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The Genetic and Environmental Structure of Fear and Anxiety in Juvenile Twins

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Abstract

Fear and anxiety are conceptualized as responses to acute or potential threat, respectively. Adult twin studies found substantial interplay between genetic and environmental factors influencing fear disorders (phobias) and anxiety disorders. Research in children, however, has largely examined these factors independently. Thus, there exists a substantial knowledge gap regarding the underlying etiologic structure of these closely-related constructs during development. Symptom counts for five fear (criticism, the unknown, death, animal, medical) and four anxiety (generalized, panic, separation, social) dimensions were obtained for 373 twin pairs ages 9–14. Multivariate twin modeling was performed to elucidate the genetic and environmental influences distributed amongst these dimensions. The best fitting model contained one genetic, two familial environmental, and two unique environmental factors shared between fear and anxiety symptoms plus dimension-specific genetic and unique environmental factors. Although several environmental factors were shared between fear and anxiety dimensions, one latent factor accounted for genetic influences across both domains. While adult studies find somewhat distinct etiological differences between anxiety and phobic disorders, the current results suggest that their relative genetic and environmental influences are not as clearly demarcated in children. These etiological distinctions are more nuanced, likely contributing to the highly diffuse symptom patterns seen during development.

Keywords

Anxiety; Fear; Twin Study; Behavioral Genetics; Heritability

Fear and anxiety are adaptive responses to acute or potential threat, respectively (Steimer, 2002). When their symptoms become dysregulated, excessive, or interfere with functioning and quality of life, they are considered clinical phobias or other anxiety disorders, respectively (American Psychiatric Association, 2013). As disorders of threat response with some shared features, psychiatric nosology traditionally includes phobias within the anxiety

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disorder domain together with generalized anxiety and panic. Both domains have roots in childhood, but commonly expand and persist into adolescence and adulthood, accounting for a substantial proportion of lifetime psychiatric illness (Kessler et al., 2005). However, due to their individually broad but partially distinguishable features and complex unfolding across development, researchers have often separately investigated various aspects of their symptomatology at different ages.

Fear represents the emotional-behavioral response to the perception of immediate danger, leading one to avoid the threat for discernible survival value (Panksepp, 2010). Phobias are common throughout adulthood (Kessler, 2005), and girls consistently report more *fears* than boys during childhood and adolescence with reliable patterns of developmental changes (Ollendick & Muris, 2015). Twin studies conducted by our group have found phobias in adults to be moderately heritable (30–40%) with phobia subtypes having overlapping genetic and environmental influences as well as subtype-specific factors (Kendler, Myers, Prescott, & Neale, 2001; Kendler Neale, Kessler, Heath, & Eaves, 1992). These overlapping influences help explain the high comorbidity amongst fears and phobias (Loken, Hettema, Aggen, & Kendler, 2014). Individual fear *symptoms* in children are also moderately heritable with modest familial environmental influences shared between twins and a greater role for unique environment (Eaves & Silberg, 2008; Eley, Rijdsdijk, Perrin, O'Connor, & Bolton, 2008; Lichtenstein & Annas, 2000). A few studies investigating the comorbidity structure of fear symptoms in children reported a common genetic factor that influenced all symptom types in addition to fear-specific factors (Eaves & Silberg, 2008; Lichtenstein & Annas, 2000).

Anxiety disorders (ADs) often have a basis in normal anxious concerns; however, the degree of anxiety and associated symptoms becomes excessive, uncontrollable, and impairing to an individual's life. The ADs are the most prevalent class of psychiatric disorders in US adults (Kessler, 2005). Similar to fears, females have higher rates of ADs throughout both childhood and adulthood (Grills-Taquechel & Ollendick, 2012). Twin studies demonstrate ADs are also moderately heritable (Hettema, Neale, & Kendler, 2001). ADs are highly comorbid with each other, and adult twin studies suggest this comorbidity may be due, in part, to genetic risk factors shared between disorders (Hettema, Prescott, Myers, Neale, & Kendler, 2005; Scherrer et al., 2000). This comorbidity pattern is also seen in children, where 40% to 60% of children with one AD are estimated to meet criteria for additional ADs (Kashani and Orvaschel, 1990; Leyfer, Gallo, Cooper-Vince, & Pincus, 2013). While the heritability of ADs has been studied extensively in adults, the genetic liability to childhood ADs has primarily focused on more anxiety-related symptoms or behaviors, often in the context of other internalizing syndromes like depression.

