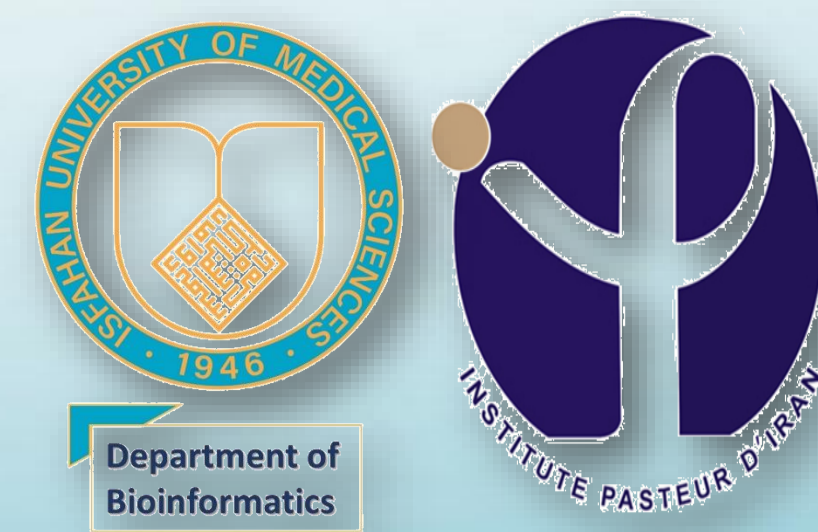




Stratified genome-wide association analysis of blood pressure traits reveal new specific loci for systolic and diastolic blood pressures



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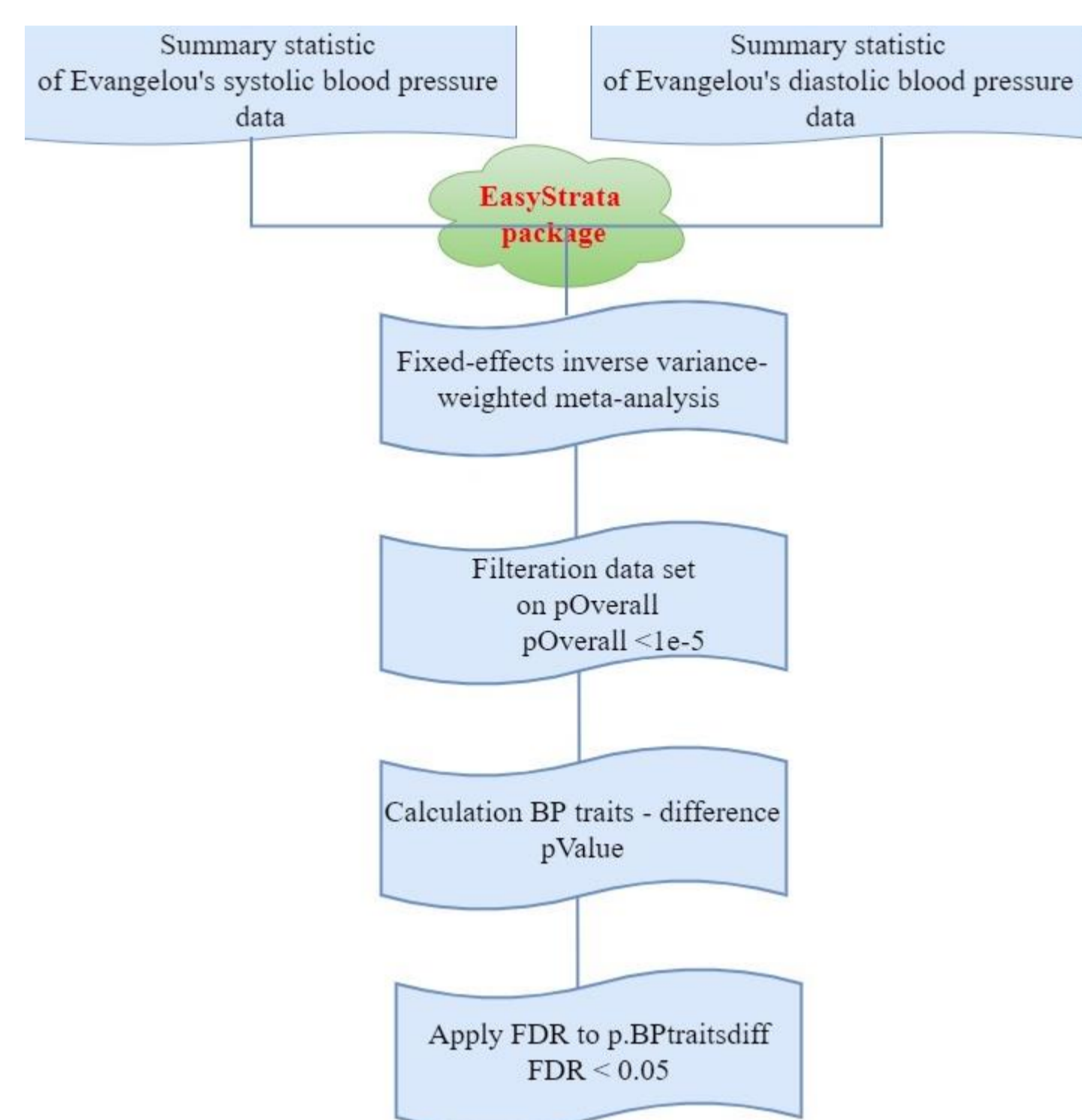
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Abstract

Systolic blood pressure (SBP) and diastolic blood pressure (DBP) are complex quantitative traits. Despite great success in reporting new loci for blood pressure traits, Evangelou et al. did not report any single nucleotide polymorphisms (SNPs) specifically associated with either SBP or DBP. Traits-specific genomic loci might provide promising potential clues for understanding the underlying biology as well as the etiology of complex diseases. Here, we report a stratified analysis of SBP and DBP and potential involved trait-specific mechanisms.

