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Heritability across different domains of trust

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ABSTRACT

Using a large sample of 1,120 twins and the multivariate ACE-Cholesky model, we estimated the heritability of trust using four distinct measures of trust – domain-specific political trust, general self-reported trust, and incentivized behavioral trust and trustworthiness. Across the different measures of trust we consider, our estimates for heritability range from 1 % to 37 %. Furthermore, the environmental correlates of trust also vary across the different measures with political trust having the largest set of environmental covariates. To reconcile the variation in the estimated heritability of trust in the literature, we provide a meta-analysis of the heritability of behavioral and stated trust.

1. Introduction

Trust and trustworthiness are the indispensable foundations of any well-functioning relationship and a society as a whole. Since not all agreements are enforceable via legal contracts, in practice, to function societies rely on trust and trustworthiness. Trustworthiness is among the main traits sought out in intimate relationships (Fletcher et al., 1999). Trust fosters economic development (Algan and Cahuc, 2013), and is the key metric in politics, marketing, education, and parenting. The long-term costs of foregone trust can be devastating. Approximately 35 % of the life expectancy gap between black and white men in the 80's in the US was due to the disclosure of the unethical and deadly experiment in which black men in Alabama were denied appropriate medical treatment for syphilis, which lowered trust in the medical profession (Alsan and Wanamaker, 2018). To this day, a half century later, black adults display more distrust in medical interventions recommended by the government. For example, they were the least willing racial group to get the COVID-19 vaccine (Deane et al., 2021).

Unfortunately, public trust in politicians is at an all-time low. Over the past 60 years, about 60 % of Americans stopped trusting that their government in Washington will do what is right always or most of the time. Public trust tumbled from 77 % of Americans trusting the government in 1964 to just 17 % in 2019 (Pew Research Center, 2021) and similar patterns have been observed in many countries all over the world. According to a recent report (OECD, 2021), in Australia fewer people trust their national government (38 %) than do not (43.8 %). The consequences are dire. On 18 July 2021, the leading medical advisor on the pandemic in the US, Dr Anthony Fauci, was quoted saying “We probably would still have polio in this country if we had the kind of false information that’s being spread now ... if we had that back decades ago, I would be certain that we’d still have polio in this country” (Tinker and Elassar, 2021). During the pandemic, it was evident that politicians all over the world were struggling to achieve the levels of political trust that would allow them to maintain health and order. Needless to say, maintaining trust is costly — approximately 35 % of US cost of labor is devoted to upholding trust and this cost has been growing during recent decades (Davidson et al., 2018).

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While the societal importance of trust is evident, a firm understanding of its foundations remains elusive. For decades researchers in various disciplines used theoretical and empirical research to investigate the antecedents and consequences of trust (Cook, 2001; Ho, 2021). With enormous amounts of money and time invested in building trusting relationships, a sensible question to ask is to what extent interpersonal differences in the tendency to trust others are explained by a combination of variation in our genes and environmental factors. The existing evidence, using twin similarity designs, provides estimates that range from 3 % to 66 % (see Table 1) of variation in trust being explained by genetic variation rather than by external factors.¹ When reported, the confidence intervals of these estimates are often wide indicating that they are not very precise. Van Lange et al. (2014) use a variety of self-report measures for trust and conclude there is no evidence they are heritable. In contrast, Sturgis et al. (2010), using a similar battery of general trust survey questions, find that 66 % of variation in trust is explained by additive genetic effects. It is not clear whether these differences across studies are driven by differences in the sample² or in how trust is measured (see Bauer and Freitag, 2017 for a discussion on the relationship between different measurement approaches).

Recent literature on trust paints a picture of a trait that is difficult to define, let alone measure (Sapienza et al., 2013). Research in political science recognizes that trust can differ across the domains and treats general social trust and political trust as separate concepts with the causal relationship between the two not yet fully understood (Newton et al., 2017; Newton and Zmerli, 2011; Sønderkov and Dinesen, 2016). This means that, the general trust questions may tell us little about trust in a different domain such as trust in politicians, which can be amplified during challenging times, like a pandemic. Ojeda (2016) measured trust in politicians and argued that genetic variation influences on political trust briefly increased after 9/11 but did not include measures of trust in other domains. From the other eight studies that investigated the heritability of trust, six used a (different across studies) general trust self-reported survey measure and two used behavioral measures based on incentivized decisions in an economic trust game (Berg et al., 1995). None used both. One challenge in interpreting this literature is that even survey and behavioral measures of trust are only very weakly correlated (Glaeser et al., 2000) and therefore seem to capture different aspects of trust, reinforcing the idea that trust is domain specific.

To overcome this problem and provide comprehensive evidence on the heritability of trust, we conduct a meta-analysis of the existing trust heritability estimates. This meta-analysis includes our own estimates based on a large sample of twins in Australia. Our estimates are a unique contribution to the literature because, using a within-sample comparison, we provide evidence on whether heritability differs across different domains of trust, as well as on the extent to which these different trust measures have the same genetic influences. Our measures of trust include stated trust in politicians, general trust stated survey measure, and behavioral measures of trust and trustworthiness. We also provide evidence that the environmental covariates of trust differ across these different measures. COVID-related income and health insecurity are one of the strongest correlates that are unique to trust in politicians. Moreover, trust in politicians is correlated with the largest number of socioeconomic and demographic measures we collected. Our data suggest that worry about pandemic outcomes is associated with reduced trust in politicians but not trust in general.

2. Data

Ethics statement: Our protocols and procedures were approved by the University of Technology Sydney Human Research Ethics Committee (application numbers ETH19–4381 and ETH20–5410) and by Twins Research Australia.

Participants. 1120 twins (18–66 years old; $M = 44.67$, $SD = 12.83$) recruited from Twins Research Australia, Australia's largest twin registry, participated in our study allowing us to create the largest twin dataset on behavioral trust.³ Our sample comprises 401 monozygotic (MZ) and 159 dizygotic (DZ) twin pairs. The majority (83 %) of twins are female, reflecting selection into the registry. Forty-two DZ pairs are mixed sex. We include these pairs in our baseline regressions and adjust for mean differences between sexes. Our sample is well-balanced (Table S1–S2). The only significant difference between MZ and DZ pairs is sex, with 14.2 % of MZ twins being male compared to 24.5 % for DZ twins. We control for sex in our analysis, and present results for same-sex pairs only for comparison. MZ and DZ twin pairs do not differ in other demographic and socioeconomic characteristics as well as trust measures.

Domain-specific stated trust in politicians. We measure trust in politicians using responses to four statements which participants could rate as true, somewhat true, or false. The statements are: “Most politicians care more about staying in power than about the interests of the people”, “Most politicians make a lot of money by misusing public office”, “Most politicians do not care what happens to people like me”, and “Most politicians do their job well most of the time” (Pop-Eleches and Pop-Eleches, 2012). For the first three questions true is coded as 0, somewhat true as 0.5, and false as 1 and for the last question the coding is reversed. The average of these four scores is our measure of trust in politicians. The internal consistency of the four scores is high (Cronbach's alpha = 0.78).

Survey general trust. Our stated trust measure is a single question from the Global Preferences Survey (Falk et al., 2018) which asks participants to rate how well the following statement describes them as a person “I assume that people have only the best intentions”, on a scale from 0 “does not describe me at all” to 10 “describes me perfectly”. We chose this instrument given the extensive validation efforts underlying the GPS (Falk et al., 2016) and the ongoing influence of the GPS on social science research.⁴ We normalize this

¹ An alternative to using twin similarity is to estimate heritability from mapped genome data for large samples. Only small sample studies have been conducted for (stated) trust, and they estimate heritability between 12–24% (Benjamin et al., 2012; Wootton et al., 2016).

² For example, in a society where all trust is enforced by strong legislation and social rules, genes may explain only a small share of variation. In this way, the influence of genetic variation is dependent on the environmental context.

