and J.R. David 2004, Funct. Ecol. 18: 700-706; Crumparker, D.W., 1974, The American Midland Naturalist 91: 118-129; David, J.R., R. Allemand, J. Van Herewege, and Y. Cohet 1983, Ecophysiology: abiotic factors. In: *The Genetics and Biology of* Drosophila (Ashburner, M., H.L. Carson, and J.N. Thompson, jr., eds.). Vol. 3d, pp. 105-170, Academic Press, London; David, J.R., P. Gibert, and B. Moreteau 2004, Evolution of reaction norms. *Phenotypic Plasticity: Functional and Conceptual Approaches* (De Witt, T.J., and S.M. Scheiner, eds.), pp. 50-63. Oxford University Press, Cary, NC; French, V., M. Feast, and L. Partridge 1998, J. Insect Physiol. 44: 1081-1089; Hegde, S.N., and M.S. Krishna 1999, Curr. Sci. 77: 178-179; Hoffmann, A.A., J.G. Sorensen, and V. Loeschcke 2003, J. Therm. Biol. 28: 175-216; James, A.C., and L. Partridge 1995, J. Evol. Biol. 8: 315-330; Lefranc, A., and J. Bundgaard 2000, Hereditas 132: 243-247; Obradović, T., S. Pavković-Lučić, and V. Kekić 2007, Growth temperature, duration of development, preadult viability and body size in *Drosophila melanogaster*. Dros. Inf. Serv. 90: *in press;* Partridge, L., A. Hoffmann, and J.S. Jones 1987, Anim. Behav. 35: 468-476; Pavković-Lučić, S., and V. Kekić 2006, Period. Biol. 108: 81-84; Prakash, S., 1967, Genetics 57: 655-663; Precht, H., J. Christophersen, and H. Hensel 1955, Temperatur und Leben. Springer. Berlin; Rose, M.R., H.B. Passananti, and M. Matos (eds.) 2004, *Methuselah Flies: A Case Study in the Evolution of Aging*. Word Scientific Publishing, Singapore; Singh, S.R., and B.N. Singh 2004, Curr. Sci. 86: 465-470; Terzić, T., M. Andjelković, and M. Stamenković-Radak 1994, Dros. Inf. Serv. 75: 164; Trotta, V., F.C.F. Calboli, M. Ziosi, D. Guerra, M.C. Pezzoli, J.R. David and S. Cavicchi 2006, BMC Evol. Biol. 6: 67.

Amplifications of orthologous DNA fragments in three *Drosophila* species endemic to India.

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The footprint of evolution is very often reflected at the molecular organisation in the closely related taxa (Takano, 1998). Such footprints can easily be traced by the identification of conserved DNA sequences across different taxa (otherwise known as orthologous DNA fragments). These conserved DNA sequences can then be utilized to reconstruct phylogenetic positions of these taxa (Goodstadt and Ponting, 2006) and to infer detailed evolutionary history of a group of closely related taxa. Thus, much attention has been paid in recent years to use of single-locus homologous DNA markers for these kinds of study. However, it has been shown that evolutionary history reconstruction through the use of multilocus DNA fragments provides robust inference to this aspect (Kopp and Barmina, 2005).

To this respect, the model organism *Drosophila* has been used to test this hypothesis in great detail. Since wide varieties of *Drosophila* species are sympatric to many tropical habitats of the globe, it is interesting to understand evolutionary history of these species and thus to correlate with ecological adaptations. Evolutionary history inferred from multilocus DNA fragments, that too using putatively neutral markers are especially important, as demographic events related to species differentiation could be inferred baring the effect of natural selection. *Drosophila* species, due to manifold advantages for use in both classical and molecular genetic work, are organisms of choice to test the differential evolutionary hypotheses and also the role of different evolutionary forces in speciation.

India harbours a wide range of *Drosophila* species. Species that are found in domestic or semi-domestic areas are often common. Among these, three different species of *Drosophila* are of fairly common in occurrence in the wild; *Drosophila ananassae*, *D. malerkotliana* and *D. melanogaster*. While the first species is fairly common in almost all seasons, *D. malerkotliana* is widely available for collection during rainy season of the year and *D. melanogaster* during winter. However, the latter species is becoming rare in the wild in India. Ecologically, *D. melanogaster* and *D. ananassae* almost utilize a similar food resource and both are found to be strictly domestic, while *D. malerkotliana* is semi-domestic and mostly seen in orchards, gardens, and places just close to human habitation, but rarely inside houses. Thus, while the almost-common ecological habitat of all the three species in India provides an opportunity to understand similarities at the DNA level, it is of high interest, on the other hand, to look for genetic dissimilarities as well, by which each have adapted to different ecological, seasonal conditions in India.

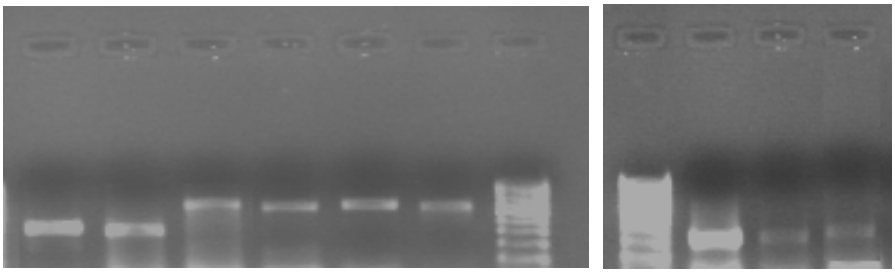

Figure 1. Agarose-gel electrophoretic pictures showing three PCR-amplified nuclear DNA fragments in the genomic DNA of three species of *Drosophila* endemic to India. L = 100 base pair DNA ladder; M1 to M 3 = *D. malerkotliana* DNA fragment no. 1 to 3; A1 to A3 = *D. ananassae* DNA fragment no. 1 to 3; ME1 to ME3 = *D. melanogaster* DNA fragment no. 1 to 3.

The present study, a part of the long-term genomic understanding of speciation history of common *Drosophila* species in India focuses on identifying common nuclear DNA fragments and utilizes these markers to understand evolutionary history of these species in India. To initiate such a kind of study, we have utilized the whole genome sequence information (Adams *et al.*, 2000) of *D. melanogaster* to design primers in the coding regions of different genes (exon parts) to amplify the flanking non-coding introns. As stated above, such types of DNA fragments serve as putatively neutral nuclear DNA markers (Das *et al.*, 2004). We have designed as many as 20 primer pairs based on the *D. melanogaster* whole genome sequence information of the X-chromosome and could successfully amplify only three fragments in all the three species so far (Figure 1). Considering a large reported divergence time among these three species (Kopp and Barmina, 2005), the data on the low amplification rate of DNA fragments across three different species is not surprising, even though the primers are designed in the coding regions of the genome. These fragments will further be sequenced followed by sequence alignments and phylogenetic tree construction which is in process in this laboratory.

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Reference: Adams, M.D. *et al.*, 2000, Science 287: 2185-2195; Das, A., S. Mohanty, and W. Stephan 2004, Genetics 168: 1975-1985; Goodstadt, L., and C.P. Ponting 2006, PLoS Comp. Biol. 2(9) e133; Kopp, A., and O. Barmina 2005, Genet. Res. 85: 23-46; Takano, T.S., 1998, Genetics 149: 959-970.