

Book Review

Genomic Diversity: Applications in Human Population Genetics Edited by Surinder S. Papiha, Ranjan Deka and Ranajit Chakraborty
Kluwer Academic/Plenum Publishers, New York
233 Spring Street, New York, N.Y. (1999)
(Hard Bound)

The reconstruction and understanding of the origin and past history of modern human is the hotly debated issue today. The subject of evolutionary history of man has been greatly explored with the use of paleontological and archeological records along with cultural and linguistic evidences. This subject has received new direction and insight with advent of new molecular genetic technology and population genetic diversity studies to construct the phylogenetic path of *Homo sapiens sapiens*, particularly the whole new power full cDNA, mtDNA and Y- Chromosome DNA polymorphism which has revolutionized the population genetics and evolutionary research.

This book which is the outcome of the symposium "Molecular Anthropology in 21st Century" held during the 14th International Congress of the Association of Anthropological Ethnological Science at Williamsburgh on July – August, 1998, seems to provide the basic groundwork of the use of molecular technology for the improved and better understanding of the problems of Human Population Genetics, Evolutionary Research and Genomic Diversity. The authors with an encyclopedic compilation of the very relevant chapters of the various contributors on the topic of genomic diversity and evolutionary research have dealt with dictum in detail in an exemplary manner.

The first chapter discusses the population studies from the Indian Subcontinent and development of this field from classical genetic markers of early 20th century to the most recent molecular genetic markers. The two types of markers have been compared to understand the origin and interrelationship of the some population groups of this subcontinent. The second chapter also outline the same subject through a case study among the five Brazilian Indian tribes, here variability in the nDNA, mtDNA and proteins has been compared which highlight the difference of results in using these

three different genetic markers for the study of phylogenies and population relationships. In the third chapter nine autosomal microsatellite polymorphic markers are potentially used for the understanding of genetic differentiation of the five Native American tribes. Chapter four by Deka et al. gives an account of trinucleotide repeat loci which have been implicated in the genesis of more than a dozen human disease, here these loci have been discussed for their population genetic properties with an emphases on the maintenance of the expended alleles in human populations. In chapter five Chris Tylar – Smith has outlined the methodological issues and complications due to the use of Y chromosomal DNA markers which includes recurrent mutation, duplication of loci, sample reliability and nomenclature. Whereas in Chapters six – eight genetic origin of some world populations with use of Y chromosomal markers has been presented. Francalacci et al. (Chapter 9) have presented a database for the variability of the control region sequence (Segment I) of the mito-chondrial DNA, to avoid the complications of sequence and polymorphic sites in different data-base, a possible use of the database for timing migrational events in the two Mediterranean Islands is also discussed. In chapters ten – twelve mitochondrial DNA studies among the populations of Europe, India and Southwest Pacific provide an excellent example of the use of these markers in evolutionary genetics. Connie J. Kolman (Chapter 13) has discussed the use of ancient DNA in the reconstruction of population origin and evolution, along with the problem of contamination in this DNA. A very interesting use of human pathogens, to address the evolu-tionary histories of pathogens as well as migra-tion patterns and evolutionary relationships of human populations. Chapter fourteen by Deininger et al. discusses the evolution, origin and structure of *Alu* events in human genome and their potential use in estimation of the root of evolutionary tree which are not possible with other markers, whereas Mayolo et al. in the chapter fifteen has presented world wide distribution of *Alu* insertions in the progesterone receptor gene. Some statistical issues pertaining to the use of microsatellite loci for molecular anthropological studies has been

discussed by Chakarborty in the sixteenth chapter.

The sum and substance of this book is that the authors have tried to highlight the extant of genomic variation in the contemporary populations, importance of this variation in gaining

insight into the evolutionary history and in understanding the genetic complexity of human beings.

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