

Online Appendix for

Friendships Moderate an Association Between a Dopamine Gene Variant and Political Ideology

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Journal of Politics 72 (4): 1189–1198 (October 2010)

Dopamine and DRD4-7R

The dopamine system affects the control of locomotion, cognition, emotion, positive reinforcement, appetite, and endocrine regulation (Missale et al. 1998). Dopamine receptors are denser in the limbic system of the brain and the anterior cortex (Golimbet et al. 2007). *DRD4* is associated with brain reward and reinforcement mechanisms (Swift et al. 2000, Golimbet et al. 2007), exploratory approach behavior in animals (Swift et al. 2000), attention disorders (Jovanovic et al. 1999, LaHoste et al. 1996, Swanson et al. 2000, Rowe et al. 1998, Smalley et al. 1998; Langley et al. 2004, McCracken et al. 2000), and novelty-seeking (Benjamin et al. 1996, Ebstein et al. 1996, Noble et al. 1998, Tomitaka et al. 1999, Strobel et al. 1999, Benjamin et al. 2000, Auerbach et al. 2001).

There is evidence that DRD4-R7 is associated with novelty seeking. In particular, Savitz and Ramesar (2004) conduct a meta-analysis of 37 studies, finding that 18 of them show higher than average novelty-seeking test scores to be significantly associated with the long allele in *DRD4*. In 94% of the cases where statistically significant results were found, the implicated

allele was the 7R allele or a longer version. Savitz and Ramesar (2004) suggest that the relationship might not always show up because of periodic latency due to interactions between different genes, gene-environment interactions, variation in genetic background, or the presence of other variables. Overall, the association between *DRD4* and novelty-seeking has been shown to be independent of ethnicity, culture, sex, or age (Ebstein et al. 1996; Benjamin et al. 1996; Tomitaka et al. 1999).

Add Health Sample

Add Health is a large publicly available study started in 1994-1995 that explores the causes of health-related behavior of adolescents in grades 7 through 12 and their outcomes in young adulthood. In addition to health-related information, a large amount of information has been collected about the personality, attitudes, relationships, religious beliefs, civic activities, and political beliefs and behaviors of the respondents. The initial wave of the study utilized a sampling design that resulted in a nationally representative study.

In Wave I of the Add Health study, researchers created a genetically informative sample of sibling pairs based on a screening of the in-school sample of 90,114 adolescents. These pairs include all adolescents that were identified as twin pairs, half siblings, or unrelated siblings raised together. Twins and half biological siblings were sampled with certainty. The Wave I sibling-pairs sample has been found to be similar in demographic composition to the full Add Health sample (Jacobson & Rowe 1998). Details on access to the study, DNA collection, and genotyping process are available at the Add Health website (Add Health Biomarker Team 2007).

The analysis of the *DRD4* 48 bp VNTR (variable number tandem repeat) in exon 3 resulted in detection of alleles with base-pair (bp) length of 379, 427, 475, 523, 571, 619, 667,

715, 763 and 811. The two most common alleles were the 475 bp (with four repeats of the 48-bp VNTR), and the 619 bp (with seven repeats of the 48-bp VNTR). Following Hopfer et al. (2005) we group the 379, 427, 475, 523, and 571 bp alleles to form the 4R grouping and 619, 667, 715, and 763 bp alleles into the 7R grouping.

Genetic Association

A significant association can mean one of three things: 1) The allele itself influences ideology; 2) the allele is in “linkage disequilibrium” (LD) with an allele at *another* locus that influences ideology; or 3) the observed association is a false positive signal due to population stratification. Given our data, we cannot differentiate between 1 and 2. In order to do so we would need additional genetic information about loci in close proximity to the locus of interest. Thus, a significant association means that either a particular allele, or one (likely) *near* it, significantly influences ideology.

Population stratification occurs because groups may have different allele frequencies due to their genetic ancestry. For example, two groups may not have mixed in the past. Through the process of natural selection or genetic drift these groups may develop different frequencies of a particular allele X. At the same time, the two groups may also develop divergent behaviors that are not influenced by allele X but completely by the environment in which they live. Once these two groups mix in a larger population, simply comparing the frequency of X to the observed behavior would lead to a spurious association.

Case-control designs compare the frequency of alleles or genotypes among subjects that exhibit a trait of interest to subjects who do not (controls may be randomly selected from the population or from groups known not to exhibit the trait). As a result, case-control designs are

vulnerable to population stratification if either group is especially prone to selection effects. A typical way to deal with this problem is to include controls for the race or ethnicity of the subject or to limit the analysis to a specific racial or ethnic group. Because we know that the 7R allele is found with substantially different frequencies in different ethnic groups (Harpending and Cochran 2002, Ding et al. 2002), we have reason to expect that population stratification could be a problem in our study.

