International Journal of Entomology Research
www.entomologyjournals.com
ISSN: 2455-4758
Received: 23-04-2022, Accepted: 08-05-2022, Published: 24-05-2022
Volume 7, Issue 5, 2022, Page No. 103-105

Phylogenetic analysis of *Luciola cruciata* and *Luciola curtithorax* using whole mitochondrial genome sequence

Ayush Baral
Department of Genomic Science, Central University of Kerala, India

Abstract

Mitochondrial genome sequences as well as their comparative analysis is important from evolutionary point of view and plays a crucial role in species identification and also can be used to monitor populations. In this study comparative mitochondrial genome analysis of two fireflies which belongs to the same genus viz., *Luciola cruciata*and Luciola curtithorax is provided. The detailed comparative analysis of mitochondrial genome of *Luciola cruciata*and Luciola curtithorax provides information of mitochondrial genome organization in both species and gives overview of variation between the both species. This study provides a useful benchmark for further study on firefly mitochondrial genome evolution and their comparative analysis.

Keywords: mitochondrial genome, *Luciola Cruciata*, luciola curtithorax, firefly, phylogeny

Introduction

Mitochondrial genome is a reach source to study evolutionary history of any organism. Due to genome rearrangement property, mitochondrial genome is become role model to study evolution and evolution related studies (Sankoff *et al*. 1992) [1]. This fundamental principle is become so useful to understand biological consequence of firefly's evolution. Fireflies are members of the Lampyridae family, which includes more than 2000 species (Ohba 2004, Lewis 2016) [2, 3] and 100 genera (Lewis & Cratsely 2008; Han *et al*. 2020) [5]. hence it is very important to understand the evolutionary pattern of firefly so that some crucial data can be extracted from the evolutionary history which will be helpful for further study. Firefly mitochondrial genome is very much important to study phylogeny and evolutionary consequences of firefly evolution. Since fireflies are widely used in biomedical researches in current times (Ayush Baral. 2022) [6] hence by studying the consequences of firefly evolution we can forward any type of information which will become useful in further research. Not only in biomedical field, fireflies also used in drug designing, technological advancement and innovation (Banu *et al*. 2017) [7] and also in toxicological studies (Trajkovska *et al*. 2005) [8].

High rate of nucleotide substitution in mitochondrial genome makes it extremely important from evolutionary point of view (Wise *et al*. 1997). Depending on this phenomenon comparative analysis can provide some important information to solve issues related with evolutionary study and population genetics. Through this type of comparison of mitochondrial genome it becomes easy to understand evolutionary dynamics and pattern of evolution. As well as, information collected from this type of study can be used in population genetics study.

In this study, comparative analysis of mitochondrial genome of two fireflies belonging to the same genus, viz., *Luciola cruciata*(LCR), and Luciola curtithorax (LCU) is put forwarded to understand the pattern of evolutionary dynamics. This study also revealed the evolutionary background and phylogeny of these two fireflies.

Method and Materials

Genome Sequence

For comparative analysis of mitochondrial genome sequence of LCR and LCU were downloaded from NCBI. Along with *Luciola cruciata*and Luciola curtithorax other eight fireflies and a suitable out-groups mitochondrial genome were taken for phylogenetic study.

Data Analysis

MEGA 10 (Tamura *et al*. 2006) is used to construct the phylogenetic tree in this comparative study.

Result

To construct phylogenetic tree, ten fireflies and one out-group's mitochondrial genomes were taken. Using the mitochondrial genome of *Luciola cruciata*(NC_022472.1), Sclerotia substriata (NC_027176.1), Luciola curtithorax (NC_038225.1), Aquatica lateralis (NC_035755.1), Pyrocoelia rufa (NC_003970.1), Aquatica lei (NC_025276.1), Pyrocoelia praetexta (NC_044790.1), Pyrocoelia thibetana (NC_044792.1), Curtos bilineatus

(NC_044789.1), and Hotaria unmunsana (NC_050947.1) phylogenetic tree is constructed to demonstrate the evolutionary history. Plexippus paykulli is used as out-group.