In a non-twin study, Muris and colleagues (1998) report substantial correlations between subscales of the Fear Survey Schedule for Children-Revised (FSSC-R; Ollendick, 1983) and the Screen for Child Anxiety-Related Emotional Disorders (SCARED; Birmaher et al., 1997). However, only a few studies of children have examined the liability structure of DSM-based anxiety dimensions (Ogliari et al., 2006) or phobic fear symptoms (Stevenson et al., 1992; Eaves & Silberg, 2008). A recent longitudinal twin study examined internalizing symptoms more broadly, reporting increasingly shared risk factors between depression and

SCARED anxiety scales with age, (Waszczuk, Zavos, Gregory, & Eley, 2014). However, no child twin studies have explored the potential sources of shared etiology of each separate anxiety dimension together with various specific fear dimensions as assessed in the FSSC-R. Given the partial distinction between risk factors for phobias and other ADs in adults, it is important to examine their childhood precursors. Furthermore, early fear and anxiety disorders are the strongest predictors of later psychiatric comorbidity (Kessler et al., 2012). Therefore, this study aimed to explicate the shared and specific risk factors (genetic, familial environment and unique environment) and their roles amongst fear and anxiety domains in youth. Based on the prior literature, significant genetic, familial environment and unique environment are predicted for fears and anxiety examined separately. Due to the moderate level of phenotypic correlation between the FSSC-R and SCARED subscales described above, differential overlap between genetic and environmental factors across these scales is predicted. By leveraging symptom sum scores rather than diagnostic criteria, the power to detect meaningful patterns of shared and specific variance is maximized.

Methods

Editorial Policies and Ethical Considerations

The Institutional Review Boards at VCU and NIMH approved this study, and parents of all participants provided informed consent before participating.

Participants

The twins included in these analyses comprised the VCU Juvenile Anxiety Study (VCU-JAS; Carney et al., 2016). Using twin families recruited by the Mid-Atlantic Twin Registry (MATR; Lilley and Silberg, 2013), VCU-JAS enrolled twins aged 9–14 across two sites (VCU and the National Institute of Mental Health; NIMH) to participate in a study of internalizing phenotypes. This age range focuses on middle-school aged children in the pre-adolescent period of increasing risk for internalizing disorders. Only Caucasian twins were recruited to minimize heterogeneity within the sample for the genetic aims of the overall study. The Institutional Review Boards at VCU and NIMH approved this study, and parents of all participants provided informed consent before participating. Self-report data available for this study came from 746 youths (N=130 monozygotic (MZ) twin pairs and N=243 dizygotic (DZ) twin pairs) consisting of 388 female and 358 male twins. Zygosity was determined using parental responses to standard questions about physical appearance of the twins and DNA testing as described in detail elsewhere (Carney et al., 2016).

Measures

Fear—The FSSC-R (Ollendick, 1983) is a widely used questionnaire for assessing common fears in children (Gullone, 1999; Myers & Winters, 2002; Ollendick & Muris, 2015). It uses a 3-point Likert scale for each of 80 feared stimuli or situations. The shortened 25-item form (FSSC-RSF) has a 5-factor structure similar to the full scale with the following means (standard deviations; Muris, Ollendick, Roelofs, & Austin, 2014): fear of failure and criticism 8.51 (2.43), fear of the unknown 7.68 (2.38), fear of animals 7.28 (2.02), fear of danger and death 12.96 (3.41), and medical fears 6.85 (2.06). A sum score was calculated for all subscales with minimal missingness (<2%).

