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COMT met Allele Differentially Predicts Risk versus Severity of Aberrant Eating in a Large Community Sample

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Abstract

Prefrontal dopamine (DA) transmission participates in the reinforcement of reward-driven behaviors like eating. Because catechol-O-methyltransferase (COMT) degrades DA and is expressed in the prefrontal cortex, variation in the *COMT* gene may modulate eating behavior. Previous studies have shown that the met allele of the *COMT* val158met single nucleotide polymorphism (SNP) is associated with Bulimia Nervosa (BN). The specific aim of this study was to test whether the met allele increased risk for, and severity of, eating disorder symptomatology in community volunteers. Caucasian adults (N = 1,003; 51.2% female) from the University of Pittsburgh Adult Health and Behavior Project (AHAB) were genotyped and completed the Eating Disorders Inventory (EDI). Logistic and Poisson regression analyses assessed genotype-dependent presence and severity of eating disorder symptomatology. The met allele was significantly associated with the presence of symptoms on the Bulimia subscale and the severity of Body Dissatisfaction scores. All EDI subscales significantly predicted BMI. To our knowledge, these are the first data indicating that the *COMT* met allele increases risk for some symptoms of disordered eating, while increasing severity of others, in a community sample. These novel findings may have important implications for understanding the etiology of heterogeneous disordered eating phenotypes.

Keywords

Catechol-O-methyltransferase gene; prefrontal cortex; dopamine; aberrant eating; eating disorders; Bulimia

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1. Introduction

Binge eating is a feature of several eating disorders, including Binge Eating Disorder (BED), Bulimia Nervosa (BN), and Anorexia Nervosa (AN) Binge-Eating/Purging Type, and affects as much as 5% of the general population (Arcelus et al., 2014; Hilbert et al., 2012; Micali et al., 2013; Mitchison et al., 2012). Defined as periods of excessive eating coupled with a subjective feeling of loss of control, binge eating is associated with clinically significant distress and disability (Striegel-Moore et al., 2001; Tanovsky-Kraff & Yanovsky, 2003; Vanucci et al., 2012). Individuals who report loss of control over eating demonstrate greater psychological comorbidity and weight gain compared to those who overeat without experiencing loss of control (Tanovsky-Kraff & Yanovsky, 2003), even among individuals without an eating disorder (Vanucci et al., 2013). Moreover, individuals who binge eat are more likely to be overweight or obese than those who do not binge eat (Striegel-Moore et al., 2001; Wilfley et al., 2000). Prospective longitudinal research has demonstrated that aberrant eating is associated with more frequent weight-related cognitive distortions, weight gain, and weight-related disease (Tanovsky-Kraff & Yanovsky, 2003). Collectively, these findings suggest that many of the mental and physical health consequences associated with eating disorders also are present in subclinical aberrant eating, highlighting the importance of exploring etiological mechanisms influencing aberrant eating among individuals without a diagnosable eating disorder.

Growing evidence suggests that dopaminergic signaling may promote and maintain aberrant eating behavior (Blumenthal & Gold, 2010; Stice & Burger, 2012). In rat models of binge eating, surges in extracellular dopamine (DA) and altered DA receptor binding within the mesolimbic dopaminergic system (MDS) following a meal are evident in rats that have developed binge-like food intake patterns (Rada et al., 2005). Further, binge eating induced changes in DA signaling have been associated with enhanced responsivity to cues of impending food reward, particularly following a period of dietary restriction (Avena, 2007). This suggests that motivation to consume palatable foods is greater under conditions of restricted access to food (Avena et al., 2005). Dietary restraint is considered an important predictor of aberrant eating (Fairburn et al., 2003), and mediates the effect of drive for thinness and body dissatisfaction on subsequent episodes of aberrant eating (Stice et al., 1998; Wilfley et al., 2000). Therefore, changes in DA signaling enhance motivation to eat following dietary restraint, and may account for the relationship between affect and weight-related cognitive distortions in aberrant eating.

