution and loadings are consistent across both the median-replaced full sample and the subsample (see Table S7). Given that the inclusion or omission of RaceInvent does not change the factor structure and its omission could weaken the theoretical and empirical power of the scale (particularly for Polygenism,

[8] We are presenting here only the three-factor solution because our final model is a three-factor model. In the first stage, we explored two, four and five-factor models, which also show similar patterns. However, the items with high uniqueness scores were weaker on theoretical grounds, and screeplot, parallel analysis, and model comparisons were all supportive of a three-factor solution.

[9] For the subsample with complete data, using these 9 items, the KMO score is .819, and the Bartlett's test of sphericity indicates a chi-square value of 401.233 with 36 degrees of freedom. Both tests confirm that subsample with complete data has enough observations with interrelated variables to proceed with factor analysis. See Online Supplement for tables using this subsample.

**Table 2** Distribution of the retained 9 items

| Variable | 1 Strongly Disagree | 2 Somewhat Disagree | 3 Somewhat Agree | 4 Strongly Agree | . Missing |
|---|---|---|---|---|---|
| | % | % | % | % | % |
| Athlete | 14.12 | 15.82 | 47.27 | 12.24 | 10.55 |
| Smart | 45.76 | 20.53 | 17.33 | 3.39 | 12.99 |
| Pure | 29.38 | 21.28 | 17.89 | 10.36 | 21.09 |
| PopDivide | 18.83 | 15.63 | 34.65 | 9.04 | 21.85 |
| GeneticsTells | 7.34 | 8.85 | 32.77 | 39.36 | 11.68 |
| Classify | 12.81 | 11.11 | 30.7 | 14.5 | 30.89 |
| RaceInvent | 26.93 | 21.47 | 27.87 | 13.37 | 10.36 |
| AllAfrican | 17.89 | 9.04 | 21.09 | 25.99 | 25.8 |
| AllShare | 2.07 | 4.33 | 28.25 | 52.17 | 13.18 |

Note: "Don't Know" coded as Missing. This distribution is before the missing values are replaced with the median values. $N = 531$

which would have only two items), we decided to retain RaceInvent. However, we discuss this item further below.

## Confirmatory Factor Analysis: Cross-Validation of the Scale

To validate the dimensions produced by the exploratory factor analysis, we performed a confirmatory factor analysis (CFA) on the second half of the randomly split sample. The nine items we used in the EFA were the observed variables of the model and the three extracted factors were the latent variables. To obtain the goodness of fit test results and build a diagram, we used Stata's "SEM" command with maximum likelihood (See Fig. 2).[10] The loadings are usually above .5, which indicate structural validity (Kline 2005).

Regarding model fit, we used the comparative fit index (CFI), Tucker-Lewis index (TLI), and the root mean square error of approximations (RMSEA). To check whether a three-factor model has a better fit than a one-factor (unidimensional) model, we compared the fit statistics of the two models and found that the three-factor model performs much better (Table 7): CFI and TLI are .910 and .865 respectively, showing a good fit; and the RMSEA is .059, which shows a modest fit. All three indices demonstrate the strength of the three-factor model over the one-factor model. The difference is all the more striking in the analysis using the subsample with complete data where the RMSEA for the one-factor model is not acceptable (.093) and neither the CFI (.834) nor TLI (.779) show a good fit, whereas the three-factor solution yields a good fit (RMSEA: .073; CFI: .910; TLI: .865) (Table S8).

[10] We also ran the models with asymptotic distribution free estimation, and the results remained the same.

## Validity and Reliability

We examined the convergent and discriminant validity of the measurement model, which are indicators for construct validity. Convergent validity indicates whether the items intended to measure the same construct are related, i.e. they converge to the same construct (Fornell and Larcker 1981; Hair et al. 2010). Discriminant validity is the degree to which one latent variable ("core determinism," for example) can be statistically differentiated from other latent variables (in our case, "category determinism" and "polygenism"). It shows whether the latent variable can explain more variance in the observed variables that are theoretically related to it than the measurement error or the other variables within the broader conceptual framework (Fornell and Larcker 1981).