Anxiety—The SCARED was developed to screen for ADs within clinical samples (Birmaher et al., 1999, 1997) but has also been widely used in community and research studies (Verhulst and van der Ende, 2006; Ramsawh et al., 2012). It assesses five types of childhood anxiety symptoms: panic/somatic 5.17 (3.86), generalized anxiety 5.94 (3.69), social anxiety 5.20 (3.42), and separation anxiety 6.00 (3.29), as well as school avoidance which was not used in these analyses. The 41-item version (Birmaher et al., 1999) assesses symptoms on a 3-point Likert scale. A sum score was calculated for each of the four subscales with minimal missingness (<2%).

Statistical analyses

Analyzing the similarity of MZ and DZ twins elucidates the roles of genetic (A), familial environmental (C), and unique environmental (E) effects. Variance is partitioned into underlying genetic and environmental influences by leveraging the difference in genetic relatedness between twin types. A reflects the latent cumulative effects of individual genetic loci influencing a trait. Familial environment (C) captures non-genetic influences that make twins more similar to each other compared to the general population. Unique environment (E) describes influences that contribute to the differences seen between co-twins including measurement error. Analyses were conducted with a maximum-likelihood approach using the OpenMx package (Neale et al., 2016).

In multivariate structural equation modeling, ACE components can be specific to each subscale (e.g., A_{s1} in Figure 1) as well as common to multiple subscales (e.g., A_{c1}). Given the substantial effects of age and sex on fear and anxiety measures, these two predictors were included as covariates in the primary analyses. Significance of individual model parameters were tested by comparing constrained submodels to a saturated model (i.e., all paths freely estimated) via the Akaike information criterion (AIC), and a likelihood ratio χ^2 test used to determine if the constrained model fits the data significantly worse than the saturated. AIC is based on twice the difference in log likelihood between higher order and submodels with a penalty for degrees of freedom, with lower AIC denoting a better balance of model fit and parsimony (Williams & Holahan, 1994).

An increasingly complex sequence of hypothetical models was fit to the data. Multivariate independent pathway models were estimated separately for the Fear and Anxiety dimensions to determine their overall etiologic structure. The final model, an independent pathway model covering both Fear and Anxiety tested the need for multiple sets of common ACE sources of covariance to explain the observed data.

Results

Fear

The Fear section of Table 1 displays the fit statistics for the modeling of the FSSC-RSF. To test for genetic and environmental factors common to all subscales, we began with a model including single common plus specific A, C, and E factors with age and sex covariates for each subscale mean. Significance of common and then specific factors were sequentially tested by iteratively constraining parameters to zero. As indicated in Table 1, Model 1b was

determined to be the best fitting and most parsimonious model. It included a single set of common ACE factors and subscale specific A and E factors. Females had the expected pattern of higher mean scores compared to males across all subscales, depicted in Figure 1 as paths from the sex moderator (triangle) loading on each subscale. A slight decrease in means as age increases for all subscales except for criticism is consistent with observed decreases in most childhood fears over development. The influence of common and specific genetic factors accounted for 10–34% of the total of variance of each subscale with the remaining variance accounted for primarily by subscale specific, unique environmental factors.

Anxiety

The Anxiety section of Table 1 displays the fit statistics for the modeling of the SCARED. Similar to Fear, we found model 1b fit best with single set of common ACE factors and subscale specific A and E. Age and sex influenced the means of each subscale in a similar pattern to Fear. Generalized anxiety was the exception for which the opposite age trend was found, consistent with clinically observed increased risk of generalized anxiety with age. The total influence of all genetic factors accounted for 18–35% of each subscale's variance with remaining variance accounted for primarily by subscale specific unique environmental factors. The genetic factor common to all subscales accounted for 5–19% of the variance for panic, generalized anxiety and separation anxiety. Only social phobia did not share genetic influences with the other symptoms. Figure 2 depicts the path estimates from the best fitting model for Anxiety.

