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Recent advances in the genetics of emotion regulation: a review

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Abstract

Recent attention has been given to the role of emotion regulation in the development and maintenance of psychopathology, and the psychosocial literature on emotion regulation has been growing rapidly over the past decade. However, knowledge about the genetic etiology of emotion regulation facets has been slower to develop. The present paper aims to briefly introduce the various constructs that fall under the umbrella of emotion regulation; provide an overview of behavioral genetic methods; summarize the empirical studies of emotion regulation twin studies; introduce molecular genetic methods; review the recent molecular genetic studies on emotion regulation; and provide future directions for research.

Emotions are a key aspect of the human experience and they can influence behavior. It is theorized that emotions have been shaped by evolutionary mechanisms to promote behaviors associated with survival such as socializing/communicating with others, avoiding danger, and seeking needed resources [1]. Generating effective responses to emotion requires the ability to regulate the experience and expression of emotions, as well as the sequence in which emotions occur [2,3]. Regulation of emotion is important for mental health. In fact, over 50% of Axis I disorders and 100% of Axis II disorders implicate emotion regulation deficiencies [4]. Thus, developing a clear understanding of influences on emotion regulation is of high relevance to the characterization and treatment of psychopathological conditions.

Emotion regulation has been conceptualized as a set of strategies employed by individuals to influence the experience of, and behavioral response to, emotion. These strategies, which may be adaptive or maladaptive, include both explicit regulation processes that require conscious effort/control and implicit regulation processes that are unconscious and automatic [5•,6,7]. Given that emotions develop temporally, there are opportunities for modification at both the antecedent and response level [8•,9]. Emotion regulation is a widely studied and broadly defined construct, thus it is not surprising that several different constructs fall under the umbrella of emotion regulation including distress tolerance [10] and attention bias [11]. Diverse methods have also been used to measure these constructs, ranging from self-report measures of emotion-regulation effectiveness and strategies [12,13], to behavioral tasks [10], to fMRI paradigms [14].

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Although the psychosocial literature on emotion regulation has developed greatly in the last two decades, the examination of the biological underpinnings is less developed. Increased understanding of the etiologic mechanisms underlying emotion regulation/dysregulation is needed to help elucidate the relationship between emotion regulation and psychopathology [15]. A paper by Canli and colleagues [8•] reviews the genetics of emotion regulation, and the current paper provides an updated review of recent studies, with a focus on the past three years of research, investigating the genetics of emotion regulation, including behavioral genetic studies (i.e. twin studies) and molecular genetic studies.

Behavioral genetic studies

Twin studies provide a means of examining the etiology of emotion regulation by quantifying both genetic (i.e. heritable) and environmental contributions. These models compare the similarity between monozygotic (MZ) twins, which share 100% of their genes, and dizygotic (DZ) twins, which share 50% of their genes, on a particular observable characteristic (phenotype). Variation existing within a phenotype can be decomposed into additive genetic factors which contribute twice as much to the correlation between MZ twins as they do for DZ twins, common environmental factors that are shared and contribute equally to the correlation between MZ and DZ twins (e.g. economic disadvantage), and specific environmental sources which encompasses unique experiences that are not shared among twins and measurement error.

There have been few twin studies on emotion regulation ([8•], Table 1 for past studies conducted since 2011), and within this literature the means of emotion regulation assessment and specific facets of the construct under examination vary greatly (e.g. different forms of self-report and behavioral measures). Most prior twin studies in this area have focused on associated traits (e.g. personality characteristics [16]) and self-report emotion regulation difficulties [17] with less emphasis on certain emotion regulation strategies [8•]. However, a growing developmental literature exists regarding individual differences in emotion regulation and temperament among infants and children that additionally suggest that the processes underlying emotion regulation are moderately heritability [18]. Overall, the literature consistently suggests a moderate degree of heritability to the processes associated with emotion regulation across the lifespan (~25–55%; [8•]). This mild to moderate heritability estimate is comparable to that found for most internalizing disorders [19].