To test the convergent and discriminant validity of the three scales, we calculated Composite Reliability (CR) (Bagozzi and Yi 1988; Fornell and Larcker 1981), the Maximum Shared Variance (MSV), and the Average Shared Variance (ASV). Discriminant validity is achieved when both Maximum Shared Variance (MSV) and the Average Shared Variance (ASV) are lower than the Average Variance Extracted (AVE) for all the constructs (Hair et al. 2010). We also checked the factor correlations and high correlations indicate that the constructs are not empirically unique enough and hence lacking discriminant validity.

The factor correlations were high (above .5, as shown in Table 8 and Table S9), and the three scales show partial convergent validity and low discriminant validity (Table 9 and Table S10). In the subsample with complete data (Table S10), category determinism has discriminant validity but the other constructs do not follow suit. Theoretically we expect that core determinism, category determinism, and polygenism are tapping different constructs, notwithstanding their resemblances. Yet the validity tests indicate that they correlate too strongly to pass the discriminant validity test. Based on this, we formed a

**Table 3** Principal component analysis results

| Components | Eigenvalues | Proportion of variance | Cumulative variance |
|---|---|---|---|
| 1 | 3.139350 | 0.348817 | 0.348817 |
| 2 | 1.229324 | 0.136592 | 0.485408 |
| 3 | 1.089892 | 0.121099 | 0.606507 |
| 4 | 0.895193 | 0.099466 | 0.705973 |
| 5 | 0.678876 | 0.075431 | 0.781404 |
| 6 | 0.598441 | 0.066493 | 0.847897 |
| 7 | 0.534773 | 0.059419 | 0.907316 |
| 8 | 0.468458 | 0.052051 | 0.959367 |
| 9 | 0.365694 | 0.040633 | 1 |

Note: The command used in Stata is "polychoricpca," hence the ordinal nature of the variable is recognized. Each principal component is a weighted linear combination of the original variables. The third column shows the proportion of variance explained. N = 525

theoretical expectation that a higher-order factor (genetic essentialism) may account for the observed correlations among the first-order factors in our model. To model this expectation, we specified a higher-order model to determine the extent to which a second factor accounts for the observed correlations among the first-order factors (Byrne 2005).

## Second-Order Factorial Models

Higher-order models examine whether there is an overarching construct that subsumes the first-order factors. Such models have been used for various psychological constructs (Black et al. 2015; DeYoung et al. 2007; Gotay et al. 2002; Taku et al. 2008; Tran et al. 2013), in communications research (Yale et al. 2015) and other fields. Because higher-order constructs may be mistaken for a unidimensional construct, a bit of clarification is in order. A higher-level construct contains the dimensions (first-order factors) extracted from the observed variables, and it is conceptually and statistically different from a unidimensional construct that is created by combining items into a single composite score (Koufteros et al. 2009). A unidimensional construct would absorb the distinct role each dimension plays in the overall construct, which would imply an underspecified model. Higher-order models, in contrast, relate each first-order factor derived from the observed variables to a second-order construct and estimate the respective coefficient for each one. In doing so, higher-order models take into account the relative significance or loading of each first-order factor in the second-order factor. Should there be multiple second-order constructs, they may be relating to a third-order construct, and so on (see also Gerbing et al. 1994). Especially when the first-order model reveals that there are multiple dimensions and that they are correlated, a higher-level model is particularly useful as it allows for estimating the contribution of each dimension to a higher-level construct. For example, core determinism, category determinism, and polygenism could load onto the broader construct of genetic essentialism differently, each with their distinct coefficients indicating the strength of correlation, effectively acting as weights. Second-order modeling allows us to preserve these multiple dimensions and take into account these weights for each dimension when estimating the score of genetic essentialism for each individual.