³ Kettlewell & Tymula (2021) describe the recruitment and study design in detail.

⁴ <https://www.briq-institute.org/global-preferences/publications>

measure of trust into a fraction by dividing the indicated number by 10.

Behavioral trust. We measured behavioral trust using a standard trust game (Berg et al., 1995). Each participant first played as the ‘sender’ and then as the ‘receiver’. As the sender, participants were given \$11 AUD (approximately \$8 USD) and told they could send any part (in \$1 increments) of this amount to another randomly chosen and unknown to them participant in the study (who is not their twin). Any amount not sent, they would get to keep. The amount sent would be tripled and the receiver would then decide how much (if anything) to return to them. Trust is measured by the fraction of the endowment sent.⁵ Before commencing with the trust game, participants needed to correctly answer a series of questions indicating that they understood the task.

Behavioral trustworthiness. We elicit trustworthiness using a strategy method (Brandts and Charness, 2011). As receivers, participants chose how much they would return to the sender for all 11 possible amounts sent (i.e., values from \$1–\$11). We quantify trustworthiness as the average fraction returned across all 11 scenarios.

3. Methodology

Estimation of heritability. We employ a classic twin study design and exploit differences in genetic similarity between MZ and DZ twin pairs (Neale, 2009). MZ twins share the same set of genetic variants whereas DZ twins, on average, share half under random mating. We use two methods to establish the genetic influence on trust: simple correlations and the so-called ACE structural models. Assuming that MZ and DZ twins are influenced by their shared environments to the same degree, a stronger correlation in trust between MZ pairs than between DZ pairs indicates that interpersonal differences in trust are partly genetic. We calculate the correlation in trust between twins, separately for MZ and DZ pairs, and then compare these correlations using standard *t*-tests. Next, by imposing additional assumptions on the correlations of the phenotype between the twin pairs, we further decompose the variance in participants’ trust into additive genetic (A), common environment (C) and unique environment (E) components. Under the assumption that these components are additive and mutually exclusive, the covariance between MZ twins is given by $cov_{MZ} = \sigma_A + \sigma_C$ and between DZ twins is given by $cov_{DZ} = 0.5\sigma_A + \sigma_C$.⁶ It is easy to solve for σ_A and σ_C , with σ_A being twice the difference in correlation between MZ and DZ pairs. This simple algebraic decomposition is intuitive but in practice does not guarantee sensible estimates (e.g., variance shares may be outside the unit interval), does not easily accommodate controls, and does not deal with multivariate decompositions (Neale, 2009). Typically, researchers use structural equation modelling (SEM) to estimate variance shares. This can generate estimates of not only the univariate pathways, but also the correlations between the A, C and E components across phenotypes (in our case, different measures of trust). We follow this tradition and estimate the multivariate ACE-Cholesky model, implemented using the *umx* package for R (Bates et al., 2019).

In addition to assuming additivity of genetic effects, the classic twin design assumes that MZ and DZ twins share ‘equal environments’, which requires that on average MZ and DZ twins are influenced by their shared environments to the same degree. While strong, numerous studies in behavioral genetics find support for this assumption, or that violations only modestly affect estimates (see Barnes et al., 2014; Felson, 2014). In our sample, the fact that MZ and DZ twins appear to have similar environmental experiences is helpful, to the extent this suggests similar upbringings for MZ and DZ pairs. Our analysis also assumes no assortative mating related to trust. If trust is positively correlated within couples due to partner selection, DZ twins are likely to share more than 50 % of their individual genes on average. If so, our estimates (and those in the existing literature) may understate the importance of genetic variation.

Meta-analysis. We searched three databases (Google Scholar, PsycINFO, and PubMed) using one or a combination of the following search terms: ‘heritability of trust’, ‘genetic basis of trust’, ‘biological basis of trust’, ‘twin study’, ‘social trust’, ‘political trust’. We conducted the search on February 20th, 2023, and our meta-analysis includes studies published up to this date as well as the estimates from this paper. The studies we found are summarized in Table 1. Because we found only one existing study for political trust and one for trustworthiness, we do not meta-analyze these estimates.⁷ We conduct our meta-analysis of stated and behavioral trust in two ways. First, we meta-analyze the ACE model using all papers that provide unconstrained ACE model estimates. The papers that constrain one of the ACE components to zero are therefore not included in this analysis. Second, we provide a meta-analysis of the raw trust measure correlations for MZ and DZ twins because this allows us to include more studies. Following Polderman et al. (2015), we transformed the ACE estimates and twin correlations to their Fisher *z*-values with their standard errors. We conducted fixed-effects meta-analysis, back-transforming the estimates at the end, using the *meta* program in Stata.

4. Results

Correlation across different measures of trust. As expected, our correlation analysis reveals that different measures of trust are poorly approximated by other trust measures (Table S3). Trust in politicians is significantly but only weakly correlated with the survey general trust measure (corr. coef. = 0.1986, $p < 0.001$) and not significantly correlated with the behavioral measures of trust (corr. coef. = 0.0395, $p = 0.221$) and trustworthiness (corr. coef. = 0.0084, $p = 0.798$). Our social trust measures – stated and behavioral – are also

⁵ The participant survey also included other behavioral tasks with monetary outcomes (see Kettlewell & Tymula (2021) for details). We followed common practice by selecting one task at random to ‘play out for real’.

⁶ Here we are additionally assuming dominant genetic (D) effects (genetic interaction effects) are zero since they cannot be identified without restricting other components.

⁷ One related study is Sutherland et al. (2020), who find that 17–29% of differences in how people evaluated the trustworthiness of others based on their appearance can be explained by genetic variation.

Table 1

Summary of twin studies on the heritability of trust.

Study	Trust measure	MZ pairs	DZ pairs	Mixed sex	Zygosity	Region	F/M	Age range	A%	C%	D%	E%	MZ	DZ
Cesarini et al. (2008)	Fraction sent in standard trust game (6 levels) (Sweden)	258	71	No	Questionnaire (self-report)	Swedish twin registry	79/21	$M = 34$ $SD=7.5$	20	12		68	0.25	-0.01
	Fraction sent in standard trust game (11 levels) (US)	278	75	No	Questionnaire (self-report)	Twins Days Festivals, OH, USA	80/20	$M = 34$ $SD=15.5$	10	8		82	0.13	-0.07
	Fraction sent back in standard trust game (Sweden)	258	71	No	Questionnaire (self-report)	Swedish twin registry	79/21	$M = 34$ $SD=7.5$	18	17		66	0.25	-0.01
	Fraction sent back in standard trust game (US)	278	75	No	Questionnaire (self-report)	Twins Days Festivals, OH, USA	80/20	$M = 34$ $SD=15.5$	17	12		71	0.13	-0.07
Hiraishi et al. (2008)	Self-reported responses to five items of generalized trust questionnaire (7-point scale)	491	138	No	Questionnaire, some by blood	Keio Twin Registry (Tokyo)	69/31	$R = 14-31$ $M = 20.3$ $SD=4.1$	31	0		69		
Sturges et al. (2010)	Self-reported responses to four items of social trust (5-point scale) (common pathway model only)	133	138	Yes	Questionnaire (9 by DNA)	Australia	62/38	$R = 15-33$	66	0		34		
	Self-reported responses to item 1: intention common + specific pathway model)	133	138	Yes	Questionnaire (9 by DNA)	Australia	62/38	$R = 15-33$	27	0		73	0.22	0.18
	Self-reported responses to item 2: advantage (common + specific pathway model)	133	138	Yes	Questionnaire (9 by DNA)	Australia	62/38	$R = 15-33$	14	30		56	0.45	0.32
	Self-reported responses to item 3: trust (common + specific pathway model)	133	138	Yes	Questionnaire (9 by DNA)	Australia	62/38	$R = 15-33$	36	0		64	0.38	0.18
	Self-reported responses to item 4: honest (common + specific pathway model)	133	138	Yes	Questionnaire (9 by DNA)	Australia	62/38	$R = 15-33$	31	0		68	0.37	0.16
Oskarsson et al. (2012)	Self-reported response to a generalised trust question (10-point scale) (Female)	667	725	No	Questionnaire and some by analysis of biosample	Swedish twin registry			39	0		61	0.37	0.19
	Self-reported response to a generalised trust question (10-point scale) (Male)	463	495	No	Questionnaire and some by analysis of biosample	Swedish twin registry			33	3		65	0.35	0.19
Van Lange et al. (2014)	Self-reported responses to three items about trust in others (7-point scale)	186	191	Yes	DNA (88 %) and questionnaire	Netherlands	55/45	$R = 17-70$ $M = 45.3$ $SD=14.1$			5	90	0.16	0.04
	Self-reported responses to three items about trust in self (7-point scale)								3		10	86	0.17	0.03
Ojeda (2016)	Self-reported response to political trust question (I trust the federal				Questionnaire (self-report)	USA (National Longitudinal Study of Adolescent Health)	53/47	Median = 22	17.64	6.76		84.64	0.21	0.32