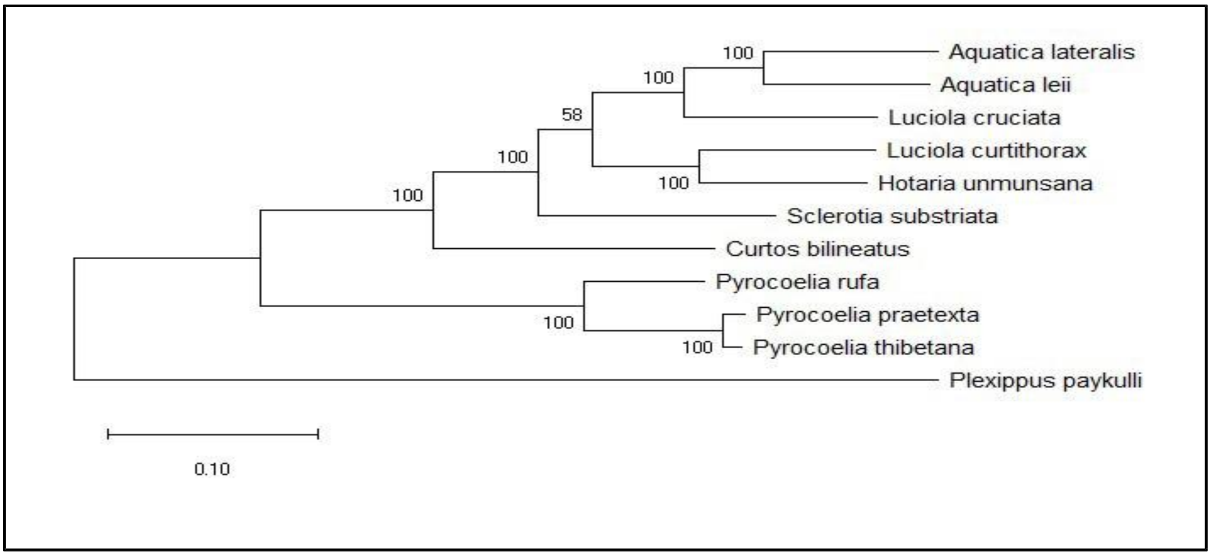

Fig 1: Phylogenetic tree depicting the mitochondrial genome of Luciola cruciata, Sclerotia substriata, Luciola curtithorax, Aquatica lateralis, Pyrocoelia rufa, Aquatica lei, Pyrocoelia praetexta, Pyrocoelia thibetana, Curtos bilineatus, Hotaria unmunsana and an out-group Plexippus paykulli. Tree was constructed in MEGA 10 with 1000 bootstrap value.

Discussion

In this study two fireflies' viz., *Luciola cruciata*(LCR) and luciola curtithorax (LCU) were chosen and through comparative analysis tried to find out convergence and divergence in mitochondrial genome of both firefly species.

In preliminary observation, phylogenetic tree shows that *Luciola cruciata*is closes to Aquatica leii followed by Aquatica lateralis and both the species belongs to different genus. On the other hand Luciola curtithorax is close to Hotaria unmunsana and it also belongs to different genus. Through evolutionary analysis we can conclude that *Luciola cruciata*is distantly related to Luciola curtithorax. Though both species taken in our study belongs to the same genus, yet divergence is present in genome (Fig 1). The result of this analysis clearly indicates that the evolution of firefly mitochondrial genome is independent with respect to other species of same genus.

Conclusion

In summary, the results of this analysis indicated that mitochondrial genome of *Luciola cruciata*and Luciola curtithorax has variations that allow them to be separated on a phylogenetic tree. In phylogenetic analysis this variation plays a critical role, hence analysed species which are belonging to same genus shows close relatedness with those fireflies which belongs to entirely different genus. Overall, our study gives idea about mitochondrial genome analysis and its importance in evolutionary studies.

Acknowledgment

Guidance throughout this research and computational facility for bioinformatic analysis was provided by Dr. Tony Grace, Assistant professor, Dept. of Genomic Science, Central University of Kerala, India.

Reference

1. Sankoff, David. "Gene order comparisons for phylogenetic inference: evolution of the mitochondrial genome." Proceedings of the National Academy of Sciences,1992:89(14):6575-6579.
2. Ohba N. "Mystery of fireflies." Yokosuka City Museum, Yokosuka (2004, in Japanese), 2004.
3. Lewis, Sara. Silent sparks: the wondrous world of fireflies. Princeton University Press, 2016.
4. Lewis, Sara M., and Christopher K. Cratsley. "Flash signal evolution, mate choice, and predation in fireflies." Annu. Rev. Entomol,2008:53:293-321.
5. Han, Taeman, *et al*. "Evolutionary history of species of the firefly subgenus Hotaria (Coleoptera, Lampyridae, Luciolinae, Luciola) inferred from DNA barcoding data." Contributions to Zoology,2020:89(2):127-145.
6. Ayush Baral. Firefly: Its importance and an inspiration for innovations. International Journal of Entomology Research,2022:7(4):126-127
7. Banu, PK Nizar, Ahmad Taher Azar, Hannah Inbarani H. "Fuzzy firefly clustering for tumour and cancer analysis." International Journal of Modelling, Identification and Control,2017:27(2):92-103.

8. Trajkovska, Snezana, *et al*. "Bioluminescence determination of enzyme activity of firefly luciferase in the presence of pesticides." Luminescence: The journal of biological and chemical luminescence,2005:20(3):192-196.
9. Wise, Cheryl A. "Comparative nuclear and mitochondrial genome diversity in humans and chimpanzees." Molecular Biology and Evolution,1997:14(7):707-716.
10. Tamura, Koichiro. "MEGA6: molecular evolutionary genetics analysis version 6.0." Molecular biology and evolution,2013:30(12):2725-2729.