The 7R polymorphism in the dopamine receptor D$_4$ gene (*DRD4*) is associated with financial risk taking in men ☆

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Abstract

Individuals exhibit substantial heterogeneity in financial risk aversion. Recent work on twins demonstrated that some variation is influenced by individual heritable differences. Despite this, there has been no study investigating possible genetic loci associated with financial risk taking in healthy individuals. Here, we examined whether there is an association between financial risk preferences, elicited experimentally in a game with real monetary payoffs, and the presence of the 7-repeat allele (7R+) in the dopamine receptor D$_4$ gene as well as the presence of the A1 allele (A1+) in the dopamine receptor D$_2$ gene in 94 young men. Although we found no association between the A1 allele and risk preferences, we did find that 7R+ men are significantly more risk loving than 7R− men. This polymorphism accounts for roughly 20% of the heritable variation in financial risk taking. We suggest that selection for the 7R allele may be for a behavioral phenotype associated with risk taking. This is consistent with previous evolutionary explanations suggesting that selection for this allele was for behaviors associated with migration and male competition, both of which entail an element of risk.
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1. Introduction

Risk preferences are central to any model of human decision making, and a number of studies have documented substantial heterogeneity in individuals' willingness to take financial risks—that is, their willingness to trade off increasing variance of returns against greater expected returns (Barsky, Juster, Kimball, & Shapiro, 1997). Some

individual variation in preferences can be explained by such demographic variables as sex (Barsky et al., 1997; Byrnes, Miller, & Schafer, 1999), age (Barsky et al., 1997; Donkers, Melenberg, & Van Soest, 2001), race (Barsky et al., 1997; Fan & Xiao, 2005), religion (Barsky et al., 1997), education (Donkers et al., 2001; Grable, 2000; Grable & Joo, 2004), and socioeconomic status (Grable, 2000; Grable & Joo, 2004). However, these variables explain only a modest share of the variation. Recent work based on samples of twins showed that risk preferences are heritable (Cesarini, Johannesson, Lichtenstein, Sandewall, & Wallace, in preparation). Approximately 25% of the individual variation in risk taking, as measured by actual pension investment decisions and elicited experimentally using a gambling task, was explained by heritable differences (Cesarini, Dawes, Johannesson, Lichtenstein, & Wallace, in press). The

challenge for behavioral scientists is to now identify the genetic loci associated with such risk preferences.

Risk preferences may be influenced by dopaminergic pathways in the brain. These pathways play a role in regulating the anticipation of rewards (Kelley, Schiltz, & Landry, 2005; Wise, 2002) as well as the motivation for obtaining rewards (Kelley, 2004) and include the ventral tegmental area, nucleus accumbens, and the prefrontal cortex. Activation of these pathways can result in increased physiological arousal and intense feelings of well-being or pleasure (Heath, 1964; Peterson, 2005), which in turn may increase an individual's propensity to take risks. Dysfunction in these pathways can affect reward processing, motivation, and, consequently, decision making. Individuals who weigh anticipated rewards heavily may be more likely to take risks since rewards induce approach-related behaviors. Two genes known to be involved in the regulation of the dopaminergic system are the dopamine receptor D_4 (DRD4) gene and the dopamine receptor D_2 (DRD2) gene.

The DRD4 gene has been investigated as a candidate gene for modulating a number of approach-related behaviors (Munafo, Yalcin, Willis-Owen, & Flint, 2008), but not financial risk taking per se. Particular interest has been paid to the 48-bp variable number of tandem repeats (VNTR) polymorphism in exon III of the DRD4 gene, which consists of 2–11 repeats (Ding et al., 2002) likely involved in modulating expression (Schoots & Van Tol, 2003). Specifically, the 7-repeat (7R+) allele is associated with decreased ligand binding (Asghari et al., 1994) and has been shown to require higher levels of dopamine to produce a response of similar magnitude as compared with smaller-sized variants (Asghari et al., 1995), although its functional significance has not been definitively characterized. This blunted response to dopamine may cause inhibitory neurons that use the 7R receptor to require increased dopamine for "normal" functioning (Swanson et al., 2000) and may thus contribute to individual differences in personality and behavioral traits that are associated with dopamine levels.

