Genetic and Environmental Origins of the Co-occurrence of Autistic Traits,

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Abstract

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Full Text

Genetic and Environmental Origins of the Co-occurrence of Autistic Traits,

Anxiety and Depression: Evidence from Meta-analysis and Twin Study

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Background: Prior twin studies have shown genetic and environmental overlap between autistic traits and internalising symptoms. However, it remains unknown whether this overlap reflects a common latent liability or similar aetiological influences operating through independent pathways. We investigated the genetic and environmental origins of the co-occurrence of autistic traits and internalising symptoms with a meta-analysis and an empirical twin study.

Methods: Study 1 meta-analysed six twin studies examining autistic traits and internalising symptoms, predominantly in Western child and adolescent samples. Study 2 applied multivariate genetic modelling to a Chinese community sample of 178 twin pairs (109 monozygotic and 69 dizygotic, aged 24–35).

Results: Study 1 showed genetic (rA = 0.42) and non-shared environmental (rE = 0.15) overlap between autistic traits and internalising symptoms, although substantial heterogeneity was observed across estimates. Study 2 was broadly consistent with the findings of Study 1. It further suggested that the co-occurrence of autistic traits, anxiety and depressive symptoms may be partly explained by a common latent factor shaped by genetic and non-shared environmental influences, although the common pathway model was only tentatively favoured over the independent pathway model.

Conclusion: Across meta-analytic and empirical twin studies, the co-occurrence of autistic traits, anxiety and depressive symptoms appears to be shaped in part by shared genetic and non-shared environmental influences across these three traits. This generally aligns with the transdiagnostic framework of psychopathology. It also highlights that individuals presenting autistic traits may benefit from screening for internalising symptoms, and vice versa.

Keywords: autistic traits; depression; anxiety; internalising symptoms; twin study;

meta-analysis

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Introduction

Autistic individuals frequently experience anxiety and depression, with a pooled prevalence of 39.6% for at least one anxiety disorder (Van Steensel et al., 2011) and 14.4% for a lifetime prevalence of depressive disorders (Hudson et al., 2019). Autistic females show even higher rates of co-occurrence than males (Martini et al., 2022; Rødgaard et al., 2021). This co-occurrence extends beyond clinical populations. Recent studies in community populations similarly demonstrated that autistic traits are associated with anxiety and depressive symptoms across the lifespan (Galán Vera et al., 2026; Liu et al., 2024; Shi & Hirai, 2024). Furthermore, this co-occurrence may arise from similar aetiological mechanisms across clinical and general populations, as molecular genetic liability for autism, depression and anxiety disorders is also associated with corresponding continuous traits (Taylor et al., 2019).

This frequent co-occurrence raises concerns about psychological well-being and treatment effectiveness for autistic individuals. For example, cognitive behavioural therapy may be less effective for internalising symptoms in youths with autistic traits or elevated autism-related genetic liability than in non-autistic peers, though evidence remains mixed across outcome measures and follow-up periods (Andersson et al., 2019; Cervin et al., 2023; Van Steensel & Bögels, 2015). Therefore, better understanding the co-occurrence may inform more effective mental health support.

The co-occurrence of autistic traits and internalising symptoms may arise from a

joint contribution of environmental and genetic influences. Environment or personality-related factors, such as stigma and loneliness associated with autistic people' s minority status and intolerance of uncertainty, have been linked to their lower life satisfaction and anxiety (van Asselt et al., 2026; Shi & Hirai, 2024). Meanwhile, a genome-wide analysis found a significant genetic correlation between internalising symptoms and autism in childhood and adolescence, suggesting common genetic bases (Jami et al., 2022). These lines of evidence together suggest a shared aetiology between autism and internalising symptoms; however, none of them assessed genetic and environmental factors simultaneously.

Twin studies are well suited to address this gap by allowing researchers to estimate the relative contribution of genes and environment. Monozygotic (MZ) twins share almost all genes, whereas dizygotic (DZ) twins share only half on

average. When raised together, higher MZ than DZ resemblance indicates genetic effects. This allows researchers to decompose phenotypic variance and covariance into additive genetic (A), shared environmental (C), and non-shared environmental (E) effects. The "A" captures the cumulative effect of inherited genetic factors; "C" reflects environmental factors shared by both twins (e.g., family housing); and "E" represents environmental influences unique to each individual, with measurement error included (Knopik et al., 2017).

Previous twin studies have examined the aetiological overlap between autistic traits and internalising symptoms. They have uncovered significant genetic, shared environmental and non-shared environmental correlations between autistic traits and

internalising symptoms consistently across childhood, adolescence and adulthood

(Hallett et al., 2009, 2010; Lundström et al., 2011; Micalizzi et al., 2016; Scherff et al., 2014). However, this line of evidence primarily characterises bivariate correlations between autistic traits and anxiety, depression, or a composite of internalising symptoms. It cannot provide a comprehensive account of the aetiological associations across all these phenotypes, while simultaneously distinguishing the unique genetic architecture of anxiety versus depression (Tabrizi et al., 2025; Waszczuk et al., 2014, 2016).

Multivariate modelling addresses this limitation by testing whether common aetiological influences underlie multiple phenotypes, while simultaneously quantifying phenotype-specific effects. To our knowledge, only one study has applied this to autistic traits, anxiety and depressive symptoms. Using a multivariate Cholesky decomposition model, it revealed that genetic and environmental factors underlying a personality trait–environmental sensitivity—also influenced anxiety, depression and autistic traits (Assary et al., 2024).

