Review

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Heca Journal of Applied Sciences

Vol. 1, No. 2, 2023

A Review on Mitochondrial Genome of Ants (Hymenoptera: Formicidae)

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Article History

Received 9 August 2023
Revised 3 September 2023
Accepted 14 September 2023
Available Online 19 September 2023

Keywords:
Ants
Mitochondrial genome
Genetic diversity
Evolutionary dynamics
Ecological interactions
Evolution
Physiology

Abstract

Ants, which are members of the Formicidae family, have been the subject of considerable scientific scrutiny due to their remarkable diversity and ecological importance. Extensive research endeavors have been directed towards understanding the complex behaviors and ecological responsibilities exhibited by these organisms. The advent of cutting-edge sequencing technology in recent times has sparked a significant breakthrough in the deciphering of mitochondrial genomes in many animals, including ants. The objective of this review paper is to provide an informative summary of the mitochondrial DNA of ants. Exploring the intricate structural aspects, we investigate the genetic diversity that exists in the mitochondrial genomes of ants. The investigation of evolutionary processes provides insight into the complex alterations that have shaped genomes throughout time. The broader ramifications of these genetic differences for the fields of ant biology and conservation are thoroughly considered. An examination is conducted on the structural characteristics, genetic variations, and evolutionary features of ant mitochondrial genomes, along with an investigation into their physiological impacts. As the molecular complexities of ant mitochondrial genomes are revealed, there is an opportunity to further explore their realm, leading to a more comprehensive comprehension of these extraordinary organisms.

1. Introduction

Ants (family Formicidae) are a remarkable and exceptionally diverse group of insects that have captivated the interest of scientists and nature advocates [1–4]. Ants exemplify a success story in the domain of terrestrial life, with more than 9,500 recognized species and an estimated total species diversity of well over 20,000 [5, 6]. Their ecological importance is unparalleled, as they perform essential roles in ecosystems. Ants undertake a wide array of roles, encompassing activities from promoting soil health and facilitating nutrient cycling to dispersing seeds and preying upon other arthropods [2, 4, 6–8].

The field of genomics has significantly transformed our understanding of the biological and evolutionary aspects of various organisms, including ants. The mitochondrial genome has emerged as a valuable instrument for investigating evolutionary histories, comprehending population genetics, and exploring ecological interactions among the genomic components of particular interest [9–17].

Mitochondrial DNA (mtDNA) is a distinctive type of genetic material found in the mitochondria of cells. Unlike nuclear DNA, which is a combination of genetic material from both parents, mtDNA is solely inherited maternally [18, 19]. Its unique characteristics, such as compressed size, rapid evolutionary rate, and lack of recombination, have rendered it an indispensable molecular marker for a wide range of phylogenetic and ecological studies [20–24].

In recent years, the introduction of next-generation sequencing technologies has facilitated the elucidation of complete mitochondrial genomes from numerous ant species. This is providing researchers with a treasure trove of data to explore the genetic complexities that govern their biology [24–28]. These exhaustive genomic datasets have not only increased our understanding of ant evolutionary relationships, but also opened new research avenues into the functional implications of mitochondrial genes and their significance to ant biology and conservation [20, 24, 25, 29].

This article intends to provide a comprehensive summary of the current state of knowledge concerning the mitochondrial genome of ants. We will examine the structural characteristics, genetic diversity, and evolutionary aspects of ant mitochondrial genomes, as well as the functional ramifications of these genomes on the physiology of ants.

2. Structural Features of Ant Mitochondrial Genomes

In terms of gene content and organization, the mitochondrial genome of ants exhibits a high degree of conservation, but it also displays intriguing variations that shed light on their evolutionary history and adaptive traits [29–32]. The mitochondrial genome of ants is typically a circular molecule ranging in size from 15.2 to 19.7 kilobases (kb) [32, 33]. It contains 37 genes, consisting of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), and two ribosomal RNA genes (rRNAs), as shown in Figure 1 [32, 34, 35]. These genes collectively contribute to the mitochondrial process of oxidative phosphorylation, which is essential for energy production [36–39]. These genes exhibit a degree of similarity not only within ants, but also among other insect species.