Allelic variation in the DRD4 dopamine gene has been associated with novelty seeking (for a review, see Munafo et al., 2008). The presence of the 7R allele itself has been associated with alcoholism (Laucht, Becker, Blomeyer, & Schmidt, 2007), behavioral disinhibition (Congdon, Lesch, & Canli, 2008), attention deficit/hyperactivity disorder (Li, Sham, Owen, & He, 2006), pathological gambling (Perez de Castro, Ibanez, Torres, Saiz-Ruiz, & Fernandez-Piqueras, 1997), and impulsivity (Eisenberg et al., 2007). While the personality trait most widely studied in relation to DRD4 is novelty seeking, many studies have failed to find significance (Munafo et al., 2008). The most recent meta-analysis conducted also failed to support a relationship between DRD4 (VNTR) and novelty seeking as well as impulsivity (Munafo et al., 2008). However, given the small effect sizes reported for DRD4 (VNTR) on personality, small differences between studies can lead to nonsignificant findings. Indeed, there was evidence of between-study heterogeneity in this

meta-analysis. The role of DRD4 (VNTR) polymorphism in personality, and specifically on approach-related behaviors, is thus inconclusive.

Another receptor for the neurotransmitter dopamine is the DRD2 gene, coded for by locus 11q23. A single-nucleotide polymorphism with two variants exists at the TaqI A locus, located downstream of DRD2 (Dubertret et al., 2004). Although its functional significance is unclear, the less frequent A1 allele has been associated with decreased D_2 receptor expression in the striatum (Noble, Blum, Ritchie, Montgomery, & Sheridan, 1991; Thompson et al., 1997), as compared with the A2 allele (but see Laruelle, Gelernter, & Innis, 1998). Carriers of the A1 allele, in contrast to carriers of the A2 allele, have diminished glucose metabolism in the brain (Noble, Gottschalk, Fallon, Ritchie, & Wu, 1997) and exhibit reduced dopaminergic activity (Berman & Noble, 1995). The A1 allele has been associated with substance abuse (Noble, 2003) impulsivity (Eisenberg et al., 2007), pathological gambling, novelty seeking, and sensation seeking (Ratsma, van der Stelt, Schoffelmeer, Westerveld And, & Boudewijn Gunning, 2001). A recent study examined the A1 allele in relation to personality scores measuring reward-related traits and found that women with the A1 allele were more responsive to rewards (Lee, Ham, Cho, Lee, & Shim, 2007). We predict that individuals with the A1 allele will be more risk loving as they may be more responsive to rewards.

Using a behavioral measure of risk involving real financial incentives, we examined the relationship between risk preferences and allelic variation in DRD4, focusing on the presence of the 7R allele, as well as allelic variation in DRD2 in 98 young men. An advantage of eliciting preferences experimentally, with financial incentives attached to performance, is that we can infer preferences from choices made by our subjects rather than rely on self-reported hypothetical decisions (Hertwig & Ortman, 2001).

2. Methods

2.1. Participants

Participants were recruited by flyers distributed at the Harvard University campus and via e-mail solicitation to undergraduate residential houses. A total of 98 male subjects between 18 and 23 years old participated in the study. Subjects were excluded if they reported current use of psychotropic medications or having a diagnosis of bipolar depression, pathological gambling, and/or attention deficit hyperactivity disorder. The ethnic composition of the sample was determined by self-report: 66 individuals reported themselves as European, 9 as Asian, 4 as Hispanic, 4 as African American, and 14 as being of other or several categories. A total of 89 individuals reported themselves as heterosexual, and 7 did as homosexual. One individual was a self-reported bisexual, and another reported having an unknown sexual orientation. Neither of these two individuals

was included in the analyses when controlling for sexual orientation. All aspects of the study were approved by Harvard University's institutional review board. Written consent was obtained from all subjects before they participated in the study.

2.2. Data collection

For data collection, subjects came to a central location. After receiving an explanation of the study procedures, each subject provided an unstimulated saliva sample by spitting through a straw into a vial. A second oral sample using 10 ml of Scope mouthwash was also obtained, and it was through this sample that we collected DNA. Participants then filled out a questionnaire including the risk measure adapted from Gneezy and Potters (1997) and background information. After completion of the questionnaire, anthropometric measures and a frontal facial photograph were obtained, as well as a final saliva sample. For more information on the hormonal analysis, see the work of Apicella et al. (2008).

