Genetic markers for hypertension – a genetic epidemiological study of 5000 Romanian individuals

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Background: During the past decades, genetic research has reached new heights as next generation sequencing has rapidly taken over and genome-wide association studies (GWAS) have broug.

The purpose of the research is to determin high-risk variants (Single-Nucleotide-Variants,SNVs) associated with hypertension (HTA) in the Romanian population.

The current presentation asseses the final results of a 3 part study comprising the first and the largest GWAS on hypertension in Romanians.

Material: Methods The total cohort includes a number of 5690 individuals, of which 2190 with hypertension and 3500 heathy controls.

Genetic testing was performed at in Iceland.

A multiple GWAS assay has been performed for the identification of variants associated with hypertension, hypertension risk factors and hypertension comorbidities.

Results: Environmental (lifestyle) risk factors, such as smoking, alcohol consumption and coffee consumption, and also pathological risk factors, as are obesity and ageing, were analyzed in association with hypertension. Tissue-specific protein expression, gene function and gene-gene interactions have been analyzed for assessing a possible biological explanation of the association between the identified related variants and HTA. Expression quantitative trait loci (eQTL) were assessed for variants in the reported locations for a better understanding of their involvement in HTA.

The results of the analysis revealed a number of over 5000 genetic variants statistically correlated with hypertension in the studied cohort, some well documented and in genes known to be involved in hypertension pathophysiology (clusters on chromosomes 1p36, 1q24, 3q24, 4p16, 5q12, 7q36, 12p12, 15q, 17q, 20q12, a.o. or CRNKL1, C19Orf12, CCDC51, C20Orf26, ZNF420, ZNF571, a.o. intragenic variants). Approx. 4100 SNVs were identified in correlation with diabetes mellitus and obesity.

Variants correlated with both hypertension and DM were identified (TBX20,ANK2, a.o. genes). Two other variant clusters ($p=10^{-4}$–10^{-3}) on chromosomes 19 (19q12) and 20 (20p11.21) revealed statistical correlations with both hypertension and obesity.

Conclusions: The present study found some important loci and clusters associated with HTA, which migh provide insights into the genetic architecture of this pathology.

The validity of these results for the Romanian population need to be confirmed by replication studies.

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