



Genetic and Environmental Influences on Biological Essentialism, Heuristic Thinking, Need for Closure, and Conservative Values: Insights From a Survey and Twin Study

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Abstract

Biological essentialism, the belief that human attributes are determined by biology, is a core component of essentialist thinking. Previous studies have shown that individual differences in essentialist thinking are associated with heuristic thinking, cognitive ability and style, conservative values, and prejudice. None, however, have examined whether biological essentialism is itself heritable, or the extent to which familial aggregation explains associations with core correlates. In order to do this, we analyzed data from a genetically informative sample of families with twins in Australia (N = 2,103), as well as general population samples from the UK (N = 501) and the US (N = 500). Genetic factors had little influence in individual differences in biological essentialism or in its relationship with heuristic thinking. Conservative values were genetically correlated with cognitive styles (i.e., need for closure and heuristic thinking). These findings support a bigger role of genes in explaining the relationship between cognitive processes and moral reasoning and ideology than they do the association between cognitive processes and essentialist thinking.

Keywords Biological essentialism · Motivated cognition · Heuristics · Moral foundations · Need for closure · Twin study

Introduction

Research and media coverage on the role of genetic factors in behavior has increased since the development of genome-wide association studies (GWAS) (Morosoli and Medland 2020). GWAS technology has also made possible the calculation of individual genetic scores, which could allow the development of genetically tailored pharmacological treatments and the screening of high-risk individuals for early intervention and prevention programs for many complex disorders (Wray et al. 2020). However, this information could influence how people understand their behavior, as well as

trigger worrying thoughts about prognosis, discrimination, or reproductive decisions (Haslam and Kvaale 2015; Lebowitz and Ahn 2017; Meiser et al. 2020). When behavior is thought to be influenced by genetic factors, people tend to: (i) view such behavior as immutable and determined; (ii) disregard non-genetic causal explanations; (iii) perceive exaggerated genetic differences between groups; and (iv) perceive partially genetically determined behaviors as natural, and therefore more acceptable (Dar-Nimrod and Heine 2011; Lynch and Griffiths 2018).

Genetic essentialism theory proposes that these negative consequences originate from essentialist biases (Dar-Nimrod and Heine 2011; Lynch et al. 2018). According to the genetic essentialism theory, people have a core cognitive predisposition to see different categories (e.g., “cats”, “Spaniards”, “elite athletes”, “lemons”) as having underlying *essences*. These essences are perceived as the true nature of something or someone which makes them what they are, even if we cannot observe them. This tendency is known as *psychological essentialism* (Gelman 2003; Medin and Ortony 1989) and given its ubiquity it is argued to be a functional universal (i.e., a core mental attribute shared by humans everywhere), even if it is endorsed to a different degree by

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different cultures (Haslam 2017; Heine and Proulx 2017). Under this framework, *genetic essentialism* (also known as *biological essentialism*) could be explained as a specific case of psychological essentialism where genes act as a placeholder for the essence. More broadly, the belief that human attributes are rooted in biology (i.e., are “natural”), instead of the product of socialization or the interaction between biological and environmental factors, is considered a key component of essentialist thinking (Bastian and Haslam 2006). Furthermore, people who endorse genetic essentialist beliefs are more likely to report racist and sexist behavior, pessimistic thoughts about expected recovery from a disease, and sympathy for eugenic practices (for a review of examples and consequences of genetic essentialist biases, see Heine et al. 2017). At this point we should clarify that the present study and the research cited so far, focus on the systematic bias to essentialize categories and not on the existence or not of actual essences. Especially in the context of biological essences, the belief that any complex human behavior is solely *determined* by the genes is erroneous. In order to better understand the causes of individual differences in essentialist biases, in the present study we aim to evaluate the relative contribution of genetic and environmental influences to not only individual differences in biological essentialism, but also to the covariance between biological essentialism and several constructs that have been previously associated with it in the literature. In the following sections we review some of the theories behind essentialist thinking and its relevance for our understanding of cognitive biases and beliefs about genetics.

Heuristic biases and motivated cognition

Heuristics are automatic, unconscious, rapid, belief-based, or low-effort mental shortcuts used to provide quick answers to complex problems or questions (Cimpian and Salomon 2014; Evans 2008). Cimpian and Salomon (2014) argued that psychological essentialism could emerge from the intuitive knowledge provided by an *inherence* heuristic, a cognitive bias that makes people look for internal explanations of human behavior. They argue that a heuristic bias towards internal explanations could gradually develop during life into fully elaborated essentialist stances, such as psychological essentialism, or genetic essentialism. Their hypothesis could in part explain findings that that essentialist thinking is associated with general intelligence, creativity, and need for closure (Cimpian and Salomon 2014). Need for closure, in particular, which is defined as the desire for simple and unambiguous answers, has been proposed to be the key psychological construct underlying essentialist biases: need for closure would motivate essentialist thinking, which in turn

could give rise to stereotyping and prejudice (Roets 2017; Roets and Van Hiel 2011a).

An alternative hypothesis is that people could be biased towards internal explanations of behavior because of personal preferences or motivation (i.e., a product of motivated cognition). That is, people can be motivated to arrive at specific, desired conclusions when evaluating evidence (Chen et al. 1999; Kunda 1990). For example, essentialist thinking might be used by conservative groups to justify and maintain pre-existing social systems of inequality and oppression (Jost and Orsolya 2005), or members of a group with a higher social status may invoke essentialism strategically in order to protect their social status or defend the existing social system (Brescoll et al. 2013; Morton et al. 2009). The motivated cognition hypothesis could explain why higher endorsement of biological essentialism is associated with more conservative values (Keller 2005), and why participants have different genetic explanations of human characteristics (i.e., race, class, individual differences, and sexual orientation) depending on their political ideology (Suhay and Jayaratne 2012). In particular, liberals tend to explain racial inequality as being the result of the environment (e.g., discrimination) whereas conservatives are more likely to see inequality as the result of stable genetic differences (Morin-Chassé et al. 2017). Interestingly, essentialist thinking, conservatism, and inherence heuristic scores have been associated with need for closure (Cimpian and Salomon 2014; Jost et al. 2003; Rhodes and Gelman 2009; Roets and Van Hiel 2006), which raises the question of how these constructs interact with each other, and whether associations are accounted for by heritable or environmental factors.