2.3. Risk preferences

We measured participants' risk preferences using an investment game with real monetary payoffs (adapted from Gneezy & Potters, 1997). Subjects were "given" a balance of $250 and asked to choose an amount, $X, between $0 and $250, to invest into a risky investment. The rest ($250−$X) was kept by the subjects. A coin flip determined the outcome of the risky investment; thus, the probability of success was 0.5. In case of failure, the money invested is lost, and the subject has $250−$X on his balance. If successful, the money invested is multiplied by 2.5, and the subject has $250+1.5X on his balance. This means that a very risk-averse individual could choose to invest $0 into the risky investment and would thus get $250 with certainty. A risk-loving individual could, on the other hand, invest all $250 into the risky investment; he then would be equally likely to receive $0 as $625 and would in expectation get $312.5. At the end of the experiment, one of the subjects was randomly drawn and paid according to the amount on his balance (e.g., according to the choices he made and the outcome of the coin flip). Subjects were told that there would be approximately 100 subjects participating in the study. Because investing is risky but offers higher returns, subjects must weigh a higher expected return against the risk of the investment. We thus used $X, the fraction invested, as our measure of risk taking.

Since only one participant is selected for actual payment, a legitimate concern is that this introduces noise in the elicitation of preferences. Camerer and Hogarth (1999), in the most comprehensive review to date on the effects of financial incentives on performance, reviewed 74 experiments with no, low, or high performance-based financial incentives. Their modal result was that incentives had no effect on mean performance, but they did note that incentives shift performance toward the equilibrium prediction in cognitively complex tasks. Independently, Smith and Walker (1993) reached a similar conclusion. They suggested a model in which the laboratory subject faces a tradeoff between decision costs and the benefits of taking the action that maximizes his expected utility, conditional on his preferences. Compared with more complex laboratory experiments, the risk elicitation measure we used is cognitively simple and ought to pose no problem of comprehension in a sample of predominantly Harvard undergraduates. Thus, introducing a small probability of winning money is likely enough to ensure that risk preferences are measured with reasonable precision.

It is also important to note that the small stake criticism against laboratory experiments most forcefully applies to experiments designed to measure social preferences (e.g., giving in dictator games). The concern is that utility maximization is influenced not only by wealth maximization but also by an individual's desire to "do the right thing" or make the "moral" choice (Levitt & List, 2007) but that such concerns will be suppressed as the opportunity cost of making the moral choice rises when stakes are sufficiently high. It is not obvious why risk preferences elicited experimentally with low stakes should be biased in a particular direction. Recent evidence also suggests that laboratory measures of risk aversion, using small stakes, predict risk taking in the field (Dohmen et al., 2005). Ultimately, noise would merely lead to attenuation bias in the estimated correlation between risk and the selected polymorphisms.

Finally, the validity of the commonly used experimental procedure where subjects play multiple rounds during an experiment and with one round being randomly selected for payment was recently tested (Laury, 2006). That work did not report differences between paying for 1 out of 10 rounds or for all 10 rounds when payments are low. This provides support for the hypothesis that behavior is not entirely contingent upon the probability that the outcome will be realized, at least in the simple experiment designed to measure risk aversion that Laury considered.

2.4. Genotyping

Buccal cell samples for DNA analysis (Feigelson et al., 2001) were obtained from 98% (96/98) of the recruited male subjects. All collected samples were shipped to the Binghamton University Laboratory of Evolutionary Anthropology and Health. DNA was extracted using an abbreviated version of the silica extraction protocol (Boom et al., 1990) described by Lum, Cann, Martinson, and Jorde (1998). All genotyping procedures were approved by Binghamton University's human subjects research review committee. Genotyping was performed for the two candidate genes only.

2.4.1. DRD4 48-bp VNTR
The human *DRD4* gene on chromosome 11 contains a 48-bp VNTR polymorphism in exon III. It varies between 2 and 11 repeats of a similar 48-bp coding region

sequence, with a trimodal distribution of 2-, 4-, and 7-repeat alleles (2R, 4R, and 7R) in most populations (Ding et al., 2002).