Within the Formicidae, the gene arrangement in ant mitochondrial genomes is relatively conserved [29, 35, 40]. The standard arrangement of genes, also known as the ancestral gene order, has been identified in a number of ant species and represents the typical organizational structure [26, 41]. Nonetheless, occasional gene duplications and rearrangements have been observed in specific lineages, suggesting that structural alterations in the mitochondrial genome may contribute to the evolutionary diversification and adaptation of ants [29, 35, 42]. Variation in gene size, especially among protein-coding genes, is a remarkable aspect of the mitochondrial genomes of ants [29, 32, 43].

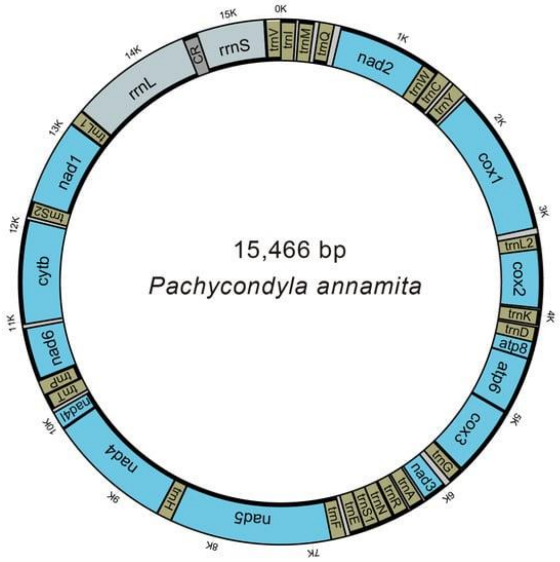

Figure 1. Organization of the mitochondrial genome of *Pachycondyla annamita* [35].

In addition, comparative analyses of mitochondrial genomes have revealed that certain ant lineages have a higher frequency of nonsynonymous substitutions in protein-coding genes. These nonsynonymous changes can affect the functional properties of proteins, suggesting that natural selection may have influenced the evolution of ant mitochondrial genes, potentially as a result of adaptations to particular ecological niches or physiological requirements [27, 29, 41, 42, 44].

Furthermore, the control region, also known as the D-loop, regulates the replication and transcription of mitochondria [45–48]. It has a high level of nucleotide variability, which makes it a useful marker for ant population genetics and phylogeography research. The D-loop region has been utilized extensively in studies aimed at resolving phylogenetic relationships among ant species and evaluating patterns of genetic diversity and differentiation within ant populations [24]. In general, the structural characteristics of ant mitochondrial genomes shed light on the evolutionary processes that shaped these ecologically diverse insects.

3. Genetic Diversity and Phylogenetic Relationships

The investigation of mitochondrial genomes has played a crucial role in the reconstruction of phylogenetic relationships among ant species and the clarification of their evolutionary history [41, 42, 49]. The study of ants and their evolutionary links poses an interesting challenge due to their extensive diversity and ecological adaptations. To tackle this complexity, researchers have turned to mitochondrial DNA as a valuable tool [27, 29, 41, 44, 50–52].

Mitochondrial markers, such as the cytochrome c oxidase

Subunit I (COI) gene, have been extensively utilized in DNA barcoding investigations for the purpose of identifying ant species. This methodology has greatly aided the expeditious and precise identification of species, rendering it an indispensable instrument for ecological and taxonomic investigations [53–55]. Furthermore, the utilization of mitochondrial sequences has been widely employed in the deduction of evolutionary links between various ant species, hence enhancing our comprehension of their evolutionary history and biogeography [26, 29, 41]. Phylogeographic investigations utilizing mitochondrial markers have provided valuable insights into the dynamics of ant populations and the occurrence of dispersal events throughout history [11, 56–59].

Furthermore, the utilization of mitochondrial genomics has been employed to examine higher-level relationships within the Formicidae family, in addition to resolving ties at the species level. Recent research utilizing a mix of mitochondrial and nuclear markers has yielded valuable insights into the evolutionary relationships across various subfamilies and tribes within the ant species [29, 32, 60]. The aforementioned findings have resulted in the modification of ant classification and enhanced our comprehension of their evolutionary connections. For example, the *Atta* genus analyzed using mitochondrial partial sequences (COI, tRNA leucine, and COII) in 2009 could be better clarified phylogenetically among its species when using the mitochondrial genome 10 years later [32].