The present study

Previous research shows that genetic factors explain to some extent the variance in individual differences in most of the constructs reviewed above. The heritability of the cognitive reflection test, a measure of tendency to commit heuristic errors, has been estimated at 61.0% (Itamar and Aner 2011). In the case of need for closure, previous studies estimate the heritability at 36.6% and suggest that the relationship between need for closure and political ideology is mostly due to genetic factors (Ksiazkiewicz et al. 2016). In relation to conservative values, as measured by binding foundations (i.e., how important in-group loyalty, obedience to authority, and the enforcement of purity sanctions are when individuals produce moral judgements), their heritability estimates range between 6 and 22% (Smith et al. 2017). Lastly, several studies have studied the role of genetic influences in prejudiced behavior and have found that genetic factors have a marked and consistent influence on prejudice with heritability estimates ranging between 20 and 50% in various prejudicial

attitudes (Barlow and Zietsch 2016). We did not find any published studies on the genetics of essentialist thinking.

While there is much debate around the pathways through which essentialist thinking, cognitive styles, and prejudice are connected (i.e., through biologically influenced general tendencies, or through environmental factors) to date no study has evaluated the genetic and environmental contributions to the relationship between them. Therefore, the present study has two objectives: (i) to test whether essentialist thinking is associated at a phenotypic level with tendency to engage in heuristic thinking, the need for closure, conservative values, and prejudice; and (ii) to evaluate the contribution of genetic and environmental factors to the relationship between these five constructs. Given the higher heritability of tendency to commit heuristic errors, in particular, and cognitive traits in general (Polderman et al. 2015), we would expect a significant contribution of genetic factors to the variability in essentialist thinking, along with significant genetic correlations between essentialist biases and heuristic thinking. This would also support the possibility of common biological pathways between these cognitive biases.

To this end, we collected data from a genetically informative sample of families with twins in Australia, as well as from general population samples from the UK and the US. First, we conducted an exploratory factor analysis in the UK and US samples to evaluate the dimensionality of the questionnaires selected to test these objectives. The factor structure was then replicated using confirmatory factor analysis in the twin sample. This led to the formulation of our phenotypic or measurement model, where phenotypic correlations were estimated to evaluate the first objective of the study. Second, we conducted a twin study in the Australian twin sample and estimated the role of genetic and environmental factors in the variation between these five constructs. This constitutes our genetic or structural model. In summary, in this study we aim to provide insight into the factors associated with individual differences in essentialist thinking, conservative values (operationalized as binding foundations), cognitive styles (i.e., tendency to commit heuristic errors, and need for cognitive closure), and genetic prejudice, operationalized as prejudice towards a partner with high genetic predisposition for a mental health condition. In doing so, we aim to elucidate the extent to which, within our sample, essentialist thinking and its correlates are explained by genetic and environmental factors.

Methods

Participants

Participants were recruited from families that had already participated in genetic research studies at QIMR Berghofer, Australia (N=2,103), and from (ii) the general population from the UK (N=501) and the US (N=500), recruited via Prolific Academic:

- (i) Participants from QIMR Berghofer were part of the Brisbane Longitudinal Adolescent Twin Study (BLATS; Wright and Martin 2004). The BLATS study began in 1992 and has been successively recruiting 12-year-old twins and their parents. They have participated in studies on the genetics of a wide range of health conditions, including psychiatric disorders. For the present study, surveys were sent to 2,236 families, of which 1,686 had at least one family member providing data.
- (ii) Participants residing in either UK or US and having fluent in English were selected via Prolific Academic, an online platform for subject recruitment that has been shown to produce high quality data from a diverse range of population (Palan and Schitter 2018). Participants were offered £4.35 for their time (the estimated duration of the survey was 40 min). There was no other selection criteria and participants entered the study on a first-come first-served basis.

The number of participants varied across different analyses due to missing data. The survey was distributed online, therefore all participants were computer literate and had access to an internet connection. Frequency data for the main demographic variables are summarized for the three samples in Table 1. All participants provided informed consent at the beginning of the survey. The Human Research Committee of QIMR Berghofer Medical Research Institute and the Human Research Ethics Committee of the University of Queensland provided approval of this study (approval numbers: P2227 and JM03024).

Measures

This study was part of a larger research project on public understanding of genetics (see Morosoli and Medland 2021). For the present study, five measures were used. A copy of them can be found in Online Appendix A.

Table 1 Description of samples based on a selection of demographic variables

| | Australia (N=2103) | United Kingdom (N=501) | United States (N=500) |
|---------------------------------------|-----------------------|------------------------------|-----------------------------|
| Age range (%) | | | |
| 15–24 | 31.1 | 22.3 | 26.0 |
| 25–34 | 44.6 | 30.9 | 35.4 |
| 35–44 | 23.0 | 17.4 | 21.0 |
| 45–54 | 0.1 | 13.8 | 9.4 |
| 55–64 | 0.8 | 12.8 | 5.0 |
| 65+ | 0.3 | 2.8 | 3.2 |
| Gender (%) | | | |
| Female | 62.6 | 62.9 | 47.6 |
| Male | 37.4 | 37.1 | 52.4 |
| Highest educational degree (%) | | | |
| Compulsory education* | 6.1 | 2.8 | 1.6 |
| Senior high school | 11.9 | 21.4 | 33.0 |
| Certificate or diploma | 26.2 | 24.1 | 17.8 |
| Undergraduate degree | 37.4 | 35.1 | 36.0 |
| Postgraduate degree | 18.3 | 16.6 | 11.6 |
| Political orientation** (%) | | | |
| Extremely left-wing | N/A | 3.7 | 13.1 |
| Left-wing | N/A | 21.7 | 24.7 |
| Somewhat left-wing | N/A | 25.4 | 20.2 |
| Centrist | N/A | 28.5 | 21.5 |
| Somewhat right-wing | N/A | 13.0 | 10.2 |
| Right-wing | N/A | 7.0 | 8.2 |
| Extremely right-wing | N/A | 0.6 | 2.0 |

* Primary and high school up to senior secondary school

** Political orientation data was not collected for Australian sample

Biological basis of behavior scale

Endorsement of biological essentialism was assessed using the biological basis of behavior scale (Bastian and Haslam 2006). The scale is composed of eight items (e.g., “The kind of person someone is can be largely attributed to their genetic inheritance”), evaluated on a 6-point Likert scale that range from *Strongly disagree* to *Strongly agree* with no neutral option.