Sufficient DNA for *DRD4* PCR amplification was extracted from 99% (95/96) of the buccal cell samples. Previous studies highlighted problems associated with consistent genotyping of the *DRD4* VNTR region (Eisenberg, Campbell, Gray, & Sorenson, 2008; Eisenberg et al., 2007; Hamarman, Fossella, Ulger, Brimacombe, & Dermody, 2004), suggesting multiple PCR runs for each sample to control for allelic dropout. Thus, the PCR was modified to reflect the high GC content (see below) and all samples that were initially scored as homozygotes were reanalyzed two additional times with different starting template concentrations to confirm genotypes. The PCR consisted of 1× Q-Solution (Qiagen), 1× buffer (Qiagen), 1 μM primer 1 (5′ GCGACTACGTGGTCTACTCG 3′), 1 μM primer 2 (5′ AGGACCCTCATGGCCTTG 3′), 200 μM deoxy-ATP, 200 μM deoxy-TTP, 200 μM deoxy-CTP, 100 μM deoxy-ITP, 100 μM deoxy-GTP, 0.3 U of HotStar Taq (Qiagen), and 1 μl of DNA template, in a total volume of 10 μl. The PCR profile began with 15 min at 95°C for enzyme activation and denaturing of template DNA followed by 40 cycles consisting of 1-min denaturation at 94°C, 1-min annealing at 55°C, and 1.5-min extension at 72°C; it finished with a 10-min extension at 72°C. Amplicons were electrophoresed through 1.4%–2.0% agarose gels containing ethidium bromide, and genotypes were determined by comparison with a 100-bp ladder. Subjects were then scored as either 7R+ (at least one allele of at least 7 repeats) or 7R− (both alleles less than 7 repeats).

2.4.2. DRD2 TaqI A

The human *DRD2* gene located on chromosome 11 contains an often studied single-nucleotide polymorphism called TaqI A. PCR amplification was successful for 97% (93/96) of the buccal cell samples. The PCR for *DRD2* consisted of 0.5 μM forward (5′ CAC GGC TGG CCA AGT TGT CTA 3′) and 0.5 μM reverse (5′ CACCTTCCT-GAGTGTCATCAA3′) primers, 200 μM deoxy-NTP, 2.5 mM MgCl₂, 0.25 U of HotStar Taq (Qiagen), 1× buffer (Qiagen), and 2.5-μl DNA template, in a total volume of 10 μl. The PCR profile began with 15 min at 95°C for enzyme activation and denaturing of template DNA followed by 40 cycles consisting of a 30-s denaturation at 94°, 30-s annealing at 55°C, and 1-min extension at 72°C; it finished with a 7-min extension at 72°C. The PCR product was digested with the TaqI enzyme overnight at 65°C as per the manufacturer's specifications (New England Biolabs). Amplicons were electrophoresed through 1.4%–2.0% agarose gels containing ethidium bromide, and genotypes were determined by comparison with a 100-bp ladder. The A1 alleles do not contain a TaqI restriction site, and so the 300-bp PCR product is not cut. In contrast, the TaqI restriction site containing A2 alleles yields 125- and 175-bp fragments after digestion. Subjects were thus scored as either A1− or A1+ based on the presence of at least one TaqI restriction site (i.e., A1/A1=A1−; A1/A2 or A2/A2=A1+).

Hardy–Weinberg (HW) equilibria were tested with the HWE program written by John Brzustowski. HW equilibrium was tested with Fisher's exact test, and *DRD4* was tested with the Markov chain algorithm (Guo & Thompson, 1992). Both DRD2 and DRD4 genotype frequencies were in accordance with HW equilibrium (DRD2: p=.1584, Fisher's exact test; DRD4: p=.717, Markov chain algorithm).

2.5. Statistical analysis

We used linear regressions (ordinary least squares) throughout. Subjects were classified according to the presence (7R+) or absence (7R−) of the 7R of *DRD4* and according to the presence of the A1 allele (A1+) of *DRD2*. We found no significant difference in the presence of 7R or A1 when comparing individuals in different ethnic groups or heterosexual men with homosexual men. We also found no significant difference in risk preferences between ethnic groups.