(continued on next page)

Table 1 (continued)

Study	Trust measure	MZ pairs	DZ pairs	Mixed sex	Zygosity	Region	F/M	Age range	A%	C%	D%	E%	MZ	DZ
	government) (5-point scale) before 911													
	Self-reported response to political trust question (I trust the federal government) (5-point scale) after 911				Questionnaire (self-report)	USA (National Longitudinal Study of Adolescent Health)	53/47	Median = 22					0.40	0.32
Wootton et al. (2016)	Self-reported responses to generalized trust (in general I think people can be trusted, yes/no)	1293	2299	Yes	Questionnaire and DNA markers	England and Wales	54/46	$M = 16.15$	35 (0, 60)		22 (0, 60)	43 (35, 52)	0.34	0.11
	Self-reported responses for trust in friends (10 items, 5-point scale)	807	1262	Yes	Questionnaire and DNA markers	England and Wales	59/41	$M = 16.47$	14 (0, 36)		36 (13, 54) ¹	50 (45, 55)	0.51	0.15
Reiman et al. (2017)	Amount sent in standard trust game (up to \$1 in 10c increments)	162	105	No	Questionnaire and some DNA testing	USA (Washington State Twin Registry)	100/0	$M = 44.52$ $SD=14.14$	30 (17, 42)	0 (0, 31)		70 (58, 83)	0.31	0.15
Weinschenk & Dawes (2019)	Self-reported response to two items about generalized trust	991	989	No		Germany			30 (15, 44)	14 (1, 25)		57 (52, 62)	0.44 (0.39, 0.49)	0.28 (0.21, 0.34)
Kettlewell & Tymula	Self-reported responses to three items about trust in politicians (3-point scale)	401	159	Yes	Questionnaire, blood, some DNA testing	Australia	83/17	$R = 18-66$ $M = 44.67$ $SD=12.83$	34.48 (6.36)	2.2 (5.18)		63.32 (3.25)	0.38 (0.04)	0.16 (0.08)
	Self-reported response to generalized trust question (11-point scale)								27.35 (5.93)	1.73 (4.30)		70.92 (3.62)	0.32 (0.05)	0.04 (0.08)
	Fraction sent in standard trust game								0.82 (4.74)	14.39 (4.77)		84.79 (3.57)	0.15 (0.05)	0.15 (0.08)
	Average fraction returned in standard trust game (strategy method)								13.91 (7.07)	8.51 (5.67)		77.59 (4.17)	0.21 (0.06)	0.17 (0.08)

Notes: We report unconstrained ACE model estimates whenever they are provided in a paper. If they are not reported, we list the estimates that were provided, usually of the best fitting among the AC(D)E models. Trust measures in bold provide the unconstrained ACE estimates and are included in the ACE model meta-analysis. For Sturges et al. (2010) we chose the item that most closely resembled general trust. *MZ pairs*: the number of monozygotic twin pairs. *DZ pairs*: the number of dizygotic twin pairs. *Mixed sex*: whether the sample included twin pairs with different sex or not. *Zygosity*: how zygosity was determined for participants. *Region*: where the study was conducted. *F/M*: percentage of females/males in the sample. *Age range*: available statistics on age distribution of sample (R =range, M =mean, SD =standard deviation). *A%*: estimated percentage of variation due to additive genetic effects. *C%*: estimated percentage of variation due to common environment effects. *D%* estimated variation due to dominant genetic effects. *E%*: estimated percentage of variation due to unique environment effects. With a classic twin design, one of ACDE needs to be constrained to equal zero (usually this is D). In the last six columns, we report confidence intervals (two values in brackets) or standard errors (single value in brackets). C indicates credible interval.

only weakly correlated (corr. coef. = 0.1347, $p = 0.000$).

Heritability of trust across different trust measures – correlation approach. Simply comparing correlations in trust between MZ and DZ twin pairs is useful for establishing whether there is likely to be any heritability or common environmental influence. If correlations are higher for MZ than DZ twins, this suggests that genetic variation plays a role. If there is no correlation, this suggests that neither genes nor common environment play a role. The correlations are also helpful for gauging the appropriateness of the structural ACE model we use later. For example, given that on average DZ twins share half of the genetic variants and MZ share all, we should expect that the correlation between MZ is not more than twice the difference between MZ and DZ if genetic effects are additive. Moreover, the correlation for MZ should be at least as large as for DZ (if not, this may indicate violation of equal environments).

We find that the correlation between sets of twin pairs varies substantially across different measures of trust (Fig. 1). Trust in politicians is significantly more correlated in MZ than DZ pairs (0.375 versus 0.163, $p = 0.017$). General trust measured using a survey question is also more strongly correlated within MZ than DZ pairs (0.317 versus 0.041, $p = 0.003$).⁸ Behavioral measure of trust paints a substantially different picture. Statistically indistinguishable correlations of behavioral trust for the MZ and DZ pairs (0.151 versus 0.152, $p = 0.992$) suggest a limited role for genetic variation and some influence of common environment. The correlations of trustworthiness are higher for MZ twins (0.214) than for DZ twins (0.168), although the difference in correlations is not statistically significant ($p = 0.631$).

Heritability of trust across different trust measures – ACE-Cholesky approach. Next, we formally decompose the variation in trust using the multivariate ACE-Cholesky approach. In Fig. 2 we summarize our estimates in terms of implied variance component shares. We estimate that in our sample 35 % of differences in political trust and 27 % of interpersonal differences in stated trust are explained by variation in genes, with negligible shares for common environment. In contrast, our genetic share estimate for behavioral trust is close to zero, with 14 % of variation explained by common environment. In our sample, genetic variation explains 14 % of interpersonal differences in behavioral trustworthiness and common environment explains 9 %.

An appeal of multivariate decomposition is that we also estimate pathways between variance components, which can be used to calculate correlations between them, such as the correlation in variation attributable to additive genetic effects between stated and political trust. These correlations are summarized in Table S4. The genetic correlation between stated and political trust is 0.34 (SE = 0.190), which indicates modest overlap in the genetic variants that explain these traits. Other genetic correlations between variance components are either small or relate to shares that explain very little variation in the trust measure (e.g., the share of variation attributable to genes for behavioral trust is practically zero so the genetic correlations with other trust measures are not informative). The correlations between unique environment variation are generally positive but small, implying that there is little overlap in the experiences that drive variation in these trust measures. The one exception is with respect to behavioral trust and trustworthiness (which have a regular correlation of 0.36); the correlation between the unique environment variance factors is 0.34 (SE = 0.043) which implies a moderate level of overlap in the unique experiences that explain the correlation between these traits.