Cognitive reflection test

Participants’ tendency to commit heuristic errors was measured with the Cognitive Reflection Test (CRT; Frederick 2005). This test contains three questions (e.g., A bat and a ball cost \$1.10 in total. The bat costs \$1.00 more than the ball. How much does the ball cost?) which are designed to trigger an “intuitive” answer (\$0.10) while the correct answer requires more cognitive effort (\$0.05). The number of correct responses indicates the tendency to rely on

deliberative rather than heuristic thinking (Frederick 2005). This variable was considered ordinal for analytic purposes.

Need for closure scale

Need for closure was measured using the 15-item version of the need for closure scale (Roets and Van Hiel 2011b). This scale includes items such as “I dislike questions which could be answered in many different ways”, or “I feel uncomfortable when I don’t understand the reason why an event occurred in my life”. Each item is evaluated on a 6-point Likert scale that ranges from *Completely disagree* to *Completely agree* and we used the sum score of the scale.

Binding foundations

Napier and Luguri (2013) proposed that 18 out of the 30 items from the Moral Foundations Questionnaire (Graham et al. 2011) could be grouped into one overarching moral drive, *binding foundations*, which in turn is strongly associated with self-identified conservatism (Strupp-Levitsky and Jost 2020). Binding foundation scores are obtained by aggregating items that measure values related to in-group loyalty and patriotism (e.g., “People should be loyal to their family members, even when they have done something wrong”), obedience to authority (e.g., “Respect for authority is something all children need to learn”), sanctity and natural order (e.g., “I would call some acts wrong on the grounds that they are unnatural”). In the Moral Foundations Questionnaire, respondents indicate how relevant each statement is for them when they decide whether something is right or wrong (from *Not at all relevant* to *Extremely relevant*), and how important it is for them when making decisions (from *Strongly disagree* to *Strongly agree*), on a 6-point Likert scale. We used bindings foundations to measure conservative values.

Prejudice

Participants were asked if they agreed or disagreed (i.e., two response options) with the following statement: “I wouldn’t choose a partner who has a strong genetic predisposition for T”, where T could be *alcohol dependence*, *depression*, or *schizophrenia*. Responses to the three questions were combined into a sum score that ranged from 0 to 3. This variable was considered ordinal for analytic purposes.

Statistical analysis

Phenotypic study

We computed factor scores after assessing dimensionality for biological basis of behavior scale, need for closure scale,

and binding foundations items instead of analyzing sum scores, following recent recommendations on questionnaire scoring (McNeish and Wolf 2020). Due to their low number of indicators, factor analysis was not conducted for cognitive reflection test scores and prejudice towards a partner (Hair and Anderson 2018). However, their internal consistency was evaluated using Cronbach's alpha and sum scores were computed. The dimensionality of biological basis of behavior scale, need for closure scale, and binding foundations items was evaluated in the following way:

- (i) Exploratory factor analysis (EFA). EFA was conducted using the psych R-package (Revelle 2020) in the samples from general population for each questionnaire independently, with oblimin rotation and maximum likelihood estimation. Suitability of the data for factor analysis was evaluated using the KMO measure and Bartlett's test (Bartlett 1937; Dziuban and Shirkey 1974). The optimal number of factors was evaluated using the scree test, parallel analysis, Velicer's MAP, Kaiser's criterion, and the VSS test (Horn 1965; Revelle and Rocklin 1979; Velicer 1976). The number of factors retained was the average number of factors recommended across dimensionality criterions. Only items with factor loadings higher than 0.50 were retained for any given factor.
- (ii) Confirmatory factor analysis (CFA). The factor structure identified in the EFA was tested in the twin sample. In order to avoid bias due to dependency of scores (Rebollo et al. 2006), CFA was conducted in OpenMx (Neale et al. 2016) which allows the use of full-information maximum likelihood to analyze data from relatives. Goodness of fit was evaluated using RMSEA, TLI, and BIC indices for each model (Akaike 1987; Hu and Bentler 1999).
- (iii) Factor scores were computed for each construct using maximum likelihood in OpenMx (Neale et al. 2016).

For our first objective, several models were tested. First, the effect of age, gender, and their interaction was regressed out from the observed scores via a linear regression using the FIML method in OpenMx. Subsequently, phenotypic correlations were calculated using the residual scores. Correlations across measures were calculated after testing if means, variances, and covariances could be constrained to be equal across twin order and twin order and zygosity. Correlations between constructs were computed in OpenMx (Neale et al. 2016). The polytomous items evaluating partner choice (four possible scores from 0 to 3) and the cognitive reflection test scores (same response range) were analyzed using a liability-threshold model (Rijsdijk and Sham 2002) and polychoric correlations were calculated. The significance of coefficients was evaluated using likelihood-based

