Genetic loading on human loving styles

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Submitted: September 17, 2007 *Accepted: November 19, 2007*

Key words: **romantic love; neurotransmitters; genetics; humans**

Neuroendocrinol Lett 2007; **28**(6):815–821 **PMID:** 18063936 NEL280607A06

Abstract

OBJECTIVES: It has been hypothesized that cerebral neurotransmitters such as dopamine and serotonin could play a role in human romantic bonding. However, no data on the genetic basis of human romantic love are currently available. To address this issue, we looked for associations between markers in neurotransmitter genes (the serotonin transporter gene, 5-HTT; the serotonin receptor 2A, 5HT2A; the dopamine D2 receptor gene, DRD2; and the dopamine D4 receptor gene, DRD4) and the six styles of love as conceptualized by Lee (Eros, Ludus, Storge, Pragma, Mania and Agape).

DESIGN: A total of 350 healthy young adults (165 males and 185 females, mean age: 24.1±3.9 years, range 18–32 years) filled the 24-item Love Attitudes Scale (LAS) and were genotyped for the following six polymorphic markers: the serotonin transporter-linked polymorphic region (5-HTTLPR), the 5HT2A T102C and C516T polymorphisms, the DRD2 *Taq*I A and *Taq*I B variants, and the DRD4 exon 3 VNTR polymorphism.

RESULTS: Statistical analysis revealed a significant association between the DRD2 *Taq*I A genotypes and "Eros" (a loving style characterized by a tendency to develop intense emotional experiences based on the physical attraction to the partner), as well as between the C516T 5HT2A polymorphism and "Mania" (a possessive and dependent romantic attachment, characterized by self-defeating emotions). These associations were present in both sexes and remained significant even after adjustment for potential confounders.

CONCLUSIONS: Our data provide the first evidence of a possible genetic loading on human loving styles.

ORIGINAL ARTICLE

INTRODUCTION

Throughout centuries, the nature of human love has been a matter of speculation for scholars from a variety of disciplines. For instance, contemporary personality and social psychologists have made important progresses to understanding the nature of close relationships and attachment styles (Furnham & Heaven 1999). Accordingly, behavioral scientists have proposed a number of taxonomies of human love that have provided additional impetus for research in the field of love types or varieties (Hendrick 2004; Moore & Leung 2002; Worobey 2001). Among the different typologies of love, one of the

most common classification scheme was developed by the Canadian sociologist Lee. Specifically, this author proposed a taxonomy named "the Color Theory of Love", and believed that social scientists could categorize love into a total of six different loving styles (Lee 1976).

The first, Eros, is an intense emotional experience based on the physical attraction to the partner. The erotic lover is prone to fall instantly and completely in love with a stranger ("love at first sight"), is powerfully attracted by a particular physical type, and enjoys expressing his or her affection through sexual contact with the beloved. The second love style, Ludus, is a game-playing love entailing deception and often played with several partners simultaneously. Differently from Eros, ludic lovers display low emotional involvement, prefer a variety of physical types, and view sexuality as an opportunity for pleasure rather than for intense emotional bonding. Storge is the third love style proposed by Lee, and refers to enduring love, or the merging of love and friendship. Storgic lover does not experience the intense emotional and physical attraction associated with Eros, prefers to engage in shared interests with the partner rather than communicate direct feelings, and tends to express his or her affection in nonsexual ways. The fourth love style, Pragma, is a practical and logical love. Pragmatic lover typically seeks a compatible individual and selects a mate based on how well a person fulfills his or her requirements. This kind of love requires a committed partner, and is believed to be not very exciting. Mania, the fifth love style, is a possessive and dependent love, characterized by self-defeating emotions, and an extreme desire to be loved by the preferred individual. Manic lovers usually try to force the partner to show reciprocation and commitment, and have an intense craving for emotional union with their beloved. As described by Lee, manic lovers are "irrational, extremely jealous, obsessive, and often unhappy". The last love style is Agape, a selfless, unconditional, and all-giving love. Agapic lover totally devotes himself or herself to the partner, even stepping aside in favour of another person who seems most likely to meet the partner's expectations. Accordingly, Agape is considered an ideal altruistic love based on the concept that everyone is worthy of love, and that loving others is a duty of every mature person.

