Abstract

Coronary Heart Disease is a condition wherein there is a buildup of plaque in the coronary artery that creates a blockade reducing the supply of oxygen to the myocardial cells. As the muscle cells begin to undergo necrosis, the body is said to be in a state of Myocardial Infarction. Even though the condition of Myocardial Infarction (MI) is extensively associated with lifestyle, recent evidence has indicated the role of genetics in the widespread occurrence of disease. Linkage Disequilibrium study of the genes associated with myocardial infarction was the foundation for a more advanced study of pharmacogenetic implications for drug efficacy and toxicity. The study aided in identification of new drug targets and in the mapping of genetic associations in various populations that hence contribute to personalized medicine. In the present study, the authors performed genome-wide association studies to compare the genes associated with Myocardial Infarction (ACE, MIA3, GATA4, ESR1) in five populations. Linkage Disequilibrium (LD) analysis was performed to understand the association of various SNP’s present on these genes. Post-retrieval of SNP genotype data of various populations from
NCBI’s 1000genomes browser, an LD plot was constructed using an online LD Link LD Analysis tool developed by National Cancer Institute. The results have indicated a dense map of single nucleotide polymorphisms (SNPs) which were linked to Myocardial Infarction and SNPs that are co-inherited in different populations. Further analysis of SNP’s using PharmGKB database suggested the SNP’s influence on drug therapy of prescribed drugs for Myocardial Infarction like Fluvastatin, Raloxifene, Letrozole, Warfarin, and Vancomycin.

References

10. Imai Y. A, 2013. Regulation of bone metabolisms by estrogen/estrogen receptors
SNP Analysis, Genome Wide Association Studies and Pharmacogenetic implications of Acute Myocardial

11. T Wei Y Toy, Yang Shen, Helen Won, Bradley Green, Rita A Sakr, Marie Will, Zhiqiang Li, Kinisha Gala, Sean Fanning, Tari A King, Clifford Hudis, David Chen, Tetiana Taran, Gabriel Hortobagyi, Geoffrey Greene, Michael Berger, José Baselga & Sarat Chandarlapaty, A, 2013. ESR1 ligand-binding domain mutations in hormone-resistant breast cancer. Nature Genetics, 45, DOI: 10.1038/ng.2822, 1439-1445.


15. Slatkin, Montgomery, Linkage disequilibrium - understanding the evolutionary past and mapping the medical future, Nat Rev Genet, 2008/06//print 96477485, Nature Publishing Group, 1471-0056, DOI: 10.1038/nrg2361


20. Bozkurt et al, Genetic variation in the renin-angiotensin system modifies the beneficial effects of ACE inhibitors on the risk of diabetes mellitus among hypertensives, J Hum Hypertens, 2008/06/19/online/2211774780, Macmillan Publishing Group 0950-9240, DOI: 10.1038/jhh.2008.62


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