Recent twin studies of emotion regulation have yielded heritability estimates comparable to those reviewed by Canli and colleagues [8•]. In a twin study of toddlers, genetic factors contributed 43% to individual differences in emotion regulation as identified by a self-report measure [20]. Similarly, in a study conducted among adult twins, heritability estimates of ~40% were found to influence affect liability and intensity of emotional experiences, specifically, anger and anxiety [21]. Furthermore, brain activity occurring during periods of time where emotion regulation is believed to be actively occurring (i.e. viewing of images) appears to be moderately heritable (45–55% [22]). Although genetic influences appear to play a significant role in emotion regulation, each of the aforementioned studies also suggests a strong influence from nonshared environmental effects (e.g. occurrences that one twin may experience yet the other does not, for example, trauma exposure). In contrast, the

contribution affiliated with shared or common environmental factors appears to be more limited in nature, thereby suggesting that experiences between twins (e.g. reared in same family) may have less of an impact on similarities identified between the pairs. Given the moderate heritability of emotion regulation, increased interest has been placed in identifying specific genes that may contribute to the processes associated with the particular construct.

Molecular genetic studies

Whereas twin studies yield an estimate of the magnitude of latent genetic effects on emotion regulation, molecular genetic association studies seek to identify specific genetic variation associated with emotion regulation. Before providing a brief overview of recent studies examining the genetics of emotion regulation in the next section, we will first review some key concepts involved in studies of molecular genetics; the interested reader is referred to more in depth articles on incorporating genetics into social science research [23•]. The majority of human genetic variation is comprised of single nucleotide polymorphisms (SNPs, pronounced 'snips'), which occur when a single nucleotide in the DNA sequence is altered, forming different alleles; when considered jointly, an organism's two alleles at each site in the genome compose their genotype. Within each gene there are many SNPs, often hundreds, and candidate gene studies in psychology have often only assayed a single or a small number of SNPs within each gene (thus capturing limited variation in each gene, and sometimes erroneously concluding that the 'gene' is not associated with the outcome of interest when it could be that the limited SNPs measured were not associated). In contrast, genome-wide association studies (GWAS) include upwards of millions of SNPs across the genome; however, this design has not been implemented to date in emotion regulation research. Another type of polymorphism is the variable number tandem repeat (VNTR) polymorphism (also referred to as microsatellite markers). Aptly named, VNTRs involve segments of repeated base pairs. Extant candidate gene studies for emotion regulation have included both types of common polymorphisms: SNPs (e.g. catechol-*O*-methyltransferase [*COMT*] Val^{158}Met), and VNTRs: (e.g. 5-HT transporter-linked polymorphic region [*5-HTTLPR*]). In the following section, we review recent articles that have empirically examined these genetic contributions to emotion regulation (see Table 2 for a review of recent molecular genetic studies of emotion regulation).

Although associations between the variants from a number of genes have been studied in relation to emotion regulation constructs, the most commonly examined genes included *5-HTT* and *COMT*. *5-HTTLPR*/rs25531 is a common *5-HTT* polymorphism. *5-HTT* has a14-repeat allele (*S*) that has lower transcriptional efficacy than the 16 repeat allele (*L*). Furthermore, the *L* allele may contain $A \rightarrow G$ substitution that makes it function like an *S* allele [24]. Therefore, genotype frequencies for the *5-HTTLPR/rs25531* polymorphism should be classified triallelically, wherein L_A/L_A are classified as L'/L', L_A/S'; L_A/L_G are classified as L'/S'; and L_G/L_G, L_G/S', S'/S' are classified as S'/S'. When classified biallelically, the *S*-like effects of L_G are not accounted for, which may result in miscoded genes and lead to discrepancies. Hence forward and in Table 1, we will discuss papers that have looked at *5-HTTLPR* biallelically and triallelically. A review of the literature demonstrates that carriers of the low transcribing allele (S' or L_G) compared to homozygous L_A/L_A carriers generally appeared to have greater emotion dysregulation, including

increased attentional biases (negative biases [25•]; positive biases [11]), lower distress tolerance [10], and increased susceptibility to certain psychopathologic conditions, such as increased depressive symptoms [12].