3. Results

Our subject pool was composed of 24 individuals with at least one 7R allele (7R+) and 70 individuals without the 7R allele (7R−) for *DRD4*. See Table 1 for summary statistics. A first test of the hypothesis comes from a mean comparison of these two groups. Regressing risk taking on a dummy variable taking a value of 1 if the individual is 7R+ and that of 0 otherwise, we found a statistically significant difference (coefficient=39.09, p=.023). On average, 7R+ individuals invest $39 more than individuals who are 7R−. This difference is illustrated graphically in Fig. 1. The R^2 from this regression is 0.05, suggesting that 5% of the variation in risk taking, or approximately a fifth of the heritable variation, is accounted for by the 7R+ polymorphism. In order to make our analysis more stringent, we also performed a Bonferroni correction. This is common when multiple hypotheses, such as multiple candidate genes, are tested. Since our p value is 0.023, our result remains significant also when corrected.

Table 1
Summary statistics

	Mean	SD	n
Risk (USD invested)	145.71	72.79	98
1 if 7R+	0.255	0.438	94
1 if A1+	0.391	0.491	92
1 if Caucasian	0.680	0.469	97
1 if Asian American	0.093	0.292	97
1 if Hispanic/Latino	0.041	0.200	97
1 if African American	0.041	0.200	97
1 if of other ethnicity	0.144	0.353	97
1 if homosexual	0.073	0.261	96
Testosterone (pg/ml)	100.40	33.59	97
Facial masculinity	−0.060	2.11	96

Ethnicity and sexual orientation data were self-reported. Facial masculinity was constructed from four standardized measures of sexual dimorphism.
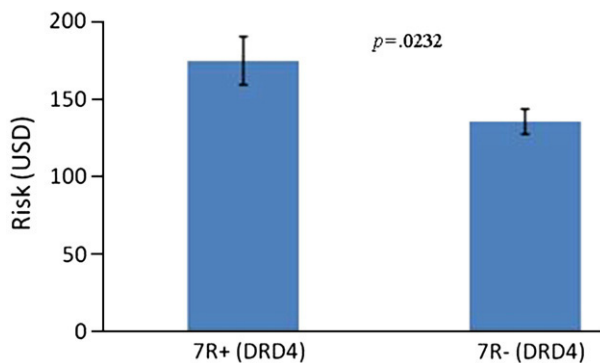
Fig. 1. Men with *DRD4* 7R+ invest more money in a financial risk game. Error bars indicate standard errors.

We have previously reported an association between risk taking and circulating testosterone, sexual orientation, and facial masculinity (Apicella et al., 2008). Moreover, there are differences in the frequency of 7R+ between populations (Chen, Burton, Greenberger, & Dmitrieva, 1999), although we did not find any difference in our sample (see Section 2.5). Controlling for these variables (e.g., circulating testosterone, facial masculinity, sexuality, and ethnicity) does not appreciably change our estimated coefficient (coefficient=36.59, p=.026).

Regression analysis revealed no significant association between the A1 allele of the TaqI A *DRD2* and risk taking. When comparing men with the A1 allele (A1+, n=36) with those without the A1 allele (A1−, n=56), the difference is nonsignificant (p=.813). The p values do not reach conventional levels of significance when other covariates are included.

4. Discussion

We found a significant correlation between the presence of the 7R allele of the *DRD4* gene and risk taking in a laboratory task. The difference in investment between individuals who are 7R+ and individuals who are 7R− is approximately half a standard deviation ($39 of $250). Our results are consistent with the hypothesis that individual variation in risk preferences may be mediated partly by allelic variants coding for differences in *DRD4* receptor gene expression in key brain areas associated with reward processing. However, we did not find carriers of the A1 allele for *DRD2* at the TaqI A locus to be more risk tolerant. These findings are consistent with the hypothesized link between reward pathways of the brain and risk taking. This is the first study to establish a correlation between a specific gene and financial risk taking in a normal (i.e., nonpathological) sample, and recent unpublished findings corroborate this link (Kuhnen & Chiao, unpublished data).