**Table 4** One-factor solutions

| | 9-item | | 8-item | |
|---|---|---|---|---|
| Variable | Factor1 | Uniqueness | Factor1 | Uniqueness |
| Athlete | 0.503 | 0.747 | 0.489 | 0.761 |
| Smart | 0.605 | 0.635 | 0.633 | 0.599 |
| Pure | 0.605 | 0.635 | 0.611 | 0.627 |
| PopDivide | 0.639 | 0.592 | 0.617 | 0.619 |
| GeneticsTells | 0.442 | 0.804 | 0.450 | 0.797 |
| Classify | 0.502 | 0.748 | 0.508 | 0.742 |
| RaceInvent [R] | 0.458 | 0.790 | | |
| AllAfrican [R] | 0.465 | 0.783 | 0.433 | 0.813 |
| Allshare [R] | 0.438 | 0.808 | 0.439 | 0.807 |

N = 525

Maintaining the three-factors derived from the nine items, we defined a second-order factor called "genetic essentialism," and had it load onto each of the first-order factors – core determinism, category determinism, polygenism – in a structural equation modelling framework (see Online Supplement for syntax). Results from the second-order model are presented in Fig. 3. Genetic essentialism as the higher-order construct loads very strongly onto the three first-order factors (factor loadings of .82, .86, and .79). Here, these coefficients can be interpreted as weights for each of the first-order factors. For example, core determinism is weighted by its factor loading of .82 in the second-order measure of genetic essentialism. The second-order factor performs much better in terms of validity and reliability. The composite reliability score for the second-order factor is .866 while it was around .50 for each of the first-order factors, and the convergent validity is established (see Table 9). The fit statistics are not of much help as the statistics of the second-order model are the same as the first-order model (correlated-factors models) because the total number of parameters estimated does not change. Yet, the indicators of validity are reassuring. We also have theoretical reasons to believe that a higher-order factor of genetic essentialism can explain the lower-order constructs. While beliefs about genes determining the traits or categories of people and beliefs about races evolving from distinct ancestral groups are conceptually distinct, it is compelling to expect that there is a common latent trait of genetic essentialism which the three first-order factors spring from.

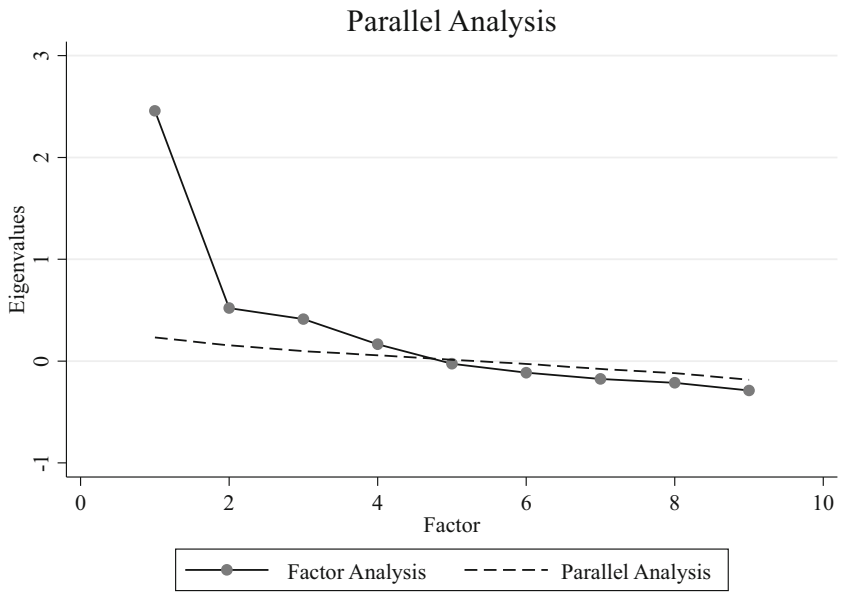


**Fig. 1** Parallel Analysis. Note: Eigenvalues are averaged over 100 replications. The figure is created with Stata software. Where the dashed line crosses the solid line indicates the highest number of factors to retain. N = 525

Hence we contend that the second-order model, our Genetic Essentialism Scale for Race (GESR), is superior. A higher order model is generally more advantageous because it is both more parsimonious and "can distinguish between residual error associated with prediction of the lower order factors by the second-order factor and measurement error associated with the observed variables" (Byrne 2005, p.27). In our case, it captures the overarching theoretical construct of genetic essentialism, while the measures of first-order factors can be used to identify its distinct but related dimensions.