The catechol-O-methyltransferase (COMT) enzyme plays an important role in terminating the action of DA following release from presynaptic terminals (Chen et al., 2004). COMT expression is most abundant in the prefrontal cortex (PFC; Dreher et al., 2009), a region strongly innervated by MDS structures that participates in response inhibition and reward-related contingency learning (Ridderinkhof, et al., 2004). Individuals who associate food more strongly with the experience of pleasure may be at greater risk for aberrant eating, and the strength of this association appears to be strongly dependent on DA processing (Mathes et al., 2009; Ridderinkhof et al., 2004). DA levels are significantly higher in *COMT* knockout mice relative to wild-type controls (Gogos et al., 1998), suggesting that COMT

may contribute to eating behavior through its effects on DA levels. Therefore, sequence variations in the *COMT* gene may predict individual differences in aberrant eating.

In humans, a functional single nucleotide polymorphism (SNP) that codes for an amino acid substitution at codon 158 of the *COMT* gene is associated with increased risk for eating disorders (val158met; Frieling et al., 2006; Mikołajczyk et al., 2005). Enzymatic activity in individuals homozygous for the methionine (met) allele is reduced by 25-75% compared to valine (val) carriers (Chen et al., 2004; Lachman et al., 1996). Lower enzymatic activity may produce elevated DA levels, enhancing DA mediated sensitivity to reward cues (Dreher et al., 2009). It is expected that carriers of the low activity met allele would be more responsive to food cues (Dreher et al., 2009), thus increasing their risk for aberrant eating. Consistent with this hypothesis, the met allele has been associated with greater activation in the ventral striatum during anticipation of food reward, and in the orbitofrontal region of the PFC following delivery of a reward (Dreher et al., 2009). Importantly, the orbitofrontal region is thought to be involved both in the encoding of stimulus value and the regulation of food intake (Kringelbach, 2005). Met allele carriers with a diagnosed eating disorder have also been shown to score higher on self-report bulimia scales relative to val homozygotes (Frieling et al., 2006). In addition, there is evidence to suggest that the met allele is preferentially transmitted to female probands with BN (Yilmaz et al., 2011). These findings indicate that variation in *COMT* could influence aberrant eating.

As of yet, it is unknown whether the *COMT* val/met polymorphism is related to aberrant eating among individuals who exhibit normative or sub-clinical aberrant eating. Although the candidate gene approach to the study of genotype-phenotype relationships has some disadvantages (e.g. difficulty with replication), the power to detect such relationships is far greater for the candidate gene approach relative to the genome wide association approach (Amos et al., 2011). Further, many of the disadvantages of the candidate gene approach can be overcome by the use of large samples (N>200) and choosing polymorphisms with known biological significance (Amos et al., 2011; Tabor et al., 2002). The *COMT* val/met SNP has well documented functional effects (Amos et al. 2011; Chen et al., 2004; Dreher et al., 2009), and has been linked to variation in several processes known to depend on prefrontal signaling (Mier et al., 2009), making it an excellent candidate for study in the context of aberrant eating. Therefore, the specific aim of the present study was to determine whether the *COMT* met allele increases risk for and severity of aberrant eating among a large sample of midlife community volunteers. It was hypothesized that met allele carriers will be more likely to exhibit aberrant eating, and have a higher body mass index (BMI).

2. Methods

2.1. Participants

Participants included 1,295 medically healthy adults from the Adult Health and Behavior Project (AHAB), an extensive registry of behavioral and biological measures collected from a mid-life community sample recruited in Western Pennsylvania between 2001 and 2005 (Erickson et al., 2013; Manuck et al., 2010). Exclusion criteria included a clinical history of neurologic illness, cardiovascular disease, cancer treatment within the previous year, schizophrenia, or other psychoses. Volunteers were also excluded if they reported current

use of insulin, glucocorticoid, antiarrhythmic, psychotropic, or prescription weight-loss medications. Data collection occurred over the course of several laboratory visits, and informed consent was obtained in accordance with the guidelines of the University of Pittsburgh Institutional Review Board. To avoid confounding by population heterogeneity, unknown extent and variability of European genetic admixture among African Americans, and race/ethnicity differences in *COMT* val158met allele frequencies (Palmatier et al., 1999), study analyses were limited to the 1081 AHAB participants of European American ancestry. Of these individuals, those who were not successfully genotyped (n = 64; 5.9%), who met criteria for an eating disorder at the time of participation (n = 1, BN), or who were missing data for any of the EDI scales (n = 13) were excluded, yielding a final sample size of 1,003.

