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An online version of the Mooney Face Test: phenotypic and genetic associations

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ABSTRACT

The Mooney Face Test is a widely used test of face perception, but was originally designed to be administered by personal interview. We have developed a three-alternative forced-choice version for online testing. We tested 397 healthy adults between the ages of 18 and 42 (M=24 years). There was a wide range of performance (64–100% correct; M=89.6%). We observed a significant sex difference favoring males (.31 standard deviation; p =.004). In addition, independently of sex, higher 2D:4D digit ratios were significantly associated with higher scores (ρ=.14, p=.006). A genome-wide association study (GWAS) for a subset of 370 participants identified an association between Mooney performance and a polymorphism in the *RAPGEF5* gene (rs1522280; $p=9.68\times10^{-8}$). This association survives a permutation test (p=.031).

1. Introduction

The cortical processing of faces encompasses a complex sequence of stages, including the visual extraction of features, the analysis of their configuration, the matching of this configuration with a possible existing memory, and the subsequent recognition of known faces (Bruce & Young, 2012). Many tests have been developed to assess various aspects of face processing (Young, Hellawell, & Hay, 1987; Duchaine & Nakayama, 2006; Burton, White, & McNeill, 2010). However, for more than half a century, neuropsychologists have recognised the value of the classic *Mooney Face Test* (Mooney, 1956, 1957; Milner, Corkin, and Teuber 1968; Newcombe & Russell, 1969; Wasserstein, Zappulla, Rosen, Gerstman, & Rock, 1987; Rizzo, Nawrot, & Zihl, 1995). The Mooney Face Test (Mooney, 1956, 1957) comprises forty black and white images in which a certain combination of pure black (shaded) and pure white (lit) parts gives rise to the image of a face (see Fig. 1). Perception of the two-tone Mooney figures is all or none: the complete percept of the face emerges suddenly from an array of patches rather than through a conscious and serial evaluation and compilation of elements. It is considered a test of holistic processing: inversion of the images makes recognition almost impossible (Kanwisher, Tong & Nakayama, 1998), confirming that the viewer is unlikely to be using isolated features to identify the hidden face.

The still-mysterious process of closure—the preconscious computation that precedes the emergence of a complete percept—seems to play an important role in the Mooney Face Test. Wasserstein, Barr, Zappulla, and Rock (2004) administered four closure tests and one face-matching test to patients with unilateral brain damage, and—by means of a factor analysis—identified two factors: a *closure* factor and a *facial discrimination* factor. They observed that the Mooney Face Test loaded more heavily on the closure factor (shared variance: 55% for left-sided cases, 62% for right-sided) than on the facial discrimination factor (shared variance: 14% and 18% for the two groups). However, Foreman (1991) reported no relationship between performance on the Mooney Face Test and performance on the Gollin Incomplete Figures Test, on the Poppelreuter test, or on a visual search task. Young, De Haan, and Newcombe (1990) reported a patient ('SP') who showed marked impairments on various tests of face processing (including the Mooney Face Test), but who could distinguish faces from other objects, whereas other prosopagnosic patients

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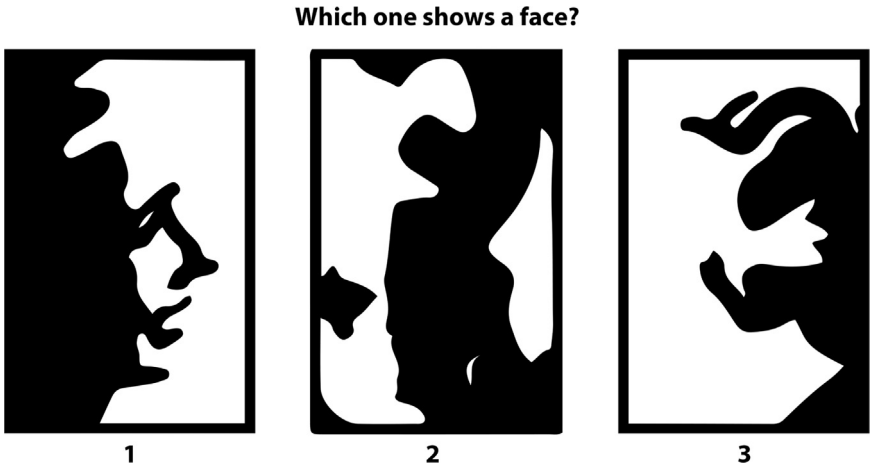