## Construct Validity

To confirm the construct validity of the GESR, we tested the relationship between the GESR and measures directly relevant to social policy. Belief in genetic essentialism may have consequences for public support of policy initiatives that address social and structural barriers for racial minorities. Previous research has shown a positive relationship between beliefs in biological and cultural essentialism among dominant racial groups and opposition to affirmative action policies (Soylu Yalcinkaya et al. 2017). Here, we focused on affirmative action in college admissions, in government hiring and contracts, and general support for programs that help racial minorities get ahead. We hypothesized that the GESR would be similarly associated with opposition to affirmative action policies. We used multivariate regression to test the relationship between the GESR and opposition to race-based policies based on responses to three questions: 1) "In general, do you support or oppose programs that make special efforts to help racial minorities get ahead?" 2) "Thinking specifically about college admissions, do you support or oppose admissions committees considering the applicants' race?" and 3) "Thinking specifically about government jobs and contracts, do you support or oppose the government considering the applicants' race in hiring and contracts?" Responses for these social policy indicators were on a 5-point scale, ranging from strongly support to strongly oppose. We controlled for sociodemographic variables, including age, gender, educational attainment, region, political inclination,[11] and frequency of communication with racial minorities.[12]

Results showed that higher scores on the GESR were significantly and positively associated with opposing the consideration of race in proactive programs (β=.650, p<.001), in college admissions (β=.894, p<.001), and in government

**Table 5** Model comparisons of different factor solutions

| # of Factors | Log likelihood | Model df | AIC | BIC |
|---|---|---|---|---|
| 1 | −150.022 | 36 | 318.044 | 356.415 |
| 2 | −77.557 | 28 | 189.115 | 261.593 |
| 3 | −25.0380 | 21 | 98.076 | 200.398 |

Notes: In order to get AIC and BIC scores, we used maximum likelihood estimation method. Three-factor solutions are Heywood cases (invalid or boundary values of uniqueness). Nonetheless, the results confirm the parallel analysis and theoretical expectations. N = 525

*AIC* Akaike Information Criterion; *BIC* Bayesian Information Criterion

[11] Our measure of political inclination uses feelings thermometer questions on a scale from 0 to 10 to rate how favorable or warm respondents feel toward the Republican Party and toward the Democratic Party. Their response toward Democrats is subtracted from their response toward Republicans in this measure.

[12] Participants were asked how often they had a conversation with someone from a different racial group (Black, Asian, Hispanic/Latino, Middle Eastern/Arab, or Native American) in the past six months. Response options ranged on a 7-point scale from "not at all" to "every day." From these 5 variables, we created a variable of mean frequency of interracial contact with any of these racial groups in the past six months.

**Table 6** Three-factor solution

| | Core Determinism | Category Determinism | Polygenism | Uniqueness |
|---|---|---|---|---|
| Variable | | | | |
| Athlete | 0.559 | | | 0.660 |
| Smart | 0.719 | | | 0.470 |
| Pure | 0.425 | | | 0.614 |
| PopDivide | | 0.519 | | 0.522 |
| GeneticsTells | | 0.525 | | 0.696 |
| Classify | | 0.675 | | 0.579 |
| RaceInvent [R] | | | 0.619 | 0.738 |
| AllAfrican [R] | | | 0.531 | 0.632 |
| AllShare [R] | | | 0.395 | 0.699 |
| EIGENVALUES | 2.45 | 0.52 | 0.41 | |
| Explained Variance | 0.89 | 0.19 | 0.15 | |

