**THE ROLE OF GENE POLYMORPHISM IN FAMILIAR CARDIOMYOPATHY**

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Cardiomyopathy manifests itself as dilated (DCM) or hypertrophic (HCM) cardiomyopathy, whereby the idiopathic forms of the disease are ascribed to unknown etiology. While the underlying cause of the disease is known to be partly genetic in nature, the contributory genes have not been fully deciphered yet. This study was designed to identify gene involved in familial (idiopathic) dDCM and HCM in the Saudi population as a study model. Accordingly, several core and large families in which at least two affected members were recruited and whole genome scan using Affymetrix 250 sty1 chip was employed to identify possible loci for homozygosity in these families. Following the identification of high density loci, we then targetted potential genes of interest to identify causative single nucleotide polymorphisms (SNPs) by sequencing the coding area of genes of interest in the family members followed by association studies in the general population. Thus far, four families have been recruited, and screened for mutations. Homozygosity mapping has indicated common loci on several genes including 1, 2, 3, 4, 9, 11, 12, 14, 19 and 20, isolating at least three of the siblings with autosomal dominant trait. The results show several chromosomal loci linked to familial dilated cardiomyopathy. While some familiar genes could be indentified on these loci, there appeared also to be new genes that have to be mined for their possible role in disease.