Fig. 1. An example of a trial from our modified Mooney Face Test. One of the three images (in this case, number 1) is an original Mooney face, and the other two are custom-made distractors.

may retain normal performance for Mooney faces while being impaired in the holistic perception of individual faces (Busigny, Joubert, Felician, Ceccaldi, & Rossion, 2010). In fMRI studies, Kanwisher et al. (1998) found much stronger responses in the fusiform face area (FFA) to upright Mooney faces than to inverted ones, while Andrews and Schluppeck (2004) found that the response in the FFA to Mooney faces was stronger when the face was actually perceived—a distinction that was not observed for the face regions of the superior temporal sulcus. Thus it remains unresolved to what extent the Mooney Face Test is a test of closure, and to what extent it is a specific test of face processing.

In neuropsychological studies, impairment on the Mooney test has been associated with damage to the right hemisphere, and to the temporal lobe in particular. Freda Newcombe, in her series of patients with unilateral focal missile wounds, found that right-hemisphere cases were impaired on the Mooney test but left-hemisphere cases did not differ significantly from controls (Newcombe & Russell, 1969; Newcombe, 1974). In a group of epileptic patients who had undergone unilateral resection of the temporal lobe, Lansdell (1968) found reduced scores on the Mooney test after right-sided resection. A similar asymmetry was observed by Wasserstein et al. (2004); see above. In its disproportionate vulnerability to right-hemisphere damage, the Mooney test resembles other tests of face perception (Hécaen, 1962; Warrington & James, 1967; Yin, 1970; Newcombe, De Haan, Ross, & Young 1989; Busigny et al., 2014).

Sex differences for the Mooney Face Test have been reported by Foreman (1991), who observed a significantly shorter reaction time for males than for females. Vigen, Goebel, and Embreem (1982) reported that sex accounts for 8.5% of the variance in performance on the Mooney Face Test, additionally observing that females' performance declines with increasing age while that of males remains the same. These results contrast with findings for other tests of face perception, where females seem to enjoy an advantage on both memory and non-memory based tests, although perhaps for female faces only (Megreya, Bindemann, & Havard, 2011).

In its classical form, the Mooney Face Test was designed to be administered by personal interview: the examinee was asked to describe for each face the sex, approximate age, orientation or position of the head etc., to show that he or she had correctly identified the face (Mooney, 1956). In the present study we set out to develop a three-alternative forced-choice version that could be used for online testing. We here report the distribution of scores for a population of young adults, and we relate individual performance on the test to sex, to Autism-Spectrum Quotient and to digit ratio.

Although the heritability of performance on the Mooney test is unknown, recent twin studies suggest a strong heritable component to performance on other tests of face processing (Wilmer et al., 2010; Zhu et al., 2010). For example, for the Cambridge Face Memory Test, Wilmer et al. (2010) found correlations of .70 and .29 for monozygotic and dizygotic twin pairs respectively. Brown et al. (2012), in a whole-genome association study, found genetic associations with increased brain activity evoked in the FFA by the presentation of affective facial expressions. However, no research has so far been conducted to find specific genetic correlates of the psychophysical ability to detect faces. Most of our participants had earlier taken part in a genome-wide association study (GWAS); we are thus in a position to report preliminary genetic associations with performance on our version of the Mooney Face Test.