Keywords: Systolic blood pressure, diastolic blood pressure, PIK3CG, SESN3, genomic loci, genome-wide association study

Materials and Methods

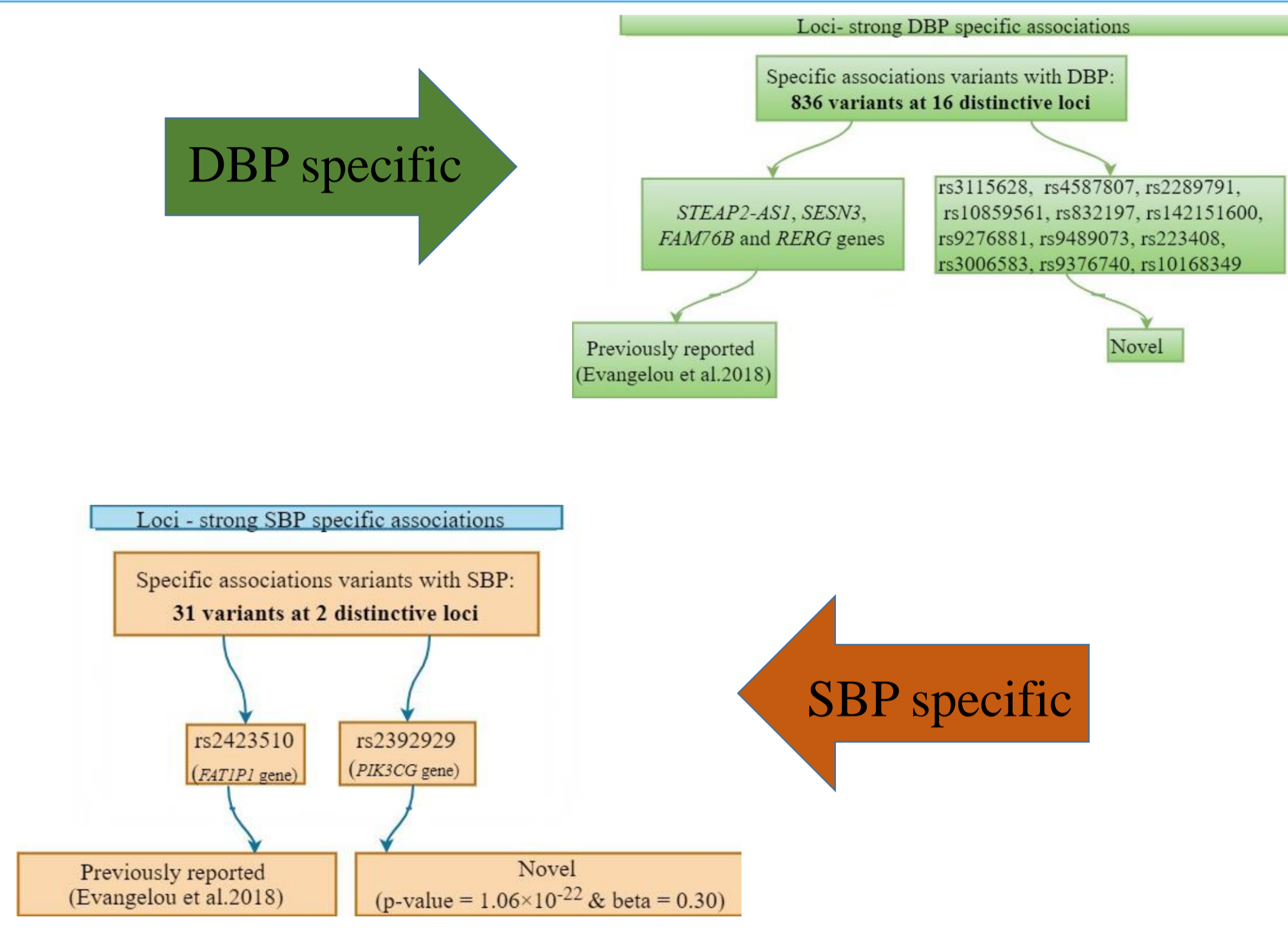


Introduction

Systolic blood pressure (SBP) and diastolic blood pressure (DBP) are determined by complex interactions between genetic background and life-course environmental factors.

The latest and largest meta-analysis of genome-wide association study of blood pressure traits has identified and validated genomic variants at 901 blood pressure-associated loci in total (Evangelou et al. 2018) but did not report any single nucleotide polymorphisms (SNPs) specifically associated with either SBP or DBP.

Results



Discussion, Conclusion and Suggestions

To the best of our knowledge, we are the first team that has identified the above-mentioned systolic and diastolic-specific loci. We identified 2 and 16 trait-specific loci for systolic and diastolic blood pressure, respectively of which, 13 loci are novel. Our findings can be followed-up to identify new biological pathways underlying the regulation of blood pressure and eventually be used to improve the control of hypertension.

References

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