The *5-HTTLPR* polymorphism has also been associated with various forms of brain reactivity. This polymorphism has been found to be associated with frontal lobe activity during emotional regulation processes [26]. Specifically, S'/S' genotype carriers of the *5-HTTLPR* responded with lower posterior insula and prefrontal brain activation during passive perception of negative emotional information but showed greater prefrontal activation and anterior insula activation during downregulation and upregulation of negative emotional responses [27]. Evidence further suggests increased amygdala activity in low efficacy allele carriers [28•,29,30]. The results on amygdala activity may provide preliminary evidence that different amygdala habituation curves may partly underlie the differences between *5-HTTLPR* genotype groups [28•].

In sum, although the preponderance of this literature, including past meta-analyses (for review, see [24,31]), suggests that the S'/L_G allele is associated with risk for poor emotion regulation, some studies did not find differences in emotion regulation between genotype groups [13,32].

Another frequently studied polymorphism with regard to emotion regulation is the *COMT* Val^{158} Met (rs4680), which is a functional SNP involving a common valine (val; high activity) to methionine (met; low activity) transition that has been associated with a 3–4 fold difference in homozygous *COMT* enzyme activity, with heterozygotes showing intermediary enzyme activity [33,34]. The *COMT* enzyme catalyzes the transfer of a methyl group from *S*-adenosylmethionine to a hydroxyl group of catecholamines (e.g. dopamine, epinephrine, and norepinephrine [34]).

Val^{158}Met is a common functional SNP in the *COMT* gene. The majority of ER genetics studies have demonstrated an association of the Val allele with increased emotional dysregulation. Carriers of the Val allele showed increased left amygdala activity in response to fearful/angry stimuli [14] and were more likely to exhibit low distress tolerance than those homologous for the Met allele [10]. Conversely, the Met allele has been associated with increased emotional management and relation [35], as well as increased self-reported emotion regulation efficacy [13]. However, these findings are not consistent across all studies; Lonsdorf *et al.* [28•] found that Met allele showed increased left amygdala activity in response to angry stimuli. Swart *et al.* [36] evidenced a positive relationship between Met homozygotes and difficulty verbalizing feelings. They additionally demonstrated an association between the Met allele and attenuated brain activation in the posterior cingulate gyrus and precuneus during valence evaluation. Surguladze and colleagues [37] found that an interaction between *5-HTTLPR* S' and Met alleles was associated with reduced connectivity in various brain regions, potentially lending to ineffective emotion regulation.

Although recent molecular genetic investigations of emotion regulation have focused on *5-HTT* and *COMT*, other genes have also been implicated in the processes associated with emotion regulation. For example, the *tryptophan hydroxylase-2 (TPH2)* gene, specifically

the GG genotype, has shown a contribution to individual differences in processing of fearful/angry faces and ability to cope with negative stimuli [38,39]. Furthermore, mouse models have demonstrated increased levels of anxiety-like behavior among mice deficient in *TPH2* [39]. Processing of negative stimuli has also been linked to *Neuropeptide Y (NPY)*. Mickey and colleagues [40] found that low expression of *NPY* increases reactivity to negative stimuli in the medial prefrontal cortex when exposed to an experimental paradigm involving negative versus neutral words. Finally, *oxytocin receptor polymorphism (OXTR)* has been implicated in the relationship between culture and emotion regulation. Although a relationship was not present for emotion reappraisal, the findings did suggest that emotion suppression could be influenced by the interplay between *OXTR* variation and culture [41].

Limitations of the extant literature and future directions

There are a limited number of twin studies on emotion regulation. Although the molecular research on emotion regulation is increasing, it is limited to candidate gene studies of a small number of genes wherein often a single polymorphism was assayed, thereby capturing very limited variation in the gene. Additionally, the literature is limited by small sample sizes, and therefore limited power, within admixed populations that can lead to erroneous conclusions about genetic effects. Technological advances in genetic sequencing as well as an emergence of evidence for a previously unrecognized role of non-coding regions of RNA have converged to support the feasibility and importance of GWAS as a promising design for molecular genetic research. GWAS studies adopt an agnostic approach, testing possible associations across the entire genome rather than selecting only a few candidate genes. This approach has the potential to identify important, previously unconsidered genetic influences on emotion regulation.