Modeling Across Fear and Anxiety

To examine whether the etiological overlap in children is similar to that reported for adults, we started with a model containing two sets of latent common ACE factors. To ensure model identification as well as a unique solution for each set of ACE common factors, we constrained one loading on each set of latent factors in order to designate one set as the 'Anxiety' set and the other as the 'Fear' set. I.e., all SCARED subscales load on the 'Anxiety' ACE factors and all subscales but criticism from FSSC-RSF do so as well, and the reverse with all FSSC-RSF and all SCARED except generalized anxiety loading onto the 'Fear' ACE set (Illustrated in the C and E diagrams in Figure 3). This allowed for all scales to remain in the analyses while also providing a unique analytic solution. Parameter estimates and model fit did not significantly differ when we examined constraining alternative pathways. When testing a single common risk source (i.e., Ac), we allowed all subscales to load onto that single source. While one of the two latent Ac factors could be eliminated without a significant deterioration in fit, we were unable to remove any of the four common environmental factors (i.e., keeping two each for Cc and Ec). The best fitting was Model 3b in Table 2 with similar effects of age and sex as before. The proportion of variance in liability accounted for by each source of variance is listed in Table 3. Figure 3 illustrates the larger role of shared genetic influences on the Anxiety subscales, with limited influence of familial environment common to all subscales and the largest proportion of unique environmental influences originating from subscale specific factors. This is reflected in Table 3 where the total genetic influences across shared and specific components account for 15–40% of the variance, whereas the total variance accounted for by common and

specific familial environment is markedly lower (0–17%); the remainder was accounted for by some common but predominantly specific unique environment (47–74%).

Discussion

We used multivariate modeling to examine the structure of genetic and environmental risk factors that underlie the associations between Fear and Anxiety domains in a juvenile twin sample. We first separately examined each domain's genetic and environmental factors. Fear and Anxiety each displayed an overall similar etiologic covariance structure across their respective dimensions that included moderate influences of genetic plus familial and unique environmental factors common to all symptoms (Figure 2). The remaining influences were due to subscale specific genetic and unique environmental effects. Prior childhood twin studies of Fear have primarily focused on the etiology of particular fears (Stevenson et al., 1992) and their longitudinal changes over development (Eaves & Silberg, 2008) or the etiology shared between fears or phobias (Lichtenstein & Annas, 2000). Whether measuring diagnoses or symptom counts, extant studies reported moderate genetic influences that were partially shared with other fears or phobias plus a predominance of unique environmental influences. Our finding of significant fear-specific genetic and unique environmental with substantially less familial environmental influences reflects prior studies examining these domains independently (Bolton et al., 2006; Eley et al., 2008; Lichtenstein & Annas, 2000; Waszczuk et al., 2014).

Within Anxiety symptom dimensions, a latent genetic factor A_c accounted for a modest proportion of variance shared by all SCARED subscales except social phobia. This is generally consistent with findings by Ogiari and colleagues (2010). Differences between these two studies are largely accounted for by our finding of an additional common familial factor C_c with modest influence on the covariance of subscales that the other study did not include in their final models. Overall, our findings of significant moderate genetic and unique environmental influences are similar to previous independent studies of social phobia, separation anxiety, and panic in children (Bolton et al., 2006; Eley et al., 2008; Scaini et al., 2012).

Considering previous twin research that examined Fear and Anxiety separately in children, our study provides novel insights into the potential etiological underpinnings responsible for the high comorbidity observed between phobic fear and anxiety domains in youth. Within the combined model (Figure 3), risk across both domains was variably influenced by a single genetic factor (A_c) in addition to more domain-specific familial environment (C_{c1} and C_{c2}), plus environment unique to each individual (E_{c1} and E_{c2}). The proportion of variance accounted for by A_c is lower for fear symptoms (3–37%) than for anxiety symptoms (14–50%). Only A_c accounts for greater than 30% of the variance for any of the subscales affecting both fear of criticism and generalized anxiety, the most genetically influenced of each scale (37% and 50% heritability, respectively). The pattern of 'same genes but, different environments' found in this study is also found in the relationship between two highly comorbid disorders in adults, major depression and generalized anxiety (Kendler et al., 1992; Kendler, Heath, Martin, & Eaves, 1987). Phobic fears, anxiety, and depression are all closely related internalizing domains, so this shared genetic influence A_c may be

indexing a broader risk factor than just Fear and Anxiety such as a global predisposition for negative affective syndromes. Previous research has demonstrated the overlapping etiology of these internalizing syndromes in children and adolescents (Waszczuk et al., 2014), whereas the adult literature shows only a partial overlap between genetic risk for internalizing disorders (Hettema et al., 2005).