Testing the equality of genetic effects. Our point estimates and their confidence intervals (reported in the notes of Fig. 2) suggest that genetic variation plays a larger role for stated and political trust than for behavioral trust. However, it is not clear whether this difference is because genetic influences are truly different, or due to sampling variation. To formally test this, we jointly estimate two versions of the ACE-Cholesky model and perform a likelihood ratio test. In the baseline, we constrain the correlations between variance components to be zero, which is akin to jointly estimating separate univariate ACE models. In the second, we additionally constrain the standardized path coefficients for the genetic pathways to be equal so that the shares of variation due to genetic variants are also equal across trust measures. The improvement in the likelihood when we allow the genetic shares to vary is not statistically significant ($p = 0.272$), which means that despite the large difference in point estimates, we cannot reject the hypothesis that the heritability of each trust measure is the same.

Additional results. In the supplement (Table S5), we show results from estimating univariate ACE-Cholesky decompositions on each trust measure, and compare the fits of models that constrain either the common environment effect to be zero (AE model) or the effect of genetic variation to be zero (CE model). The best fitting models (according to AIC) for stated and political trust are AE specifications and we can formally reject the CE specification. The estimated genetic shares are similar to our multivariate decompositions (29 % and 37 % respectively). For behavioral trust, the best fitting model is CE; however, we cannot formally reject ACE or AE. The ACE specification implies that genetic differences explain 3 % of the variation. For behavioral trustworthiness, the ACE specification has the best fit and the estimated genetic share is identical to the multivariate decomposition (14 %).

We report results for same-sex pairs only in Tables S6–S7. One reason for this exercise is that the equal environments assumption may be more tenable without mixed sex pairs. A second reason is that genetic variants and environment may be differently important for males and females. However, since there are relatively few male-male pairs in our sample (57 MZ, 18 DZ), we lack adequate statistical power to differentiate these estimates and therefore interpret differences as suggestive.

For political and stated general trust, we estimate for females that 35 % and 29 % of variation is due to genetic differences

⁸ When the correlation coefficient is more than twice as large for MZ than DZ twins, this can indicate the presence of dominance genetics effects (D), which occur when the expression of the two inherited gene variants at a particular locus depend on an interaction effect between them. However, in the classic twin design D effects can only be identified by restricting the common family environment effect to zero. We estimated this ADE model for general stated trust but found the AIC statistic was higher than the constrained AE specification, implying a worse fit of the data. The ADE model estimated total variation due to genes equal to 30.36%, entirely due to dominance genetic effects. This is a similar degree of genetic heritability to our reported estimates. Further, using a t-test test, we cannot statistically reject that the correlation is twice as large or smaller ($p = 0.151$), which justifies our use of models with additive genetic effects only.

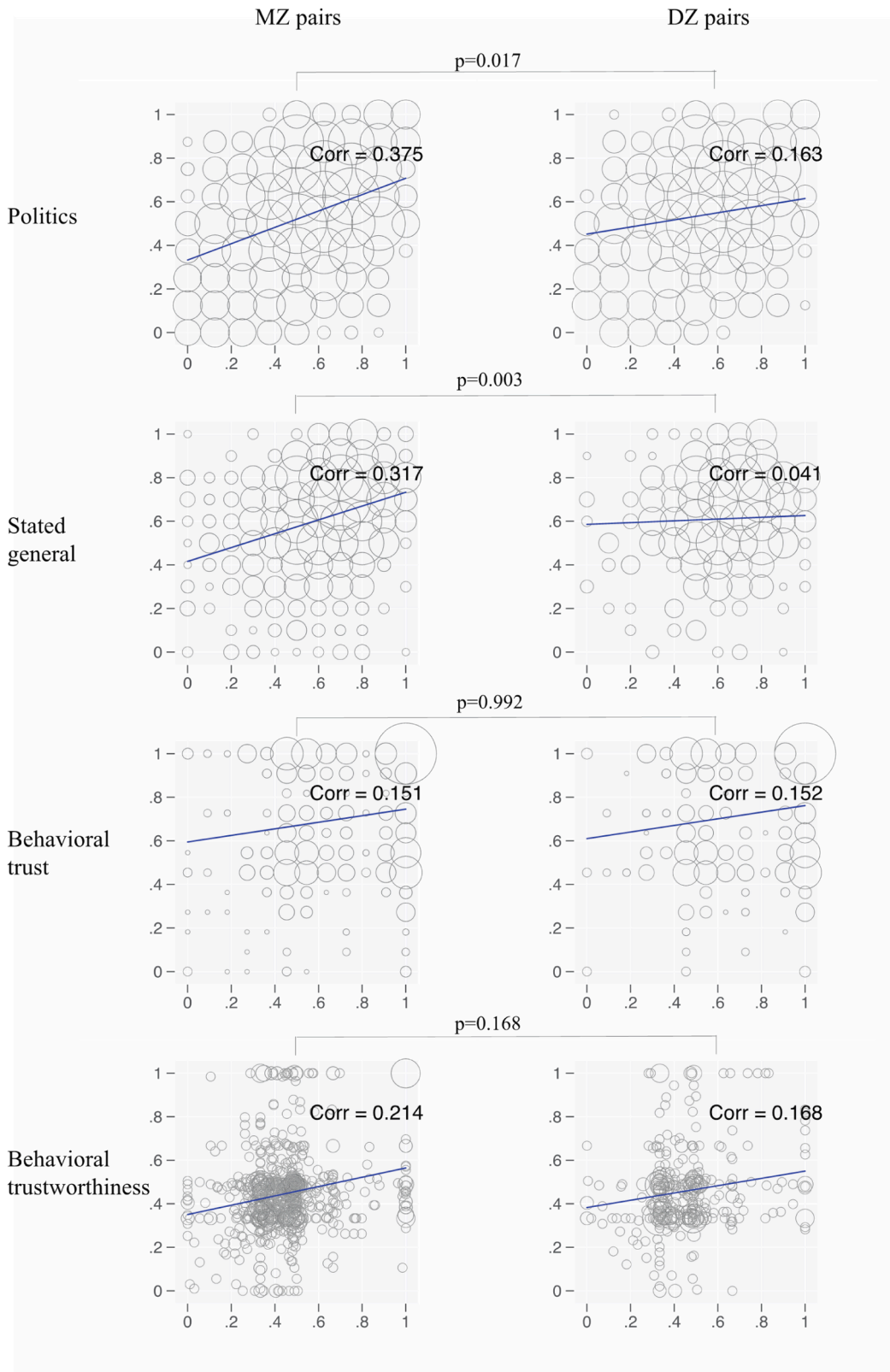


Fig. 1. Twin pair trust correlations.

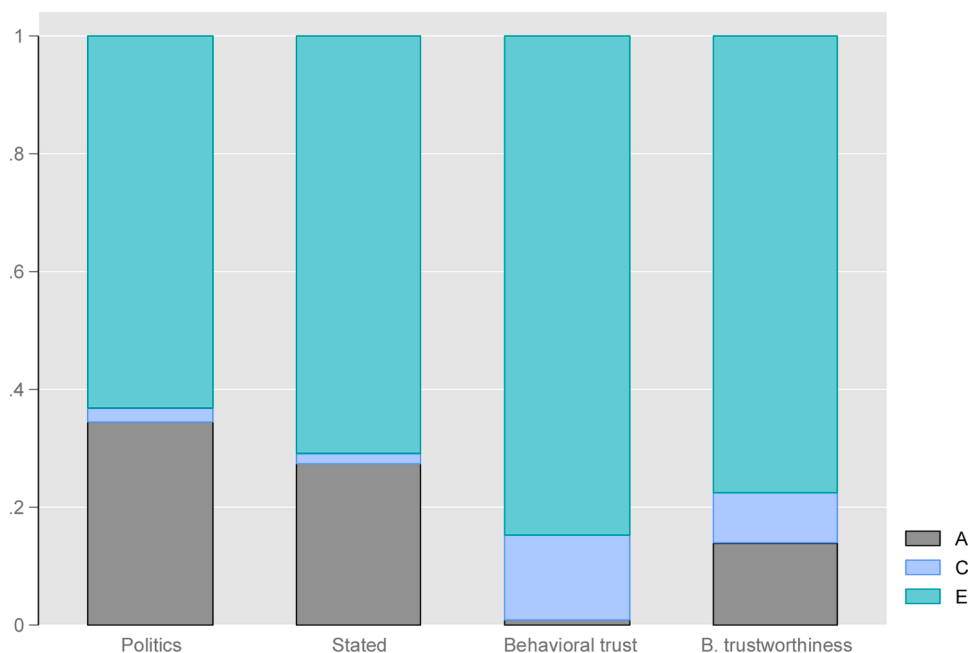


Fig. 2. Proportion of variance explained by additive genes and environment.