Note: Estimation Method: Principal Factor Method. Rotation Method: Promax Oblique Rotation. Blanks represent factor loadings less than .30. The number in the cells for each factor indicates "Rotated Factor Loadings." Variances are post-rotation unique variances, factoring in the correlations among factors. N = 525

hiring and contracts (β=.610, p<.001) (Table S11). These findings support our hypothesis, and indicate construct validity for the GESR. Furthermore, these associations indicate that even when controlling for the effects of interracial contact, political inclination, and other sociodemographic factors, belief in genetic essentialism is associated with opposition to social policies intended to address racial inequality, and consequently, the belief

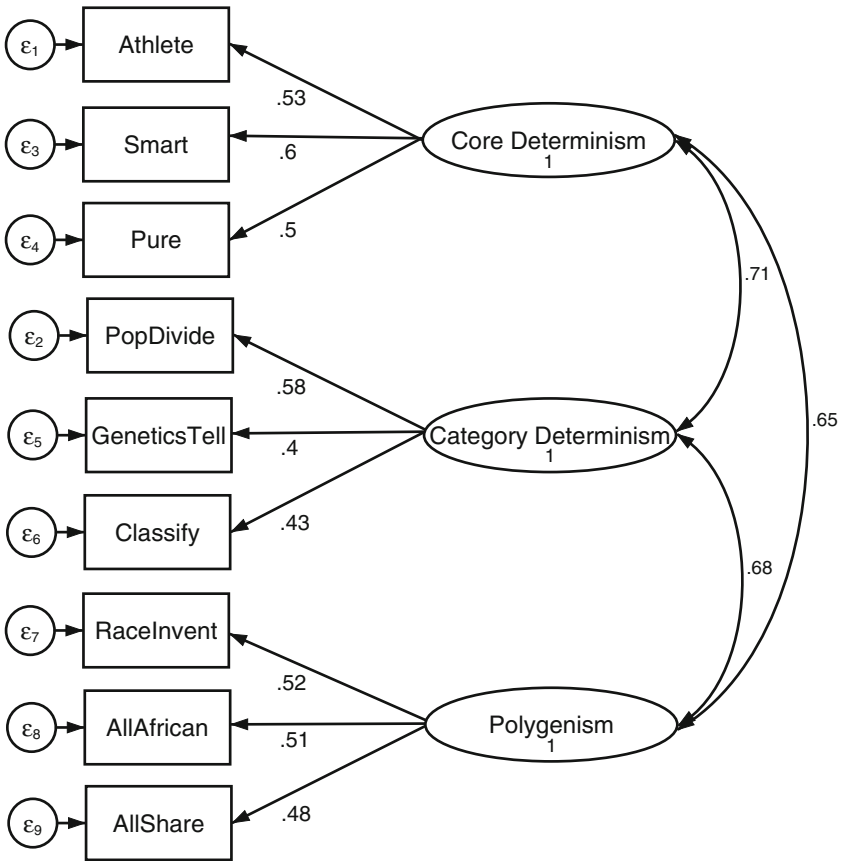


**Fig. 2** Confirmatory Factor Analysis Results with the Second Half of the Sample. Note: The loadings are standardized. Estimation method is maximum likelihood. The observed items are treated as interval data for ML. Variances of the latent variables are fixed at 1. All the loadings are significant (p < .001). The figure is created in the Structural Equation Modeling Builder in Stata. *N* = 537

**Table 7** Comparison of Fit between a one-factor and three-factor model in CFA

| Fit Statistics | One-factor model | Three-factor model | Cut-off for good fit |
|---|---|---|---|
| Comparative Fit Index (CFI) | 0.852 | 0.910 | CFI ≥0.90 |
| Tucker-Lewis Index (TLI) | 0.803 | 0.865 | TLI ≥ 0.90 |
| Root Mean Square Error of Approximations | 0.072 | 0.059 | RMSEA <0.08 |

Notes: Tucker-Lewis Index is also known as (Non) Normed Fit Index. See Hu and Bentler (1999) for reference to cutoff criteria. N = 537

system has practical implications for policy initiatives to stem the effects of structural racism.