Table A1. Summary Statistics

<i>Variable</i>	<i>Mean / Incidence</i>	<i>Variable</i>	<i>Incidence</i>
<i>Very Liberal</i>	1.7%	<i>0 Friends</i>	27.6%
<i>Liberal</i>	15.4%	<i>1 Friend</i>	4.1%
<i>Moderate</i>	57.4%	<i>2 Friends</i>	4.7%
<i>Conservative</i>	21.9%	<i>3 Friends</i>	5.3%
<i>Very Conservative</i>	3.5%	<i>4 Friends</i>	7.3%
<i>White</i>	70.9%	<i>5 Friends</i>	9.4%
<i>Male</i>	47.8%	<i>6 Friends</i>	7.2%
<i>0 7R Alleles</i>	62.0%	<i>7 Friends</i>	7.3%
<i>1 7R Allele</i>	33.1%	<i>8 Friends</i>	6.8%
<i>2 7R Alleles</i>	4.9%	<i>9 Friends</i>	9.6%
<i>Average Age</i>	21.9	<i>10 Friends</i>	10.7%

Table A2. Quantitative Disequilibrium Transmission Test of a Direct Association Between *DRD4* and Political Ideology

	Estimate (standard error)	p-value
<i>Intercept</i>	2.84 (0.23)	0.00
<i>Between-family component of DRD4-7R (b)</i>	-0.05 (0.04)	0.12
<i>Within-family component of DRD4-7R (w)</i>	0.09 (0.07)	0.18
<i>Age</i>	0.00 (0.01)	0.66
<i>Male</i>	-0.05 (0.04)	0.15
<i>Deviance</i>	1119.55	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that *DRD4-7R* is not directly associated with political ideology. Null deviance = 1123.28.

Table A3. Quantitative Disequilibrium Transmission Test of a Direct Association Between *DRD4* and Number of Friends

	Estimate (standard error)	p-value
<i>Intercept</i>	9.21 (1.09)	0.00
<i>Between-family component of DRD4-7R (b)</i>	-0.23 (0.17)	0.16
<i>Within-family component of DRD4-7R (w)</i>	0.16 (0.33)	0.63
<i>Age</i>	-0.20 (0.05)	0.00
<i>Male</i>	-0.39 (0.17)	0.02
<i>Deviance</i>	25125.3	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that *DRD4-7R* is not directly associated with the number of friends. Null deviance = 25455.3.

Table A4. Quantitative Disequilibrium Transmission Test of an Association Between *DRD4* and Political Ideology, Including an Interaction with Dichotomous Friendship

	Estimate (standard error)	p-value
<i>Intercept</i>	2.82 (0.24)	0.00
<i>Between-family component of DRD4-7R (b)</i>	-0.05 (0.04)	0.12
<i>Within-family component of DRD4-7R (w)</i>	-0.19 (0.13)	0.14
<i>Any Friends? (1 = Yes, 0 = No)</i>	-0.01 (0.04)	0.74
<i>Age</i>	0.00 (0.01)	0.65
<i>Male</i>	-0.05 (0.04)	0.16
<i>w*Any Friends</i>	0.37 (0.16)	0.02
<i>Deviance</i>	1116.54	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that the interaction effect is robust to different specifications of the friendship variable. Null deviance = 1123.28.

Table A5. Regression Model Testing the Direct Association Between Number of Friends and Political Ideology

	Estimate (standard error)	p-value
<i>Intercept</i>	2.82 (0.24)	0.00
<i>Friendships</i>	-0.00 (0.00)	0.93
<i>Age</i>	0.00 (0.01)	0.69
<i>Male</i>	-0.05 (0.04)	0.17
<i>Deviance</i>	1122.01	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that there is no direct relationship between number of friends and ideology. Null deviance = 1123.28.

Table A6. Quantitative Disequilibrium Transmission Test of an Association Between *DRD4* and Political Ideology, Including an Interaction with Number of Male Friendships

	Estimate (standard error)	p-value
<i>Intercept</i>	2.77 (0.24)	0.00
<i>Between-family component of DRD4-7R (b)</i>	-0.05 (0.04)	0.13
<i>Within-family component of DRD4-7R (w)</i>	-0.07 (0.11)	0.53
<i>Male Friendships</i>	0.02 (0.01)	0.11
<i>Age</i>	0.01 (0.01)	0.54
<i>Male</i>	-0.06 (0.04)	0.09
<i>w*Male Friendships</i>	0.09 (0.04)	0.04
<i>Deviance</i>	1116.97	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that the interaction term remains positive and significant when we restrict the analysis to male friendships. Null deviance = 1123.28.

Table A7. Quantitative Disequilibrium Transmission Test of an Association Between *DRD4* and Political Ideology, Including an Interaction with Number of Female Friendships

	Estimate (standard error)	p-value
<i>Intercept</i>	2.91 (0.24)	0.00
<i>Between-family component of DRD4-7R (b)</i>	-0.05 (0.04)	0.12
<i>Within-family component of DRD4-7R (w)</i>	-0.03 (0.10)	0.80
<i>Female Friendships</i>	-0.01 (0.01)	0.15
<i>Age</i>	0.00 (0.01)	0.78
<i>Male</i>	-0.06 (0.04)	0.09
<i>w*Female Friendships</i>	0.05 (0.04)	0.15
<i>Deviance</i>	1117.40	
<i>N</i>	1941	

Note: This table can be read like an ordinary regression except that the variable coding for *DRD4* is divided into two variables to control for population stratification. The between-family component represents the average number of *DRD4-7R* alleles among all observed members of the subject's family, while the within-family component indicates the excess number of *DRD4-7R* alleles relative to the family average. The results show that the interaction term remains positive when we restrict the analysis to female friendships, and the coefficient on this term does not differ significantly from the coefficient for male friendships shown in the model in Table A6. Null deviance = 1123.28.

Appendix References

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