2. Materials and methods

2.1. Participants

Our 397 participants (252 female) were a subset of a cohort of 1060 who had previously completed a battery of perceptual tests in our laboratory as part of the PERGENIC project (Goodbourn et al., 2012, 2014; Lawrance-Owen et al., 2014; Bosten et al., 2014a, 2014b). Participants were healthy young adults between the ages of 18 and 42 ($M=24$ years), all of European descent. The majority were students from the University of Cambridge. Although the present tests were conducted online, all the participants were known to us from their previous visit to the laboratory. In the PERGENIC study, other potentially relevant phenotypic data were collected, including handedness, personality, Autism-Spectrum Quotient (AQ), and digit ratio. Ethical permission for the study was given by the Cambridge Psychology Research Ethics Committee.

2.2. Materials

We developed a three-alternative forced-choice version of the Mooney test for online testing, using the original 40 Mooney faces (Mooney, 1957) but adding distractor images that were created by rearranging the components of the original Mooney faces until—in a pilot study—participants did not recognise them as faces (see Fig. 1). The participants of the pilot study are not part of the sample reported here.

Each trial contained three frames in a horizontal array: one frame contained the target Mooney face, and two frames contained distractor images. The position of the target image among the three frames was random.

2.3. Procedure

The present data were collected online. Although no time limit was set or advertised, participants were instructed to respond as quickly as possible, using the numeric keys on their keyboard to indicate which frame showed a face (either 1, 2, or 3). Upon the participant's response, the next trial was presented after a 600-ms interval consisting of a blank screen. No feedback was given, except on the first trial, which was explicitly a practice trial. Before beginning the test, participants subjectively rated their face recognition ability on a scale of 1 to 10, where 1 represents very poor, and 10 represents very good face recognition ability. Data analysis was performed using *R*.

We had genetic information available for 378 participants. Saliva samples were collected at the time of the original PERGENIC study using the Oragene OG-500 kit (DNA Genotek Inc, Ottawa, ON, Canada) and DNA was extracted according to the manufacturer's protocols. Genotyping was performed by Cambridge Genomic Services using the HumanOmniExpress BeadChip (Illumina, San Diego, CA, USA). For further details of the acquisition and processing of genetic material, see Lawrance-Owen et al. (2013) and Goodbourn et al. (2014). For our set of participants, eight samples (of 378) were excluded from the genetic analysis: one because of a genotypic sex anomaly, and seven because they were related to another participant. Thus the final genetic analysis was based on 370 participants. Quality control for individual single nucleotide polymorphisms (SNPs) excluded markers with more than 2% missing genotypes (12,706 SNPs) and markers with a minor allele frequency below 5% (125,086 SNPs). This left 595,410 SNPs in the analysis. Using the software PLINK v1.07 (Purcell et al., 2007) and assuming an additive genetic effect, we performed an association analysis with four covariates: sex, and the first three principal components reflecting genetic variation in our cohort (to control for stratification in the population).

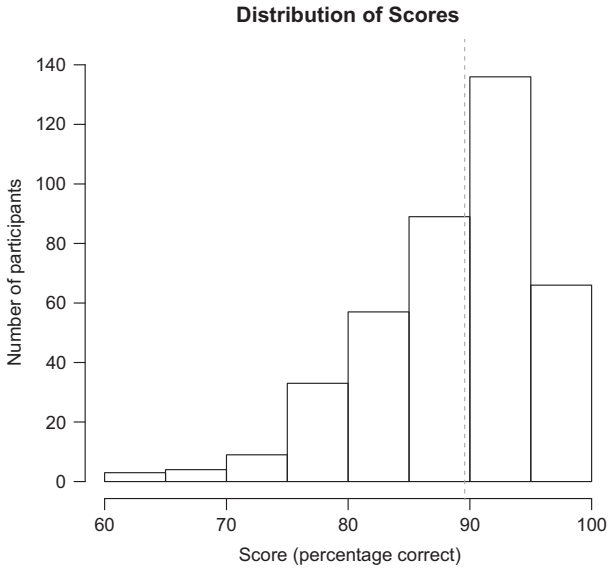

Fig. 2. The distribution of scores (as percentage correct) on our Mooney Face Test for our sample. The dashed, vertical line marks the sample mean at 89.6% correct.