Beyond Cholesky decomposition, behavioural geneticists have developed more informative hypothesis-testing frameworks for shared aetiology: the independent pathway model (IPM) and common pathway model (CPM) (Knopik et al., 2017; Loehlin, 1996). Both models partition common and phenotype-specific effects, but make different assumptions about how shared influences operate. The IPM assumes that common genetic and environmental factors influence each phenotype directly through separate pathways, whereas the CPM assumes that they act indirectly through

a single latent trait. Comparing these models allows direct evaluations of whether the co-occurrence of autistic traits, anxiety, and depression reflects a common underlying liability or shared influences operating through distinct pathways.

The present research investigated the genetic and environmental origins underlying the co-occurrence of autistic traits, anxiety and depression in two steps. Study 1 meta-analysed existing twin studies to provide an overall assessment

of genetic and environmental overlap between autistic traits and internalising symptoms. We further examined whether this overlap varied across anxiety, depression and a composite of multiple internalising symptoms. Study 2 used a Chinese young adult twin sample to examine whether the shared aetiology of autistic traits, anxiety and depression was better explained by the CPM or the IPM. We hypothesised that the CPM would provide a better account of the covariance among the three traits than the IPM, supporting the presence of a common underlying liability.

Study 1

Methods

Systematic literature search

Following PRISMA guidelines (Page et al., 2021), we conducted a systematic literature search up to the 30th of June 2025, using PubMed, PsycINFO, Scopus and Web of Science. We acknowledge that the literature search and meta-analysis were not prospectively registered, and no formal protocol was registered before screening, data extraction or analysis. The following search query was used for PubMed and adapted for other databases:

("*Autism Spectrum Disorder"[MeSH Terms] OR "Autistic Traits"[Title/Abstract] OR autis*[Title/Abstract] OR ASD[Title/Abstract]) AND ("Anxiety Disorders" [MeSH Terms] OR "Anxiety" [MeSH Terms] OR anxiet*[Title/Abstract] OR depress*[Title/Abstract] OR internali*[Title/Abstract]) AND ("Twin Study" [Publication Type] OR "twins" [Title/Abstract] OR "twin study" [Title/Abstract] OR "co-twin" [Title/Abstract] OR "cross-twin cross-trait" [Title/Abstract] OR CTCT[Title/Abstract])

We included studies that: (i) recruited MZ and DZ human twin pairs of any age; (ii) assessed autistic traits using validated quantitative measures; (iii) assessed internalising symptoms (i.e., anxiety, depression or a composite internalising score) via validated quantitative measures; (iv) reported, or allowed computation for, additive genetic correlations (rA), shared environmental correlation (rC), and non-shared environmental correlation (rE) between autistic traits and internalizing symptoms; and (v) were published as peer-reviewed, English-language full-text articles. We excluded studies that: (i) involved non-human samples; (ii) lacked twin-specific analyses; (iii) did not report sufficient information to extract or compute the required data; (iv) were reviews, meta-analyses, commentaries, or conference abstracts.

The initial search yielded 200 unique results. Titles and abstracts were screened according to the inclusion criteria, resulting in 44 papers for full-text review. After further screening, six articles met all criteria and were included (Supplementary Fig. 1).

Two reviewers assessed the methodological quality and risk of bias of included

studies using the Joanna Briggs Institute Critical Appraisal Checklist for Analytical Cross-

Sectional Studies (Barker et al., 2026), and disagreements were resolved through discussion (Supplementary Table 1).

Data coding

We employed a standardised extraction procedure to extract (i) study characteristics (author, year of publication, country/registry); (ii) sample characteristics (MZ/DZ twin counts, age groups); (iii) instrument used for autistic traits and internalising symptoms; (iv) additive genetic correlations (rA), shared environmental correlation (rC), and non-shared environmental correlation (rE) for each trait pair. Extracted data were cross-checked for consistency.

When sample sizes varied for parameters within a study, to avoid overestimating the precision of pooled estimates, we conservatively used the smallest available sample size for that correlation. For research reporting sex-specific correlations, we applied Fisher' s Z transformation to each coefficient, calculated a weighted average by sample sizes and back-transformed them to Pearson' s r (Borenstein et al., 2009). We treated each unique combination of cohort, age group, and/or instrument as a separate entry, even within the same study, to preserve specificity and maximise data use (Table 1).

Data analysis

We conducted random-effect meta-analyses of correlation coefficients (rA, rC, rE) in R 4.5.2 using the *meta* package (v8.2.0). To account for dependency between entries from the same cohort, either across different ages or internalising symptoms, we fitted a three-level random-effect meta-analysis with cohort specified as the clustering variable. Random-effect models were fitted using restricted maximum-likelihood

estimation (REML). Coefficients were transformed to Fisher' s z to stabilise variance, weighted by the number of twin pairs and back-transformed to Pearson' s r for interpretation. For all pooled estimates, we obtained 95% confidence intervals. We assessed the between-entry heterogeneity using Cochran' s Q, the proportion of variance due to heterogeneity (I^2), and the between-study variance (τ^2).

Using the same approach, we conducted subgroup meta-analysis to calculate pooled estimates separately for the correlations between autistic traits and each indicator of internalising symptoms: anxiety (ANX), depression (DEP), and the composite of multiple symptoms (INT). Given the small number of studies per subgroup, Hartung-Knapp adjustment was used when estimating confidence intervals (Knapp & Hartung, 2003).