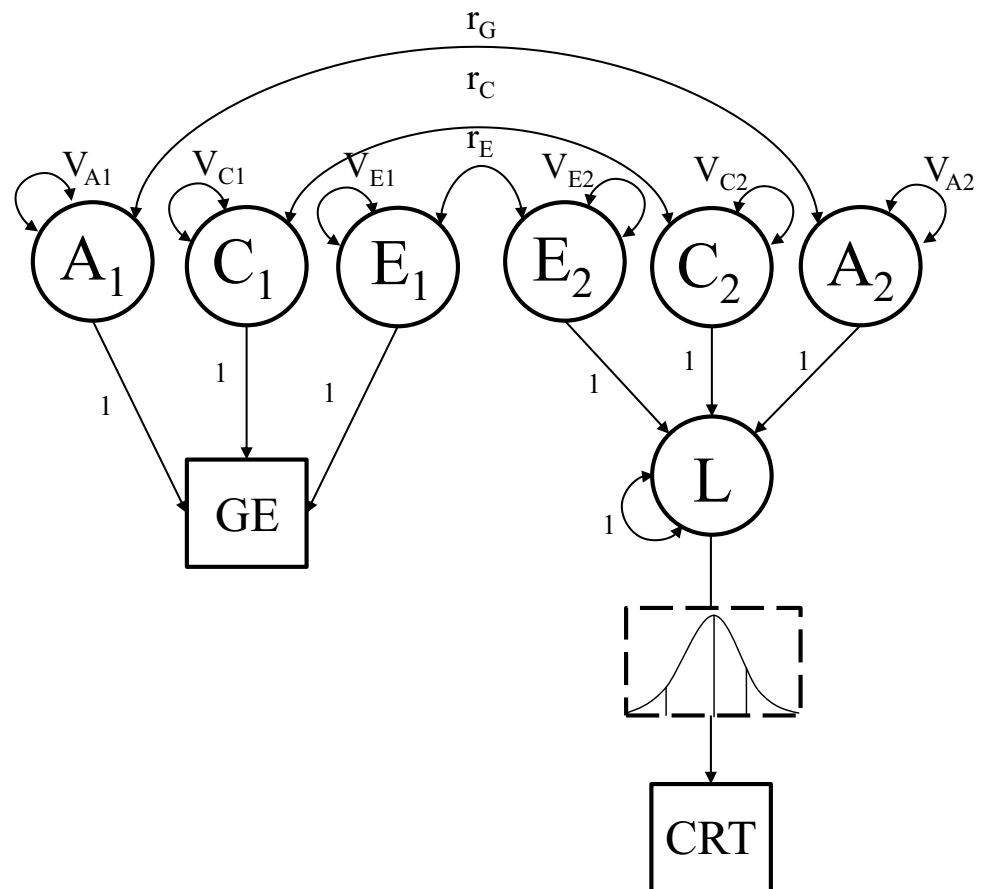
95% confidence intervals (Neale and Miller 1997). Data preparation, as well as descriptive and preliminary analysis, were conducted in R v4.0.3 (R Core Team 2020).

Genetic study

For our second objective, within-trait and cross-trait cross-twin correlations were estimated within a model where variances and means were constrained to be equal across zygosity groups. Twin zygosity was determined using genome-wide genotyping (95% of participants) while a standardized questionnaire was used for the remaining 5% of participants, with an accuracy of approximately 98% (Heath et al. 2003). The appropriateness of multivariate genetic modelling was evaluated based on three criteria: (i) the phenotypic correlation between two given phenotypes was statistically significant from zero and higher than 0.10; (ii) the cross-twin cross-trait correlation for MZ pairs was higher than for DZ pairs; and (iii) the cross-twin cross-trait correlation in MZ pairs was significantly different from zero. These requisites ensure that there is a meaningful covariance to decompose and that the constructs are influenced by genetic or family factors to some extent, which is an underlying assumption of the classical twin design.

Bivariate genetic models were fit to each pair of measures that met these requirements (9 bivariate analyses in total). Given that no specific causal order between variables was hypothesized, we estimated a correlated factors model that does not assume ordering of the variables (Loehlin 1996; see Fig. 1). Structural Equation Models (SEM) were fitted to raw data using full information maximum likelihood (FIML) with the R-package OpenMx v2.18.1 (Neale et al. 2016). All genetic models using the direct variance method (Verhulst et al. 2019). V_C was not modelled when r_{DZ} was less than half of r_{MZ} . In those cases, V_D was modelled instead. In addition, V_D was only modelled if V_A was significantly different from zero. In the cases where only V_D was significantly different from zero, V_D was dropped from the model and only V_A was estimated instead, since significant dominance genetic variance in the absence of additive genetic variance is highly unlikely (McGue and Christensen 1997). Goodness of fit was evaluated by comparing the genetic model against a saturated model using a log-likelihood ratio test (LRT) and by evaluating the RMSEA and TLI indices of each model (Akaike 1987; Hu and Bentler 1999). The accuracy of the obtained parameters was assessed using likelihood-based 95% confidence intervals (Neale and Miller 1997). We direct the reader to Barlow (2019) for a very accessible review on the use of twin studies for psychological research and its basic assumptions.

Fig. 1 Path diagram of the bivariate model with the latent factors A, C, and E and their influence on the liability (L) to cognitive reflection (CRT), as modeled in the liability-threshold model, and on genetic essentialism (GE). Variables in circles represent latent variables or factors. Variables in boxes represent observed (measured) variables. Single-headed arrows (paths) represent causal relationship between the latent and observed variables. Double-headed arrows define correlations between variables



Results

Phenotypic study

Bartlett's test for sphericity and Measure of Sampling Adequacy suggested that EFA was appropriate for the biological basis of behavior scale, the need for closure scale, and the binding foundations items in the combined UK and US sample. EFA showed that a 2-factor structure had the best fit for the three questionnaires:

The two factors extracted for the *biological basis of behavior scale* separated positively-worded items (4 indicators) and negatively-worded items (4 indicators). We interpret the first factor as 'degree to which someone believes that there are kinds of people and these are genetically determined' and we will refer to this factor as *genetic essentialism*. Items in the second factor referred to the 'degree to which someone rejects the idea of any genetic influence on any human trait' and we will refer to this factor as *genetic indeterminism*.

The two factors in the *need for closure scale* grouped items measuring close-mindedness, and dislike for ambiguity and unpredictability (9 indicators), labelled *need for*

predictability, and items measuring need for order and routine (3 indicators), or *need for order*. Factor loadings of three items of the need for closure scale were below the 0.50 cut-off and were excluded from subsequent analyses. Most *binding foundations items* loaded into one factor, labelled conservative values, which included items measuring respect for authority, patriotism, and traditional values (9 indicators). The second factor (2 indicators) grouped two items measuring the importance of being loyal to the group. This factor was dismissed as the number of indicators was below the minimum recommended for factor analysis (Hair et al. 2018). There were also six items with factor loadings below the 0.50 cut-off which were excluded from subsequent analyses. A complete list of which items loaded into which factors and detailed results from factor extraction can be found in Appendix B.