Lee's classification scheme of loving styles is of particular interest inasmuch as it has generated considerable research activity and widely used measurements instruments, the most well-known being the Love Attitudes Scale (LAS) (Hendrick & Hendrick 1986; Hendrick *et al.*, 1998). Nonetheless, while a number of studies have been conducted into the psychological constructs associated with measures of the six loving styles (Heaven *et al.*, 2004; Wan *et al.*, 2000; Woll 1989), no data are currently available on the possible neurogenetic substrates underlying the different love varieties. This information gap is surprising, in view of the growing evidences implicating the cerebral monoaminergic signalling systems in the sentiment of human love.

Indeed, a reduced functionality of the serotonin transporter has been previously related to obsessive romantic thoughts (Marazziti *et al.*, 1999). Additionally, the dopaminergic circuits implicated in the neuronal reward pathways have been demonstrated to play an important role in the feelings and behaviors of romantic love (Aron *et al.*, 2005; Bartels & Zeki 2004; Fisher *et al.*, 2002). Of interest, neurobiological evidences implicating dopamine neurotransmission in human love have striking parallels in animal investigations (Gingrich *et al.*, 2000; Liu & Wang 2003).

Hypothesizing about a possible influence of genetic factors related to the neurotransmitter systems on loving styles, it seemed of interest to examine the association of polymorphisms in four genes involved in the serotonergic and dopaminergic pathways (the serotonin transporter gene, 5-HTT; the serotonin receptor 2A, 5HT2A; the dopamine D2 receptor gene, DRD2; and the dopamine D4 receptor gene, DRD4) with the six styles of love as measured by the LAS (Hendrick *et al.*, 1998). The investigated polymorphisms were the serotonin transporter-linked polymorphic region (5-HTTLPR), the T102C and C516T polymorphisms of the 5HT2A receptor gene, the DRD2 *Taq*I A and *Taq*I B variants, and the DRD4 exon 3 VNTR polymorphism.

MATERIALS AND METHODS

Study participants

A total of 350 healthy young adults (165 males and 185 females, mean age: 24.1±3.9 years, range 18–32 years) were recruited by posters and word-of-mouth inviting to participate in a study of "genetic bases of loving style". The great majority of the participants (91%) were university or postgraduate students, the remaining 9% being office employers or factory workers. Potential participants were required to be medically healthy. Subjects with a history of heavy cigarette smoking, alcohol or drug dependence were excluded from the present investigation.

Before enrolment in the study, candidates were thoroughly screened for current or past psychiatric conditions. During this first-line assessment, subjects were also asked to complete a series of rating scales that included the Beck Depression Inventory (BDI), the State-Trait Anxiety Inventory (STAI), and the Yale-Brown Obsessive-Compulsive Rating Scale (Y-BOCS).

Axis-I and axis-II disorders, axis-I diagnosis of first degree relatives and psychotropic medication intake led to immediate exclusion from the study. In addition, only subjects who did not show an abnormal scoring at psychometric instruments were considered for participation. The cutoff points used for defining abnormal scores were in accordance with previous studies (O'Leary *et al.*, 2000; Peres *et al.*, 2001; Nuttin *et al.*, 2003; Wang *et al.*, 2005). Specifically, all study participants showed BDI scores <16, trait- and state-anxiety scores <46, and Y-BOCS scores lower than or equal to 7.

