8. FUTURE PROSPECTIVES

With the advent of 21st century, a major leap into the genetics of CAD has been witnessed which is highlighted by a tremendous rate of progress in technological breakthroughs synchronous to a better disease understanding with the advancement in both the divisions complementing each other. Advancements in the field of CAD genetics have been achieved with collaboration studies and data sharing. Thus it was no surprise that such collaborative work identified more than 60 receptive loci which played a crucial role in disease understanding. Not only previously well established mechanisms related to disease were highlighted, such collaborative work also revealed novel pathways that are associated with atherosclerosis. Such work has also pointed out the immense relevance of population genetic studies and providing with valuable data on relationship between already established or recently identified risk factors and CAD. Comparative analysis of such reports with single patient data can help us to identify and narrow down individuals who are at high risk and thus preventive measures can be executed early on.

Although the progress has been remarkable, many milestones are yet to be achieved to augment the clinical utility of the expertise gained. As of now, it is paramount to identify and recognize the remaining susceptibility loci for CAD for a better profiling. The next step can be proving the clinical applications of the data gained through clinical testing and implementing strict observations and government policies for CAD prevention.

In order to explain the effect of genetic variations in an individual, all genetic studies require large sample size for generating a far more accurate data for comparative analysis. This need can be met by setting up mega-biobanks which have adequate facilities and expertise to store and handle such large data (at least one half million participants). The data can be generated from currently available bio-banks such as UK Biobank, the China KadoorieBiobank, the Million Veteran Program, and the National Institutes of Health Precision Medicine Initiative cohort (Chen, Chen et al. 2011; Allen, Sudlow et al. 2014; Gaziano, Concato et al. 2016; Shah, Arnett et al. 2016). Thus, large scale population studies should be encouraged as they provide vital information on gene prevalence and build a solid foundation for comparative analysis. Apart from the utilities stated above, installing such biobanks will be advantageous as it will allow us to understand the clinical utility of genetic risk scores. Also there is a dire need to correlate
the cellular mechanisms with the genetic associations in the general pool. Such knowledge will not only spearhead further research in this domain but will also act as an impetus for future drug targeting and novel therapeutic agents. Combining such information with ongoing initiatives such as the ENCODE (ENCyclopedia Of DNA Elements), GTEx (Genotype-Tissue Expression), and Roadmap Epigenomics projects, which are carefully documenting the complex and abundant regulatory regions of the genome across all human cell types (Tak and Farnham 2015) will definitely yield better results.

Epistasis has also been postulated to play an important role in gene-gene, gene-environment and gene-gender interactions and thus might play an eminent role in elucidating CAD risk. Nonetheless, such studies will provide excellent opportunities for carrying out future work. The effect of gender and the influence of sex hormones, difference in anatomical and physiological fat distribution, lipid metabolism, insulin resistance and cardiovascular function should be deciphered conclusively. This will lead to an early adoption of healthy behaviors for combating CAD epidemic. Also combining the non-invasive imaging techniques with the genetic variation analysis will provide important breakthroughs in our understanding of the molecular basis of CAD.

There is a lot of scope for the nutrigenetics and nutrigenomics. The former deals with studying the impact of SNPs in the food metabolism and the latter are concerned to explore the effect of food bioactive compounds on gene function and regulation. This will help in identifying population subgroups having differential responses to diet therefore, having a tailored dietary regimen.

Although the understanding of majority of the available information is yet to be utilized as a therapeutic agent which targets such gene loci, rapid advancement in the path of translation for other susceptibility loci, such as PCSK9 gives us considerable comfort that this expansion is foreseeable in the future. It is anticipated that such ventures will give us an insight into these mechanisms and pave way for groundbreaking opportunities to further curtail and possibly eradicate CAD hazard in the 21st century.