## Discussion

People continue to endorse racial essentialism (Morning 2011; Tawa 2018; Williams and Eberhardt 2008). The well-cited finding of the Human Genome Project that all humans are 99.9% identical seems unlikely to stem those beliefs; if anything, the research and technologies the project has fostered may increase racial essentialism (Bolnick 2008; Fullwiley 2007; Ossorio and Duster 2005; Phelan et al. 2014; Phelan et al. 2013; Roberts 2011). Given the negative social consequences of racial essentialism (Bastian and Haslam 2006; Chao et al. 2013; Tawa 2016; Williams and Eberhardt 2008), it is important to understand how these beliefs may be influenced by the range of technologies, medicines, and tests the genomic revolution has fostered. Yet doing so is hampered by the lack of a scale that specifically focuses on genetic essentialism, rather than other forms of essentialist belief that may not be as strongly influenced by new genomic discoveries.

In this paper, we developed and validated a new scale that improves upon existing measures by 1) using items that specify genetic causes as responsible for essential group differences; 2) focusing on beliefs about race rather than assuming that genetic essentialist beliefs are consistent across different types of groups and characteristics; 3) recognizing and accounting for the multidimensionality of the construct; and 4) not focusing on specific races (e.g. Whites and Blacks), which renders it appropriate for studying beliefs about different racial groups and in different regional contexts. Furthermore, our study relies on original survey data gathered from a nationwide sample of 1069 native-born White Americans, and benefits from the insights of 115 earlier qualitative interviews. By developing new survey items based on those insights, we contribute to deeper theoretical understanding of the dimensions of genetic essentialist beliefs about race, as well as offering a practical solution for measuring the concept.

Our analysis, which uses 9-items, first revealed a three-factor measure, with factors which we call "core determinism," "category determinism," and "polygenism." After recognizing the high correlations and low discriminant validity in the factors, we used advanced modelling techniques to test for a second-order factor model. The data demonstrate that a second-order model with three-first order factors is superior to the correlated-factors (first-order factors) model in terms of validity and reliability. That is to say, our measure of genetic essentialism, the GESR, is a second-order construct representing the broader construct from which the three factors derive. It is different from a unidimensional model, as we showed, in that it accounts for the distinct contributions from each factor rather than treating each item or dimension equally.

Of the final nine items used in our scale, one item appeared to be volatile; RaceInvent had a high uniqueness score and it loaded onto polygenism in the median-replaced dataset yet onto category determinism in the dataset where the missing values were dropped, which renders it a possibly complex item. In other preliminary analyses (not shown), RaceInvent cross-loaded onto both factors. We examined the factor structure with and without RaceInvent and found out that the three-factor structure and the loadings do not change with omission of RaceInvent. We decided to keep it in the analysis to make sure we have three items per factor and also because of its theoretical relevance to the construct of genetic essentialism. Part of the volatility inherent in the variable RaceInvent may relate to its wording – "Races are groups societies invent" – which is broad and, when reverse coded, gets to the heart of what the different dimensions of genetic essentialism share, the belief that races are genetically determined at their core. One way to overcome the issue of volatility with this variable may be to use a statement that is more tailored to a specific

**Table 8** Correlations among the first-order factors

| Factor Names | Correlation Among Factors | | |
|---|---|---|---|
| | F1 | F2 | F3 |
| F1 = Core Determinism | 1 | | |
| F2 = Category Determinism | 0.578 | 1 | |
| F3 = Polygenism | 0.578 | 0.546 | 1 |

Note: The sample is the first half of the randomly split sample used for EFA. These correlations are produced by structural equation modeling where factors are loading onto items as shown in Table 6. $N = 525$