The results from this study suggest that one underlying mechanism responsible for heterogeneity in financial risk preferences is the dopamine system—more specifically, allelic variation in the *DRD4* dopamine receptor gene. The D_4 receptor, expressed by this gene, in part mediates the physiological actions of dopamine, and the 7R allele is known to have a blunted response to dopamine (Asghari et al., 1995). Dopamine itself is closely related to reward-seeking behaviors (Arias-Carrion & Poppel, 2007), although the mechanisms by which it affects reward-related decision making are still unclear.

Indeed, neuroimaging studies exploring the neural correlates of financial risk taking have implicated dopaminergic pathways. For instance, ventral striatum activation, including the nucleus accumbens, correlates with the magnitude of anticipated monetary reward and predicts risky investment decisions (Knutson, Adams, Fong, & Hommer, 2001; Knutson & Bossaerts, 2007; Knutson, Taylor, Kaufman, Peterson, & Glover, 2005; Kuhnen & Knutson, 2005). Some studies also demonstrated increased ventral striatal activity as the probability of obtaining monetary rewards increases (Abler, Walter, Erk, Kammerer, & Spitzer, 2006; Yacubian et al., 2006), but one study did not (Knutson & Cooper, 2005). Similarly, medial prefrontal activity is correlated with increased probability of monetary reward (Knutson & Cooper, 2005; Yacubian et al., 2006).

It has been proposed that there exist two separate neural systems that value monetary reward (McClure, Laibson, Loewenstein, & Cohen, 2004). One such system values immediate monetary reward and is marked by increased activation in the ventral striatum and areas of the medial prefrontal cortex relative to the lateral prefrontal and parietal cortices (McClure et al., 2004). The converse was found for the second system, which values delayed rewards. In this system, greater activation is seen in the lateral prefrontal and parietal cortices relative to the ventral striatum and medial prefrontal cortex (McClure et al., 2004). This finding may help explain why we did not find an association between the TaqI A polymorphism of the *DRD2* gene and risk taking in our study. The *DRD2* gene codes for D_2 receptors that play a relatively more prominent role in the striatum, while the *DRD4* gene codes for D_4 receptors that play a relatively more prominent role in cortical regions not limited to the prefrontal cortex (see Eisenberg et al., 2007). Participants in our task were aware that winnings would only be received at the completion of the entire study and, in this sense, expected that rewards were delayed. Thus, the null result found for TaqI A of *DRD2* may be due to the delayed nature of the risk task itself. Therefore, future work should examine the possible role of *DRD2* on financial risk taking where outcomes are immediately supplied. Finally, it is worth noting that TaqI A is a nonfunctional polymorphism with a history of inconsistent results when related to phenotypic variation. This may be the case because it is susceptible to confounding due to varying linkage patterns by lineage and/or population stratification (Hutchison, Stallings, McGeary, & Bryan, 2004). That is, both phenotypic values and allele frequencies might vary between populations, while the polymorphism itself does not cause the phenotypic variation.

This is particularly nefarious when the underlying population structure is unknown.

Although our results suggest that reward system function may be influenced by the D_4 dopamine receptor gene, we have no measure of dopamine activity in the brain, and, consequently, the mechanism we propose is speculative. The findings reported here are only suggestive of an association and necessitate future work integrating both molecular- and cellular-level data with behavior. Specifically, research should examine neural activity in conjunction with allelic variation in *DRD4* to better understand the mechanism(s) by which polymorphisms in this gene influence financial risk taking. We emphasize the exploratory nature of the results reported here and the need for replication studies involving larger and more diverse populations, where both sexes are examined.

As noted by Cesarini et al. (in press) and Camerer (2003), a few stable correlates to experimentally elicited preferences have been found. The results reported here suggest that one reason is that some of the studied variation is genetic in origin and that the underlying genetic variation maps to observable variables imperfectly. Beyond shedding light on an important source of variation, the results serve as a useful reminder that the parent–offspring correlation (Charles & Hurst, 2003) in risk preferences is likely the result of a collection of heterogeneous mechanisms, including genetic inheritance. We know of only one study that linked a gene with behavior in an experimental game. Knafo et al. (2007) reported an association between the amount of money donated in a dictator game and variants of the AVPR1 gene.