3. Results

The range of scores on our modified Mooney Face Test was wide (see Fig. 2). The mean proportion correct was 89.6% (i.e. 34.9 trials out of 39; SD=.07%), with a minimum score of 64% (i.e. 25 trials correct), and a maximum of 100% (i.e. 39 trials correct). 30 participants achieved the maximum score. The distribution was not normal (Kolmogorov–Smirnov $D=3.20$, $p \approx 4.40 \times 10^{-18}$), exhibiting a leftward skew of $-.89$. Split-half reliability, calculated using Guttman's λ_6 (Guttman, 1945; Revelle and Zinbarg, 2009), was .69. An item analysis showed that two items were solved by all participants, but that no item was impossible. We observed a significant positive correlation between performance and subjectively rated ability to recognise faces (Spearman's $\rho=.21$, $p=2.24 \times 10^{-5}$). Performance did not correlate with age or with overall time taken.

Mooney (1957) provided a ranking of his forty stimuli according to the proportion of participants who responded correctly. We performed a Spearman correlation between his measure of item difficulty and an analogous ranking of our own test items. Although our own testing was by forced choice, and thus the difficulty of each item depended on both the target and the distractors, there was a significant correlation (Spearman's $\rho=.56$, $p=2.09 \times 10^{-5}$) between our ranking of difficulty and Mooney's ranking of difficulty.

Significant sex differences were observed: although the distributions for men and women overlap substantially (see Fig. 3), our male participants show a significant advantage (Mann–Whitney $U=15{,}127.5$, $p=.004$). The male advantage is equivalent to .31 standard deviations. Sex differences accounted for 2% of the variance in our sample.

In the original PERGENIC study, participants rated their handedness on a Likert scale ranging from 1 ("strongly disagree") to 5 ("strongly agree") in response to two questions: "I always use my right hand when writing", and "I always throw a ball with my right hand". These measures did not correlate with performance on our version of the Mooney Face Test. Nor was there any significant correlation with the Big Five personality traits as indexed by the Mini-IPIP (Donnellan, Oswald, Baird, & Lucas, 2006). For a subset of 316 participants (203 female), scores were available for the Autism-Spectrum Quotient (Baron-Cohen, Wheelwright, Skinner,

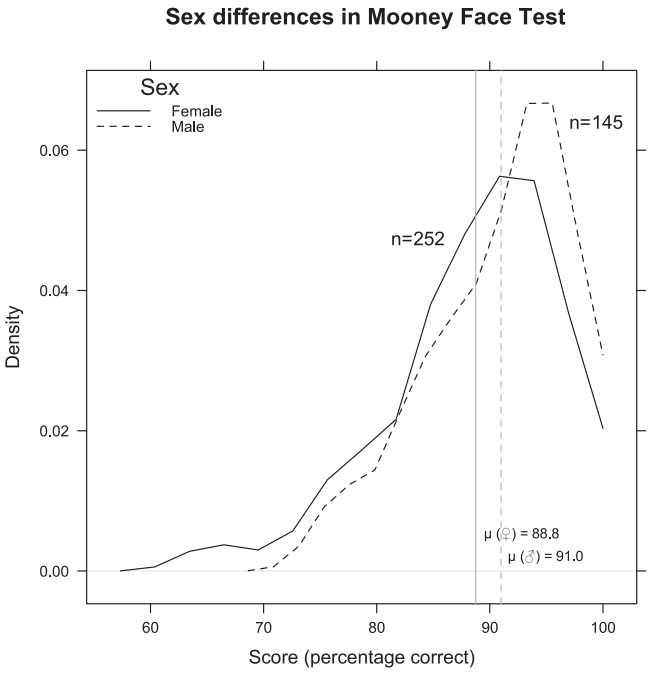

Fig. 3. The probability density of scores (in percentage correct) for our modified Mooney Face Test, plotted separately for females (solid line) and males (dashed line). The vertical lines represent the mean score in percentage for females (left, $\mu(\varphi)$) and males (right, $\mu(\sigma)$). Males score on average .31 standard deviation, or 2.2%, higher than females ($p=.004$).