2.2. Measures

2.2.1. Eating Disorders Inventory (EDI)—Participants completed the Drive for Thinness, Bulimia, and Body Dissatisfaction subscales of the EDI (Garner et al., 1983). The EDI and its subscales have been shown to possess adequate internal consistency (Cronbach's □ ranging from 0.82 to 0.90), construct validity, and discriminant validity (Espelage et al., 2003; Garner et al., 1983). Further, the EDI has been shown to be useful for identifying at-risk individuals in healthy samples who display subthreshold symptoms of either AN or BN (Engelson & Laberg, 2001; Klemchuk et al., 1990; Shoemaker et al., 1994). Respondents indicate on a 6-point scale the extent to which a statement applies to their eating-related thoughts or behavior, ranging from "never" to "always." The present study utilized the full 0-6 scale with untransformed scores for all analyses.

2.2.2. Structured Clinical Interview for DSM-IV-TR Disorders (SCID) (First et al., 1996)—Participants were interviewed using the SCID for lifetime and current history of DSM-IV Axis I disorders by masters or doctoral level clinicians, and consensus diagnoses were determined by a licensed clinical psychologist (JDF).

2.2.3. BMI—Height and weight were measured, and used to calculate BMI ((weight[lbs]/height[in^2]) × 703).

2.3. Genotyping

DNA was isolated from white blood cells using the PureGene kit (Gentra Systems, Minneapolis, MN, USA). The genomic region of interest was amplified using polymerase chain reaction. The *COMT* val/met SNP was genotyped using florescence polarization (Chen et al. 1999). Consistent with previous studies (Frieling et al., 2006), the met/met genotype was coded as 1, the val/met genotype was coded 0.5, and the val/val genotype was coded 0.

2.4. Analytic plan

Preliminary analyses indicated that scores on the EDI subscales were positively skewed and zero-inflated, and were thus in violation of the assumptions of Ordinary Least Squares (OLS) regression. Violation of these assumptions can lead to biased estimates of regression coefficients, limiting interpretability of results (Cohen et al., 2003). An alternative to OLS,

the two-process hurdle model, accounts for positive skew by assuming a logistic regression model for zero vs. non-zero responses and a Poisson distribution for the non-zero responses (Atkins & Gallop, 2007; McDowell, 2003). Regression coefficients were separately estimated for comparisons of zero responses to any responses and for comparisons among all non-zero responses (i.e. severity of symptoms among those who endorse them; McDowell, 2003). As such, the hurdle model provides a method for determining whether the factors that contribute to the occurrence of symptoms differ from those that contribute to the severity of symptoms, which may help elucidate the processes underlying heterogeneity in symptom presentation among individuals with aberrant eating.

To test the first component of the hurdle model, scores for each of the EDI subscales were dummy coded to compare zero responses to non-zero responses. Three logistic regression analyses were utilized to estimate the effect of *COMT* genotype on risk for symptoms captured by the Bulimia, Drive for Thinness, and Body Dissatisfaction subscales. To test the second component of the hurdle model, Poisson regression analyses were utilized to estimate the effect of *COMT* genotype on severity of symptoms on the Bulimia, Drive for Thinness, and Body Dissatisfaction subscales among only those individuals endorsing these symptoms (Bulimia: $n = 275$; Drive for Thinness: $n = 607$; Body Dissatisfaction: $n = 863$). Wald's Chi-square values are reported for models in which the independent variable was analyzed at three levels (e.g., *COMT* genotype: met/met vs. val/met vs. val/val), while incident rate ratios (IRR) are reported for models in which independent variables were analyzed dichotomously (e.g., *COMT* genotype: met/met and val/met vs. val/val). IRR statistics reflect the likelihood of reporting symptoms as a function of genotype. To correct for possible alpha inflation due to multiple comparisons, the significance threshold was adjusted for all six primary analyses utilizing the Bonferroni method, yielding an adjusted *p*-value of 0.008.

