



Category: Animal genomics

A study on climatic adaptation of dipteran mitochondrial protein coding genes

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Abstract

Diptera, the true flies are frequently found in nature and their habitat is found all over the world including Antarctica and Polar Regions. The number of documented species for order diptera is quite high and thought to be 14% of the total animal present in the earth [1]. Most of the study in diptera has focused on the taxa of economic and medical importance, such as the fruit flies *Ceratitis capitata* and *Bactrocera spp.* (Tephritidae), which are serious agricultural pests; the blowflies (Calliphoridae) and oestrid flies (Oestridae), which can cause myiasis; the anopheles mosquitoes (Culicidae), are the vectors of malaria; and leaf-miners (Agromyzidae), vegetable and horticultural pests [2]. Insect mitochondrion consists of 13 protein coding genes, 22 tRNAs and 2 rRNAs, are the remnant portion of alpha-proteobacteria is responsible for simultaneous function of energy production and thermoregulation of the cell through the bi-genomic system thus different adaptability in different climatic condition might have compensated by complementary changes in the both genomes [3,4]. In this study we have collected complete mitochondrial genome and occurrence data of one hundred thirteen such dipteran insects from different databases and literature survey. Our understanding of the genetic basis of climatic adaptation in diptera is limited to the basic information on the occurrence location of those species and mito genetic factors underlying changes in conspicuous phenotypes. To examine this hypothesis, we have taken an approach of Nucleotide substitution analysis for 13 protein coding genes of mitochondrial DNA individually and combined by different software for monophyletic group as well as paraphyletic group of dipteran species. Moreover, we have also calculated codon adaptation index for all dipteran mitochondrial protein coding genes. Following this work, we have classified our sample organisms according to their location data from GBIF (<https://www.gbif.org>). Finally, result suggests that dipteran insects from different regions are gone through distinct selection process and even our outcome also indicate that dipteran mitochondrial genes from different climatic condition shows differential efficacy in their translation process.

References

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