Martin, & Clubley, 2001). The mean was 17.85 and the standard deviation 7.94 (range 3–39). There was no significant relationship with performance on our Mooney test (Spearman's $\rho=.02$, $p=.651$); and this remained the case when we accounted for sex, by first removing its influence from the raw scores of both AQ and Mooney performance by linear regression, and then performing a Spearman correlation using the residuals from the regression analyses as the x and y variables ($\rho=.01$, $p=.967$).

Digit ratio, the ratio of the lengths of the index and ring fingers, or second and fourth digits (the 2D:4D ratio), is believed to be a biomarker for exposure to prenatal androgen: exposure to higher

amounts of testosterone leads to a lower ratio and, it is supposed, to more masculine traits (Manning, Scutt, Wilson, & Lewis-Jones, 1998; Zheng & Cohn, 2011; Lawrance-Owen et al., 2013). A positive association between digit ratio and the magnitude of the Face Inversion Effect has recently been reported by Leow and Davis (2012). For our sample, digit ratio—after the influence of sex had been removed from both variables by linear regression—was significantly correlated with performance on our Mooney Face Test: a higher digit ratio was associated with higher performance (Spearman's $\rho = .14$, $p = .006$).

A whole-genome analysis was performed using the software PLINK (Purcell et al., 2007), entering the ranks of the Mooney scores and using the four covariates described above in Section 2.3. This regression analysis revealed one SNP to be highly associated with performance on our Mooney test ($p = 9.68 \times 10^{-8}$): rs1522280, a marker located on chromosome 7, in the first intron of the gene *RAPGEF5*. In a genome-wide association study, the correction needed for multiple testing depends on the number and identity of SNPs that are genotyped, and on the linkage between SNPs in the population tested. We used the Genetic Type 1 Error Calculator (Li, Yeung, Cherny, & Sham, 2012) to calculate the number of independent tests that we had to correct for in our analysis. The calculated number of independent tests was 339,116 and the probability value required for significance at an alpha level of $\alpha = .05$ was 1.47×10^{-7}. The result for rs1522280 at $p = 9.68 \times 10^{-8}$ satisfies this threshold.

An independent approach to assessing significance in a whole-genome association study is to use a permutation procedure to derive empirical *p*-values. This gives values that are inherently corrected for multiple testing. We ran a permutation test on the data using PLINK (Purcell et al., 2007)[1]: phenotypes are shuffled amongst participants, while the genotypes are left untouched. Thus, multiple permutations of the original dataset are created, generating data under the null hypothesis. Subsequently, for every SNP, empirical *p*-values are calculated, which give the probability that any *p*-value for any SNP in the permuted analysis was larger than the originally observed *p*-value for rs1522280. We performed 50,000 permutations in total: the association between Mooney performance and rs1522280 was significant at the $\alpha = .05$ level ($p = .031$).

Table 1 shows summary statistics for the three alleles at rs1522280 and Fig. 4 shows the distributions of scores for the three genotypes. We follow dbSNP convention by reporting the reverse strand alleles. Participants who are homozygous for the major allele ('AA') score on average .37 standard deviation higher than participants who are heterozygous ('GA'), who in turn score on average .62 standard deviation higher than participants who are homozygous for the minor allele ('GG'). The minor allele frequency was .31 in the sample used for the present analysis. Our SNP rs1522280 is in Hardy–Weinberg equilibrium ($p = .54$).