Finally, in light of research demonstrating that age (van Lenthe et al., 2000; Rand & Kuldau, 1992) and gender (Striegel-Moore et al., 2010) are associated with AN and BN prevalence rates and BMI, all analyses included these as covariates.

3. Results

3.1. Sample characteristics

The sample ($N = 1,003$) included Caucasian adults (51.2% female) between 30 and 54 years of age (M=44.62, SD=6.85) with an average BMI in the overweight range ($M = 27.03$, SD=5.36). Consistent with prior research (Field et al., 1997; Rolls et al., 1991; Striegel-Moore et al., 2010), women were significantly more likely than men to endorse symptoms on the Bulimia (OR (1, 1002) = 1.906, $p < 0.01$), Drive for Thinness (OR (1, 1002) = 2.792, $p < 0.01$) and Body Dissatisfaction (OR (1, 1002) = 3.577, $p < 0.01$) subscales. Women also had higher scores on the Drive for Thinness (IRR (1, 605) = 0.574, $p < 0.01$) and Body Dissatisfaction subscales (IRR (1, 861) = 0.521, $p < 0.01$) relative to men. However, gender was not associated with the severity of symptoms reported on the Bulimia subscale (IRR (1, 273) = 0.595, $p = 0.95$). Men had higher BMI compared to women (F (1, 1002) = 22.211, p = <0.01). Age was not associated with presence or severity of symptoms on the Bulimia (OR (1, 1002) = 0.992, $p = 0.46$; IRR (1, 273) = 0.995, $p = 0.47$), Drive for Thinness (OR (1,

1002) = 0.964, p = 0.85; *IRR* (1, 604) = 0.996, p = 0.40), or Body Dissatisfaction (*OR* (1, 1002) = 0.993, p = 0.62; *IRR* (1, 861) = 1.004, p = 0.24) subscales. Age also did not predict BMI (F (1, 1002) = 0.539, p = 0.46). Table 1 depicts the association between DSM-IV-TR (APA, 2000) Axis-I diagnoses and scores on the EDI subscales. Allele distributions were in Hardy-Weinberg equilibrium (X^2 (1, 1002) = 2.03, p = 0.15).

3.2. Primary analyses: effect of COMT val/met genotype on EDI scores and BMI

Table 2 depicts results from the logistic regression models predicting risk for any symptoms on the EDI, while Table 3 depicts results from the Poisson regression models predicting severity of these symptoms. As shown in Table 2, the *COMT* val/met SNP was significantly associated with risk for bulimic symptomatology such that individuals carrying the met allele were more likely to report symptoms on the Bulimia subscale compared to non-carriers. The relationship between *COMT* genotype and risk for Drive for Thinness scores did not survive correction for multiple comparisons. Finally, *COMT* genotype was not associated with increased likelihood of reporting symptoms on the Body Dissatisfaction subscale.

In contrast to the effect of *COMT* genotype on *risk* for aberrant eating, results of the Poisson regression analyses indicated that among individuals who endorsed items on the EDI, met allele carriers had more severe Body Dissatisfaction scores, but not more severe Bulimia or Drive for Thinness scores than non-carriers (see Table 3). Specifically, the incident rate for Body Dissatisfaction scores among individuals with the val/val genotype was 0.835 times that of individuals with the met/met genotype. Among individuals with the val/met genotype, the incident rate for Body Dissatisfaction was 0.854 times that of individuals with the met/met genotype.

