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.

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