Next, we fitted multilevel meta-regression models with the *metafor* package (v4.8.0) to test whether the genetic and environmental correlations varied across

the three internalising phenotypes (ANX, DEP, INT). The internalising phenotypes were entered as a categorical moderator, with REML estimation applied. Cohorts were treated as a clustering variable in the multilevel model to account for covariance among entries from the same cohort. Pairwise differences were tested on Fisher' s z scale, and p-values were adjusted using Bonferroni correction.

We made funnel plots for each correlation coefficient. Separate plots by internalising phenotype and by cohort were generated when at least three estimates were available. Formal tests of funnel plot asymmetry were not conducted because of the small number of available studies (Sterne et al., 2011). The completed PRISMA

checklist is provided in Supplementary Table 2.

Results

Small to moderate effect sizes were observed for the pooled additive genetic and non-shared environmental correlations between autistic traits and internalising symptoms: rA = 0.42, 95% CI [0.24, 0.57], $p < .001$; rE = 0.15 [0.11, 0.19], $p < .001$. However, there was substantial heterogeneity across estimates ($Q_A(11) = 1715$, $p < .001$, ${I_A}^2 = 99\%$; $Q_E(11) = 164$, $p < .001$, ${I_E}^2 = 93\%$), indicating considerable variability across entries. The pooled shared environmental correlation was very high, rC = 1 [0.75, 1.00], $p = .015$. Given the boundary estimate and extreme heterogeneity across entries ($Q_C(9) = 319972$, $p < .001$, ${I_C}^2 = 100\%$), the pooled shared environmental correlation may reflect statistical boundary or numerical instability issues rather than a genuine effect and should therefore be interpreted with caution. Fig. 1 shows pooled estimates for all internalising symptoms combined, as well as for anxiety, depression and the composite of multiple symptoms, separately.

For rA, rC and rE, the multilevel meta-regression analyses revealed negligible differences across anxiety, depression and the composite of internalising symptoms after Bonferroni correction (Supplementary Table 3). Funnel plots are presented in Supplementary Fig. 2-3.

Study 2

Methods

Participants

Participants were drawn from the Beijing Twin Study (BeTwiSt), a longitudinal

twin sample in Beijing followed from adolescence into adulthood (Chen et al., 2013).

The present study used data from 194 twin pairs (50.7% female, aged 24-35)

collected in 2023. We excluded nine pairs without zygosity information, one opposite-sex twin pair and six pairs for incomplete data (i.e., only one twin responded). In the final sample of 178 same-sex twin pairs, 165 pairs' zygosity was determined by DNA testing with classification accuracy approaching 100%. For the remaining 13 pairs without DNA data, zygosity was determined using a validated questionnaire assessing physical similarity and frequency of mistaken identity between co-twins, which yields 91% predictive accuracy (Chen et al., 2010). The study was approved by the Ethics Committee of the Institute of Psychology, Chinese Academy of Sciences. All participants provided informed consent and received compensation of about 30 US dollars.

Measures

Autistic traits (AUT). We measured autistic traits using the validated Chinese version of Autism-Spectrum Quotient (AQ) (Baron-Cohen et al., 2001; Zhang et al., 2016). The AQ is a 50-item questionnaire for autistic traits in adults with five subfactors: social skills, attention switching, imagination, attention to detail, and communication. Items were rated on a 4-point Likert scale ("definitely agree" to "definitely disagree") and dichotomously coded (0 = absence, 1 = presence of an autistic trait). Higher total scores indicate greater autistic traits. Internal consistency in this sample was acceptable (McDonald' s $\omega = 0.88$, Cronbach' s $\alpha = 0.65$).

Trait anxiety (ANX). We measured trait anxiety using the Chinese version of the

Trait Anxiety Inventory (TAI; Spielberger et al., 1971). It consists of 20 items that reflect individuals' general anxiety tendencies, with good reliability and concurrent validity (Shek, 1993). Participants responded on a 4-point Likert scale (1-4), ranging from "almost never" to "almost always" . Higher scores indicate greater trait anxiety. Internal consistency was excellent in this sample (McDonald' s $\omega = 0.94$, Cronbach' s α =0.92).

Depressive symptoms (DEP). We measured depressive symptoms using a Chinese version of the original Beck Depression Inventory (BDI), a widely used 21-item self-report scale developed to assess the intensity of depressive symptoms (Beck et al., 1961; Shek, 1991). Each item describes a specific symptom and is rated on a 4-point scale (0-3), with higher scores reflecting greater intensity. Internal consistency in this sample was excellent (McDonald' s $\omega = 0.95$, Cronbach' s $\alpha = 0.91$).

Data analysis

Data preparation. As the raw scores deviate mildly from normality (Table 2), we applied the Yeo-Johnson transformation (Yeo & Johnson, 2000). We standardised all variables to facilitate interpretation and meet the assumption of twin modelling (Neale & Cardon, 1992). Before modelling, age and sex were regressed out, following standard practice in twin analyses (McGue & Bouchard, 1984).

Twin correlations. For anxiety, depression and autistic traits, we calculated intraclass correlation coefficients (ICCs) separately for MZ and DZ pairs to assess twin similarity. A higher ICC between MZ twins suggests a genetic influence. We also computed cross-twin cross-trait (CTCT) correlations between Twin 1' s score on one

trait and Twin 2' s score on another trait. Greater CTCT correlations in MZ pairs indicate potential genetic covariance between the two traits.

