



1: [Hypertension](#). 2007 Dec;50(6):1126-33. Epub 2007 Oct 15.

[Links](#)

## Cross-talk of expression quantitative trait loci within 2 interacting blood pressure quantitative trait loci.

[Lee NH](#), [Haas BJ](#), [Letwin NE](#), [Frank BC](#), [Luu TV](#), [Sun Q](#), [House CD](#), [Yerga-Woolwine S](#), [Farms P](#), [Manickavasagam E](#), [Joe B](#).

Department of Pharmacology and Physiology, George Washington University, Washington, DC, USA. [phmnhl@gwumc.edu](mailto:phmnhl@gwumc.edu)

Genetic dissection of the S rat genome has provided strong evidence for the presence of 2 interacting blood pressure quantitative trait loci (QTLs), termed QTL1 and QTL2, on rat chromosome 5. However, the identities of the underlying interacting genetic factors remain unknown. Further experiments targeted to identify the interacting genetic factors by the substitution mapping approach alone are difficult because of the interdependency of natural recombinations to occur at the 2 QTLs. We hypothesized that the interacting genetic factors underlying these 2 QTLs may interact at the level of gene transcription and thereby represent expression QTLs or eQTLs. To detect these interacting expression QTLs, a custom QTL chip containing the annotated genes within QTL1 and QTL2 was developed and used to conduct a transcriptional profiling study of S and 2 congenic strains that retain either 1 or both of the QTLs. The results uncovered an interaction between 2 transcription factor genes, *Dmrta2* and *Nfia*. Furthermore, the "biological signature" elicited by these 2 transcription factors was differential between the congenic strain that retained Lewis alleles at both QTL1 and QTL2 compared with the congenic strain that retained Lewis alleles at QTL1 alone. A network of transcription factors potentially affecting blood pressure could be traced, lending support to our hypothesis.

PMID: 17938377 [PubMed - in process]