Supplemental Information

Aging and a genetic *KIBRA* polymorphism interactively affect feedback- and observation-based probabilistic classification learning

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Supplemental Methods: Genotyping

All SNP genotyping was performed using the TaqMan 5'-exonuclease allelic discriminiation assay. The sequences of primers and TaqMan probes for the SNP genotyping were designed and synthesized by Applied Biosystems (Foster City, CA; assay ID: C___7452370_1_). Experimental conditions followed the manufacturer's instructions.

BDNF (rs6265). The nonsynonymous *BDNF* (Val66Met, dbSNP: rs6265) single-nucleotide polymorphism was genotyped using the TaqMan 5'-exonuclease assay in a 384-well microtiter plate format as described elsewhere (e.g., Hariri et al., 2003). The frequencies of the three BNDF rs6265 genotypes were 63.1% for Val/Val, 33.8% for Val/Met, and 3.1% for Met/Met in the older group. The corresponding distribution in the younger group was 65% for Val/Val, 28.8% for Val/ Met, and 6.8% for Met/Met. The genotypic distributions did not deviate significantly from those expected according to Hardy–Weinberg equilibrium (HWE) in either age group, all χ^2s < 0.22; all *p*s > 0.05. For analysis purposes, and in accordance with previous reports, participants were grouped into "val/val" and "any met" carriers (e.g., Li et al., 2010).

DARPP-32 (rs907094). Genotyping was performed on 384-well microtiter plates in 5 µl reaction volumes. For each reaction we combined 10 ng DNA template, 5 TaqMan genotyping assay and 5 TaqMan Genotyping Master Mix. Thermal cycling was done on a PTC-240 PCR instrument using the following cycling conditions: pre-amplification phase at 50 °C (2 min), initial denaturation at 95 °C (10 min), followed by 45 cycles of denaturation at 95 °C (15 s), annealing and extension at 60 °C (60 s). Participants were grouped into "A/A" and "any G" carriers (Frank, Doll, Oas-Terpstra, & Moreno, 2009). The frequencies of the genotypes among the older adults were 53.8%, 35.4% and 10.8% for the A/A, A/G and G/G alleles and 57.5%, 35.0% and 7.5% among the younger adults. The observed counts genotypes did not differ from that expected according to HWE in either age group; all χ^2s < 1.1; all *p*s > 0.05

DAT VNTR. For the DAT VNTR, we genotyped the 40-base-pair VNTR in the 3′ untranslated region following previously published procedures (Lim et al., 2006). Product amplification was achieved by polymerase chain reaction (PCR) on 96-well microtiter plates in 10 µl reaction volumes. For each reaction we combined 1.5 mM of each primer, 50 ng/ml of DNA template, 0.25 mM dNTPs, 0.25U Taq polymerase and Q solution (QIAGEN Ltd; Hilden, Germany). Thermal cycling was done on an MJ Research Thermo

Cycler PTC-240 using the following cycling conditions: initial denaturation at 94 °C (3 min), followed by 35 cycles of denaturation at 94 °C (45 s), annealing at 70 °C (90 s), and extension at 72 °C (35 s), followed by a final extension step at 72 °C (6 min). Genotypes were called after visualization of amplification products on a Shimadzu MCE-202 MultiNA instrument (Shimadzu Corporation, Kyoto, Japan) using the DNA 500 kit following the manufacturer's protocol. In this assay, the 9-repeat allele ran at approximately 430 bp, while the 10-repeat allele ran at approximately 470 bp. The DAT VNTR genotypes were grouped into "any 9" and "10/10" carriers (Li et al., 2013). The frequencies of older adults carrying the different alleles were 49.2% for 10/10, 43.1% for 9/10, and 7.7% for 9/9. The distribution of genotypes among the younger adults was 46.25%, 42.5% and 11.25% for 10/10, 9/10 and 9/9 repeats, respectively. The observed counts genotypes did not differ from that expected according to HWE in either age group; all χ^2s < 0.11; all *p*s > 0.05.

Supplemental Figures

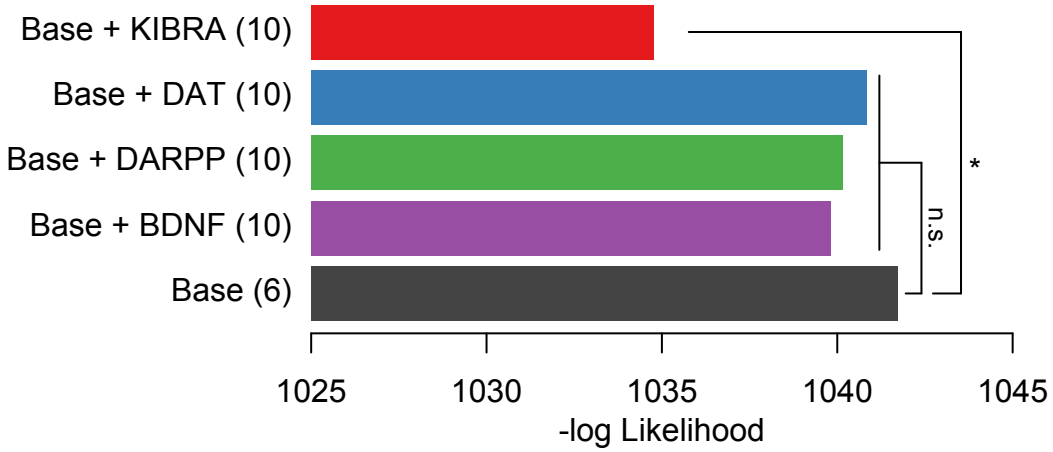

Figure S1: ***Effects of BDNF, DARPP-32, DAT and KIBRA polymorphisms on performance***. The 'Base' model (grey bar) included fixed effects for Age Group, Condition, and their interaction, plus a random effects term for the subject-wise intercepts. This model was compared to four models including genetic factors. Each of the comparison models included all factors of the Base model, plus the main and interaction effects of the respective genetic factor, see model names. Numbers in brackets behind model names indicate the degrees of freedom. The x-axis shows the negative log likelihood (lower numbers indicate better model fit). Comparisons were done using χ^2 log likelihood ratio tests as implemented in R. n.s.: non-significant. *: Model comparison is significant at $p < .05$, corrected for 4 multiple comparisons.