Univariate genetic modelling. We fitted univariate ACE models to decompose the trait variance into A, C and E components. We specified full ACE models and then compared them against nested AE, CE and E models to identify the most parsimonious model.

Bivariate genetic modelling. Bivariate twin models were used to estimate the sources of covariance. We fitted correlated factors models that decompose each trait variance into A, C and E components while estimating cross-trait correlations between the corresponding components (rA, rC, rE; Supplementary Fig.4). Nested AE, CE and E models were evaluated and compared against the full model. We then calculated the proportion of phenotypic correlations accounted for by A, C and E.

Multivariate genetic modelling. To examine the shared aetiology of autistic traits, anxiety and depression, we fitted the independent pathway model (IPM, Supplementary Fig. 5) and the common pathway model (CPM, Supplementary Fig. 6). We compared the model fit between CPM and IPM to determine which model provided a better account for the observed data. After identifying the preferred model, we compared the full ACE model with its nested AE, CE and E sub-models.

Model fit evaluation. We evaluated all the model fits using OpenMx (v2.22.11) in R. We conducted parameter estimation using the full information maximum likelihood estimation, which accommodates raw continuous data and provides robust parameters and fit indices. Model fits were compared via the chi-square (χ^2) difference test and

Akaike' s Information Criterion (AIC). A non-significant χ^2 difference indicates equivalent fit to the data (Bollen, 1989). When χ^2 differences are non-significant, lower AIC values were considered the criterion for choosing the optimal model (Akaike, 1987). Sensitivity analysis was conducted by repeating the main analyses after excluding twin pairs with only questionnaire-based zygosity information.

Statistical Power for Genetic Analyses. We estimated the minimum detectable effect size for our sample using the package *pwr* (v1.3.0) in R. With a sample size of $N = 178$ and 1 degree of freedom (df) (i.e., estimating one effect each time), path parameters with standardised estimates $\geq .186$ could be detected with adequate statistical power (80%), at a significance level of $\alpha = .10$. For model comparison between the IPM and the CPM ($\Delta dfs = 6$;

Supplementary Table 9), the minimum detectable effect size was $w = .250$ at a $\alpha = .10$ and 80% power. We then calculated the threshold of the test statistics (χ^2) according to the formula $\chi^2 = w^2 \times N$. This yielded a χ^2 value of 11.13. Therefore, a model fit difference ($\Delta - 2LL$) between the IPM and CPM of 11.13 or greater would have adequate power for model comparison.

Results

Descriptive statistics

The final sample included 178 same-sex twin pairs (51.7% female; age range: 24-35, $M = 28.85$, $SD = 2.48$), comprising 109 monozygotic (MZ) and 69 dizygotic (DZ) pairs (see Supplementary Table 4 for additional sample characteristics). Table 2 presents descriptive statistics, including means, standard deviations, skewness, kurtosis, and phenotypic correlations.

Twin correlations

For autistic traits, the ICC for MZ twins was moderate (rMZ = 0.299 [0.118, 0,461]), but small and non-significant for DZ twins (rDZ = 0.173 [-0.064, 0.392]). Similar patterns emerged for anxiety (rMZ = 0.256 [0.073, 0.423]; rDZ = 0.078 [-0.160, 0.307]) and depression (rMZ =0.297 [0.116, 0.458]; rDZ = 0.047 [-0.189, 0.279]). The higher ICC estimates observed for MZ twins than DZ twins across all traits descriptively suggest genetic contributions to all three traits. Notably, this interpretation should be made cautiously as all DZ confidence intervals included zero. The CTCT correlations ranged from small to moderate in both MZ and DZ twins (Supplementary Table 5); however, as most confidence intervals included zero, we cannot make meaningful comparisons between MZ and DZ twins. This also limits the ability to reliably distinguish additive genetic effects from shared environmental effects. Consequently, estimates of additive genetic and shared environmental effects in subsequent genetic modelling should be interpreted cautiously.

Univariate modelling

Univariate model-fitting results revealed that the AE models provided a better fit than the full ACE models and other sub-models across autistic traits, anxiety and depressive symptoms (Supplementary Table 6). Standardised estimates from the AE models showed modest additive genetic effects and large non-shared environmental effects across all three traits. Additive genetic components accounted for 30.8% [14.4%, 45.3%]) of variance in autistic traits, 25.0% [8.1%, 40.3%] in anxiety and 25.3% [7.5%, 41.4%] in depression. Non-shared environmental factors explained the remaining

variance, contributing 69.2% [54.7%, 85.6%] in autistic traits, 75.0% [59.7%, 91.9%] in anxiety and 74.7% [58.6%, 92.5%] in depression. To note, these es-

timates for non-shared environmental factors also incorporated measurement error besides true environmental influences unique to individuals.

Bivariate modelling

Consistent with univariate modelling results, bivariate model comparisons also indicated that the AE models provided the best fit for both the association between autistic traits and anxiety and that between autistic traits and depression (Supplementary Table 7). Supplementary Table 8 presents the estimates for genetic and non-shared environmental effects based on the best-fitting models. Moderate genetic correlations were observed between autistic traits and anxiety (rA = 0.438) and between autistic traits and depression (rA = 0.453), indicating that common genetic factors partly underlie the co-occurrence. However, given the wide confidence intervals with lower boundaries slightly below zero, these genetic correlations require cautious interpretation. We also found modest-to-moderate non-shared environmental correlations between autistic traits and both anxiety and depression (rE_AUT-ANX = .425, rE_AUT-DEP = 0.263).