Notes: Stacked bars correspond to the proportion of variation explained for each trust phenotype by additive genetic effects (A), common environment (C) and unique environment (E). ACE estimates obtained using the umx program for R. A estimates (percent) and 95 % confidence intervals are: Trust politics, 34.48 [26.17, 45.09]; trust stated, 27.35 [17.10, 38.15]; behavioral trust, 0.82 [0.00, 1.73] and trustworthiness behavioral, 13.91 [2.75, 28.67]. Confidence intervals are obtained using non-parametric bootstrap with 1000 replications. Full estimation results are in the Supplementary Material (Table S4).

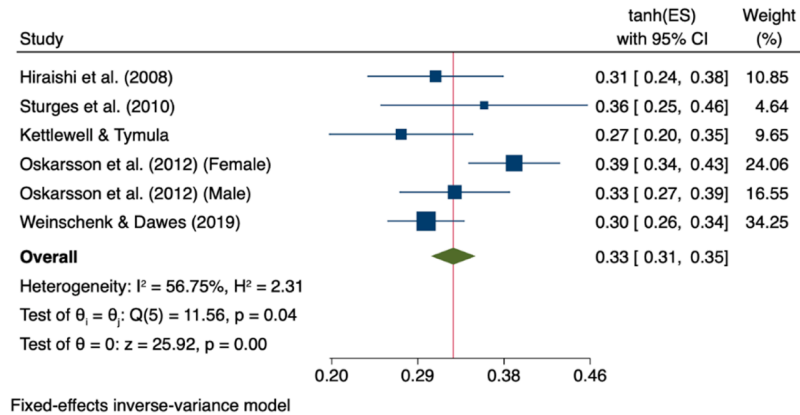
Table 2

Correlations between residualized trust and covariates.

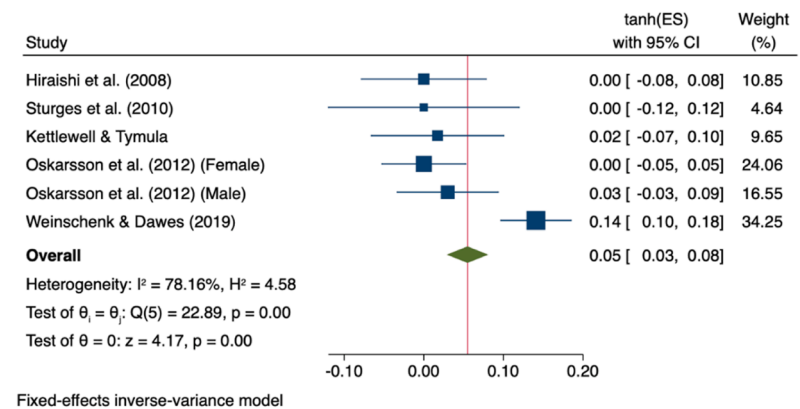
Variable	Politics		Stated		Behavioral		Trustworthiness	
	Corr	q-val	Corr	q-val	Corr	q-val	Corr	q-val
Age	0.113	0.001	<i>0.065</i>	<i>0.098</i>	0.012	1.000	0.052	1.000
Male	0.028	0.364	−0.047	0.210	0.029	1.000	0.014	1.000
Aus born	−0.011	0.619	0.032	0.352	0.035	1.000	−0.022	1.000
Live city	0.021	0.560	−0.029	0.438	−0.025	1.000	−0.012	1.000
Married/defacto	0.099	0.003	0.137	0.001	0.046	1.000	0.014	1.000
Household size	−0.019	0.560	<i>0.078</i>	<i>0.098</i>	0.064	0.504	−0.006	1.000
Num. dep. children	0.013	0.619	0.075	0.055	0.063	0.504	0.002	1.000
University	0.113	0.001	−0.003	0.836	−0.032	1.000	−0.048	1.000
Employed	0.004	0.672	−0.034	0.438	−0.021	1.000	0.017	1.000
Retired	0.006	0.672	0.020	0.652	0.008	1.000	0.022	1.000
Income	0.119	0.003	0.027	0.511	0.086	0.341	0.049	1.000
Financial security	0.186	0.001	0.063	0.176	−0.009	1.000	0.017	1.000
LT health condition	−0.171	0.001	−0.104	0.044	−0.043	1.000	−0.013	1.000
Covid worry	−0.100	0.005	−0.045	0.325	−0.020	1.000	−0.001	1.000
Covid risk	−0.106	0.004	0.001	0.836	−0.004	1.000	0.019	1.000
Covid mortality	−0.175	0.001	−0.082	0.148	0.005	1.000	0.068	1.000
Covid job loss	−0.133	0.001	−0.013	0.750	0.013	1.000	−0.003	1.000
Covid reduced income	0.012	0.619	−0.045	0.325	0.087	0.341	0.053	1.000
Covid work home	0.044	0.227	0.028	0.438	−0.018	1.000	0.031	1.000
Covid reduced hours	−0.032	0.364	−0.062	0.176	−0.016	1.000	−0.011	1.000
Covid friends	−0.038	0.267	0.023	0.511	0.023	1.000	−0.032	1.000

Notes: Estimates from non-missing values from a full sample of 802 monozygotic twins (See Table S1 for observation counts). Correlation cells show the pairwise correlation between the covariate and the residualized trust measure (residual obtained after estimating a linear regression controlling for twin pair’s trust). FDR q-values as described in Anderson (2008) are used to test for statistical significance (adjusted for multiple hypotheses) after obtaining standard errors via non-parametric bootstrap with 1000 replications clustered at the twin pair level. P-values without adjustment for multiple hypothesis testing are in Table S8. Estimates in bold are significant at the 5 % level and estimates in italics at 10 %.

A component



C component



E component

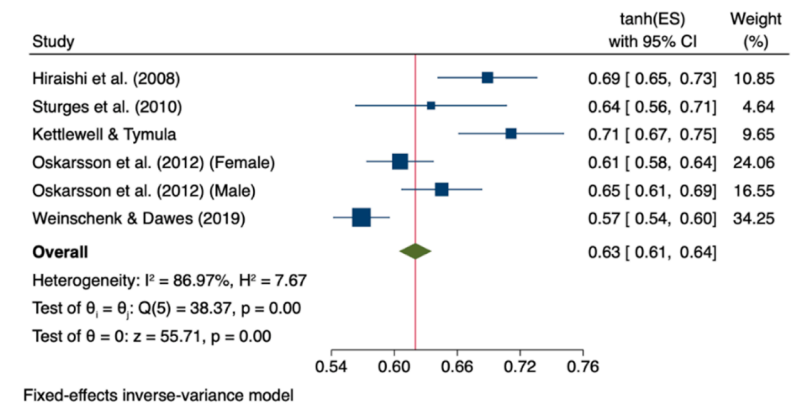


Fig. 3. Meta-analysis of the heritability of survey-measured general trust in the ACE model. For each ACE component, the estimated effect sizes and their 95 % confidence intervals are presented in the “tanh(ES)” column and graphically as squares and lines, respectively. The inverse-variance weight that each estimate received in the meta-analysis is in column “weight” and also represented by the size of the square. The red line and the diamond represent the meta-analytic estimate.