After these exclusions, participants were required to fill the short-form of the Love Attitudes Scale (Hendrick *et al*., 1998). This is a revised version of the earlier LAS scale (Hendrick & Hendrick 1986), consisting of 24 items with four items for each of the six love styles. Participants were asked to rate each item on a five-point Likert scale from "strongly disagree" (score 1) to "strongly agree" (score 5). The validity and reliability of this scale to measure the six love styles have been demonstrated in previous studies (Heaven *et al*., 2004; Wan *et al*., 2000, Woll 1989). This instrument has strong psychometric properties and is considered to be suitable for researchers who need a brief love scale in relationship measures (Hendrick *et al*., 1998). Current relationship status was assessed by self-report questionnaire and coded as 1 ("having a current loving relationship") or 0 ("no current loving relationship"). All study participants were Caucasians. All subjects provided their written informed consent to participate in the study, which was conducted with the ethical requirements defined in the Helsinki Declaration.

Genotyping

Genomic DNA was extracted from saliva samples collected in Oragene kits according to the manufacturer's instructions (DNA Genotek Inc.). Genotyping of insertion/deletion polymorphism in the promoter region of the serotonin transporter gene (5-HTTLPR) was performed as described by Lesch *et al*., (1996). Products were subjected to electrophoresis on 3.5% agarose gel and visualized under ultraviolet light after ethidium bromide staining. DNA bands were classified as long (L=528 bp) and short (S=484 bp).

Genotyping of the T102C polymorphism of the 5HT2A receptor gene was done according to the PCR method described by Warren *et al*., (1993). The amplified products were digested with the endonuclease *Msp*I. Digested products were resolved by electrophoresis and visualized under UV light. The 102T allele PCR products remained uncut, with a single DNA band of 342 bp, whereas the 102C allele yielded two distinct fragments of 216 bp and 126 bp. The sequence containing the C516T variant in the 5HT2A gene was amplified by PCR using primers described by Arranz *et al*., (1995). The amplified products were digested with *Sau96*I restriction enzyme and the genotype was determined after electrophoresis on ethidium bromide stained 2% agarose gels. The 516C allele showed fragments of 109 and 86 bp, whereas the 516T allele remained uncut 195 bp.

Subjects were genotyped for *Taq*I A and *Taq*I B restriction fragment length polymorphisms of the DRD2 gene according to the previously described methods. Specifically, for the *Taq*I A variant, we followed the protocol of Grandy *et al*., (1993). Two alleles were obtained: the Al allele (the uncleaved 310 bp fragment) and the A2 allele (the cleaved 180 bp and 130 bp fragments). The primers and methods for determining DRD2 *Taq*I B alleles described by Spitz *et al*., (1998) were utilized. Two alleles were identified: the B1 allele (the uncleaved 459 bp fragment) and the B2 allele (the cleaved 267 bp and 192 bp fragments).

Finally, for the DRD4 exon 3 typing, a PCR was carried out with primers and conditions reported previously (Macciardi *et al*., 1994). As this polymorphism is particularly complex, depending on a seven-allele system from DRD4*2 to DRD4*8 (Van Tol *et al*., 1991), we pooled DRD4 variants into short (alleles 2–4) and long (alleles 5–8), as done previously (Cusin *et al*., 2002). Genotyping was checked by two readers who were blinded to all psychometric data.

Statistical analysis

Data were expressed as frequencies and percentages or as means ± standard deviations (SD). As none of the continuous variables was statistically significantly different from a normal distribution at the 5% level according to Kolmogorov-Smirnov tests, only parametric analyses were performed in the present study. The categorical data were analyzed by $\chi 2$ tests. For comparison of continuous variables between two groups, the differences were evaluated using the Student's *t* test. A test for deviation from the Hardy-Weinberg equilibrium was performed using online resources (http://www.kursus.kvl.dk/shares/vetgen/_Popgen/genetik/applets/kitest.htm). Correlations between variables were evaluated using Pearson's correlation coefficients. The hypothesis that loving style scores differed across the investigated genotypes was tested using ANOVA (including polynomial contrast analysis for trend), and by ANCOVA after considering the confounding effects of age, current relationship status, and psychometric indexes. Analyses were conducted separately in males and females participants. SPSS 11.0 software (SPSS Inc.) was used in all statistical analyses. All significance tests for comparison were two-tailed, and results were considered significant at $p<0.05$.