Incorporating self-report and behavioral measures of emotion regulation into GWAS samples is a promising future direction for elucidating mechanisms underlying emotion regulation. It is important to note, however, that due to the complexities of genetic studies, caution is warranted when conducting genetics research without the proper background or collaborative team. Dick and colleagues [23•] provide a helpful review of the current stage of research integrating genetics and social science in which they address some issues faced when incorporating genetics into the social sciences and offer recommendations for effective integration. Studies examining the genetics of emotion regulation to date have been informative at the behavioral and molecular levels of genetics, but remain varied and, at times, contradictory. Expanding our current methodologies to include examination of emotion regulation at the genome-wide level in well-powered studies provides promising possibilities for understanding the etiologic mechanisms underlying emotion regulation and associated psychopathology.

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Table 1

Recent twin studies of emotion regulation.

Author information	Population (*N*, ethnic breakdown, age, gender)	ER measurement	Major finding
Wang *et al.* (2014)	*N* = 304 same-sex twin pairs (140 MZ and 164 DZ) -Mean age of 2.99 years (SD = .08) - Ethnicity: 85.4% Caucasian, 3.2% Black, 2% Asian, 7.3% Mixed, 2.2% Other	Behavior Rating Scale (BRS) of the Bayley Scale of Infant Development-II	The results demonstrate a significant influence from genetic factors (43%) and from nonshared environmental factors (48%) on individual differences in emotion regulation. Shared effects contributed 9% (not significant).
Coccoro *et al.* (2012)	*N* = 301 (182 MZ and 119 DZ) twin pairs from the Vietnam Era Twin (VET) Registry - Mean age of 44.1 (SD = 2.9) - Caucasian (94.1%)	Affect Liability Scale (ALS) and Affect Intensity Measure (AIM)	ALS Depression and ALS Anger mood shift scores suggest a significant nonadditive genetic influence (29% and 27%, respectively). ALS Anxiety mood shift and AIM scores also showed a significant pattern of additive genetic influence (25% and 40%, respectively).
Kanakam *et al.* (2013)	*N* = 70 - 51 twins with an eating disorder diagnosis - 19 of unaffected co-twins - 16 concordant pairs (14 MZ and 2 DZ pairs) - 19 discordant pairs (11 MZ and 8 DZ pairs)	Difficulties in Emotion Regulation Scale; Reading the Mind in the Eyes test; Emotional Stroop task	For emotion recognition and social attentional bias, MZ twins had significant within-pair similarity in comparison to DZ twins suggesting a genetic influence to these particular processes underlying emotion regulation.
Weinberg *et al.* (2014)	*N* = 479 (244 MZ, 235 DZ) - Mean age of 29.39 (SD = 4.84) - 242 males - 237 females - Ethnicitiy: Caucasian, 96.5%; African American, 0.6%; Hispanic, 0.4%; Native American, 0.8%; mixed race, 0.8%; other/missing, 1.3%	Viewing 90 pictures (30 pleasant, 30 neutral and 30 unpleasant) from the International Affective Picture System	MZ twin correlations were significantly greater than DZ twin correlations for all picture type s within the centroparietal P300 observed between 300 and 600 ms and genetic influence accounted for 45–55% of the variance.

Table 2

Recent molecular studies of emotion regulation.