Table 3

Meta-analytic correlations of stated and behavioral trust within MZ and DZ pairs. Confidence intervals in brackets.

	MZ pairs	DZ pairs	2*(MZ-DZ)
Stated general trust	0.36 [0.34, 0.39]	0.16 [0.13, 0.19]	0.39 [0.35, 0.43]
Behavioral trust	0.19 [0.14, 0.25]	0.08 [−0.01, 0.18]	0.25 [0.13, 0.36]

Notes: Estimates are based on fixed effects meta-analysis. Included studies are reported in Table 1. Raw MZ/DZ correlations are transformed to Fisher z-values with their standard errors given by $1/\sqrt{n-3}$ where n is the number of twin pairs for the relevant correlation, and back transformed to obtain the reported confidence intervals. 2*(MZ-DZ) is the within study difference in correlations. For this analysis, an approximate standard error is

calculated by $\sqrt{\frac{(1-r_{MZ}^2)^2}{n_{MZ}-3} + \frac{(1-r_{DZ}^2)^2}{n_{DZ}-3}}$ for each study (see Bonett & Wright (2000)) where r_i is the correlation and n_i is the number of twin pairs.

respectively, and the rest to unique environment, similar to our main results. Our estimates are similar for males (36 % and 35 %). For behavioral trust, we estimate no role for genetic variation and 12 % to common environment for females according to the ACE specification. Interestingly, for males the estimates attribute 27 % of variation to differences in genes. A surprising finding is that for behavioral trustworthiness, we do not estimate any role for genetic variation for either gender, which contrasts with our pooled results. This is particularly the case for our (small) sample of males; there, we estimate that 34 % of variation is due to common environment and can formally reject the AE specification. Overall, our results make us less certain about the true heritability of behavioral trustworthiness and point to gender as a potentially interesting moderator to explore in datasets with more males.

Environmental correlates: Since unique environment explains most of the variation in all trust measures (63 – 85 %), we investigated what parts of the environment predict trust. Table 2 reports the pairwise correlations between trust (net of twin’s trust) and key covariates for MZ twins.⁹ There is surprisingly little overlap in the correlates across different measures of trust. After adjusting for multiple hypotheses, none of the correlations are significant for behavioral trust or trustworthiness. People who are older, in better health and married or in de facto relationships, exhibit higher political and stated general trust while higher income and financial security increases with political trust only. Additionally, particularly interesting is the unique role of COVID-19 on political trust, with negative correlations with worry, risk beliefs and having experienced job loss, ranging from -0.10 to -0.18.

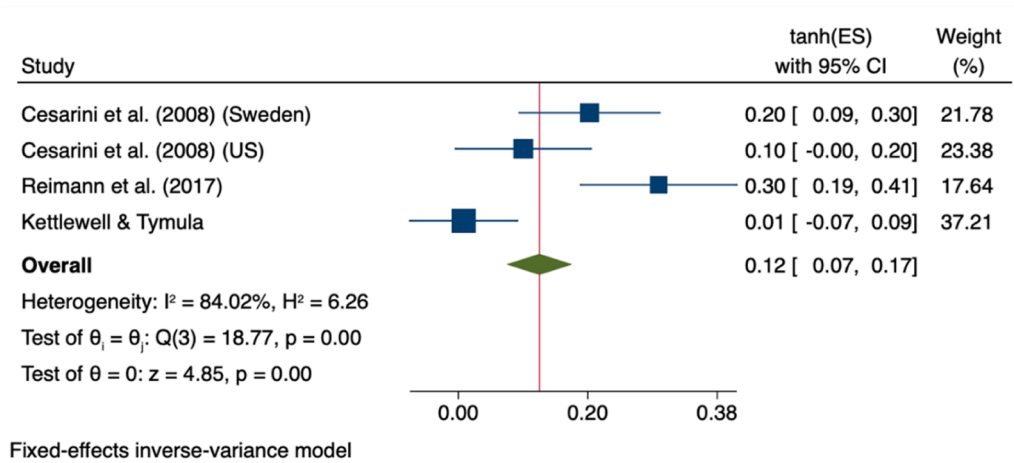
Meta-analysis. Finally, to provide more robust evidence on the heritability of trust, we meta-analyzed the existing literature using the studies listed in Table 1. Fig. 3 presents the forest plots of the studies that provided unconstrained ACE model estimates for stated general trust. We meta-estimate that 33 % of the variation is due to genetic differences, 5 % due to common environment, and 63 % due to unique environment. Based on six papers that provide correlations for MZ and DZ pairs, we find that the meta-analytic correlation for MZ pairs is 0.36 with [0.34 – 0.39] confidence interval which is slightly more than double of the correlation for DZ pairs (0.16 with [0.13, 0.19] confidence interval) (Fig. 5, Table 3). We also present estimates using the simple Falconer decomposition formula, $2*(r_{MZ} - r_{DZ})$, which allows us to include some studies that do not report unconstrained ACE model results, and obtain a slightly higher estimate for the role of genetic variation (39 %).

The meta-analysis reveals that the genetic influences in behavioral trust are lower (Figs. 4 and 5). We meta-estimate that 12 % of the variation is due to genetic differences (significantly less than for the stated general trust), 10 % due to common environment, and 79 % due to unique environmental factors (significantly more than for the stated general trust). Based on three papers that provide correlations of behavioral trust, we meta-estimate that for MZ pairs the correlation is equal to 0.19 with [0.14, 0.25] confidence interval, which is lower than for DZ pairs (0.08 with [−0.01, 0.18] confidence interval) (Fig. 6, Table 3). The Falconer heritability estimate is higher than that obtained using the ACE model estimates (0.25 with [0.13, 0.36] confidence interval), which is driven by much larger estimates for one study.

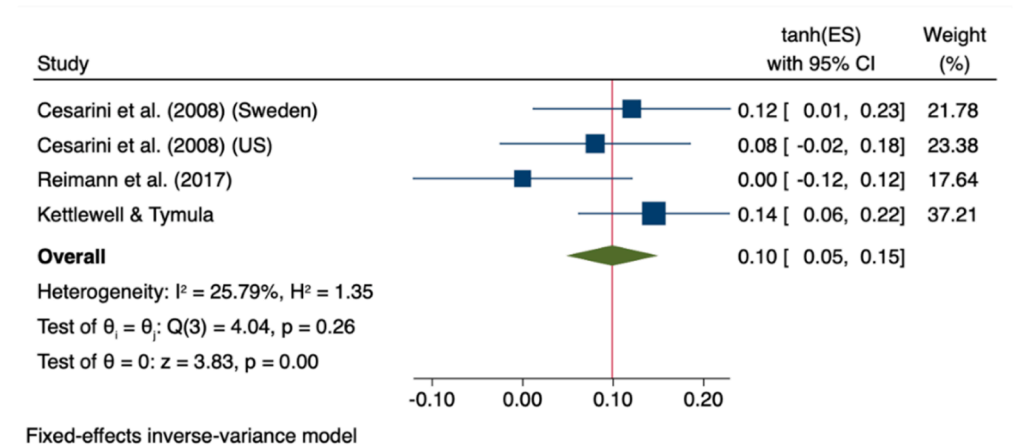
Measurement error. The results from the meta-analysis, including our study, suggest genetic differences explain less variation in behavioral trust than stated generalized trust. One potential explanation for this is that there is more noise in behavioral trust, which forms part of the unique environment variance share, and attenuates estimates for A and C components of the ACE model. While it is difficult to directly address measurement error without repeat measures of the outcome variables (like in e.g., Beauchamp et al., 2017), here we briefly consider how much of the variance in behavioral trust would need to be attributable to classical measurement error to equalize the meta-estimates under the assumptions of the classical twin study decomposition. Taking our meta-estimate of 12 % for behavioral trust, measurement error would need to explain ~64 % of the variation for this to instead be equal to our meta-estimate for stated generalized trust of 33 % (see Supplementary Material for workings). This is even higher if stated trust is measured with error. We are not aware of estimates on the usual degree of error in trust game behavior, but this exercise suggests it would need to be considerable for genes to play an equal role in these different measures of trust.