Finally, *COMT* genotype did not predict BMI (ΔF (1, 996) = 1.667, p = 0.20) above and beyond the effect of age and gender, but scores on the EDI subscales were associated with higher BMI (Bulimia: ΔF (1, 996) = 92.589, p = <0.01; Drive for Thinness: ΔF (1, 996) = 78.698, p = <0.01; Body Dissatisfaction: ΔF (1, 996) = 423.227, p = <0.01; Table 4). Including any current or past Axis-I diagnoses as covariates in each model did not change results. See Table 1 for all diagnoses that were significantly associated with each EDI subscale.

3.3. Secondary analyses

To further explore the extent to which results from primary analyses might be explained by the presence of Axis-I diagnoses that commonly co-occur with eating disorder symptomatology, analyses were re-run excluding individuals who, at the time of assessment, had a history of an eating disorder, were in a depressive episode, met criteria for drug abuse or dependence, and/or met criteria for alcohol dependence (n = 76). Utilizing the standard significance threshold of p = 0.05, the met allele remained a significant predictor of presence of symptoms on the Bulimia subscale (*OR* (1, 926) = 1.853, p = 0.004), and severity of Body Dissatisfaction scores (Wald's X^2 (1, 794) = 9.224, p = 0.01). As before, the met allele was not significantly associated with presence of symptoms on the Drive for Thinness (*OR* (1, 926) = 1.435, p = 0.075) and Body Dissatisfaction (*OR* (1, 926) = 1.736, p = 0.054)

subscales, or severity of Bulimia (Wald's X^2 (1, 255) = 1.171, p = 0.557) and Drive for Thinness (Wald's X^2 (1, 563) = 3.336, p = 0.186) scores.

4. Discussion

The present investigation demonstrated that individuals carrying the met allele of the *COMT* val158met SNP were 87% more likely than individuals with the val/val genotype to report symptoms on the Bulimia subscale. Interestingly, the *COMT* val/met SNP was not predictive of the severity of symptoms captured by the Bulimia subscale, suggesting that *COMT* variation may be specifically related to risk but not severity of these symptoms. In contrast, the met allele was associated with severity of, but not risk for, body dissatisfaction. Specifically, the number and severity of symptoms endorsed by individuals homozygous for the met allele was about 19% higher than the number of symptoms report by individuals with either the val/met or val/val genotype. Further, correction for presence or history of any Axis I diagnosis did not eliminate the relationship between *COMT* genotype and likelihood of reporting symptoms on the Bulimia subscale or severity of symptoms on the Body Dissatisfaction subscale, indicating that the observed associations are not better explained by comorbid psychopathology.

The observation that the met allele is associated with risk for symptoms associated with BN is consistent with previous candidate gene studies examining the relationship between the *COMT* val/met SNP and bulimic symptomatology (Frieling et al., 2006; Yilmaz et al., 2011). Given that the met allele is associated with reduced enzymatic degradation of DA in the PFC (Dreher et al., 2009), it is possible that met allele carriers are more responsive to rewards like food and have greater difficulty exerting top-down control of behavior driven by midbrain DA activation (Carr & Sesack, 2000; Dreher et al., 2009; Yacubian et al., 2007). Furthermore, preliminary evidence suggests that impaired functional connectivity in fronto-striatal networks during a reward processing task predicts persistence of binge eating following treatment for BED (Balodis et al., 2014). Therefore, abnormalities in dopaminergic processing in prefrontal regions may contribute to risk for BN or BN-spectrum symptomatology through weakened coupling between prefrontal and midbrain regions, which may increase the frequency of impulsive dietary behaviors (e.g. bingeing, purging, excessive exercise). This hypothesis warrants further empirical testing.