Factor structure was then replicated using CFA in the twin sample. Factor structure of biological basis scale and need for closure scale showed identical goodness of fit (CFI = 0.93, TLI = 0.92 and RMSEA = 0.04), while the factor structure of binding foundations showed only marginal fit to the data (CFI = 0.81, TLI = 0.78 and RMSEA = 0.06). As

Table 2 Phenotypic correlation matrix across all measures

| | Genetic essentialism (1) | Genetic indeterminism (2) | Need for predictability (3) | Need for order (4) | Conservative values (5) | Cognitive reflection test (6) | Prejudice (7) |
|-----|---------------------------------|---------------------------------|---------------------------------|---------------------------|---------------------------------|-------------------------------|-----------------------|
| (1) | 1 | − 0.64 [− 0.68, − 0.60] | 0.15 [0.09, 0.21] | 0.19 [0.13, 0.25] | 0.47 [0.42, 0.51] | − 0.23 [− 0.29, − 0.17] | 0.11 [0.05, 0.17] |
| (2) | − 0.24* [− 0.24, − 0.19] | 1 | 0.05 [0.02, 0.11] | 0.07 [0.01, 0.13] | 0.12 [0.06, 0.18] | − 0.06 [− 0.12, 0.00] | 0.09 [0.03, 0.15] |
| (3) | 0.19* [0.13, 0.22] | 0.07 [0.03, 0.12] | 1 | 0.66 [0.62, 0.69] | 0.22 [0.16, 0.28] | − 0.08 [− 0.14, − 0.02] | 0.13 [0.07, 0.19] |
| (4) | 0.15* [0.11, 0.20] | 0.03 [− 0.01, 0.08] | 00.50* [00.46, 00.53] | 1 | 0.32 [0.26, 0.37] | − 0.14 [− 0.20, − 0.08] | 0.13 [0.07, 0.19] |
| (5) | .22* [0.17, 0.26] | 0.08 [0.03, 0.13] | 00.16* [00.11, 00.20] | 0.20* [0.15, 0.24] | 1 | − 0.30 [− 0.35, − 0.24] | 0.20 [0.14, 0.26] |
| (6) | − .10* [− 0.16, − 0.05] | − 0.10* [− 0.12, − 0.04] | − 0.11* [− 0.16, − 0.06] | − 0.06 [− 0.11, − 0.01] | − 0.25* [− 0.30, − 0.20] | 1 | − 0.06 [− 0.12, 0.01] |
| (7) | 0.16* [0.11, 0.22] | 0.00 [− 0.05, 0.05] | 0.12* [0.07, 0.17] | 0.09 [0.04, 0.15] | 0.16* [0.11, 0.22] | − 0.09 [− 0.16, − 0.03] | 1 |

Phenotypic correlations across phenotypes in the twin sample presented below the diagonal and in the combined UK and US sample above the diagonal. Correlations were corrected for age, gender, and their interaction. 1 = genetic essentialism; 2 = genetic indeterminism; 3 = need for predictability; 4 = need for order; 5 = conservative values; 6 = cognitive reflection test; 7 = prejudice towards a partner with high genetic predisposition for mental health condition

* In bold, phenotypic correlations that met our criteria for genetic modelling

a final step, factor scores were computed for those participants with less than 20% missing data within questionnaire. Finally, Cronbach's alpha for cognitive reflection test and prejudice in the combined UK and US sample was 0.76 and 0.78, respectively, while in the twin sample reliability values were 0.73 and 0.81.

Next, phenotypic correlations across all constructs were computed (see Table 2). Most phenotypic correlations in the twin sample were significantly different from zero. Correlations ranged in magnitude from − 0.06 [− 0.11, − 0.01], between cognitive reflection and genetic essentialism, to − 0.25 [− 0.30, − 0.20] between conservative values and cognitive reflection. Correlations were lower in the twin sample than in the general population sample on average. In the twin sample, at least one factor of each construct was significantly correlated with the other measures. Genetic essentialism was significantly associated with every other construct. Need for predictability was significantly correlated with every construct, except genetic indeterminism. Conservative values were associated with all construct except genetic indeterminism. Finally, cognitive reflection test scores were significantly correlated with all the other measures except for need for order, and prejudice. Out of the 21 combinations of two traits, 14 were statistically significant from zero in the twin sample (in bold and with an asterisk in Table 2) and were further evaluated for the genetic study.

Genetic study

Assumption testing

Data was available for 2103 twins. The *minimum* number of complete twins for any given analysis was 493 twin pairs (229 MZ pairs, and 264 DZ pairs) and 841 unpaired individual twins (315 MZ participants, and 526 DZ participants). There was no evidence of statistically significant differences in thresholds, means, or variances across twin order or zygosity. MZ and DZ intra-twin correlation patterns suggested that an ADE model would fit all phenotypes best except for conservative values, where correlation patterns did suggest influence of V_C . Within-trait and cross-trait twin correlations for MZ and DZ pairs can be found in Table 3. Based on the cross-twin cross-trait correlations, bivariate genetic analyses were only conducted for 9 out of the 14 combinations of traits. That is, genetic factors did not explain the association between genetic essentialism and cognitive reflection test scores, need for predictability, and prejudice, neither did they explain the association between cognitive reflection test scores and prejudice.