While our best fitting model included multiple C and E factors, they only partially distinguished between Fear and Anxiety domains. Although significant in the separate analyses of Fear and Anxiety, when examined in the combined model, familial environment was not as strongly influential, and the pattern that emerged was not simply overall Fear versus Anxiety. As Figure 3 shows, Cc_1 specifically affects fear of death and medical fears with only modest influences on Anxiety. At the level of content, both death and medical fears may relate to threats to bodily integrity. On the other hand, only separation anxiety and fear of the unknown load onto Cc_2 with negligible remaining effects. One may speculate these might represent responses related to separation from a caregiver who provides security from unknown threatening situations. These are distinguishable from potential identifiable threats such as animals and social interactions. Notably, familial environment plays little role in comorbidity of internalizing disorders in adults (Kendler, 1996). As seen previously, middle childhood seems to be a developmental stage in which family influences peak on many behavioral outcomes.

The only common factors to show an arguable overall distinction between the domains were the unique environmental influences. Figure 3 shows all the Anxiety dimensions clustering together on Ec_1 and all the Fear dimensions on Ec_2 with minimal cross loadings from the other domain (represented by dashed lines in the figure). Fear is a more primitive, instinctive defensive reaction primarily involving the amygdala and its recruitment of other subcortical regions that develop early, while Anxiety requires more complex responses dependent upon cortical involvement which develops later (LeDoux & Pine, 2016). Furthermore, given that normative fears are variably expressed within certain developmental windows (fear of strangers, separation, the dark, animals, etc.), it is hypothetically more likely for their environmental influences to cluster according to exposures by age that make them more highly correlated with each other than with environmental influences on anxiety symptoms. That is, while their predisposing genetic influences largely overlap, their environmental influences may be differentially moderated by age and neurodevelopmental stage.

Our results further suggest that the etiological structure of Fear and Anxiety in children is not as clearly differentiated as in adults. Prior adult twin studies suggest a continuity of risk factors from fears to the corresponding phobias (Kendler et al., 1992). Furthermore, both adult phenotypic (Krueger, 1999) and twin (Hettema et al., 2005) studies find correlated but partially distinct structural relationships between phobias and other anxiety disorders. Thus, while our finding of moderate levels of genetic influences common to all subscales is not unexpected, the degree of sharing seen here is notable. This reflects, and likely helps explain, clinical observations in which children are substantially more likely to have a complex, changing pattern of syndromes compared to adults (Grills-taquechel et al., 2012; Kashani et al., 1990; Kessler, 2005; Leyfer et al., 2013).

The results of this analysis should be interpreted within the context of several limitations. First, fear and anxiety symptoms are transient in nature, especially within children who commonly outgrow them. While the use of symptom measures limits generalizability beyond the age range they are designed to investigate, most studies in children use measures similar to these, allowing a relative comparison across the current literature. Although it might limit generalizability to clinical samples, such a dimensional approach increases the statistical power to detect the influences of etiologic significance over use of less prevalent psychiatric diagnoses. Second, we opted to control for age and sex effects in the analyses rather than split our sample and conduct age- or sex-specific analyses. Furthermore, this sample does not possess sufficient power to examine qualitative sex effects on sources of variance; we estimate a peak power of 0.45 to detect a correlation of 0.2 between male and female genetic factors. However, previous studies have indicated conflicting results regarding age and sex having a moderating effect on the variance of fear and anxiety measures (Eaves & Silberg, 2008; A Ogliari et al., 2006; Scaini et al., 2012); thus, we covaried for them at the means level to minimize these biases. Finally, generalizability is also limited due to the exclusive use of Caucasian twin pairs driven by the aim to minimize genetic heterogeneity introduced when sampling from multiple ethnicities. Most prior twin studies were also conducted in Caucasian twins, maximizing our comparability with them.

