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Chromosomal Inversion Polymorphism in Studying Phylogenetics

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ABSTRACT: Chromosomal inversion polymorphism is very common in natural populations of insects, plants, bacteria and humans. Association of Chromosomal inversions with several genomic disorder have been reported in human which may occur due to misalignment and/or rearrangement of chromosomes during synapsis. The presence of salivary gland chromosomes in Drosophila make itone of the best studied systems in cyto-as well molecular genetic studies to understand the causes of genetic variations especially the inversions with respect to environmental conditions, altitudinal and latitudinal clines, natural as well as balancing selection, adaptation and speciation. Inversions are known to suppress recombination in heterozygotes, as a result of which the genes present within the chromosomes escape in forming new allelic combinations. In Drosophila, inversions were reported to have positive correlation with growth rate, body size, environmental stress resistance ability, relative fitness and also metabolic pathways e.g. insulin signalling. The inversions are of different types based on their position and frequency of occurrence and are found to be species specific. There is also increasing evidence that chromosomal inversions may facilitate speciation event by increasing genetic variation, species specific adaptation and ultimately leading to reproductive isolation. Therefore, chromosomal inversions could be used as an evolutionary marker in studying population genetics such as gene flow, demographic history and in establishing the phylogenetic relationship among Drosophila species. As India harbours lots of Drosophila species due to its diversified ecological conditions, our study aims to explore both population genetics and phylogenetic of Indian Drosophila species by analysing their chromosomal inversion polymorphism and karyotype. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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