Twin models

At the univariate level, the seven constructs showed some degree of genetic influence, with cognitive reflection test scores showing the strongest genetic influence ($V_A = 59\%$) and genetic essentialism showing the weakest ($V_A = 17\%$). The low genetic influence on genetic essentialism along with

Table 3 Cross-twin cross-trait correlations for each combination of measures and within-trait correlations

| Cross-twin cross-trait correlations | | | | | | | |
|-------------------------------------|--------------------------|---------------------------|-----------------------------|---------------------|-------------------------|-------------------------------|-----------------------|
| | Genetic essentialism (1) | Genetic indeterminism (2) | Need for predictability (3) | Need for order (4) | Conservative values (5) | Cognitive reflection test (6) | Prejudice (7) |
| 1 | – | – 0.03 [– 0.04, 0.05] | 0.10 [0.02, 0.18] | 0.06 [– 0.02, 0.14] | 0.21 [0.13, 0.28] | – 0.10 [– 0.18, – 0.02] | 0.17 [0.07, 0.26] |
| 2 | – 0.15 [– 0.22, – 0.07] | – | | | | – 0.16 [– 0.24, – 0.07] | |
| 3 | 0.09 [0.01, 0.12] | | – | 0.26 [0.17, 0.34] | 0.08 [0.01, 0.16] | – 0.11 [– 0.19, – 0.03] | – 0.02 [– 0.12, 0.08] |
| 4 | 0.08 [0.00, 0.17] | | 0.03 [– 0.06, 0.12] | – | 0.16 [0.08, 0.23] | | |
| 5 | 0.05 [– 0.04, 0.13] | | 0.02 [– 0.06, 0.10] | 0.03 [– 0.06, 0.11] | – | – 0.25 [– 0.32, – 0.18] | 0.03 [– 0.05, 0.12] |
| 6 | – 0.12 [– 0.21, – 0.03] | 0.05 [– 0.04, 0.13] | – 0.07 [– 0.16, 0.01] | | – 0.12 [– 0.21, – 0.11] | – | |
| 7 | 0.10 [0.00, 0.19] | | 0.04 [– 0.06, 0.13] | | 0.09 [– 0.01, 0.19] | | – |
| Within-trait correlations | | | | | | | |
| | 1 | 2 | 3 | 4 | 5* | 6 | 7 |
| MZ | 0.19 [0.07, 0.30] | 0.15 [0.02, 0.26] | 0.32 [0.20, 0.42] | 0.36 [0.25, 0.45] | 0.56 [0.52, 0.57] | 0.63 [0.53, 0.72] | 0.38 [0.22, 0.52] |
| DZ | 0.04 [– 0.07, 0.16] | 0.06 [– 0.04, 0.17] | 0.11 [0.00, 0.22] | 0.09 [– 0.03, 0.20] | 0.37 [0.27, 0.46] | 0.17 [0.04, 0.30] | 0.16 [0.00, 0.33] |

Top panel: Cross-trait correlations for MZ pairs presented above the diagonal and below the diagonal for DZ pairs. Bottom panel: within-trait correlations. Shaded cells indicate combinations of phenotypes where there was no evidence of genetic influence in their covariance

* Only conservative values indicated influence of shared-environmental factors

no influence of shared-environment suggests that individual differences in these beliefs (within the current population) are mostly due to the participants' unique experiences. In general, the genetic correlations were moderate to high while the environmental correlations were low, with the exception of need for predictability and need for order (see Table 4). We found significant genetic and environmental correlations between genetic essentialism and (i) the need for predictability; (ii) conservative values; and (iii) prejudice, which points towards shared sources of genetic and environmental variation, which could also be consistent with a causal relationship between a genetic tendency towards essentialist thinking and those variables (De Moor et al. 2008). These correlations were positive, indicating that factors associated with higher endorsement of genetic essentialism are associated with more conservative values and prejudice in the context of mental health genetics. We also found significant genetic and environmental correlations between conservative values and need for predictability, and a significant genetic correlation between conservative values and cognitive reflection test scores. This correlation was negative, indicating that tendency to commit heuristic errors and conservative values might share genetic pathways, and that the factors associated with committing *less* heuristic errors would be associated with endorsing *less* conservative values.

Genetic bivariate models showed good fit: RMSEA values were between 0.00 and 0.01, TLI values between 0.97 and 1, and the LRT did not show differences between the saturated model and the fitted model. Variance components, correlations, and percentage of variance explained by each component for the nine bivariate comparisons are also presented in Table 4.

Discussion

Summary

In this study, we estimated the genetic and environmental contributions to individual differences in biological essentialism, a core facet of essentialist thinking. In addition, we also estimated the genetic and environmental contributions to the relationship between essentialism and heuristic thinking, need for closure, conservative values, and prejudice. By using genetically informative data, we were able to provide some information about which of these variables are influenced by genetic factors and whether they share a proportion of their genetic or environmental pathways. The first main finding of this study is that we confirmed that genetic essentialism is associated with specific components of need for

Table 4 Standardized variance components and genetic and environmental correlations from best fitting bivariate twin model between phenotypes. Variance components on the diagonal (shaded). Genetic (r_A) and environmental correlations (r_E) on the lower triangle of the

matrices. Proportion of variance explained by either genetic factors or unique environmental factors presented on the upper triangle of the matrices

| A | Genetic essentialism (1) | Genetic indeterminism (2) | Need for predictability (3) | Need for order (4) | Conservative values (5) | Cognitive reflection test (6) | Prejudice (7) |
|-----|--------------------------|---------------------------|-----------------------------|--------------------|-------------------------|-------------------------------|-------------------|
| (1) | 0.17 [0.10, 0.28] | | 67.0% [24.0, 100] | | 84.8% [54.9, 100] | | 91.8% [69.0, 100] |
| (2) | | 0.17 [0.06, 0.27] | | | | 95.4% [64.9, 100] | |
| (3) | 0.55 [0.19, 1.0] | | 0.31 [0.20, 0.36] | 44.5% [28.0, 59.4] | 56.8% [13.3, 94.8] | 83.5% [56.3, 100] | |
| (4) | | | 0.69 [0.46, 0.53] | 0.32 [0.22, 0.42] | 72.1% [39.6, 100] | | |
| (5) | 0.74 [0.43, 1.0] | | 0.27 [0.06, 0.55] | 0.42 [0.21, 0.80] | 0.35 [0.12, 0.59] | 96.2% [72.7, 100] | |
| (6) | | -0.32 [-0.64, -0.07] | -0.18 [-0.39, 0.00] | | -0.51 [-0.86, -0.33] | 0.59 [0.48, 0.68] | |
| (7) | 0.68 [0.35, 1.0] | | | | | | 0.36 [0.21, 0.49] |
| E | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| (1) | 0.83 [0.72, 0.93] | | 33.0% [0.0, 76.0] | | 15.2% [0.00, 45.1] | | 8.2% [0.0, 31.0] |
| (2) | | 0.83 [0.73, 0.94] | | | | 4.6% [0.0, 35.1] | |
| (3) | 0.08 [0.00, 0.18] | | 0.69 [0.59, 0.80] | 55.5% [40.6, 72.0] | 43.2% [5.2, 86.6] | 16.5% [0.0, 43.7] | |
| (4) | | | 0.41 [0.32, 0.49] | 0.68 [0.58, 0.78] | 27.9% [0.0, 60.4] | | |
| (5) | 0.05 [0.00, 0.16] | | 0.12 [0.01, 0.23] | 0.10 [0.00, 0.21] | 0.44 [0.37, 0.53] | 3.8% [0.0, 27.3] | |
| (6) | | 0.01 [-0.12, 0.14] | 0.03 [-0.10, 0.16] | | -0.02 [-0.16, 0.11] | 0.41 [0.32, 0.51] | |
| (7) | -0.02 [-0.15, 0.10] | | | | | | 0.64 [0.51, 0.79] |