Common vs independent pathway models

Model-fit statistics are presented in Supplementary Table 9. The chi-square difference between the IPM and CPM was non-significant ($\Delta\chi^2 = 1.37$, $p = .968$) and below the pre-specified power threshold of 11.13. However, the CPM showed a lower AIC value, providing tentative support for a shared latent factor underlying the

covariance among autistic traits, anxiety and depression. Among the CPM sub-models, the AE model (aeCPM) showed the lowest AIC value and did not differ significantly from the full model, thereby being considered optimal.

In aeCPM, the specific genetic path for anxiety (as2 in Fig. 2a) approximated zero. We therefore fixed as2 to zero and tested a more parsimonious sub-model (aeCPM2; Fig. 2b). The aeCPM2 model showed no significant deviation from the aeCPM model and a lower AIC value. Thus, the aeCPM2 model was considered the final optimal model.

Results of the aeCPM2 model showed that autistic traits, anxiety and depression covaried through a shared latent factor, with its influence on each trait manifested at both genetic and non-shared environmental levels (Table 3). This common latent factor explained 21.6% of phenotypic variance in autistic traits, with trait-specific genetic and environmental effects playing a larger role. The contribution of the common factor to depression explained nearly half (47.1%) of its phenotypic variance. For anxiety, the common latent factor was the predominant (85.3%) source of its phenotypic variance, while trait-specific influences accounted for only 14.7%.

In summary, the common latent factor accounted for substantial variance in both anxiety and depressive symptoms, but only moderate variance in autistic

traits. Results of the sensitivity analysis excluding twins without DNA-based zygosity were highly consistent with these full-sample findings (Supplementary Tables 10, 11; Supplementary Fig. 7).

General Discussion

This research examined why autistic traits frequently co-occur with anxiety and depression using a sequential two-study design. The meta-analysis in Study 1 showed that autistic traits and internalising symptoms are associated via common genetic and environmental influences. Study 2 empirically tested these associations in an independent twin sample and observed patterns broadly consistent. It further showed that autistic traits, anxiety, and depression may reflect a broader underlying vulnerability shaped by both genetic and non-shared environmental factors. Importantly, Study 2, as the first evidence from a non-Western sample, extended the generalisability of these findings.

Theoretical interpretation

Both studies uncovered genetic and non-shared environmental overlap between autistic traits and internalising symptoms with generally comparable effect sizes, except for a larger non-shared environmental correlation between autistic traits and anxiety in Study 2. However, Study 1 synthesised predominantly Western child and adolescent samples, and Study 2 examined a Chinese adult sample. Given these substantial differences in age, culture and measurement instruments, the convergence should be interpreted as evidence for broadly similar patterns of association rather than identical aetiological processes across development or populations.

Extending prior work, Study 2 suggested a common latent factor bridges the genetic and non-shared environmental links among anxiety, depression and autistic traits. Previous studies proposed environmental sensitivity and intelligence as candidates for this shared liability. Assary et al. (2024) found that genetic and

environmental influences on environmental sensitivity explained 2% of the variance in anxiety, 12% in depression and 11% in autistic traits. Another study found that genetic, but not environmental, effects on intelligence partly explained variations (3–4%) in autistic traits and anxiety (Bruins et al., 2024). However, these proportions are much smaller than the variance accounted for by the latent factor in the current study (21%–89%), suggesting that the shared liability may encompass broader psychosocial and neurobiological processes.

A notable difference between the two studies was the stronger non-shared environmental correlation between autistic traits and anxiety in Study 2 ($rE = 0.43$) versus Study 1 ($rE = 0.10$). One possible explanation is the cross-cultural differences. Chinese culture emphasises social harmony and minimising interpersonal conflict (Wei & Li, 2013). This could be associated with increased sensitivity to interpersonal differences related to autistic traits (e.g., differences in communi-

cation, reciprocity, or flexibility), which potentially heightens the environmental pathways linking anxiety to autistic traits. However, this interpretation remains speculative, as cultural variables were not directly measured, and the Chinese sample recruited from a single city may lack broader representativeness.

The discrepancy may also reflect developmental and methodological differences. Non-shared environmental effect on internalising symptoms increases with age (Nivard et al., 2015; Petkus et al., 2016). Self-report measures typically yield higher non-shared environmental estimates than parent-report measures (Chen et al., 2015; Nivard et al., 2015). While Study 2 examined adults using self-report measures, most

samples in Study 1 involved parent-report symptoms in childhood and adolescence (Hallett et al., 2009; Lundström et al., 2011). Additionally, the modest sample size, slightly imbalanced MZ-to-DZ ratio and wide confidence intervals for twin correlations further warrant cautious interpretation. These considerations suggest that culturally sensitive approaches might be useful for understanding the aetiological overlap between anxiety and autistic traits; however, more conclusive interpretation requires future cross-cultural twin studies with larger developmentally matched samples, balanced MZ-to-DZ ratios, and direct cultural variables measured.