The examination of mitochondrial DNA has played a crucial role in uncovering the genetic variability and evolutionary connections within ant species. Ant mitochondrial genomes have provided significant molecular insights, contributing to a deeper comprehension of their evolutionary trajectory [29, 41, 61, 62]. Furthermore, these findings have advanced the fields of taxonomy, ecology, and conservation.

4. Functional Implications of Ant Mitochondrial Genes

The mitochondrial genome of ants plays a pivotal role in providing essential cellular functions, primarily centered around energy production and regulation. It has been known in general that through oxidative phosphorylation, mitochondria generate adenosine triphosphate (ATP), the primary energy currency of cells, crucial for powering various physiological processes [63–66].

4.1. Energy Production and Metabolism

The principal role of the mitochondrial genome is to encode essential constituents of the electron transport chain (ETC) and the ATP synthase complex. The Electron Transport Chain (ETC) is comprised of several protein complexes that are encoded by genes located in the mitochondria. Its primary function is to promote the movement of electrons and protons across the inner mitochondrial membrane, thereby producing a gradient of protons [67–69]. The ATP synthase complex utilizes the proton gradient to facilitate the synthesis of ATP, thereby meeting the energy requirements of the cell [65, 70]. Ants, as organisms that exhibit high levels of activity and efficiency, necessitate significant amounts of energy to engage in foraging, constructing nests, and executing intricate social actions. Thus, the mitochondrial genome and its functional components play a crucial role in supplying the requisite energy resources to support these demanding operations.

4.2. Oxidative Stress Management

Mitochondria are the primary source of reactive oxygen species (ROS), which are natural byproducts of cellular respiration [71]. The mitochondrial genome also encodes several antioxidant enzymes that help mitigate oxidative stress [72–74]. Two genes (Prx3 and Sod2) in the mitochondria of parthenogenic ant *Platythyrea punctata* are reported to express antioxidant enzymes (Peroxiredoxin 3 and Superoxide dismutase 2, respectively) [75].

The balance between ROS production and antioxidant defenses is critical for cellular health and longevity [76]. Ants living in challenging environments, such as those exposed to pollutants or extreme temperature fluctuations, may experience increased oxidative stress, making the functionality of mitochondrial genes involved in antioxidant pathways vital for their survival and well-being.

Overall, the mitochondrial genome of ants serves a broader purpose beyond its primary function in energy generation and oxidative stress regulation. The operation of mitochondrial genes is intricately linked to the energetic requirements of ants' intricate lifestyles and the ecological obstacles they encounter. As the comprehension of the functional significance of mitochondrial genes in ants expands, significant insights are acquired regarding the complex interrelationships between genetics and physiology that contribute to the biological characteristics of these social insects.

5. Future Prospects

The study of the mitochondrial genome in ants has made significant strides in advancing our understanding of their biology and evolution. Looking ahead, several future prospects and challenges lie ahead in this exciting field of research. The future prospects of studying the mitochondrial genome in ants are promising, offering vast potential for unraveling the mysteries of ant biology and evolution.

6. Conclusions

Ants exhibit a remarkable level of diversity and ecological prowess, making them a topic of considerable scientific fascination. The use of next-generation sequencing technology has greatly enhanced our comprehension of mitochondrial genomes in diverse organisms, including ants. The examination of ants and their evolutionary connections is a compelling endeavor, given their significant range of variations and ecological adaptations. To address this intricate issue, researchers have turned to mitochondrial DNA as a valuable tool.

Author Contributions: Conceptualization, B.J.K.; methodology, B.J.K.; validation, T.E.T.; formal analysis, B.J.K.; investigation, B.J.K.; resources, B.J.K.; data curation, B.J.K.; writing—original draft preparation, B.J.K., R.K. A.H.A. and J.M.E.M.; writing—review and editing, B.J.K. and T.E.T; visualization, B.J.K.; supervision, T.E.T., R.K. and J.M.E.M.; project administration, T.E.T.; funding acquisition, T.E.T. All authors have read and agreed to the published version of the manuscript.

Funding: The authors wish to express their gratitude to the Ministry of Education, Culture, Research, and Technology of the Republic of Indonesia for their support through the Doctoral Dissertation Research scheme, as facilitated by Master Contract No. 158/E5/PG.02.00.PL/2023 dated 19 June 2023, along with its subsequent Derivative Contract, No. 1803/UN12.13/LT/2023 dated 27 June 2023.

Data Availability Statement: The data used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Conflicts of Interest: The authors declare no conflict of interest.

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