For those participants in the present sample for whom we hold both Autism-Spectrum Quotient and valid genotypic data ($N = 293$), there was no relationship between AQ and rs1522280 in the gene *RAPGEF5* (Spearman's $\rho = -.05$, $p = .438$).

A quantile–quantile plot shows no evidence of spuriously high signals due to technical error or population stratification (Fig. 5A). To make sure that the calling algorithm for SNPs was successful for rs1522280, we plotted the signal intensity of the two alleles for all individuals: the cluster plot shows three clearly distinct groups without overlap (Fig. 5B).

Using IMPUTE (Howie, Donnelly & Marchini, 2009; Howie, Marchini, & Stephens, 2011) and the 1000 genomes phased haplotypes (The 1000 Genomes Project Consortium, 2010), we imputed a 2.0 Mb region centred on rs1522280. The resulting association between performance on the Mooney test and this region is shown in the regional Manhattan plot of Fig. 5C. None of the imputed SNPs were more highly associated with performance on our Mooney test than was rs1522280.

[1] http://pngu.mgh.harvard.edu/~purcell/plink/perm.shtml.

Table 1
Summary statistics for the subset of 370 participants for whom we had genetic data. For each genotype, the table shows the total number of participants, the separate totals for females and males, the mean age, and the mean percentage score on our Mooney Face Test.

Genotype	AA	AG	GG
N	174	164	32
Females	121	95	19
Males	53	69	13
Mean age (and SD)	24.1 (4.46)	23.8 (3.91)	25.0 (4.06)
Mooney % score (and SD)	91.17 (6.20)	88.49 (7.34)	83.97 (9.07)

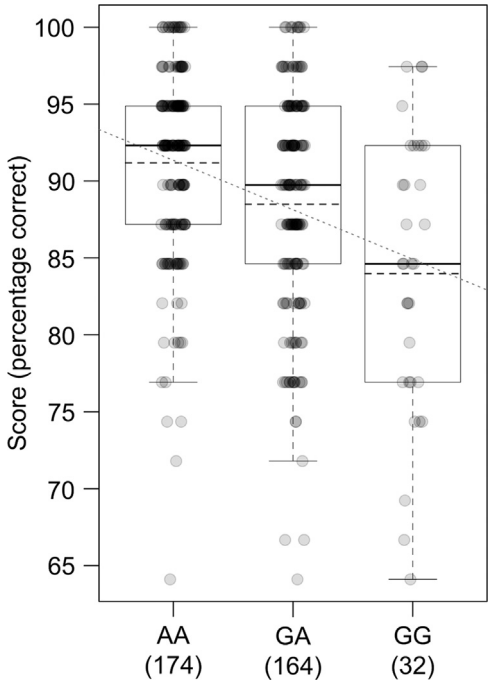

Fig. 4. Plot showing the distributions of percentage scores on our Mooney Face Test for the three possible genotypes at rs1522280: homozygous major ("AA", 174 participants), heterozygous ("GA", 164 participants) and homozygous minor ("GG", 32 participants). For each of the three groups, the boxes show the median (solid horizontal line) and the mean (dashed horizontal line) percentage of correct trials. The mean values are 91.2% (AA), 88.5% (GA), and 84.0% correct (GG). The diagonal, dotted grey line shows the least squares regression line as fitted to the data.

4. Discussion

By adopting a three-alternative forced-choice paradigm, we have been able to develop a version of the Mooney Face Test that is suitable for online administration. Using this version, a much larger group of participants can be reached than could easily be examined by personal interview. We find a wide range of performance on the test, indicating marked individual differences, and we report several correlates of performance.