⁹ To tease out the variation in trust due to unique environment, we first regress own trust on co-twin’s trust by estimating $Y_{ij} = \alpha + \beta Y_{kj} + \epsilon_{ij}$, where Y_{ij} is the trust of twin i in family j and Y_{kj} is the trust of twin k in family j (i.e., the co-twin). The fitted values $\hat{\beta}$ reflect the correlation between Y_{ij} and Y_{kj} , which for MZ twins captures genes (A) and common environment (C). The residuals $\hat{\epsilon}_{ij}$ therefore reflect the variation in Y_{ij} due to everything else i.e., unique environment. Those residuals then serve as our adjusted measures of trust, which are then used for the pairwise correlations with each covariate. We report the correlations for the full sample, without residualizing trust, in Appendix Tables S9-S10.

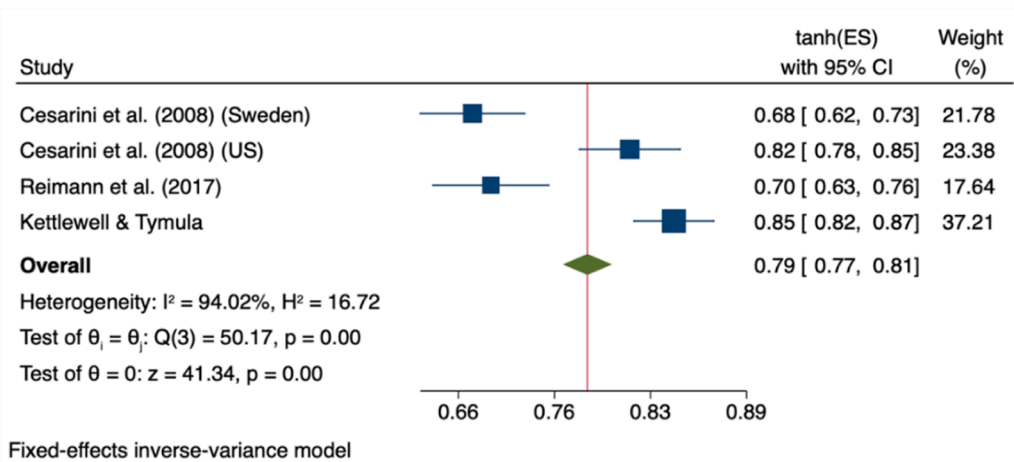
A component



C component



E component



(caption on next page)

Fig. 4. Meta-analysis of the heritability of behavioral trust in the ACE model. For each ACE component, the estimated effect sizes and their 95 % confidence intervals are presented in the “tanh(ES)” column and graphically as squares and lines, respectively. The inverse-variance weight that each estimate received in the meta-analysis is in column “weight” and also represented by the size of the square. The red line and the diamond represent the meta-analytic estimate.

5. Discussion

We contribute to a still relatively small literature that uses twin variation to estimate heritability of trust attitudes and behavior (Table 1). This literature has provided inconsistent point estimates, often with wide confidence intervals, for the heritability of trust, which is unsurprising given differences in the way trust has been measured across studies. We shed light on this variation in the literature in two ways. We are the first study to measure the heritability of trust in the same sample using different trust measures. This allows us to check if the heritability of different measures of trust indeed varies. Moreover, we conduct the first meta-analysis of the heritability of trust which provides more precise evidence on the degree to which trust is heritable.

By decomposing the variation in trust across domains in a multivariate framework, we shed new light on the genetic correlations across these measures. Our results suggest that the correlation between political and stated general trust is partly explained by the same underlying genetic variants (genetic correlation = 0.35), but most other correlations are small or correspond to only weakly correlated phenotypes. Such information on the structure of trust variables can be helpful in maximizing the usefulness of information from molecular genetics. For example, our results suggest that a polygenic score for stated general trust will partly, but not completely, capture the genetic predisposition towards trust in politicians as well.

To aggregate all the existing information on the heritability of trust, we provide the first meta-analysis. Our meta-estimates indicate that the heritability of behavioral trust is in the range of 7 to 17 % while for the stated trust it is 31 to 35 %. This indicates that the degree to which interpersonal differences in trust are due to genetic variation depends on how trust is measured. This is consistent with the findings that these measures are only weakly correlated (corr. coeff. = 0.1347 in our study) and our data showing that they have no overlap in their environmental and socioeconomic correlates. Several studies have compared the external validity of stated and behaviorally measured trust (Banerjee et al., 2021; Falk et al., 2018; Galizzi and Navarro-Martinez, 2019), but ours is the first to compare their genetic foundations. We did not meta-analyze the heritability of political trust or trustworthiness because we found only two studies for each. For political trust our heritability estimate is almost twice as high as in Ojeda (2016) (34% vs 18 %) and not statistically different from the meta-analytic heritability of stated general trust. We estimate the heritability of trustworthiness to be 14 %, which is similar to 17–18 % estimated in (Cesarini et al., 2008).

Economists often favor the trust game over self-reported measures of trust behavior as it measures trusting behavior under controlled conditions, rather than relying on self-beliefs that may be difficult to compare across individuals. However, the interpretation of trust measured in this way may be contentious, with some evidence that behavior in the trust game has low predictive power for past and field social behaviors (Galizzi and Navarro-Martinez, 2019). It also does not strongly correlate with self-reported generalized trust (Alós-Ferrer and Farolfi, 2019). Our results are consistent with differences in trust game behavior being largely driven by unobserved idiosyncratic factors, with genetic variation playing a fairly limited role, at least relative to qualitative measures of trust. To the extent this is due to different degrees of measurement error, our result may reflect a weakness in the one-shot trust game as a general measure of trust. We note, however, that recent research has found that while cooperative behavior in a single round of the Prisoner’s Dilemma (a behavioral game involving trust) is uncorrelated with stated trust, repeated behavior is significantly correlated (Gill and Rosokha, 2020). It may be that behavior across multiple rounds of the trust game would uncover a trait that is more explainable by genetic variation and less idiosyncratic; something that could be investigated in future research.

We estimate that about 34 % of interpersonal differences in political trust is explainable by genetic variation and 63 % is explained by environment that is unique to a twin. The environment common to twins plays only a small role (0–10 % based on confidence interval), suggesting that the degree of trust placed in politicians is not strongly influenced by family upbringing. Overall, people with higher financial security and those who finished university have higher trust in politicians. Political trust, unlike general trust measures, is also highly correlated with beliefs about current events. Our dataset was collected during a pandemic and we found that people who are more worried about health and economic losses due to COVID-19 distrust politicians more. This finding emphasizes the importance of trust in political leaders in times of crisis.

Declaration of competing interest

The authors declare that they have no relevant or material financial interests that relate to the research described in this paper.

Data availability

Data will be made available on request.