Results also differ in shared environmental effects. Study 2 found no significant shared environmental effect on all three phenotypes, and consequently no meaningful shared environmental correlations were expected. In contrast, Study 1 provided evidence of significant shared environmental correlations. This may partly reflect age differences. Most studies included in Study 1 were based on children and adolescents, whereas Study 2 examined adults. Previous twin studies of late adolescents and adults have also reported negligible shared environmental influences on autistic traits, anxiety, and depression (Assary et al., 2024; Lundström et al., 2011). However, this age effect should be interpreted cautiously. The modest sample size and relatively small number of DZ pairs in Study 2 limited power to detect shared environmental effects, and non-significant DZ correlations reduced the ability to distinguish shared environmental from genetic influences.

Additionally, the shared environmental correlations observed in Study 1 were accompanied by substantial heterogeneity. The estimates approaching one in many

entries may not indicate complete shared environmental overlap but rather a statistical boundary or numeric instability. Therefore, the current study cannot support definitive conclusions about differences in shared environmental effects across samples.

Clinical implications

The CPM suggests that a common aetiological factor partly explains the co-variation among autistic traits, anxiety and depressive symptoms. This aligns with the transdiagnostic model of psychopathology that co-occurring psychiatric phenotypes arise from underlying liabilities transcending traditional diagnostic boundaries (Krueger & Eaton, 2015). The genetic influence on this common factor is consistent with molecular genetic evidence showing genetic correlations between autism and internalising symptoms (Jami et al., 2022; Salenius et al., 2024; Thorp et al., 2021). The non-shared environmental influence further suggests individual-specific experiences (e.g., loneliness and bullying victimisation) may link to the covariation between these traits (Hymas et al., 2024; Trundle et al., 2023).

Clinically, these findings suggest that the co-occurrence of autistic traits and internalising symptoms is not incidental. Individuals with elevated autistic traits may benefit from routine assessments of anxiety and depression, and vice versa. Such assessment may be particularly important because anxiety and depression associated with autism-related liability may differ in their responsiveness to treatment (Andersson et al., 2019; Cervin et al., 2023).

These implications should be regarded as tentative, as the generalisability of findings from a community sample to clinical populations remains to be established.

Nevertheless, existing evidence supporting continuity between community and clinical presentations of autistic traits, anxiety and depression suggests that the observed patterns may have relevance beyond general populations (Bralten et al., 2018; Plomin et al., 2016; Taylor et al., 2019; Thorp et al., 2021).

Limitations and future directions

Our study has several limitations. First, the meta-analysis in Study 1 was restricted to six studies spanning different ages, countries and diverse measurements. Some reported relatively low internal consistency for their measurement (e.g., Cronbach' s $\alpha = .55 - .58$ for affective problems in Micalizzi et al., 2016), which may attenuate estimated associations and contribute to heterogeneity across estimates. The substantial heterogeneity and wide confidence intervals underscore the uncertainty of these estimates. Therefore, the findings should not be interpreted as conclusive evidence regarding the aetiological relationships between autistic traits and internalising symptoms. The limited study number also precluded further stratification or subgroup analyses, particularly those testing the potential confounding effect of age, and prevented statistical assessments of publication bias, such as Egger' s test. More twin studies across diverse cohorts are needed to facilitate a more robust meta-analytic evaluation.

Second, the Chinese adult twin sample in Study 2 was modest in size and included relatively few DZ pairs, although such MZ-to-DZ imbalances are common

in Chinese and other Asian populations (Ding et al., 2013; Hall, 2003; Tong et al., 1997). Consequently, the study may lack sufficient statistical power to detect small additive

genetic or shared environmental effects (Verhulst, 2017), and to reliably distinguish between the IPM and CPM. Moreover, the modest sample size resulted in wide confidence intervals for twin correlation estimates, heritability and non-shared environmental effects, although the point estimates were comparable to those reported in the previous study of adult twins (Lundström et al., 2011). Many confidence intervals of twin correlations included zero, making it difficult to reliably distinguish additive genetic effects from shared-environmental effects and further reducing the precision of subsequent twin modelling. Also, the limited sample size and the modest sex-specific twin pairs (e.g., 32 male DZ pairs) precluded us from examining potential sex differences in genetic and environmental effects, which typically required over 1,000 twin pairs (Verhulst, 2017). Therefore, our findings should be considered preliminary and require replication in larger twin samples with a more balanced zygosity ratio.

Third, all measures of Study 2 relied on self-report questionnaires, which are susceptible to response biases. Shared method variance may also inflate phenotypic correlations, potentially biasing the aetiological estimates. Future studies should employ multi-method measurement, for instance, including informant reports and interview-based symptom assessments in addition to self-report measures.

Finally, the multivariate twin analyses in Study 2 were not pre-registered. Thus, the post-hoc model modifications should be interpreted as exploratory. In addition, our selection between the CPM and IPM mainly relied on differences in AIC values, without significant chi-square differences. Given these conditions and the uncertainty

in path estimates introduced by the limited power, our findings should be regarded as preliminary. Future replications with independent twin samples are warranted.

Conclusion

This study combined a meta-analysis of existing twin studies with data from a Chinese twin sample to examine the aetiological overlap among autistic traits, anxiety and depression. Across both studies, the co-occurrence of these phenotypes was accounted for by genetic and non-shared environmental influences. Furthermore, findings from the CPM suggest that this overlap may be partly explained by a common latent liability shaped by both genes and non-shared environments. These findings advance our understanding of the co-occurrence of autistic traits and internalising symptoms and are broadly consistent with transdiagnostic models of psychopathology. They highlight the importance of considering anxiety and depression in the assessment and treatment of individuals with elevated autistic traits, and vice versa.

