



Category: Bioinformatics

Is ecological source important in phylogenomics analysis: a pilot study involving 17 *Drosophila* species using multilocus approach

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Abstract

For over a century, the fruit fly *Drosophila* has accomplished itself as a resourceful experimental model organism in the field of biological research. It has a long history of being scrutinized by biologists for evolutionary studies either through cytogenetic, phylogenetic or comparative genomics analysis. Next Generation Sequencing (NGS) technologies are also bringing a revolutionary shift in phylogenetic exploration as now whole genome can be utilized for the analysis. The goal of the present study is to examine the robustness of the molecular markers which are frequently been employed in resolving the phylogeny of *Drosophila* genus. Ten protein coding nuclear loci were utilized to infer the phylogenetic relationships across 17 taxonomically known species including four Indian *Drosophila* and one *Zaprionus* species as outgroup in the present study, including *Adh*, *Amy-p*, *Cypc*, *Gld*, *Gpdh*, *IARS*, *Marf*, *per* and *tim* and *Xdh*. The DNA sequences of selected nuclear genes in four Indian *Drosophila* and *Zaprionus* species were retrieved from whole genome sequences (WGS) generated by us through Next Generation Sequencing Technology on Illumina platform. The selected genes were predicted using Augustus as gene prediction program. Neighbour joining, Maximum likelihood and Bayesian phylogenetic methods were employed in order to reconstruct and compare the evolutionary history. Our phylogenetic trees reconstructed using *Adh*, *Amy*, *Gld*, *Gpdh*, *Xdh* shows results which were in concordance with previous studies as Indian species were placed closer with their respective group/ subgroups members. However, phylogenies obtained using *Marf*, *Cypc*, *IARS*, *per* and *tim* genes showed that Indian species were forming a separate clade rather than occupying their own taxonomical position, thereby, confirming their close evolutionary relationship. This could be due to the ecological factors that are bringing remarkable variation in the sequence of these marker genes. So, the present study reveals that ecological origin of the study species should be contemplated while ascertaining its phylogenetic positions.

References

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