at follow up. There was a mean rating of 82% for helpfulness of the intervention and 86% for likelihood to continue using the techniques. There were no significant effects of intervention on state anxiety and covid-related lifestyle disruption as both groups showed remission reflected in significant main effects of time. There were no significant effects of the intervention on emotional cognition on the Emotional Categorisation Task or the Emotional Recall Task. **Conclusion:** Online behavioural activation administered by non-therapists was effective in reducing symptoms of depression and increasing activation, although this was not reflected in changes to automatic emotional cognition. State anxiety and covid lifestyle disruption seemed to show significant spontaneous remission during our period of testing, indicating that covid-related anxiety, disruption and stress may be temporary. The intervention was rated as highly acceptable by participants experiencing depression. This study suggests that this online behavioural activation intervention can be effective despite the constraints of social distancing and that it has the potential to be cheaply disseminated during a global public health emergency when administered by non-therapists.

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Familial environment modifies association of DNA methyltransferases gene variants and cognitive functioning

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The study of cognitive functioning and cognitive deficit is becoming increasingly relevant today due to an increased frequency of cognitive decline and neurodegenerative disorders even in the middle age. In turn, the level of cognitive functioning is the basis of life success and individual self-realization. It is established that the mechanisms underlying individual predisposition to individual cognitive functioning are complex, and genetic, epigenetic and environmental factors play a significant role. Together with the data on associated SNPs [1], recent findings point to a significant role of epigenetic mechanisms in cognitive development. Since environmental factors [2] and DNA methyltransferases are responsible for certain epigenetic changes in DNA methylation profile [3], the present study aimed to examine the main effect of DNA methyltransferases gene (*DNMT1*, *DNMT3A*, *DNMT3B*) variants on cognitive abilities and to detect gene-by-environment interaction models explaining individual variance in cognitive functioning in mentally healthy young adults from Russia.

The study consisted of 897 mentally healthy individuals (79% women; 19.74±1.51 years) of Caucasian origin (428 Russians, 200 Tatars, 117 Udmurts, and 152 of mixed ethnicity) from Russia. The assessment of cognitive abilities ("number sense", 3D mental rotation, non-verbal intelligence, working memory) was performed using the Battery of cognitive tests developed at International Laboratory for Interdisciplinary Investigations into Individual Differences in Learning (InLab) (Department of Psychology, Goldsmiths, University of London). The genotyping of *DNMT1* rs10418707, DNMT3A rs1550117, DNMT3B rs2424932 gene SNPs was performed via PCR-based KASP genotyping technology on "CFX96" DNA Analyzer (BioRad, USA). Statistical analysis included multiple linear regression followed by FDR-correction for multiple testing (PLINK v.1.09). Genotypes and 13 environmental parameters served as independent factors and cognitive abilities as dependent variable.

We failed to observe the main effect of examined gene variants in individual differences in cognitive functioning after correction for multiple comparisons. However, the GxE analysis revealed statistically significant models, which explained individual variances in the level of non-verbal intelligence: 1) *DNMT1* rs10418707 and rearing in bilingual family ($\beta = 4.28$; $P = 0.003$); 2) *DNMT3A* rs1550117 and increased family income in childhood ($\beta = 16.7$; $P = 0.008$); 3) *DNMT3B* rs2424932 and rearing in a full family ($\beta = -4.61$; $P = 0.023$); 4) *DNMT3B* rs2424932 and paternal age at child's birth ($\beta = -0.13$; $P = 0.037$). In turn, the income level modulated the association of *DNMT1* rs10418707 ($\beta = -2.34$; $P = 0.017$) and *DNMT3B* rs2424932 ($\beta = -1.75$; $P = 0.025$) with working memory, which is impaired in neurodegenerative diseases associated with cognitive decline.

Our findings indicate a significant role of interaction between rearing specificity (including family income in childhood, bilingual rearing and the involvement of both parents in individual's development) and genetic predisposition mediated by variants in the genes responsible for the changes in DNA methylation profile in cognitive functioning.

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