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Declaration of generative AI use

During the preparation of this work, the authors used Grammarly and ChatGPT (version 5) in order to improve the phrasing and check grammar. After using these tools, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

Glossary

Twin study: A design comparing monozygotic and dizygotic twins to estimate genetic and environmental contributions to individual differences in traits or behavior.

Additive genetic factors (A): Genetic effects that sum across alleles and contribute to trait variation.

Shared environmental factors (C): Environmental influences that make individuals in the same family more similar.

Non-shared environmental factors (E): Environmental influences that are unique to each individual and thus contribute to differences between members of the same family.

Genetic correlation: The extent to which genetic influences on one trait correlate with those on another trait.

Shared environmental correlation: The extent to which shared environmental influences on one trait correlate with those on another trait.

Non-shared environmental correlation: The extent to which non-shared environmental influences on one trait correlate with those on another trait.

Cross-twin cross-trait correlation: The correlation between one twin's level on trait A and their co-twin' s level on trait B. Such a correlation is used to infer genetic (or environmental) effects on the phenotypic correlation between traits A and B.

Univariate twin model: A structural equation model decomposes the variance of a single trait into genetic influences, shared environmental influences and non-shared

environmental influences, with non-shared environmental effects also including measurement errors.

Bivariate correlated factor model: A structural equation model that estimates the covariance between two traits by modelling correlations between their

genetic, shared environmental, and non-shared environmental components.

Common pathway model: A structural equation model where a single latent variable accounts for the covariance between multiple traits and is itself influenced by genetic and environmental factors. Each trait also has its own specific A, C, and E components, which capture influences unique to that trait beyond the common pathway.

Independent pathway model: A structural equation model where the same genetic factor, shared environmental factor and non-shared environmental factor directly affect multiple traits, without loading onto a single common latent variable. Each trait also has its own specific A, C, and E components that capture unique influences not shared with other traits.

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Tables

Table 1. Summary of Twin Studies on Autistic Traits (AUT) and Anxiety (ANX), Depression (DEP) or a Composite of Internalising Symptoms (INT)

Twin cohort[a]	Nationality	Age	N total (% female)	N_{MZ} pairs	N_{DZ} pairs	AUT measure[b]	Internalising measure[b]	Internalising Construct	rA[g]	rC[g]	rE
Hallett et al. (2009)	TEDS	British	8	6466 (53%)	1193	2039	CAST-31 (P)	ARBQ	ANX[c]	0.12	0.96	0.07
			9	6466 (53%)	1193	2039	CAST-20 (T)	SDQ-Emo (T)	INT	0.19	1.00[f]	0.25
Hallett et al. (2010)	TEDS	British	7–8	11325 (52%)	2028	3635	CAST-31 (P)	SDQ-Emo	INT	0.17	1.00[f]	0.08
			12	11185 (53%)	2020	3570	CAST-31 (P)	SDQ-Emo	INT	0.17	0.22	0.14
Lundström et al. (2011)	CATSS	Swedish	9, 12	11222 (49%)	1562	3823	A-TAC-12	A-TAC-6	ANX	0.53	0.95	0.07
	SATSA	Swedish	26–52	18349 (60%)	2310	4909	A-TAC-12	DSM4-GAD	ANX	0.51	0.82	0.10
							A-TAC-12	DSM4-DEP	DEP	0.53	0.76	0.21
Scherf et al. (2014)[e]	TEDS	British	12, 14	4516 (54%)	841	1417	AQ (P)	SDQ-Emo	INT	0.20	1.00[f]	0.16

Twin cohort[a]	Nationality	Age	N total (% female)	N_{MZ} pairs	N_{DZ} pairs	AUT measure[b]	Internalising measure[b]	Measured Construct	rA[g]	rC[g]	rE
Micali et al. (2016)	BJTP	American	2	620 (47%)	143	167	CBCL PDD	CBCL Aff	DEP	0.27	1.00[f]	0.24
			3	608 (47%)	137	167	CBCL PDD	CBCL Aff	DEP	0.56	1.00[f]	0.17
Assary et al. (2024)	TEDS	British	17	5888 (58%)	518	1039	AQ (S)	ARBQ	ANX	0.35	–[d]	0.18
				5888 (58%)	518	1039	AQ (S)	MFQ-13	DEP	0.41	–[d]	0.17

Note:

a. Abbreviations for twin cohorts:

TEDS: Twins Early Development Study

CATSS: Child and Adolescent Twin Study in Sweden

SATGE: Study of Twin Adults: Genes and Environment

BUTP: The Boston University Twin Project

b. Abbreviations for measurement instruments:

CAST-31 (P): parent-reported 31-item Childhood Asperger Syndrome Test.

CAST-21 (T): teacher-reported shortened 20-item Childhood Asperger Syndrome Test.

ARBQ: parent-reported Anxiety Related Behaviours Questionnaire.

SDQ-emo: the Emotional scale of the Strengths and Difficulties Questionnaire (T labelled as teacher-reported).

A-TAC-12: 12 items chosen from the Autism -Tics, ADHD, and other Comorbidities inventory (A-TAC) assessing the DSM-IV algorithm for the identification of autism.

A-TAC-6: 6 items chosen from the A-TAC assessing anxiety.

DSM4-GAD: 6 DSM-IV-based items used to identify generalised anxiety disorder.

DSM4-DEP: 9 DSM-IV-based items used to identify possible major depression.

AQ (P): abridged 24-item version of the parent-reported Autism Spectrum Quotient (AQ).