RESULTS

Demographical characteristics, psychometric indexes, and mean scores on the loving measures for males and females are presented in Table 1. Men were found to score significantly higher than women on Mania and Agape dimensions, while females showed significantly higher scores on Pragma. These gender differences on loving styles are fully consistent with those previously reported by Heaven *et al*., (2004).

None of the correlation coefficients between psychometric indexes and loving scores reached significance neither in the entire study cohort nor when the analyses were conducted separately by gender, with the only exception being the significant positive relationship between Mania and BDI scores in the subgroup of males having a current loving relationship ($n=126$; $r=0.34$, $p<0.001$).

The scores on the six love dimensions in men and women sorted by genotypes of the investigated

Table 1. Demographic characteristics, psychometric indexes, and mean scores on loving styles for men and women.

	Males (n=165)	Females (n=185)	p-value
Age, years	24.4±4.1	23.8±3.8	0.18
Current loving relationship	126(76.4%)	146(80.2%)	0.46
BDI	6.0±3.9	6.5±4.9	0.19
STAI trait	35.2±6.2	35.6±6.6	0.31
STAI state	34.8±6.4	35.9±6.5	0.36
Y-BOCS	3.2±1.8	3.5±1.9	0.33
Eros	12.9±4.4	12.4±4.3	0.20
Ludus	9.5±3.9	9.7±4.2	0.71
Storge	11.9±5.0	12.4±4.7	0.42
Pragma	7.2±2.7	9.2±3.8	<0.001
Mania	12.7±4.9	11.0±4.4	<0.001
Agape	12.5±4.6	10.1±4.1	<0.001

p-values were calculated using χ^2 analysis or the Student's t test, as appropriate

polymorphisms are shown in Table 2. The distribution of each genotype was consistent with the Hardy-Weinberg equilibrium.

One-way ANOVA revealed a statistically significant association between the DRD2 *Taq*I A genotypes and Eros (Eros scores by genotype in males, A1A1: 17.1±2.0, A1A2: 14.0±4.1, A2A2: 11.2±4.3, one-way ANOVA: p<0.001, p for trend <0.001; Eros scores by genotype in females, A1A1: 15.8±3.1, A1A2: 11.5±4.3, A2A2: 12.5±4.3; one-way ANOVA: p=0.001, p for trend =0.003), as well as between the C516T 5HT2A polymorphism and Mania (Mania scores by genotype in males, CC: 15.5±6.4, CT: 14.9±3.7, TT: 11.9±5.1; one-way ANOVA: p=0.002, p for trend <0.001; Mania scores by genotype in females, CC: 17.5±3.5, CT: 14.2±3.2, TT: 9.8±4.2; one-way ANOVA: p<0.001, p for trend <0.001). These associations were present in both sexes and remained significant even when analyzed by ANCOVA after adjustment for age, psychometric indexes, and current relationship status (Table 2). There was, however, no significant relationship between the investigated polymorphisms and BDI, STAI or Y-BOCS scores in both sexes (data not shown).

DISCUSSION

Love is a central experience of human life, and there has been growing interest into the neurobiological bases of romantic love (Esch & Stefano 2005a) as well as its correlations with human health (Esch & Stefano 2005b) and stress reactions (Stefano & Esch 2005). Increasing evidence has suggested that the dopamine reward pathway and its interaction with the serotonin system could play a role in human mating system and its related behavioral aspects (Aron *et al.*, 2005, Marazziti *et al.*, 1999). However, the extent to which genetic makeup modulates loving styles in humans has been to date a neglected area of research. Although it appears unlikely that a single gene may serve as a predictor of loving styles, it is possible that if the candidate genes are examined in combination, in the form of a genetic profile, researchers may be able to gain a clearer picture of the extent to which genetics could play a role in a complex behavior that results from a host of environmental and psychological factors.

To the best of our knowledge, this is the first study investigating the influence of neurotransmitter gene polymorphisms on the six different loving styles as quantified using a psychometrically sound instrument such as the LAS (Hendrick *et al.,* 1998). We observed significant differences in Eros (a loving style characterized by a tendency to develop intense emotional experiences based on the physical attraction to the partner) scores across DRD2 *Taq*I A genotypes, as well as a relationship between the 5HT2A C516T genotype status and Mania (a possessive and dependent romantic attachment). Notably, these associations were identified using a study design that controlled for the potential confounders of age, gender, scores of anxiety and depression, and current relationship status.

