Plan Overview

A Data Management Plan created using DMPTool

Title: Genome-wide association analysis_ novel blood pressure loci_biological insights_ cardiovascular risk

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Project abstract:

Elevated blood pressure is the leading heritable risk factor for cardiovascular disease worldwide. We report genetic association of blood pressure (systolic, diastolic, pulse pressure) among UK Biobank participants of European ancestry with independent replication in other cohorts, and robust validation of 107 independent loci. We also identify new independent variants at 11 previously reported blood pressure loci. In combination with results from a range of *in silico* functional analyses and wet bench experiments, our findings highlight new biological pathways for blood pressure regulation enriched for genes expressed in vascular tissues and identify potential therapeutic targets for hypertension. Results from genetic risk score models raise the possibility of a precision medicine approach through early lifestyle intervention to offset the impact of blood pressure–raising genetic variants on future cardiovascular disease risk

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Copyright information:

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This study used data from the UK Biological Database and required genotyping using the custom Affymetrix UK BiLEVE axiom array of the UKB subset UK BiLEVE study. Quantitative data were generated for this study

(1) By applying k-means clustering to the principal-component analysis (PCA) data, a total of N = 145,315 Europeans remained. We used kinship data to exclude first- and second-degree relatives, with N = 141,647 unrelated individuals remaining.

(2) There were 76,554 hypertensive cases, and the 64,384 remaining participants were treated as non-hypertensive controls. This sample size is slightly larger than the N = 140,866 used in the main analyses, as participants with only one BP measurement but with reported BP-lowering medication could be included as hypertensive.

(3) The European exome consortium (N = 161,926) and CHARGE consortium (N = 119,792) gave a total of N = 281,718 independent replication samples for the exome analysis.

(4) For the GWAS discovery, there were ~9.8 million SNVs with MAF ≥1% and INFO >0.1. We considered for follow-up any SNVs with $P < 1 \times 10{-}6$ for any of the three BP traits. For the exome discovery, there were 149,026 exome SNVs that were polymorphic with INFO >0.1.

Metadata analysis was performed within METAL software using fixed effects inverse variance weighted metadata analysis and with .YUV files, saving this image. For GWAS, we performed linear regression analyses of three continuous, drug-adjusted BP features for all measured and imputed genetic variation under an additive genetic model using SNPTEST software and saved in .txt format.

In this paper, we combine a large single discovery sample with standardized BP measurements and intensive 1000 genomes and UK10K estimation to produce a high quality dataset of approximately 9.8 million variants. In total, we include GWAS data from 330,956 individuals and heterozygous SNVs from a total of 422,604 individuals. once published, they are publicly available without restriction.

The data from this study allow reuse, redistribution or creation of new tools, datasets or products that allow commercial use commercial use and knowledge sharing.

Sort data by data type, phenotype data, experiment data, save as .txt file and archive file directory. The generated archive files will be automatically synchronized to the specified storage system according to the storage path information.