CBCL-PDD: 13 items from the Child Behaviour Checklist (CBCL) Pervasive Developmental Problems DSM-Oriented Scale, consistent with DSM diagnostic criteria for autism.

CBCL-Aff: 10 items from the CBCL Affective Problems DSM-Oriented Scale relating to major depressive disorder.

AQ (S): 13-item abbreviated self-reported AQ.

MFQ-13: 13 items from the short Mood and Feeling questionnaires.

c. It is originally conceptualised as measuring a composite of internalising traits. However, as the questionnaire was used to assess anxiety-related behaviour, we decided to put it in the anxiety estimation group.

d. The final model in Assary et al. (2024) did not include the C components. As a result, rC was not estimated.

e. The original values in Scherff et al. (2014) were reported separately for males and females. To obtain a single estimate, we computed a weighted average using Fisher' s z-transformed correlations and the respective sample sizes for each sex. As the reported rC for females in Scherff et al. (2014) was 1.00, which is undefined under Fisher' s z-transformation. We substituted it with an adjusted value of 0.999999, calculated by subtracting a small constant ($\epsilon = 0.000001$) from 1.00 to enable Fisher' s z-transformation. The estimated rA for female and rC for male are non-significant.

f. The rCs in these samples were 1.00, which is undefined under Fisher' s z-transformation. When carrying out the meta-analysis, we substituted them with an adjusted value of 0.999999, calculated by subtracting a small constant ($\epsilon = 0.000001$) from 1.00 to enable Fisher' s z-transformation.

g. Grey font indicates non-significant estimates extracted from the original studies, where the 95% confidence intervals included zero.

Table 2. Descriptive statistics and phenotypic correlations across the three traits

	N	Mean	SD	Min	Max	Range	Skewness	Kurtosis	1	2	3
AUT	355	21.28	5.47	7	35	28	-0.19	-0.46	—		
ANX	356	40.62	9.57	20	74	54	0.32	-0.14	0.43***	—	
DEP	356	8.25	8.68	0	47	47	1.55	2.62	0.30***	0.67***	—

Note:

AUT = autistic traits; ANX = anxiety; DEP = depression; N = number of participants; SD = Standard Deviation. $^{***}p < .001$

Table 3. Standardised variance decomposition for Autistic Traits (AUT), Anxiety (ANX), and Depression (DEP) in the best-fitting common pathway model

Traits	common A	specific A	common E	specific E
AUT	0.068 [0.023, 0.132]	0.245 [0.106, 0.375]	0.148 [0.089, 0.225]	0.540 [0.409, 0.693]
ANX	0.268 [0.105, 0.415]	Fixed to 0	0.585 [0.390, 0.853]	0.147 [<.001[b], 0.310]
DEP	0.148 [0.052, 0.267]	0.054 [<.001[a], 0.169]	0.323 [0.234, 0.445]	0.475 [0.332, 0.631]

Note:

All estimates are accompanied by 95% confidence intervals, reported in square brackets.

A: Additive genetic components.

E: Non-shared environmental components.

Values displayed as <.001 indicate estimates very close to zero. The exact values corresponding to the superscripted values are: a = 1.2607348×10^{-5}, b = 6.9830024×10^{-7}

Figure Captions

Figure 1. Meta-analytic Forest Plots for rA, rC and rE Across Studies.

Each panel represents a meta-analysis forest plot for one of the three correlation components:

rA (additive genetic correlation), rC (shared environmental correlation), and rE (non-shared

environmental correlation), estimating the association between autistic traits (AUT) and three

internalising constructs: ANX (Anxiety), DEP (Depression), and INT (Composite internalising

symptoms). Each row within a panel represents a sample included in the meta-analysis, showing the

correlation coefficient (COR), 95% confidence interval (95%-CI), and the study' s weight in the

pooled estimate. Pooled estimates were calculated using a random-effects model, with heterogeneity

statistics reported as I^2 (percentage of total variation due to heterogeneity), τ^2 (between-study

variance), and p-values for heterogeneity tests. Cohort and measurement abbreviations are defined

in Table 1.

Figure 2. Standardised Path Coefficients of the Best-Fitting Common Pathway Model

This figure illustrates the standardised path coefficients from a common pathway model

examining the shared aetiological structure underlying Autistic traits (AUT), Anxiety (ANX) and

Depression (DEP). Panel A shows the full AE common pathway model (aeCPM), in which the trait

variance is decomposed to additive genetic effects (A) and non-shared environmental effects (E).

Panel B shows the aeCPM2 model, with the corresponding path (as_2) fixed to zero and therefore

omitted in this figure. Trait-specific additive genetic paths are denoted by $as_{1\text{-}3}$, and trait-specific

non-shared environmental effects are denoted by $es_{1\text{-}3}$. All path coefficients are presented with 95%

confidence intervals (CI), shown in square brackets. Values displayed as <.001 indicate estimates

very close to zero. The exact values corresponding to the superscripted values are: $a = 1.0947563 \times 10^{-6}$, $b = 1.0951218 \times 10^{-6}$, $c = 1.0951239 \times 10^{-6}$, $d = 8.1024789 \times 10^{-9}$, $e = 4.0785092 \times 10^{-6}$, $f = 0.99999998$, $g = 3.3302190 \times 10^{-6}$, and $h = 8.8355414 \times 10^{-7}$.

Note: Figure translations are in progress. See original paper for figures.