System				
Author information	**Population (*N*, ethnic breakdown, age, gender)**	**ER measurement**	**Gene/SNP**	**Major finding**
Serotonin: synaptic availability of serotonin has been widely implicated in the modulation of mood states and anxiety disorders and thus became a primary target for candidate gene research in psychiatry.				
Pergamin-Hight *et al.* (2012)	Meta-analysis: Total *N* = 807 - 11 samples from 10 published articles - Demographic breakdown unspecified	Meta-analysis of: - Attention bias - Selective attention - Dot-probe - Posner - Spatial cueing task - Stroop	*5-HTTLPR*	Low efficacy genotype (SS/SL_G) showed a significant attention bias toward negative stimuli, whereas no bias emerged for the intermediate (SL_A/L_AL_G) and high (L_AL_A) genotypes. Combed analyses of *S*-allele carriers also revealed a significant attention bias toward negative stimuli.
Amstadter *et al.* (2012)	*N* = 218 10–14-year-old youths - Mean age of 12.1 years (SD = . 90) - 44.5% female - 51.4% European American	Distress Intolerance - Behavioral Indicator of Resiliency and Distress (BIRD)	*5-HTTLPR*	The *S* allele was associated with low distress tolerance. Exploratory analyses revealed that emotional abuse moderated the relationship between the *5-HTTLPR* and distress tolerance.
Beevers *et al.* (2011)	*N* = 140 - Mean age of 23.15 years (SD = 5.6) - 94% male - 25 Hispanic (17.9%); 12 African American or Black (8.6%); six American Indian or Alaska Native (4.3%); four Asian, Native Hawaiian, or other Pacific Islander (2.9%); three other (2.1%); and 90 Caucasian (64.3%)	Eye-tracking methodology	*5-HTTLPR, rs25531*	Visual gaze of S/L_G allele carriers indicated an attentional bias toward positive emotional content stimuli, whereas L_A homozygotes' gaze did not vary according to emotional content of stimuli.
Outhred *et al.* (2014)	*N* = 36 healthy Caucasian females - Mean age of 25.08 years (SD = 6.49)	fMRI following placebo or escitalopram treatment	*5-HTTLPR*	*5-HTTLPR S* allele load moderated the acute effects of escitalopram, such that individuals with the greatest number of low-expressing *S* alleles experienced more robust shifts in left amygdala signaling (i.e. decreased signal to positive stimuli, increased signal to negative stimuli) while processing emotional stimuli compared to those with fewer *S* alleles.
Hagen *et al.* (2011)	*N* = 68 20-41-year-old Caucasians - Mean age of 31 (SD = 6)	fMRI during an implicit facial expression processing task	*5-HTTLPR*	The results suggest that the increased amygdala response observed in *S*-allele carriers to emotional faces is primarily driven by

		System		
Author information	**Population (*N*, ethnic breakdown, age, gender)**	**ER measurement**	**Gene/SNP**	**Major finding**
	- 23 males			an increased response to emotional faces rather than a decreased response to neutral faces or an increased resting baseline.
Ford *et al.* (2014)	*N* = 205 9–15-year-old youths - Mean age of 12.09 - 62% female - 74% White; 7% African American/ Black; 4% Latino/ Hispanic; 4% Asian/ Island Pacific; 11% other/multiracial	Cognitive reappraisal - Emotion Regulation Questionnaire Stress - Adolescent Life Events Questionnaire Depressive symptoms - Children's Depression Inventory	*5-HTTLPR*	At-risk children (*S*-allele carriers in high-stress contexts) exhibited more depressive symptoms than other groups. Notably, however, at-risk children who used effective emotion regulation did not exhibit increased depressive symptoms, even in the presence of the high-risk allele.
Lin *et al.* (2014)	*N* = 150 18–65 years old	Social cognition - MSCEIT Neurocognitive function - MATRICS	*TPH2*	*TPH2 T* homozygotes performed significantly better on an emotional management subtest compared to those with the *G* allele. Subjects with the *COMT* Met and *TPH2* variation surpassed all other examined groups in emotional relation, emotional management, and the managing emotion branch.
Lonsdorf *et al.* (2011)	*N* = 54 - 29 females ages 20–31 years old - Mean age of 24.11 years (SD = 1.6)	- Passive viewing task - fMRI	*5-HTTLPR*	This study demonstrated an effect of *5-HTTLPR* on higher right amygdala reactivity (*S*-carrier > *L/L*) to angry faces.
Firk *et al.* (2012)	*N* = 30 Caucasians - 15 *s/s* allele carriers (mean age of 20.9 [SD = 1.5]) - *I/I* allele carriers (mean age of 20 [SD = 1.6])	- Downregulation - Passive viewing of negative emotional pictures - fMRI	*5-HTTLPR*	*S/S* allele carriers had lower posterior insula and prefrontal brain activation during passive perception of negative emotional information compared to the *L/L* allele carriers, but showed greater prefrontal activation and anterior insula activation during downregulation and upregulation of negative emotional responses.
Weiss *et al.* (2014)	*N* = 289 female Caucasians ages 18–59 years old - Mean age of 22.8 (SD = 4.6)	Self-report Emotional Ability Scale (SEAS)	*5-HTTLPR*	*5-HTTLPR* was related to individual's self-estimated effectiveness of emotion. Members of the heterozygous (*S/L*) group more effectively rated their intra-personal emotion perception than both homozygous groups (*S/S* and *L/L*).
Grossman *et al.* (2011)	*N* = 48 7-month-old infants - Mean age of 221 days - 24 females	Neutral, happy and fearful face stimuli	*5-HTTLPR*	*5-HTTLPR* variants were associated with differences in infants' brain responses to happy faces over fronto-temporal regions. *5-HTTLPR* was also