Conclusions

The findings of this analysis have implications for investigating the risk mechanisms underlying fear and anxiety symptoms in childhood and beyond. From a trans-diagnostic perspective, these findings help explain and potentially validate the high rates of internalizing comorbidity found in children. Longitudinal research in developmental psychopathology could also benefit from incorporating both threat response domains given their close links in childhood. Studies in adults show a clearer distinction between the two domains and their sources of covariation, while their expression in children is more diffuse and malleable. From an etiological perspective this could be due to the greater degree of shared genetic influences expressed during child development coupled with developmentally specific environmental influences that help disentangle fear and anxiety. A longitudinal study extending into late adolescence would further inform the temporal unfolding of fear and anxiety risk factors as they merge into those seen in adulthood. Finally, more effective gene-finding investigations of fear and anxiety disorders such as genome-wide association studies (GWAS) could be designed to incorporate these shared genetic influences. Two prior GWAS, one for childhood anxiety related behaviors (Trzaskowski et al., 2013) and another for adult anxiety disorders (Otowa et al., 2016), have utilized this strategy. Similar efforts are being undertaken on a much larger scale by the Psychiatric Genomics Consortium Anxiety Disorders Working Group (PGC-ANX).

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Figure 1.

Best fitting model for FSSC-RSF subscales. The model contains 1 common additive genetic factor (Ac₁), 1 common familial environmental factor (Cc₁), and 1 common unique environmental factor (Ec₁). Only subscale specific additive genetic and unique environmental factors were found to be significant and retained in the final model. Path coefficients representing standardized estimates are listed above 95% confidence intervals for each path for fear of failure and criticism (CRIT), fear of the unknown (UNKN), fear of animals (ANML), fear of danger and death (DEATH), and medical fears (MED). Triangles

in the middle figure denote age and sex moderators on the means for all subscales with 95% CIs listed below the standardized path estimate.

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Figure 2.

Best fitting model for SCARED subscales. The model contains 1 common additive genetic factor (Ac_1), 1 common familial environmental factor (Cc_1), and 1 common unique environmental factor (Ec_1). Only subscale specific additive genetic, and unique environmental factors were found to be significant and retained in the final model. Path coefficients representing standardized estimates are listed above the 95% confidence intervals (CIs) for each path for panic disorder (PAN), generalized anxiety disorder (GAD), social phobia (SOC), and separation anxiety (SEP).

Figure 3.

Best fitting model for Fear and Anxiety dimensions. The model contains one common additive genetic factor (Ac_1), two common familial environmental factors (Cc_1 and Cc_2), and two common unique environmental factors (Ec_1 and Ec_2). Only subscale specific additive genetic and unique environmental factors were found to be significant and retained in the final model. The darker lines indicate a stronger influence of the latent factor on the

observed variable. Lighter lines indicate a standardized path estimate less than 0.10. Table 3 provides the proportion of variance accounted for by each of these pathways.

Table 1

Model-Fitting Results for Multivariate Independent Pathway Models of Fear and Anxiety

Fear							
Model	Common Factors	Specific Factors	EP	df/	Model Fit		<i>P</i>
					-2LL/	AIC/	
1	A ₁ C ₁ E ₁	All ACE	45	3612	15553.6	15643.6	-
1a	A₁C₁E₁	All AE	40	5	0.0	-10.0	.999
1b	A ₁ C ₁ E ₁	All CE	40	5	5.0	-5.0	.413
1c	A ₁ C ₁ E ₁	All E	35	10	15.6	-4.4	.110
2	C ₁ E ₁	All ACE	40	5	16.1	6.1	.000
3	A ₁ E ₁	All ACE	40	5	7.2	-2.8	.204
4	A ₁ C ₁	All ACE	40	5	161.2	151.2	.000
5	-	All ACE	30	15	902.1	872.1	.000
Anxiety							
1	A ₁ C ₁ E ₁	All ACE	36	2900	14824.0	14896.0	-
1a	A₁C₁E₁	All AE	32	4	0.0	-8.0	.999
1b	A ₁ C ₁ E ₁	All CE	32	4	13.6	5.7	.008
1c	A ₁ C ₁ E ₁	All E	28	8	28.6	12.7	.000
2	C ₁ E ₁	All ACE	32	4	9.4	1.4	.005
3	A ₁ E ₁	All ACE	32	4	12.1	4.1	.001
4	A ₁ C ₁	All ACE	32	4	127.4	119.4	.000
5	-	All ACE	24	12	720.1	696.1	.000

Abbreviations: EP=estimated parameters, df/ = degrees of freedom for full model and change in degrees of freedom for submodels, -2LL/ = twice the negative log likelihood of full model and change in -2LL of submodels compared to full, AIC/ = Akaike information criterion of full model and change in AIC of submodels compared to full model. For AIC and -2LL, smaller or more negative s indicate a better fit compared to the full model (Model 1). *p* is related to the statistical difference of -2LL values between full and sub models. Bold designates the overall best fitting model.