No studies to date have specifically explored how variation in prefrontal DA availability might differentially contribute to severity of, but not risk for, body dissatisfaction. Unlike the symptoms captured on the Bulimia and Drive for Thinness scales, symptoms on the Body Dissatisfaction scale are less behavioral in nature and may therefore be more distally related to dopaminergic processing, given that DA signaling is more closely related to behavioral control and motivation (Wise, 2004). Therefore, the effect of *COMT* genotype on risk for body dissatisfaction may not become evident unless other risk factors such as depressed mood are present, which may explain the lack of an association between *COMT* genotype and risk of body dissatisfaction in the present study. Candidate gene studies in other clinical populations have also demonstrated that there may be unique genetic influences on risk, severity, progression, and clinical presentation of a given phenotype (Goghari & Sponheim, 2008; Laucht et al., 2008; Parsa et al., 2013). For instance, variation

in the gene encoding apolipoprotein 1 was found to predict progression of, but not risk for, chronic kidney disease (Parsa et al., 2013). This indicates that it is possible for single genetic polymorphism to exert a differential effect on risk for, and severity of, a single symptom domain, as was demonstrated in the present study.

There are several limitations that should be considered when interpreting these results, including the low incidence of eating pathology, constricted variance in the EDI scores, method of phenotype assessment, and the cross-sectional nature of the study. Given that individuals in the current sample were selected on the basis of being in generally good health, there was minimal representation of aberrant eating. It might have been preferable to evaluate eating behavior more generally, such as size, frequency, and content of dietary intake, which would vary even in a non-clinical sample. Changes in dietary patterns are likely to precede the onset of a diagnosable eating disorder (Fairburn & Harrison, 2003), suggesting that genetic variation may have a more proximal influence on eating behavior that may subsequently lead to the development of eating disorder symptomatology (e.g. overvaluation of weight, negative expectancies about food, binge eating; Bulik et al., 2007). In addition, the EDI tends to assess dissatisfaction with body parts that are typically more of a concern for women (e.g. hips, thighs), and therefore may not be the most appropriate measure of this construct among males. Finally, the exclusion of all non-Caucasian individuals from the sample may limit the generalizability of the reported results, though it was necessary to do so in order to minimize the confounding effects of population stratification.

In summary, the present investigation provided evidence that the *COMT* val/met SNP is differentially predictive of risk for and severity of various features of aberrant eating. These findings may have important implications for understanding the mechanisms underlying heterogeneity in symptom presentation among those exhibiting aberrant eating. Future studies could utilize prospective longitudinal assessment methods to confirm the present findings, as well as expand what is known about the role of dopaminergic processing in the development, severity, and progression of aberrant eating behavior through the use of functional imaging techniques.

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Highlights

- Little is known about the role of prefrontal dopamine signaling in sub-clinical aberrant eating.
- We examined the effect of the *COMT* val/met SNP on aberrant eating in a large community sample of adults.
- Using hurdle modeling, we analyzed differential effects on risk and severity of aberrant eating.
- The met allele predicted risk for bulimic symptoms and drive for thinness but not body dissatisfaction.
- The met allele predicted severity of body dissatisfaction only.

Table 1

Associations between DSM-IV-TR diagnoses and likelihood of reporting symptoms on the Bulimia, Drive for Thinness, and Body Dissatisfaction subscales of the Eating Disorders Inventory.

Diagnosis		Bulimia		Drive for Thinness		Body Dissatisfaction	
	n (%)	X^2	*p*	X^2	*p*	X^2	*p*
Current Axis-I	130 (13.0)	**12.710**	**<0.001**	2.564	0.065	1.265	0.161
Past Axis-I	253 (25.2)	**9.722**	**0.001**	**7.376**	**0.004**	**3.923**	**0.028**
Current MDE	7 (0.7)	0.004	0.616	**6.306**	**0.017**	4.902	0.061
Past MDE	151 (15.0)	2.194	0.085	1.429	0.134	1.673	0.120
Current AUD	71 (7.1)	**5.460**	**0.011**	0.999	0.191	0.551	0.278
Past AUD	293 (29.2)	**6.233**	**0.007**	**5.754**	**0.010**	0.176	0.376
Current Drug Use Disorder	33 (3.3)	2.606	0.073	2.575	0.079	0.076	0.469
Past Drug Use Disorder	222 (22.1)	2.503	0.066	4.051	0.027	0.001	0.538
Past AN	7 (0.7)	3.130	0.094	1.873	0.165	1.144	0.348
Past BN	8 (0.8)	0.405	0.384	0.708	0.326	0.014	0.690
Past BED	4 (0.4)	1.021	0.304	2.620	0.134	0.651	0.548