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Author information	**Population (*N*, ethnic breakdown, age, gender)**	**ER measurement**	**Gene/SNP**	**Major finding**
				associated with infants' smiling and laughter.
Waring *et al.* (2014)	*N* = 26 61–86 years old - Mean age of 70.52 (SD = 5.79) - 14 women	- Face-word emotion conflict task - fMRI	*5-HTTLPR*	No significant differences between *S* carriers and *L* homozygotes in the behavioral emotion task. However, *5-HTTLPR* was demonstrated to play a role in neuro, with S carriers demonstrating impared emotional conflict adaption.
Catecholamines: the functional catechol-O-methyltransferase (COMT; metabolizing enzyme of norepinephrine and dopamine) val^{158}met polymorphism has been found to be associated with anxiety disorders and depression as well as with neural correlates of emotional processing, with, however, contradictory results.				
Domschke *et al.* (2012)	- *N* = 85 - Male subjects were significantly older (*M* = 40.2, SD = 8.7) than female participants (*M* = 35.5, SD = 10.3, *t*(83) = 2.22, *p* = .029	- Face-matching task - fMRI	*COMT* val^{158}met	In an allele-dose fashion, the *COMT* 158val allele was associated with increased predominantly left-sided amygdala activity in response to fearful/angry facial stimuli. This effect was only noted in the female probands.
Amstadter et al. (2012)	*N* = 218 10–14-year-old youths - Average age of 12.1 years (SD = .90) - 44.5% female - 51.4% European American	Distress Intolerance - Behavioral Indicator of Resiliency and Distress (BIRD) Emotional abuse Childhood Trauma Questionnaire-Short Form (CTQ)	*COMT* val^{158}met	Individuals who were Val allele carriers of the *COMT* Val^{158}Met polymorphism were more likely to discontinue a distressing task than those homologous for the Met allele. Quitting the task was especially likely in adolescents with both a history of emotional abuse and the s/s genotype of *5-HTTLPR.*
Swart *et al.* (2011)	*N* = 40 right-handed participants - Mean age of 21.5 (SD = 6.2) - 26 females - 14 males	- Bermond-Vorst Alexithymia Questionnaire (BVAQ) - fMRI	*COMT* val^{158}met	Individuals with homologous Met alleles reported increased difficulty in verbalizing affect. The Met allele was also associated with attenuated brain activation in posterior cingulate gyrus and precuneus during valence evaluation.
Lin *et al.* (2014)	*N* = 150 18–65 years old	Social cognition - MSCEIT Neurocognitive function - MATRICS	*COMT* val^{158}met	Subjects carrying the Met allele of *COMT* outperformed Val homozygotes in managing emotions branch and emotional relation subtask. Subjects with the COMT Met and TPH2 variation surpassed all other groups in managing emotion branch, emotional relation subtask, and emotional management subtask.
Lonsdorf *et al.* (2011)	*N* =54 20–31 years old - 29 females - Mean age of 24.11 (SD = 1.6)	- Passive viewing task - fMRI	*COMT* val^{158}met	This study demonstrated an effect of *COMT* on higher right amygdala reactivity (met/met > val-carrier) to angry faces. The