**Table 9** Validity tests

| | CR | MSV | ASV | AVE | Convergent Validity | Discriminant Validity |
|---|---|---|---|---|---|---|
| | | | | | CR > AVE | MSV < AVE |
| **Thresholds** | >.7 | | | >.5 | AVE > .5 | ASV < AVE |
| **First-Order Model** | | | | | | |
| **Factor** | | | | | | |
| Core Determinism | 0.559 | 0.505 | 0.465 | 0.298 | partially | no |
| Category Determinism | 0.466 | 0.505 | 0.487 | 0.228 | partially | no |
| Polygenism | 0.497 | 0.468 | 0.446 | 0.251 | partially | no |
| **Second-Order Model** | | | | | | |
| Genetic Essentialism | 0.866 | | | 0.678 | yes | |

Note: The tests are run using the factor loadings on the first-order factors from the CFA using the second random half, and loadings from the second-order model for the second-order factor. N = 537. We used the command 'condisc' for the validity tests (see Mehmetoglu 2015).

*CR* Composite Reliability; *MSV* Maximum Shared Squared Variance; *ASV* Average Shared Squared Variance; *AVE* Average Variance Extracted

dimension. As polygenism was left with only two items in our subsample analysis, we suggest that future work consider supplementing the GESR with one of Tawa's (2017) items from his "speciation" factor: "Each racial group has their own Adam and Eve, or their own ancestral parents." This item captures an important aspect of polygenist belief and including it may prevent the polygenism dimension from having insufficient items in some iterations. We suggest continuing to use RaceInvent, as adding the new item could crystallize the polygenism construct and allow RaceInvent to more strongly load onto category determinism.

To create the GESR in future analyses, researchers should use latent factor modeling (structural equation modeling) and specify the items in each factor to take its second-order