We suggest that selection for the 7R allele may have arisen partly due to its effects on increased risk taking. This claim is compatible with a number of evolutionary explanations previously offered. It has been estimated that the 7R allele is substantially younger than the ancestral 4R allele, and its frequency increased over the past 40,000–50,000 years under positive selection (Ding et al., 2002; Wang et al., 2004); it now likely exists as a balanced polymorphism (Ding et al., 2002). The reported associations between 7R allele and personality traits, such as novelty seeking and impulsivity, as well as world distributions of 7R + frequency, where it is rare in East Asians and Kung Bushmen, moderate in Europeans and Africans, and common in South American Indians (Chen et al., 1999), have provided the basis for the main evolutionary hypotheses that explain selection on *DRD4*.

The first evolutionary explanation is that selection might have been for migratory behavior (Chen et al., 1999), which may have led to the exodus out of Africa. Indeed, the long allele is more common among nomads than in settled populations (Chen et al., 1999), and it is associated with better health in nomads, but not sedentary individuals of the same population (Eisenberg et al., 2008). A similar explanation is that selection may have been for a "response-ready" phenotype during critical periods, such as times of food scarcity (Ding et al., 2002). This response-ready adaptation might have also played a role in the migration out of Africa, but subsequent selection would have been environment dependent (Wang et al., 2004). The migration morph does not explain why the 7R allele may have persisted at low frequencies long before the migration out of Africa (Harpending & Cochran, 2002), and although a response-ready phenotype could be advantageous in many environments, the characterization of such a phenotype remains ambiguous.

The other major evolutionary explanation for human variation in *DRD4* is one involving sexual selection. In male competitive societies, men who carried the 7R allele may have enjoyed a greater reproductive advantage in both resource competition and direct competitions with other men over mates (Harpending & Cochran, 2002). This advantage would have increased after the advent of agriculture (Harpending & Cochran, 2002). In preagricultural societies, much male reproductive effort likely went to parenting effort rather than mating effort compared with low-density agricultural societies, where males have more free time to compete with other males (Harpending & Cochran, 2002). Since competitions are risky, bearers of the 7R allele may have had an advantage if they were impulsive and unpredictable (Harpending & Cochran, 2002). Since women also have the 7R allele, it may be that the effect of the 7R allele in men on aggression, competition, and risk taking is testosterone dependent, although we found no significant interaction between testosterone and 7R+ on risk preferences among men (*p*=.983) when controlling for testosterone and 7R+. Future work with women should examine the role of the 7R allele on risk, competition, and aggression.

Our assertion that selection for the 7R allele may have been for a risky behavioral phenotype is complementary to all the aforementioned explanations. Taking financial risks is a recent phenomenon in human history, although risk taking itself is not. Decision making is central to both survival and fitness, and all decisions, including whether to migrate out of Africa and explore new ecological niches, engage in direct male–male competition, or invest money in a particular stock, entail some degree of risk. As previously mentioned, low levels of the 7R allele may have persisted in low frequency for much of human history, and, indeed, risk taking is a strategy that is advantageous under many conditions although the potential payoffs can be greater in some environments (e.g., in those environments where resources are scarce and when the possible rewards, such as increased access to mates, are high). Our suggestion is also in line with the finding that the allele is likely frequency dependent (Ding et al., 2002; Eisenberg et al., 2008; Harpending & Cochran, 2002; Wilson, 1994) since the payoffs of many risky behaviors, especially those involving direct competition, depend on (1) how others respond to the behavior and (2) the frequency of risk takers in the population.

Regardless of the evolutionary dynamics that led to the emergence of the 7R allele and its maintenance, the fact is that this polymorphism is a quantitatively important source

of individual variation in our risk-taking task. The effect of this polymorphism on risk taking is very high compared with those found for other complex phenotypes. The 7R allele explains 5% of the variation in risk preferences, or about a fifth of the estimated heritability of financial risk taking previously reported (Cesarini et al., in press), although the laboratory measure of risk used for this heritability estimate is different from the measure used here. The remaining 80% of the heritability still remains unexplained. Future work should examine other variants of the *DRD4* gene besides the 7R allele, as well as other candidate genes, gene environment interactions, and epigenetics. Since testosterone is also a predictor of financial risk (Apicella et al., 2008) and testosterone levels are partly heritable, we propose that future work examine genes that influence androgen exposure.

Acknowledgments

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