The dopamine D2 receptor is a G protein-coupled receptor located in the postsynaptic dopaminergic neurons that is centrally involved in reward-mediating mesocorticolimbic pathways (Bonci & Hopf 2005). Our results point toward an association between the DRD2 *Taq*I A polymorphism and the Eros dimension on the LAS. Specifically, we observed a trend for higher scores on Eros according to the number of the A1 alleles. It should be noted that the A1 allele has been previously shown to be associated with low DRD2 density in human brain both from in vitro (Noble *et al.*, 1991; Thompson *et al.*, 1997) and in vivo studies (Pohjalainen *et al.*, 1998) compared with the A2 allele. Under these circumstances, it seems reasonable to hypothesize that such a reduced number of dopamine binding sites could result in a deficiently functioning of the dopaminergic reward system (Wu *et al.*, 2000), such that individuals carrying the A1 allele would experience enhanced reward when engaged in pleasant experiences such as romantic and physical attraction, sexual consummation, and related phenomena. This could be in line with several facets of Eros, such as the seeking of emotional intimacy and sexual involvement fairly early in a relationship (Lee 1976). It is also noteworthy that the DRD2 gene has been increasingly implicated in the genetic mechanisms underlying addiction (Noble 2000). This is also consistent with some of the addictive features associated with Eros, including the intense need for daily contact with the beloved, or the wishing to maintain the relationship exclusive (Lee 1976).

Table 2. Love style scores according to the genotypes of the investigated polymorphisms in men and women.

