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I a G Ba S a C : T R D a R 3 *(DRD3)* G

Ch Zha , e J t g f, g P g a gh J e , X a Zh a

a Ce te f r Br a a C g t ve e es, f P s g a C g t ve e es, Be j g Ke a r t r f Beh av r a Me t a e th a P K - D / ve r a st t tef r Br a Rese ar h, P e g ve rs t , Be j g, e Dep a rtme t f P s g , h he ve rs t , X j a g, f Ch a Ce tref r pe a E m Z e Rese ar h a g Rese ar h Ce tref r Br a F t a a P s g a e e, he h e ve rs t , a g g, a h Ke a r t r f Re r e B g a B te h g ve ste r Ch a (Mt. str f E at), N rth est ve rs t , h a a , Ch a

f g e r st r a tes th e mp r t a e f *DRD3* e r 9 as a g e et as sf r a f r m t a p re t g v - a ff e re e es s a e ar g .

I

Social conformity occurs when people change their opinions to act in accordance with others [1]. This phenomenon is highly pervasive, as conforming to the social group enables us to learn about the value of an object or

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is known about the genetic basis underlying individual differences in social conformity. The purpose of this study was to investigate to what extent the dopamine receptor 3 gene (DRD3)affects conforming behavior.

Previous studies have strongly implicated the dopaminergic system in reward-related incentive learning, such as reinforcement learning and social conformity [6]. On the one hand, studies have demonstrated that reinforce-

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corrected-to-normal vision. They provided written informed consents prior to the experiments. This study was performed in accordance with the Declaration of Helsinki and approved by the Ethics Committee of the Department of Psychology of Peking University. One participant was excluded from the analysis because she did not respond to a large number of questions (>25%); 3 other participants were excluded because of their psychiatric history or severe psychiatric symptoms (>3 SD) as assessed by the Symptom Checklist-90 [30, 31]. It is important to note that including these participants did not change the pattern of the results.

Genotyping

Genomic DNA was extracted from 3–5 hair follicle cells of each participant via the Chelex-100 method [32]. The Ser9Gly in the *DRD3* gene was amplified by polymerase chain reaction (PCR), with the upstream primer 5 "-AGGTGTAGTTCAGGTG-3 "and the downstream primer 5 "-TCATTGCTCTATCTCC-3 ". The PCR was carried out with an initial 4-min denaturation at 94°C, followed by 35 cycles of 94°C for 30 s, 55.5°C for 30 s, 72°C for 35 s, and a final extension period at 72°C for 5 min. The PCR product was digested by the restriction enzyme *Hae*III (Fermentas) at 37°C overnight. The digestion system contained 1.0 µl PCR products, 0.40 µl (10 U/µl) *Hae*III, 0.40 µl R buffer, and 3.2 µl H_2O. The incubated mixture was analyzed using 8% polyacrylamide gel electrophoresis at 220 V for 3.5 h, followed by silver staining. The gen-

dicated the participants' own judgments rather than their explicit memory of their previous ratings or the group's ratings. All of the participants were debriefed after the experiment. No one reported any suspicion of the cover story or the task in the postexperiment interviews.

One hundred twenty digital color photographs of Chinese young adults (aged 18–35 years, 60 females) with a slight smile and moderate attractiveness (mean = 4.97, SD = 0.96) were used. These photos were drawn from a database [34] and additionally from the Internet. All the photos were taken in similar styles.

The group ratings were preprogrammed by an adaptive algorithm to ensure that the deviation (i.e. the difference between the participants' initial ratings and group ratings during the first session) ranged from –4 to 4, and the conflict level (i.e. the absolute value of the deviation) ranged from 0 to 4. The deviation (and the conflict level) was 0 in 40 trials. For the remaining 80 trials, each conflict level (i.e. 1, 2, 3, and 4) had 20 trials and each deviation level (i.e. ±1, ±2, ±3, and ±4) had approximately 10 trials. The average number of trials for each deviation level ranged from 9.70 to 10.28 across the participants.

R

Raw Conformity Score

Behavioral data were analyzed according to the procedures described by Klucharev et al. [3]. For each participant, we performed a regression analysis, with the deviation as a single predicator and the rating change (i.e. the difference between the participants' initial ratings and the second ratings) as the outcome variable, to generate individual standardized coefficients (β), which were used as a raw conformity score (i.e. an index of the individual tendency to conform) [35]. The mean raw conformity score (mean ± SD: 0.263 ± 0.095, range 0.016–0.511) was significantly higher than zero [$t(147) = 33.726$, $p < 0.001$], indicating that overall the participants changed their ratings of attractiveness in accordance with the group's ratings [3, 35].