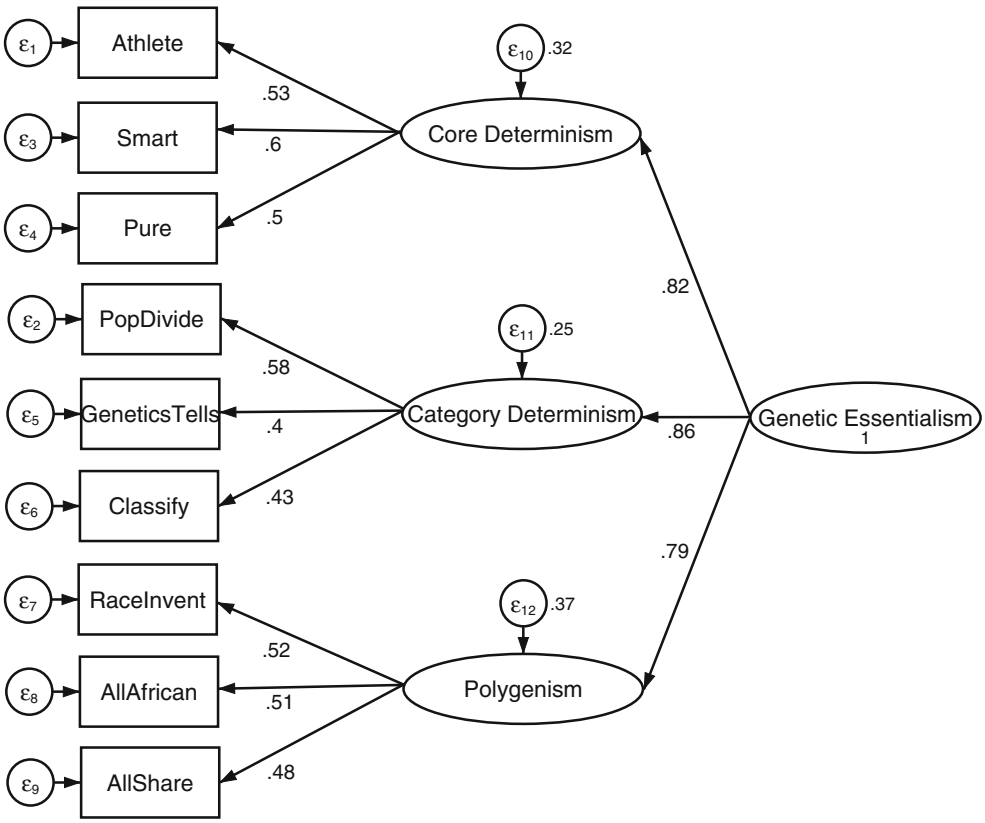


**Fig. 3** Second-Order Factorial Model Results on the Second Half of the Sample. Note: The loadings are standardized. Estimation method is maximum likelihood (ML). The observed items are treated as interval data for ML. Model Constraints: "core determinism" is anchored on "Athlete," "category determinism" is anchored on "PopDivide," "polygenism" is anchored on "RaceInvent," and "genetic essentialism" is anchored on "core determinism." All the loadings are significant ($p < .001$). The figure is created in the Structural Equation Modeling Builder in Stata. N = 537

structure into consideration.[13] Researchers should not assume that the dimensions (first-order factors) are interchangeable with the superordinate construct of genetic essentialism or that including them is optional (see Polites et al. 2012). Based on our analysis, we cannot recommend using the first-order factors separately as variables or as independent subscales because our data did not confirm their validity as first-order constructs; however, we encourage further assessment of their validity and reliability. Construct validity tests indicating that the three dimensions may operate differently despite their strong correlations, as well as theoretical distinctions among these dimensions, warrant additional testing of the first-order constructs.

A limitation of this study is the large number of cases with missing values on one or more of the key items that comprise genetic essentialism. We coded as missing "Don't Know" responses, which ranged from 9 to 30% on the 9 items we used in the scale. We addressed this issue using two strategies: 1) replacing the missing values with the median values, and 2) using the subset of cases where we have observations for every item in the analysis. Since both strategies yielded similar results in exploratory factor analysis, we proceeded with analysis using the sample where missing cases were replaced with the median values as it provides a larger sample, while we also showed the results with the subsample which did not have any missing data in the online supplement. We are confident in our findings because we were able to validate the factor structure in both the median-replaced data and the subsample with no missing values. However, the large number of missing values on these items suggests that some of them may be statements about which respondents do not feel knowledgeable. To future researchers who are planning to use the nine indicators we used to construct GESR, we recommend omitting the "Don't Know" option from the response choices. A 5-point Likert scale with a neutral option in the middle would likely provide higher quality data.[14]

Although we benefit from a large, nationwide sample, our study is limited to non-Hispanic White native-born Americans, and specifically to those who were willing to take genetic ancestry tests but had not done so. We hope that future research will apply this work in other contexts and test the validity of our scale with other samples.

The GESR is suited to empirically analyzing the impact of genomic research and technologies such as pharmacogenomics, direct-to-consumer genetic testing, and race-based and personalized medicines on conceptions of race. In addition to exposure to these technologies and products themselves, the GESR can be used to analyze the impact of mass media reporting of these innovations. The scale can also be used to examine whether genetic essentialist beliefs are a mediating factor between exposure to genomic research and social attitudes or behaviors, such as racial interactions, support for progressive social policies, and racial equality. We also hope the GESR can be validated in different national contexts so that it can be used in representative surveys comparing the extent of genetic essentialist beliefs about race around the world. Those who advocate for eliminating race questions from the census or other national surveys argue that doing so will promote racial equality and avoid reifying race (American Anthropological Association 1997; Fullilove 1998; Simon 2008); comparative research using the GESR can determine whether countries that eliminate race questions see lower rates of genetic essentialism. As research expands on the social impact of the genomic revolution, in the United States and around the world, we foresee many applications for research involving this scale.

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## Compliance with Ethical Standards

**Conflict of Interest** On behalf of all authors, the corresponding author states that there is no conflict of interest.

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[13] Please refer to the Online Supplement for how to generate the scale in a structural model.

[14] For further information on the number of categories in agree-disagree scales, see Revilla et al. (2014).

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