	Men (n=165)					Women (n=185)				
5-HTTLPR	LL (n=48)	LS (n=77)	SS (n=40)	p-value ANOVA	p-value ANCOVA	LL (n=59)	LS (n=89)	SS (n=37)	p-value ANOVA	p-value ANCOVA
Eros	13.3±4.1	12.9±4.3	12.7±4.3	0.84	0.68	12.0±4.2	12.7±4.3	12.1±4.7	0.56	0.89
Ludus	9.8±3.9	9.3±4.0	9.4±3.7	0.78	0.60	9.3±4.7	10.0±4.6	9.4±4.6	0.59	0.83
Storge	11.4±4.7	11.8±4.9	12.9±5.3	0.37	0.07	12.8±4.9	12.4±4.7	11.6±4.0	0.50	0.34
Pragma	7.1±2.7	7.0±2.7	7.7±2.7	0.38	0.41	9.6±4.5	8.8±3.1	9.3±3.9	0.45	0.74
Mania	12.1±4.6	13.0±5.0	13.1±5.0	0.50	0.30	11.8±4.5	10.4±4.3	11.1±4.5	0.13	0.24
Agape	12.1±4.8	12.5±4.8	12.8±3.9	0.72	0.55	10.5±4.4	10.3±4.2	8.8±2.5	0.11	0.14
5HT2A T102C	TT (n=38)	TC (n=70)	CC (n=57)	p-value ANOVA	p-value ANCOVA	TT (n=43)	TC (n=81)	CC (n=61)	p-value ANOVA	p-value ANCOVA
Eros	12.4±4.8	13.2±4.2	13.1±4.4	0.63	0.38	12.9±4.4	11.9±4.5	12.6±4.0	0.42	0.72
Ludus	9.8±4.4	9.5±3.9	9.4±3.7	0.89	0.55	9.4±5.1	9.6±4.3	10.0±4.8	0.81	0.77
Storge	13.2±5.1	11.6±4.9	11.5±5.0	0.22	0.19	13.2±4.8	12.2±4.6	12.1±4.6	0.42	0.25
Pragma	8.0±3.1	7.2±2.6	6.7±2.6	0.08	0.06	9.8±4.2	9.0±3.6	8.9±3.6	0.43	0.35
Mania	12.7±5.2	13.0±4.5	12.6±5.3	0.88	0.98	10.1±4.4	11.5±4.5	10.8±4.2	0.23	0.78
Agape	13.6±4.8	11.7±4.6	12.7±4.4	0.11	0.31	9.5±4.5	10.7±4.0	9.6±3.7	0.18	0.96
5HT2A C516T	CC (n=2)	CT (n=42)	TT (n=121)	p-value ANOVA	p-value ANCOVA	CC (n=2)	CT (n=49)	TT (n=134)	p-value ANOVA	p-value ANCOVA
Eros		13.5±4.4	12.8±4.4	0.61	0.56	16.0±5.6	12.0±4.2	12.4±4.3	0.41	0.64
Ludus	13.5±2.1	9.5±4.0	9.5±3.9	0.35	0.80	10.5±6.4	9.5±4.6	9.8±4.7	0.93	0.86
Storge	9.0±0.0	11.9±5.2	12.0±4.9	0.68	0.54	16.5±0.7	12.2±4.5	12.4±4.8	0.44	0.54
Pragma	6.5±2.1	7.9±3.5	7.0±2.4	0.20	0.19	11.0±4.2	9.3±3.9	9.1±3.8	0.76	0.49
Mania	**15.5±6.4**	**14.9±3.7**	**11.9±5.1**	**0.002**	**0.004**	**17.5±3.5**	**14.2±3.2**	**9.8±4.2**	**<0.001**	**<0.001**
Agape	9.0±7.1	12.7±4.1	12.4±4.7	0.52	0.88	11.5±3.5	10.0±3.9	10.1±4.1	0.87	0.58
DRD2 TaqI A	A1A1 (n=16)	A1A2 (n=70)	A2A2 (n=79)	p-value ANOVA	p-value ANCOVA	A1A1 (n=17)	A1A2 (n=73)	A2A2 (n=95)	p-value ANOVA	p-value ANCOVA
Eros	**17.1±2.0**	**14.0±4.1**	**11.2±4.3**	**<0.001**	**<0.001**	**15.8±3.1**	**11.5±4.3**	**12.5±4.3**	**0.001**	**0.012**
Ludus	10.1±3.9	9.7±3.9	9.3±3.9	0.73	0.43	11.4±5.2	9.1±4.5	9.8±4.6	0.17	0.76
Storge	10.7±4.9	12.4±4.6	11.9±5.3	0.48	0.90	12.1±4.4	12.5±4.9	12.4±4.6	0.94	0.97
Pragma	7.1±2.3	7.5±3.1	7.1±2.4	0.57	0.73	8.8±4.4	8.7±3.4	9.6±3.9	0.28	0.25
Mania	14.1±5.1	13.2±4.6	12.1±5.2	0.22	0.07	10.1±4.2	10.7±4.3	11.3±4.6	0.45	0.34
Agape	12.1±4.9	12.7±4.5	12.3±4.6	0.81	0.96	9.5±3.8	10.4±4.1	9.9±4.1	0.62	0.46
DRD2 TaqI B	B1B1 (n=31)	B1B2 (n=46)	B2B2 (n=88)	p-value ANOVA	p-value ANCOVA	B1B1 (n=38)	B1B2 (n=50)	B2B2 (n=97)	p-value ANOVA	p-value ANCOVA
Eros	14.4±4.1	12.0±4.3	13.0±4.4	0.06	0.15	13.1±4.2	11.5±4.4	12.7±4.3	0.17	0.22
Ludus	9.4±3.3	8.8±3.1	9.9±4.4	0.29	0.46	9.7±5.1	9.7±4.2	9.7±4.8	0.99	0.77
Storge	12.6±4.9	11.1±5.3	12.1±4.8	0.37	0.95	12.7±4.6	13.1±4.3	11.9±4.9	0.29	0.23
Pragma	7.1±2.8	6.8±2.6	7.4±2.8	0.42	0.45	9.0±4.1	9.2±3.8	9.3±3.7	0.93	0.95
Mania	12.6±5.1	12.5±5.5	12.9±4.6	0.89	0.84	10.3±4.1	10.7±4.6	11.4±4.5	0.42	0.44
Agape	12.3±5.1	12.3±4.2	12.6±4.7	0.91	0.70	9.5±3.8	10.9±4.7	9.9±3.8	0.20	0.83
DRD4 Exon 3 VNTR	LL (n=120)	LS (n=38)	SS (n=7)	p-value ANOVA	p-value ANCOVA	LL (n=136)	LS (n=43)	SS (n=6)	p-value ANOVA	p-value ANCOVA
Eros	13.1±4.3	12.8±4.7	12.0±3.7	0.79	0.50	12.3±4.3	12.1±4.4	15.5±5.0	0.20	0.45
Ludus	9.5±3.8	9.4±4.0	10.3±5.4	0.84	0.97	9.6±4.6	9.7±4.9	10.5±5.1	0.91	0.84
Storge	11.9±4.9	11.8±5.4	12.6±5.7	0.93	0.99	12.4±4.8	12.1±4.2	14.3±5.1	0.57	0.92
Pragma	7.2±2.7	7.6±2.8	5.8±1.7	0.26	0.84	9.3±3.8	9.1±3.8	8.2±3.1	0.75	0.42
Mania	12.7±4.9	12.5±4.8	14.6±5.8	0.58	0.66	10.7±4.5	11.4±4.1	13.7±5.0	0.32	0.59
Agape	12.4±4.5	12.3±4.8	14.2±4.6	0.57	0.60	10.2±4.2	9.4±3.6	10.3±3.8	0.50	0.34