We also used a simple reinforcement learning algorithm (Rescorla-Wagner) to model the rating change between the initial and second ratings. The Rescorla-Wagner rule probes learning through a prediction error signal [36, 37]. Unlike typical reinforcement learning models in which each stimulus is repeated several times, the learning model in our study was based on only 2 observations per face stimulus. Thus, the prediction error signal was defined as the difference between the participants' initial ratings and group ratings during the first session (i.e. deviation). The prediction error signal could be used to subsequently update the second ratings weighted by a fixed learning rate (i.e. α: $\text{rating}_2 = \text{rating}_1 + \alpha \cdot \text{deviation}$). We fitted the Rescorla-Wagner model to the participants' second ratings using a linear regression model to derive the best-fitting model parameter (α). Because there were only 2 observations for each face stimulus, the parameter α was mathematically equivalent to the raw conformity score. Consequently, we focused on the raw conformity score in the following analysis.

Tab 1. Effect of the DRD3 Ser9Gly polymorphism on conforming behavior

	Raw conformity score	Adjusted conformity score	Corrected conformity score	Probability of conforming adjustments, %
Ser/Ser	0.251±0.099	0.067±0.099	0.090±0.109	43.7±7.8
Ser/Gly	0.263±0.088	0.076±0.088	0.101±0.101	44.0±6.7
Gly/Gly	0.314±0.086	0.125±0.076	0.160±0.084	48.5±6.9

Values are presented as means ± SD.

To examine the relationship between the DRD3 Ser9Gly polymorphism and an individual's conformity score, we performed a regression analysis with the genotype (0 = Ser/Ser, 1 = Ser/Gly, and 2 = Gly/Gly) as a single predictor of the raw conformity score. The result indicated that the polymorphism accounted for a significant proportion of the variance in the conformity score [$F(1, 146) = 5.292$, $p = 0.023$, $\beta = 0.187$, $R^2 = 0.035$, and adjusted $R^2 = 0.028$]. Individuals with a greater number of Gly alleles, which are associated with a higher dopamine affinity of the D_3 receptor, were more likely to change their ratings in accordance with the group's ratings (table 1). ANOVA with the genotype as a between-participant factor also showed a significant main effect of genotype [$F(2, 145) = 3.272$, $p = 0.041$]. A post hoc t test revealed that the Gly/Gly carriers conformed significantly more than the Ser/Gly carriers (uncorrected $p = 0.034$) and the Ser/Ser carriers (uncorrected $p = 0.015$), although the difference between the Gly/Gly carriers and the Ser/Gly carriers became nonsignificant with Bonferroni's correction ($p = 0.135$). It is important to note that ANOVAs with genotype as a between-participant factor revealed no main effect of genotype on the initial ratings [$F(2, 145) < 1$] or on the second ratings [$F(2, 145) < 1$], suggesting that the significant genotype effect observed above resulted from differential impacts of conformity in different groups.

Adjusted Conformity Score

It is important to note that the adaptive algorithm was constrained such that the deviation was limited to a range

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activity during social conflict, which increases the learning rate during social interaction. Individuals with the Gly allele are thus likely to weight the group opinion more when updating the value of an object or event. Whether the dopamine-enhanced conformity is due to an increased incentive salience of conformity or an enhanced learning ability is a question for future research.

A recent work by Kitayama et al. [45] reported that the dopamine receptor 4 gene (DRD4) interacted with culture to affect social orientation. Compared to noncarriers, carries of alleles linked to increased dopamine signaling showed higher levels of acquisition of cultural norms and values; that is, carriers in individualist cultures were more independent and less interdependent than carriers in collectivist cultures, but no cultural differences were apparent between noncarriers. One might wonder to what extent the current study extends our understanding of the relationship between dopaminergic genes and normative behaviors beyond the study of Kitayama et al. [45]. People in collectivist cultures showed higher levels of conformity than those in individualist cultures [46]. Both DRD4,examined by Kitayama et al. [45], and DRD3,investigated in the current study, may contribute to this conformity in collectivist cultures. However, Kitayama et al. [45] also showed that carriers of alleles linked to increased dopamine signaling would be more likely to behave in socially normative ways than noncarriers in individualist cultures (i.e. being more independent). As higher independence was found to be associated with less conformity [47], the pattern in individualist cultures [45] is different from the findings of positive associations between dopamine signaling and conforming behavior in pharmacological and genetic studies on individuals in individualist cultures (e.g. individuals in Denmark [10] or Germany

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