Contribution of Important Candidate Gene Networks and Inflammatory Markers to Metabolic Syndrome

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Abstract

Introduction: The objectives of the present study were three. Build a metabolic syndrome (MetS) hypothesized gene network; Identify the most important inflammatory and/or prothrombotic markers that contribute to MetS; Test the association of candidate genes identified in gene networks with latent factors of MetS in the setting of the Hypertension Genetic Epidemiology Network (HyperGEN) data.

Methods: First, genes related to MetS were identified by searching the NCBI database through “Gene” Entrez search for genes related to the each MetS domain. In addition, "inflammation" genes were also identified and annotated if they contributed to other MetS domains. Second, a literature review was performed for inflammatory and/or prothrombotic markers to report association and cutoff thresholds among these markers and MetS components. Finally the association tests of selected candidate genes with the latent factor from the HyperGEN study were performed using linear mixed effects model.

Results: The curated literature search produced 123 genes as probable candidate genes for MetS. The gene network represents a prior hypothesis that these genes may interact in the pathway(s) for developing MetS. A group of inflammation markers were identified as important markers related to MetS. In this work we reported their literature thresholds for identifying the high risk individuals for MetS. The association test of candidate genes in the HyperGEN dataset showed that IL18, GHR, DPP4, LIPC and ALMS1 gene polymorphisms were associated significantly with factors similar as the predicted domains of the MetS gene network.

Conclusion: MetS gene networks identified represent a prior hypothesis that these genes may interact in the pathway for developing MetS. We suggest this study to be followed by testing gene x gene interactions of these candidate genes.