		System		
Author information	**Population (*N*, ethnic breakdown, age, gender)**	**ER measurement**	**Gene/SNP**	**Major finding**
				results did not support differences between *COMT* genotype groups.
Weiss *et al.* (2014)	*N* = 289 female Caucasians ages 18–59 years old - Mean age of 22.8 (SD = 4.6)	Self-report Emotional Ability Scale (SEAS)	*COMT* val^{158}met	The *COMT* Met-allele was associated with everyday emotion regulation efficacy. Women homozygous for the Val-allele had the lowest emotion regulation efficacy scores.
Grossman *et al.* (2011)	*N* = 48 7-month-old infants - Mean age of 221 days - 24 females	Neutral, happy and fearful face stimuli	*COMT* val^{158}met	*COMT* variants were associated with differences in infants' brain responses to fearful faces in centro-parietal regions. Variation in *COMT* was also associated with differences in infants' behavioral recovery from distress.
Zhang *et al.* (2014)	*N* = 281 6-month-old infants from urban area of China - 151 males - 130 females	Mother–child interaction during the free play session - Self-regulation coded as directing visual attention away from the stimulus	*5HTTLPR, MAOA*	Infants homozygous for the long allele variant of *5-HTTPLR* shower greater self-regulation compared to infants homozygous and heterozygous for the short allele variant. A significant effect was not found for the *MAOA*-uVNTR polymorphism on self-regulation although a significant interaction effect was found between the *MAOA*-uVNTR and *5-HTTPLR* polymorphism.
Waider *et al.* (2011)	Meta-analysis: reviews role of ~27 studies, number of participants in each not included	- Tridimensional Personality Questionnaire (TPQ) - NEO Personality Inventory (NEO-PI-R) - Face-Processing Task - Mouse models of TPH2 deficiency	*TPH2*	Results show significant associations between *TPH2* variants, anxiety-related traits, and emotional instability. Further, *TPH2* allelic variation was also found to influence individual differences on performance of a face-processing task (angry and fearful faces). Mouse models also demonstrate that deficits in *TPH2* are associated with greater levels of anxiety-like behavior.
Erika Szily (2012)	*N* = 260	Emotion Appraisal Questionnaire	*TPH2*	Participants with the *TPH2 GG* compared to the *TT* genotype obtained higher appraisal scores for goal-conduciveness and lower on coping ability suggesting that participants with the *GG* genotype may perceive that fear and sadness possess a greater influence on their goals and that they have less ability to cope.

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Author information	**Population (*N*, ethnic breakdown, age, gender)**	**ER measurement**	**Gene/SNP**	**Major finding**
Neuropeptide Y: neuropeptide Y(NPY) is an amino acid neuropeptide that acts as a neurotransmitter. NPY is thought to be associated with adaptation to stress and stress-related disorders.				
Mickey *et al.* (2011)	*N* = 93 - Mean age of 29 (SD = 9) - 52% male - 70 participants genotyped and 58 were classified NPY genotype	- Viewed negative (versus neutral) words - fMRI	Neuropeptide Y	Negative words were associated with activation in the medial prefrontal cortex and that increased activity was inversely related to predicted NPY expression (low versus high).
Oxytocin receptor: the oxytocin receptor (OXTR) functions as a receptor for the hormone and neurotransmitter oxytocin that ahs been associated with stress response and a number of mental health disorders.				
Kim *et al.* (2011)	Total *N* = 251 *N* = 99 Koreans - Mean age of 22.42 - 58 females - 41 males age = 22.42) *N* = 152 Americans - Mean age of 19.31 - 60 males - 92 females	Emotion Regulation Questionnaire	*OXTR*	The gene-culture interaction was not present for cognitive reappraisal yet gene-culture interaction effects with *OXTR* on emotional suppression were found. Although Koreans possessing the *GG* genotype were more likely to utilize emotion suppression compared to those with the *AA* genotype, American possessing the *AA* genotype endorsed greater emotional suppression suggesting that culture may influence on gene expression of emotion regulation.