Note: ^a $V_C=0.21$ [0.00, 0.39]

closure (i.e., need for predictability and close-mindedness; $r=0.19$ [0.13, 0.22]), conservative values ($r=0.22$ [0.17, 0.26]), the tendency to commit heuristic errors ($r=-0.10$ [-0.16, -0.05]), and prejudice ($r=0.16$ [0.11, 0.22]). These findings replicate those of Keller (2005) and extend them to show how genetic essentialism is also associated with heuristic thinking and conservative values as measured by binding foundations.

The second main finding is that genetic essentialism is mostly explained by non-shared environment ($V_E=0.83$), with additive genetic effects explaining just under 20% of the variance ($V_A=0.17$). We also found significant genetic and environmental correlations between genetic essentialism, need for predictability, and conservative values. This would be compatible with a causal relationship between them. That is, if need for predictability causally influenced genetic essentialism, all genetic and environmental factors that influence need for predictability would also influence, through the causal chain, essentialist thinking. That is, genetic and environmental correlations between the two traits must be significant (De Moor et al. 2008).

Comparison with previous investigations

This study provided the first estimate of the heritability of any measure of essentialist thinking therefore no comparison is possible. For the other measures, we found very similar estimates to those previously published. We found a heritability estimate of 31–32% [20.0, 36.0] for need for predictability and need for order, very close to the 36% estimate by Ksiazkiewicz et al. (2016) for the whole of need for closure scale. We also found a heritability estimate of 59% [48.0, 68.0] for the cognitive reflection test, where Itamar and Aner (2011) found it to be 61%. Moreover, Lewis et al. (2014), using a generalized measure of prejudice, reported a heritability estimate of 38%. We found that our own specific measure of genetic prejudice in the context of mental health, had a heritability of 36% [21.0, 49.0]. The only exception was the heritability estimate for binding foundations (which we use as a proxy for conservatism). Smith et al. (2017) found heritability estimates for a binding foundations sum score that ranged from 6 to 22%, depending on gender and on wave of data collection, while we found a heritability of 35% [12.0, 59.0]. We believe that both estimates are valid and discrepancy in the results may be driven by different

sample size. Smith et al. (2017) estimated the heritability in two samples of 586 and 588 twins, while our analyses are based on data from 2,103 twins. This provides us with confidence in the reliability of our estimates. We also found influence of shared environmental factors in binding foundations while Smith et al. (2017) did not. This is also expected when sample size increases, as shared-environmental influences require more statistical power to be detected (Keller and Coventry 2005).

Interpretation of findings and implications

Essentialist thinking is a pervasive, persistent reasoning bias, which has been shown to vary across individuals, topics, and cultures. Our findings support the idea that individual differences in essentialist beliefs, at least the ones about biological essences, are more likely to stem from unique experiences rather than cognitive traits influenced by genetic factors or even shared environmental influences. Given the moderate to high heritability previously found in cognitive ability and style (such as need for closure), and the lack of genetic correlation between genetic essentialism and cognitive reflection scores, individual differences are more likely to be due to socialization processes rather than shared biological pathways with heuristic processes (at least in the sample under study).

The findings regarding significant genetic and environmental correlations between genetic essentialism and (i) need for predictability ($r_A = 0.55$ [0.19, 1], $r_E = 0.08$ [0.00, 0.18]), and (ii) conservative values ($r_A = 0.74$ [0.43, 1], $r_E = 0.05$ [0, 0.16]) provide some support to the hypothesis of need for closure underlying essentialist categorization and conservative ideologies (Roets and Van Hiel 2011a). However, these results must be taken with caution given that environmental correlations estimates and phenotypic correlations were very low. Also, the cross-twin cross-trait correlations between genetic essentialism and need for predictability were almost identical between MZ and DZ pairs ($r_{MZ} = 0.10$ [0.02, 0.18], $r_{DZ} = 0.09$ [0.01, 0.12]), and additive genetic factors cannot be disentangled from shared-environment. Interestingly, despite a moderate heritability estimate for genetic prejudice, the only statistically significant genetic correlation was found between prejudice and genetic essentialism. While most important factors driving individual differences in this specific measure of genetic prejudice ($V_E = 64\%$), there is some degree of familial aggregation ($V_A = 36\%$). These familial factors are genetically correlated with those of genetic essentialism ($r_A = 0.68$ [0.35, 1]), but not with those underlying need for predictability, need for order, conservative values, or cognitive reflection, which does not support the hypothesis of need for closure and conservative ideologies underlying this particular type of

prejudice (Roets and Van Hiel 2011a). A possible avenue of enquiry could be evaluating how participants' family history and genetic risk scores correlate with their beliefs about a biological basis of behavior. Another finding that should be further explored is the significant genetic correlation between conservative values and cognitive reflection test, with genetic factors explaining the majority of the moderate phenotypic correlation between the two traits ($r_A = -0.25$ [-0.30, -0.20]). This supports some genetic overlap between conservative moral and heuristic thinking, which in turn support previous literature on low-effort thought promoting political conservatism (Eidelman et al. 2012). Furthermore, the significant genetic correlation between conservative values and need for predictability ($r_A = 0.27$ [0.06, 0.55]), is coherent with previous hypothesis regarding a possible association between right-wing orientation and greater neural sensitivity to threat, which potentially underlies both need for closure and conservatism (Jost and Amodio 2012). However, common unique-environmental factors also explain the phenotypic correlation between need for predictability and conservative values ($r_{Ph} = 0.16$ [0.11, 0.20]; $r_E = 0.12$ [0.01, 0.23]).