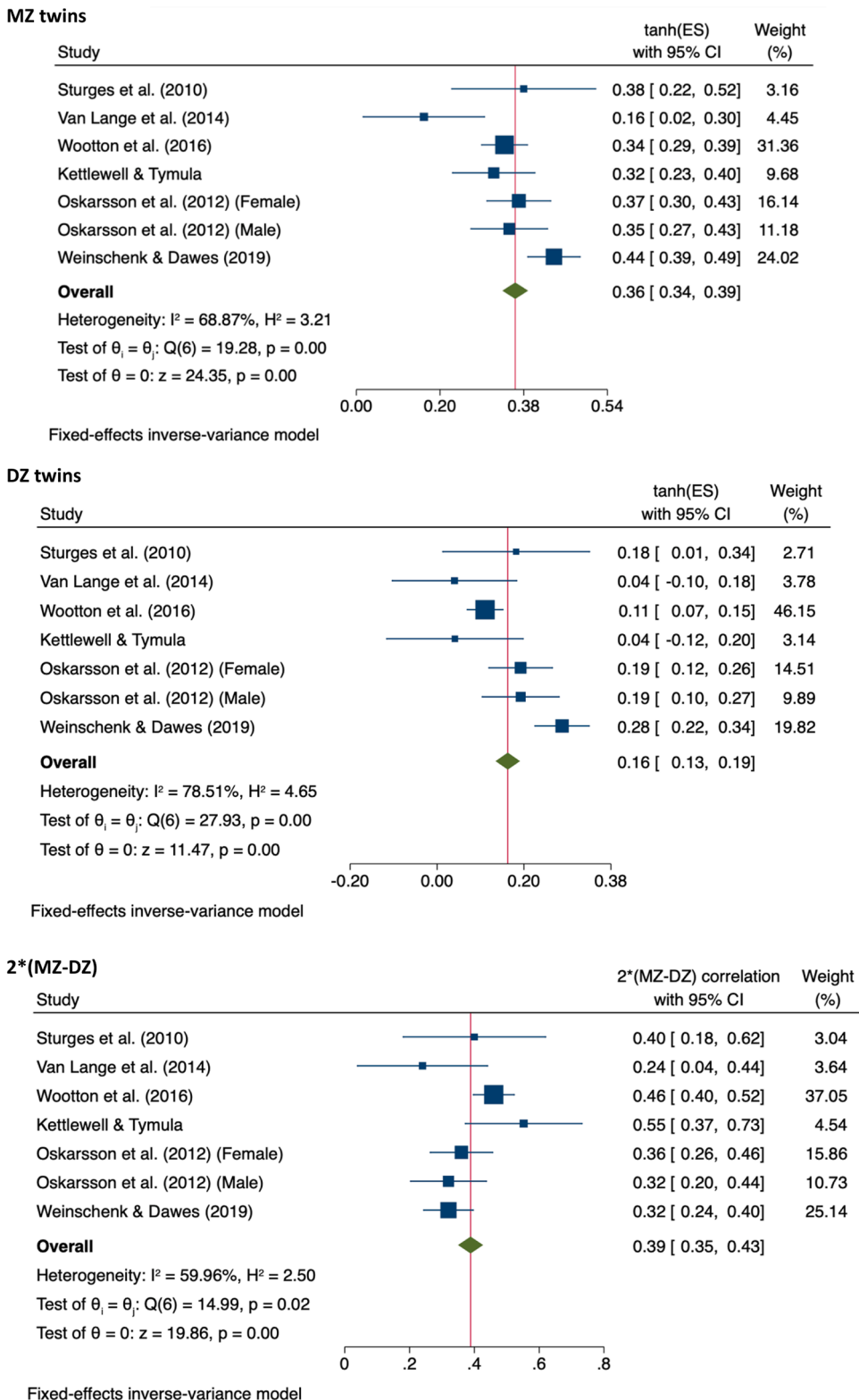
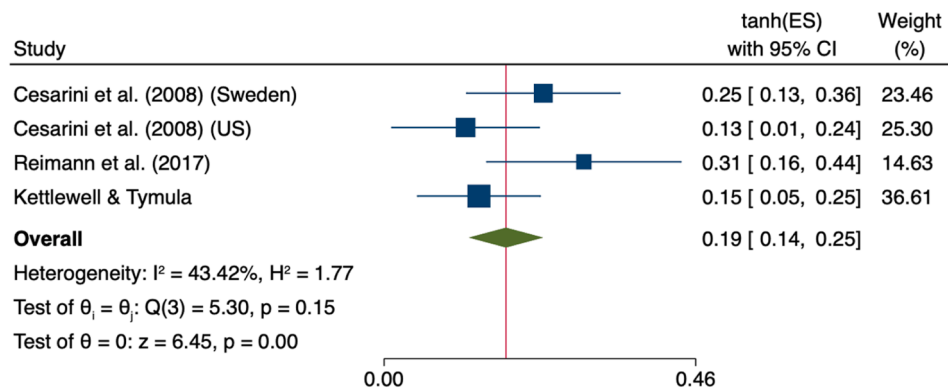


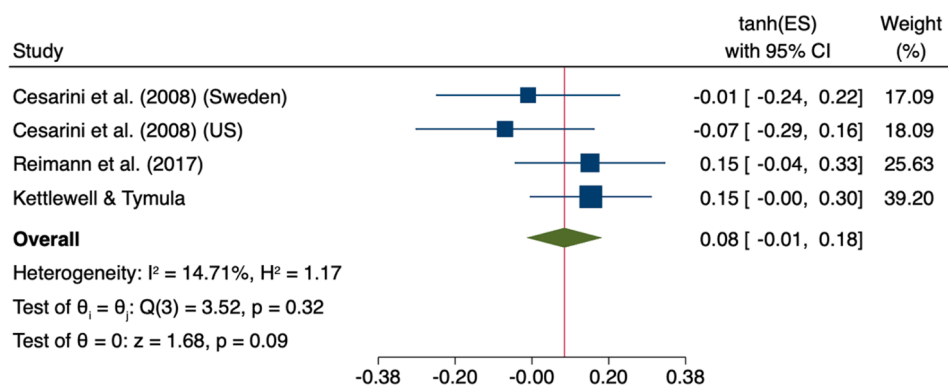
Fig. 5. Meta analysis of twin pair trust correlations (stated general). For each ACE component, the estimated effect sizes and their 95 % confidence intervals are presented in the “tanh(ES)” and “2*(MZ-DZ)” column and graphically as squares and lines, respectively. The inverse-variance weight that each estimate received in the meta-analysis is in column “weight” and also represented by the size of the square. The red line and the diamond represent the meta-analytic estimate.

MZ twins



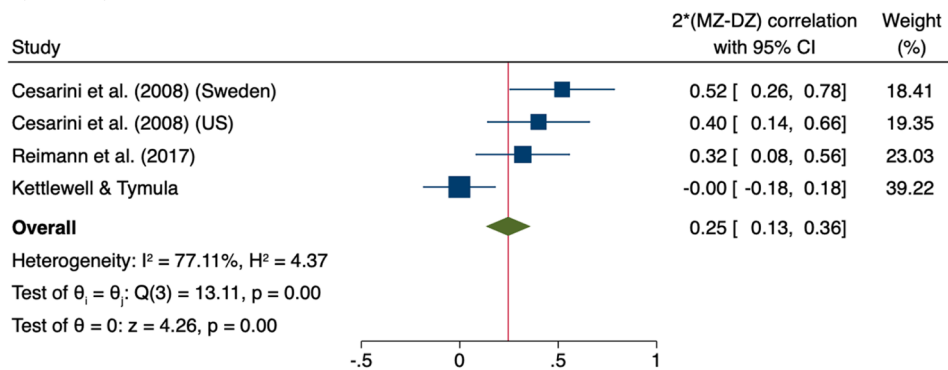
Fixed-effects inverse-variance model

DZ twins



Fixed-effects inverse-variance model

2*(MZ-DZ)



Fixed-effects inverse-variance model

Fig. 6. Meta analysis of twin pair trust correlations (behavioral trust). For each ACE component, the estimated effect sizes and their 95 % confidence intervals are presented in the “tanh(ES)” and “2*(MZ-DZ)” column and graphically as squares and lines, respectively. The inverse-variance weight that each estimate received in the meta-analysis is in column “weight” and also represented by the size of the square. The red line and the diamond represent the meta-analytic estimate.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.jebo.2024.02.008](https://doi.org/10.1016/j.jebo.2024.02.008).

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