Note. Current and past Axis-I categories do not include alcohol or drug use disorders. Alcohol and drug use disorder categories include both abuse and dependence. Current and past Axis-I categories are not necessarily mutually exclusive. All *p*-values are 1-sided. DSM-IV-TR = Diagnostic and Statistical Manual of Mental Disorders-Fourth Edition, Text Revision (APA, 2000); MDE = Major Depressive Episode; AUD = Alcohol Use Disorder; AN = Anorexia Nervosa; BN = Bulimia Nervosa; BED = Binge Eating Disorder. P-values less than .05 are in bold type.

Table 2

Effect of *COMT* val158met genotype on presence of symptoms on the Bulimia, Drive for Thinness, and Body Dissatisfaction subscales of the Eating Disorders Inventory (EDI).

EDI Subscale	Block X^2	*p*	*OR*	*p*	95% CI
Bulimia	21.457	<0.001			
Block 1					
Age			0.992	0.426	0.972-1.012
Gender			1.932	<0.001	1.453-2.569
Block 2	9.739	0.002			
COMT val/met			1.920	0.002	1.272-2.896
Drive for Thinness	60.684	<0.001			
Block 1					
Age			0.997	0.793	0.979-1.017
Gender			2.784	<0.001	2.142-3.619
Block 2	3.881	0.049			
COMT val/met			1.467	0.049	1.001-2.149
Body Dissatisfaction	44.350	<0.001			
Block 1					
Age			0.991	0.497	0.965-1.018
Gender			3.602	<0.001	2.409-5.386
Block 2	2.188	0.139			
COMT val/met			1.496	0.141	0.875-2.557

Note. Genotypes coded additively in all analyses.

Table 3

Effect of *COMT* genotype on severity of symptoms on the Bulimia, Drive for Thinness, and Body Dissatisfaction subscales of the Eating Disorders Inventory (EDI).

EDI Subscale	Wald's X^2	*p*	*IRR*	*p*	95% CI	*M (SD)*
Bulimia	1.264	0.531				
COMT val/val			1.078	0.551	0.842-1.380	2.610 (1.732)
COMT val/met			0.954	0.674	0.767-1.187	2.331 (1.823)
COMT met/met			---	---	---	2.456 (1.888)
Drive for Thinness	3.146	0.207				
COMT val/val			0.847	0.097	0.696-1.031	3.721 (3.550)
COMT val/met			0.964	0.669	0.817-1.139	4.388 (3.816)
COMT met/met			---	---	---	4.551 (4.011)
Body Dissatisfaction	9.658	0.008				
COMT val/val			0.836	0.006	0.735-0.950	9.194 (7.226)
COMT val/met			0.854	0.006	0.764-0.955	9.537 (7.236)
COMT met/met			---	---	---	11.305 (7.967)

Note. The met/met genotype was designated as the reference group for Poisson analyses. X^2 = chi square. *IRR* = incident rate ratio. CI = confidence interval.

Table 4

Mean BMI among those with and without eating disorder symptomatology.

EDI subscale	*N*	*M (SD)*	Range
COMT			
met/met	200	27.52 (5.56)	17.9–48.4
val/met	520	26.91 (5.13)	16.7–51.7
val/val	280	26.92 (5.64)	17.4–49.6
Bulimia			
Present	275	29.33 (6.16)	19.4–48.8
Absent	725	26.16 (4.75)	16.7–51.7
Drive for Thinness			
Present	606	28.16 (5.67)	16.7–51.7
Absent	394	25.30 (4.31)	17.4-48.8
Body Dissatisfaction			
Present	860	27.57 (5.44)	16.7–51.7
Absent	140	23.75 (3.33)	17.4-41.1

Note. BMI was analyzed as a continuous variable, but is presented above by dichotomized EDI subscale scores for ease of interpretation. BMI data were missing for three participants.