Limitations and directions for future studies

This study has several limitations. All the work we present is cross-sectional. Experimental and longitudinal designs should be used to explore causal relationship between these constructs. Our choice of measures is also a potential limitation. We decided to focus on biological essentialism given our particular interest in motivated cognition in the context of genetics. Other facets of essentialist thinking (i.e., discreteness, informativeness of human attributes; see Bastian and Haslam 2006) may be influenced by genetic and environmental factors in a different way. In addition, the fact that positive or negative wording of items lead to different factor structures casts some doubts about the internal validity of the scale: even in simple items, there is a substantial construct-irrelevant variance associated with negatively worded items (Gnamb and Schroeders 2020). Moreover, despite the moderately high phenotypic correlation between the two factors, and them having the same heritability point estimate (but no genetic correlation), the reliability of the whole scale is lower than for the *genetic essentialism* factor in both the UK and US sample and the Australian sample (0.34 vs 0.88, and 0.42 vs 0.78, respectively). This reinforces our decision to use of factor scores as a measure of biological essentialism, especially given that the factor structure replicated in an independent sample, suggesting that the relationship between the variables is stable at least across samples from different Western countries.

In addition, our measure of tendency towards heuristic thinking was also simplistic. A more specific measure of the inherence heuristic is required to fully examine the proposal by Cimpian and Salomon (2014) that the inherence heuristic, in particular, underlies essentialist thinking. In regards to the choice of mental health conditions to measure prejudice, we opted to obtain a sum score across conditions to control for potential bias due to personal experience with the condition. Regarding the twin design, our models did not estimate a full genetic model (i.e., V_A , V_C or V_D , and V_E components). This was due to most phenotypes showing correlation patterns incompatible with either significant additive genetic influences in the presence of dominance effects, or no genetic influences at all. Further, the decision to not model V_D when V_A was not significantly different from zero might have led to an underestimation of V_A . Modelling broad-sense heritability where V_A and V_D are estimated jointly could have taken this into account, but we argue that it would have significantly increased the complexity of the present study in exchange for a low gain in precision. Finally, our twin sample consists of participants with previous experience in genetic research and that actively participate in genetic studies. This selection bias may influence the relationship we found between the constructs. However, the factor structure of three of the questionnaires was replicated across countries as well as the same direction of association, which increases our confidence in our results.

Conclusion

Using a survey and twin design we were able to provide indirect insight into the shared mechanisms underlying the relationship between essentialist beliefs, heuristic thinking, need for closure, conservative values, and prejudice. Our findings suggest that individual differences in biological essentialism are weakly influenced by genetic factors, and that there is some evidence of shared familial factors underlying biological essentialism, need for closure, and conservative values. However, this was not the case for tendency to commit heuristic errors and biological essentialism, which does not support the auxiliary theory of biological essentialism being strongly dependent on heuristic biases. Conversely, conservative values show significant genetic correlations with cognitive styles (i.e., need for closure and heuristic thinking) suggesting shared biological pathways between them. However, environmental factors were also shown to be important in this relationship and as such, purely biological explanations of the relationship between cognitive styles and conservatism would fall short. Our findings regarding the factors underlying individual differences in beliefs about the biological basis of behavior are of special relevance in mental health genetics. The significant contribution of

unique environmental factors to the variability of biological essentialism is consistent with personal experiences having a major role on people's theories about the development of mental health conditions, such as the findings of clinicians holding different explanations of mental health conditions depending on their training (e.g., clinicians with a biomedical training leaning towards biogenetical explanations of the conditions) (Haslam and Kvaale 2015). More recently, one survey study in general population found that genetic essentialism, but not literacy, directly predicted deterministic understandings of news headlines about genetic science. However, literacy seems to indirectly mitigate these unwarranted effects (Dar-Nimrod et al. 2021). The major role played by non-shared environment might also reflect the importance contextual cues from prompting essentialist responses, opening the door to developing specific 'debiassing' algorithms to prevent essentialist interpretations of genetic explanations. Some examples of such debiasing algorithms are the proposals by Kahneman (2012) to correct for regression to the mean in intuitive predictions, to debunk scientific myths by Lewandowsky et al. (2012), or to correct hindsight and confirmation biases in decision making in health care by Chapman and Elstein (2000). These specific debiasing algorithms could be presented within news articles or information brochures. Furthermore, theories about mental health are associated with perceived usefulness of genetic information in mental health, potential for stigma and discrimination, and worrying thoughts about prognosis or reproductive decisions, among others (Haslam and Kvaale 2015; Lebowitz and Ahn 2017; Meiser et al. 2020; Morosoli et al. 2021). A better understanding of the mechanisms underlying public understanding of genetics is paramount for a successful and implementation of genetic technologies in health care (Lewis and Vassos 2020; Morosoli et al. 2019).

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Data Availability Data and code available upon request.

Declarations

Conflicts of interest JJ Morosoli, FK Barlow, L Colodro-Conde, and SE Medland declare that they have no conflict of interest.

Ethical Approval All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards. Ethical approval was obtained from the Human Research Committee of QIMR Berghofer Medical Research Institute and the Human Research Ethics Committee of the University of Queensland (approval numbers: P2227 and JM03024).

Informed Consent Informed consent was obtained from all individual participants included in the study. Participants signed informed consent regarding publishing their data.

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