Multilocus nuclear DNA markers for population genetic study in *Drosophila malerkotliana.*

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In recent years, major emphasis has been given in the use of multilocus nuclear DNA markers for inference of population evolutionary history of species (Das *et al.*, 2004). Such markers provide stable inferences on population history of *Drosophila ananassae* and could ascertain both genetic drift and natural selection in different genomic regions of this species (Baines *et al.*, 2004; Das *et al.*, 2004). These approaches have also been followed in population genetic studies of other different taxa out of the *Drosophila* model.

D. malerkotliana is a member of the *ananassae* subgroup of the *D. melanogaster* species group (Bock, 1980). This species belongs to the *bipectinata* species complex that consists of four closely related species - *D. bipectinata*, *D. parabipectinata*, *D. malerkotliana* and *D. pseudoananassae* (Singh and Singh, 2001). Evolutionary history of this species complex has been inferred recently using molecular markers (Kopp and Barmina, 2005) with both mitochondrial and nuclear loci. This study revealed that the four members of this species complex have diverged only 283,000 to 385,000 years ago. The later study had made the member of this species complex very interesting. India is presumed to be the homeland to *D. malerkotliana* (species name synonym to a place in Eastern Punjab, Malerkotla) (Tsacas *et al.*, 1981). Interestingly, this species has been introduced to the rest of the world relatively recently; to the Afro-tropical regions and the Seychelles during the 20th century (Louis and David, 1986), to Brazil in 1970s (Val and Sene, 1980; Santos *et al.*, 2003) and to Mexico and Cuba probably during 1980s (Chassagnard *et al.*, 1989). Recent reports confirm its invasion into North America, plausibly through range expansions from the South (Birdsley, 2003; Medeiros *et al.*, 2003). Parts of these hypotheses are substantiated by a recent study on correlation of genome size variation to colonization events (Nardon *et al.*, 2005). Thus, *D. malerkotliana* appears to be an interesting species to understand genetic mechanisms of adaptation to new environments.

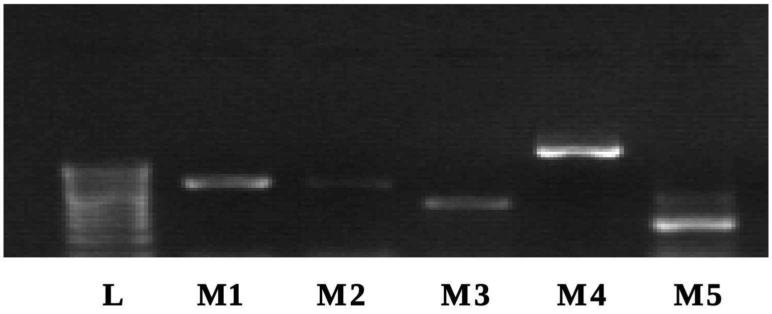

Figure 1. Agarose-gel electrophoretic pictures showing five PCR-amplified nuclear DNA fragments in the genomic DNA of *Drosophila malerkotliana*. L = 100 basepair DNA ladder; M1 = Marker 1; M2 = Marker 2; M3 = Marker 3; M4 = Marker 4; M5 = Marker 5.

In order to initiate population genetic study in India with multilocus nuclear DNA markers, we have utilized the published whole genome sequence information of *D. melanogaster* and designed EPIC (exon priming intron crossing) primers in both the forward and reverse directions. Nuclear DNA of *D. malerkotliana* from an Indian natural population sample was isolated, and amplifications of different fragments were tested. Out of 20 sets of primers tested we have obtained amplifications for five fragments (Figure 1). The extreme left of the picture contains the 100 base pair ladder for comparison. The first, second and fourth fragment are the largest ones (about 800-900 nucleotide base pair length), while the third and fifth fragments are of intermediate size (about 400 to 600 bp). The sizes of these fragments are within the limit of such fragments used for population genetics studies (Das *et al.*, 2004). However, detail sequencing of all these five fragments and further detection of single nucleotide polymorphisms (SNPs) through comparison of about 10 individuals with DNA sequence assembly and alignments will further confirm their utilization in population genetic analyses. This preliminary work is currently under process in our laboratory.

Acknowledgments: We thank the Department of Science and Technology, Government of India for an extramural research project to SM. We also thank the Vice Chancellor, JIITU for extending facilities in the department for carrying out research on *Drosophila*.

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Endemic inversions in Brazilian populations of *Drosophila melanogaster*.

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Introduction

Drosophila melanogaster is a cosmopolitan species with a very large area of distribution (Keller, 2007). It is natural that, exploiting a wide range of climatic conditions, *D. melanogaster* exhibits a large variability in morphologic and genetic characters. One such character is chromosomal inversion polymorphism (Krimbas and Powell, 1992; Lemeunier and Aulard, 1992; Powell, 1997). *D. melanogaster* chromosomal inversions can be categorized as cosmopolitan (common and rare) and endemic (recurrent and unique), depending on the geographical distribution and frequency (Mettler *et al.*, 1977). Cosmopolitan inversions are those that have been observed in populations from all parts of species' geographical range. Endemic inversions are geographically restricted. Recurrent endemic inversions are observed more than once in a given population or may be observed in adjacent populations, while unique endemic inversions are observed only in a single individual from a single population (Mettler *et al.*, 1977). Inoue and Igarashi (1994) also described recurrent inversions as `polymorphic endemics'. Comparisons of the endemic inversions found by