The observed sex differences confirm those reported by Foreman (1991) for the classical version of the Mooney test. Interestingly, a higher digit ratio (associated with exposure to *lower* levels of prenatal androgen) is associated with higher performance on our Mooney test, while simultaneously the sex difference shows males outperforming females. This correlation of

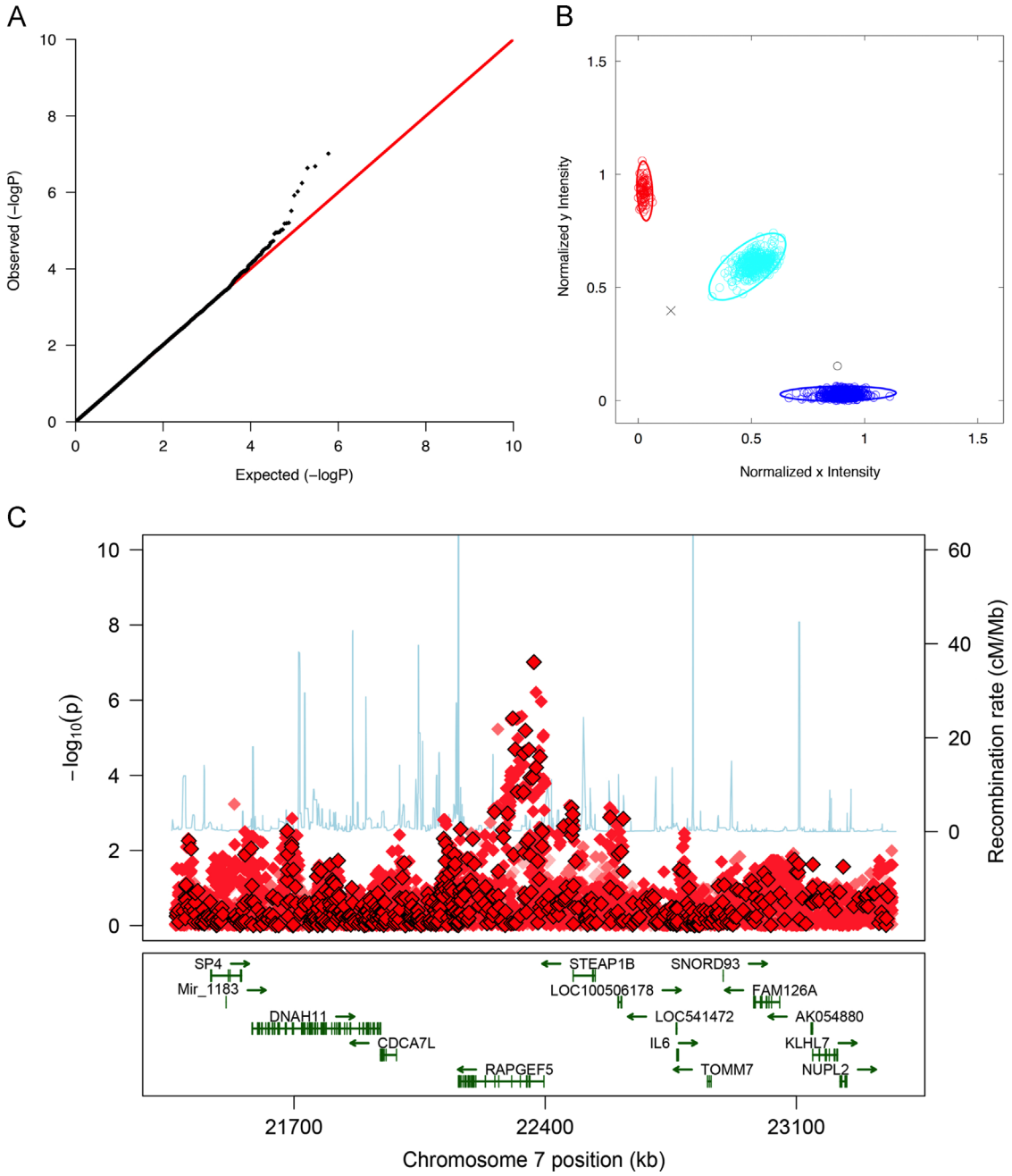

Fig. 5. Genetic results. Panel A shows the quantile–quantile plot of the observed *p*-values (solid points) against the *p*-values expected under the null hypothesis of no genome-wide association (solid line): the uppermost point (SNP rs1522280) deviates substantially from the expected value. Panel B shows a cluster plot of signal intensity used for calling the different genotypic groups for rs1522280. The plot shows three well-defined groups without overlap, indicating that the genotypic groups were properly called. Circles represent individuals; crosses represent individuals excluded from the genetic analysis; black circles are individuals with missing genotypic calls for rs1522280. Panel C shows a regional Manhattan plot for the region surrounding rs1522280, including the imputation results. The main panel shows the imputed region of 2 Mb centred around SNP rs1522280, which is at position 22,368,678 on chromosome 7. Red diamonds represent individual SNPs: those with black borders were genotyped; those without borders were imputed (their saturation corresponds to the imputation quality). The *X*-axis shows the position of the SNPs (in kb), and the *Y*-axis shows the $-\log_{10}(p)$ significance values for the associations. The faint blue line shows the recombination rate of SNPs; its scale is on the *Y*-axis on the right. In the lowermost panel horizontal green lines show the genes at their respective positions in the region; solid green rectangles indicate exons. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

performance with digit ratio is present only when sex is added as a covariate. It thus seems that—individually—both digit ratio and sex are associated with performance, yet they confound one another when entered together in an analysis.

The lack of correlation between the Mooney Face Test and Autism-Spectrum Quotient is rather surprising, given that people with explicit autism have been reported to be impaired not only on tests that require the Gestalt principle of closure (Brosnan, Scott, Fox, & Pye, 2004; Bölte, Holtmann, Poustka, Scheurich, & Schmidt, 2007), but also on some tests of face processing, including the Mooney test itself (Sun et al., 2012; Weigelt, Koldewyn, & Kanwisher, 2012).