Bold text indicates statistical significant associations. P values were calculated by one-way ANOVA, and by ANCOVA after adjustment for age, psychometric indexes, and current relationship status.

The second important finding of our study was the significant association between the C516T 5HT2A variant and Mania, a loving style characterized by a high degree of emotional dependency. Of note, over the last decade, the gene encoding serotonin receptor 2A has been implicated as a functional candidate in a variety of neuropsychiatric phenotypes including affective and anxiety disorders (Norton & Owen 2005). It is also worth noting that the same polymorphism in the 5HT2A gene has been previously associated with obsessive-compulsive disorder (Meira-Lima *et al*., 2004). With regard of human love, obsessive romantic ruminations have been previously related to a reduced functionality of the serotonin transporter (Marazziti *et al*., 1999).

Taken together, we believe that the results of our study add to the increasing amount of data implicating a role for dopaminergic and serotonergic pathways in human mating systems. Our investigation may also have implications for biological investigations of love. To date, in fact, most researchers have explored the relationships between the six love varieties and personality characteristics as well as attachment styles (Heaven *et al*., 2004; Wan *et al*., 2000, Woll 1989), thus focusing mainly on the psychological facets of human love. However, our data point toward a possible role for genetic factors in an individual's love attitudes.

While our preliminary findings provide intriguing biological insights into the nature of human love, we are aware that our study has several important limitations that should caution against over-interpretation. The complex nature of human love is probably the chief limitation when studying the genetics of different loving varieties. Obviously, the interindividual differences in loving styles can not be fully explained by biological factors, and hence genetic, psychological, social, and environmental factors should all be considered in future studies, possibly in a multivariate manner. In addition, future work should incorporate rating of loving styles by other individuals (i.e. partners or lovers) to establish the full extent to which loving styles are predicted by other factors. Another potential drawback of this report relies in its cross-sectional approach, which leaves unanswered the extent to which a longitudinal design would have delivered the same results. A third limitation that merits consideration regards the possible non-representativeness of our sample, which consisted mainly of students who may differ from the general population in a number of ways, for example in intellectual background. Finally, it is well-known that ethnic origin is a frequent cause of stratification bias in genetic association studies (Cusin *et al*., 2002).

Given the study caveats, we nonetheless believe that our present report provides preliminary evidence of a possible genetic loading on human loving styles. Further studies with a larger number of individuals are recommended to confirm and expand our findings.

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