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INVESTIGATION OF THE INTERPLAY BETWEEN GENETIC AND ENVIRONMENTAL RISK FACTORS FOR SMOKING BEHAVIOUR

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Smoking-behaviour is influenced by environmental and genetic risk factors. Established epidemiological risk factors include early age at onset (AaO), depression, positive family history (FH+) of depression/alcohol-dependence, low education, older birth cohort, and male gender. Genome-wide-association-studies (GWAS) have identified genetic risk variants for smoking-behaviour. In the present study we investigated correlations between these epidemiological and genetic risk factors and smoking-behaviour in a large population-based German sample. Genetic risk was defined in terms of a polygenic score – the accumulated effect of seven independent genetic risk markers for smoking-behaviour identified through GWAS.

The sample comprised 1736 individuals (815 males, 921 females). Dependent variables were: *smoking-duration*, *nicotine-dependence*, *cigarettes-per-day*, *ever-smoking*, and *smoking-cessation*. The effect of the epidemiological risk factors, the polygenic risk score, and their combined effect on the smoking-behaviours was tested via linear or logistic regression analyses.

The following associations were detected: AaO and birth cohort with *smoking-duration* (p=0.004; p<0.001); AaO, education and FH+ depression with *nicotine-dependence* (p=0.002; p=0.092); sex and AaO with *cigarettes-per-day* (p=0.020; p<0.001); FH+ alcohol dependence with *ever-smoking* (p=0.049); and birth cohort and education with *smoking-cessation* (p=0.001; p=0.029). The polygenic risk score showed a trend towards association with *nicotine-dependence* (p=0.113) and *cigarettes-per-day* (p=0.109). In the combined analyses, the polygenic risk score improved the regression model for *nicotine-dependence*, *cigarettes-per-day*, and *smoking-cessation*.

The addition of GWAS information concerning genetic risk factors explained an increased fraction of the smoking behaviours nicotine dependence, CPD, and smoking cessation. Future studies are warranted to elucidate the biological correlates of these genetic risk factors.