Although our sample is relatively small by the standards of whole-genome association studies, we tentatively identify a genetic correlate of performance on the Mooney Face Test: rs1522280 on chromosome 7, which is situated within the *RAPGEF5* gene. The protein encoded by this gene is a guanine nucleotide exchange factor (GEF). The molecule serves as an activator of RAS proteins, a

subfamily of GTPases that function as GTP/GDP-regulated switches in signal transduction, cycling between inactive (GDP-bound) and active (GTP-bound) states (Rebhun, Castro, & Quilliam, 2000). It is interesting that data from the Allen Brain Atlas (Hawrylycz et al., 2012) show that *RAPGEF5* is over-expressed in the fusiform gyrus (right hemisphere; *z*-score=2.408) but heavily under-expressed in the inferior occipital gyrus (right hemisphere; *z*-score -3.856). Both these structures are thought to play roles in detecting the invariant features of a face (Haxby & Gobbini, 2011).

Few genetic correlates of specific cognitive functions have so far been reported (Donohoe, Deary, Glahn, Malhotra, & Burdick, 2012). Why might a genetic correlate have nevertheless emerged in the present study? Perceptual closure on the Mooney test exhibits an all-or-none characteristic; and it might thus index a relatively low-level process—a process that is more likely to be influenced by an individual genetic polymorphism than would be higher-level aspects of face perception. However, in the absence of a replication sample, our suggestion of an association between *RAPGEF5* and the Mooney test must remain preliminary. It would be interesting in future studies to relate *RAPGEF5* not only to phenotypic performance but also to morphological and physiological measures such as the thickness of fusiform cortex and BOLD responses during processing of faces.

Our results suggest that online administration of the Mooney test is practical and would facilitate the use of larger samples that may reveal further genetic correlates of performance. However, the present test could be improved by an increase in the number of trials: such a modification would allow a test–retest study of reliability using different subsets of items. At present, reliability is difficult to assess, since an image once recognised is very likely to be identified quickly on second presentation. Since 7.6% of our participants achieved the maximum score, a second modification would be to shorten the time allowed for each trial, with the expectation of reducing ceiling effects.

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