Table 2

Model Fitting Results for Independent Pathway Model Including All Symptom Clusters

Model	Common Factors	Specific Factors	EP	df/	Model Fit		
					-2LL/	AIC/	P
1	A ₁ A ₂ C ₁ C ₂ E ₁ E ₂	All ACE	102	6481	30146.6	30350.6	-
2	A ₁ A ₂ C ₁ E ₁ E ₂	All ACE	95	7	-85.2	-99.2	.999
3	A ₁ C ₁ C ₂ E ₁ E ₂	All ACE	95	7	-121.8	-135.8	.999
3a	A ₁ C ₁ C ₂ E ₁ E ₂	All CE	86	16	-106.5	-138.5	.032
3b	A₁C₁C₂E₁E₂	All AE	86	16	-121.8	-153.8	.999
3c	A ₁ C ₁ C ₂ E ₁ E ₂	All E	77	25	-77.6	-127.6	< .001
4*	A ₁ A ₂ C ₁ C ₂ E ₁	All ACE	95	7	-	-	-
5	A ₁ C ₁ E ₁	All ACE	81	21	-41.2	-83.2	.999
6	C ₁ E ₁	All ACE	72	30	50.3	18.3	.014
7	A ₁ E ₁	All ACE	72	30	24.2	-35.8	.762
8	A ₁ C ₁	All ACE	72	30	234.9	174.9	< .001
9	-	All ACE	54	48	1853.2	1757.2	< .001

Table 3 shows the fit statistics for all models tested. Common Factors are the ACE latent factors shared between all observed variables. Specific Factors are the nine sets of ACE latent factors that each only load onto one observed variable, respectively. Specific factors were tested by dropping a class at a time (e.g., all specific A latent factors dropped at same time). Bold designates the overall best fitting model.

* Model 4 was unable to converge to a final solution

Proportion of Variance in Liability to Anxiety and Fear Symptom Clusters from Common and Specific Genetic and Environmental Risk Factors*

Table 3

Symptom Cluster	Genetic Factors		Familial Environmental Factors			Unique Environmental Factors				
	Ac	As	Total	Cc ₁	Cc ₂	Total	Ec ₁	Ec ₂	Es	Total
PAN	.28	.12	.40	.03	.02	.05	.16	.00	.39	.55
GAD	.50	.03	.53	.00	-	.00	.12	-	.35	.47
SEP	.21	.12	.33	.02	.10	.12	.21	.04	.30	.55
SOC	.14	.26	.40	.02	.00	.02	.18	.02	.38	.58
CRIT	.37	.00	.37	-	.00	.00	-	.19	.44	.63
UNKN	.14	.00	.14	.02	.15	.17	.04	.27	.38	.69
ANML	.03	.18	.21	.06	.01	.07	.00	.18	.54	.72
DEATH	.14	.02	.16	.10	.00	.10	.00	.15	.59	.74
MED	.15	.04	.19	.15	.00	.15	.00	.26	.30	.66

Panic disorder (PAN), generalized anxiety disorder (GAD), social phobia (SOC) and separation anxiety (SEP), fear of failure and criticism (CRIT), fear of the unknown (UNKN), fear of animals (ANML), fear of danger and death (DEATH), and medical fears (MED), Ac (Common A factor), As (Specific A factor), Cc₁ (First Common C factor), Cc₂ (Second Common C factor), Ec₁ (First Common E factor), Ec₂ (Second Common E factor) Es (Specific E factor). Bolded columns designate proportion of total variance accounted for by the combined common and specific etiological sources of variance for each subscale.

* Best-fitting IPM model 3b from Table 3