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# Insect Mitochondrial Genomics: Structure, Evolution and Applications in Phylogeny and Pest Management

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## ABSTRACT

Insect mitochondrial genomics is an important tool for investigating genome organisation, evolutionary relationships and applications in pest management. Insects possess compact mitochondrial genomes of approximately 15–18 kb, encoding 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs and a non-coding control region. These genomes are maternally inherited, show limited recombination and evolve rapidly, making them informative for phylogenetic and comparative studies. Advances in next-generation sequencing have greatly increased the availability of complete insect mitochondrial genomes, revealing variation in genome structure, including gene rearrangements, nucleotide compositional bias, control-region duplication and genome fragmentation. While these features provide useful phylogenetic signal, they may complicate deep-level inference. Mitochondrial genomics also supports species identification, detection of cryptic taxa, monitoring of invasive pests and insecticide resistance, contributing to pest management and biosecurity.

## INTRODUCTION

Insect mitochondrial genomics has become an important tool in evolutionary biology, systematics and applied entomology. Insects possess compact, circular mitochondrial genomes, typically 15–18 kb in size, encoding 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs and a non-coding control region (Cameron, 2014). These genomes are maternally inherited, evolve rapidly and show little recombination, making them highly informative for phylogenetic and comparative studies. Early research largely relied on single mitochondrial genes, particularly the COI gene used in DNA barcoding, which is effective for species identification but limited in resolving deeper evolutionary relationships (Hebert *et al*., 2003). The widespread adoption of next-generation sequencing technologies has greatly increased the availability of complete insect mitochondrial genomes, enabling large-scale comparative analyses. These studies have revealed substantial variation in genome organisation, including gene rearrangements, nucleotide compositional bias and, in some lineages, control-region duplication and genome fragmentation. While such features provide valuable phylogenetic signal at lower taxonomic levels, they may also complicate deeper phylogenetic inference. Beyond evolutionary research, insect mitochondrial genomics has important applications in pest identification, monitoring of invasive species and support of integrated pest management strategies (Cameron, 2014; Boore, 1997).

### Organisation and Structure of Insect Mitochondrial Genomes

Insect mitochondrial genomes are typically small, circular DNA molecules ranging from approximately 15 to 18 kb in length. Despite minor variation among taxa, they exhibit a highly conserved gene complement consisting of 37 genes, including 13 protein-coding genes, 22 transfer RNAs and two ribosomal RNAs, along with a non-coding control region. Most genes are encoded on one strand, although strand distribution may vary slightly among different insect lineages (Boore 1999). The control region, often referred to as the A+T-rich region, plays a key role in the initiation of replication and transcription and shows considerable length and sequence variability. Insect mitochondrial genomes generally display strong A+T nucleotide bias, which influences codon usage patterns and overall genome composition. Although the basic organisation is conserved, variations in gene order, particularly involving tRNA genes, are common and provide important insights into mitochondrial genome evolution and phylogenetic relationships (Zhang *et al*., 1997).

### Evolutionary Features of Insect Mitochondrial Genomes

Insect mitochondrial genomes exhibit a range of evolutionary features that reflect both functional constraints and lineage-specific adaptations. One of the most prominent characteristics is strong nucleotide compositional bias, typically towards adenine and thymine, which influences codon usage patterns and amino acid composition of mitochondrial proteins. Evolutionary rates among mitochondrial genes are not uniform, with protein-coding genes showing varying levels of selective pressure depending on their functional roles within the oxidative phosphorylation pathway. Gene rearrangements, particularly involving transfer RNA genes, are common in many insect lineages and are thought to arise mainly through tandem duplication and subsequent gene loss. These rearrangements can provide valuable phylogenetic signal at lower and intermediate taxonomic levels. However, evolutionary rate heterogeneity among lineages and compositional bias may obscure deeper evolutionary relationships (Cameron, 2014; Hassanin *et al*., 2005). Together, these features highlight the dynamic nature of insect mitochondrial genome evolution and underscore the need for careful analytical approaches in comparative and phylogenetic studies.

## Gene Rearrangements in Insect Mitochondrial Genomes

Gene rearrangements are a prominent feature of insect mitochondrial genomes and represent an important aspect of their structural evolution. Although the overall gene content remains conserved, changes in gene order, particularly involving transfer RNA genes, are frequently observed across diverse insect lineages. The most widely accepted mechanism explaining these rearrangements is the tandem duplication–random loss (TDRL) model, whereby gene blocks are duplicated and subsequently reduced through differential gene loss. In some cases, inversions and transpositions have also been reported, further contributing to genome reorganisation. Gene rearrangements often show clade-specific patterns and can therefore serve as synapomorphic characters in phylogenetic analyses (Boore, 1999; Cameron, 2014). However, the occurrence of multiple rearrangement events and convergence may complicate evolutionary interpretation. Despite these challenges, mitochondrial gene order remains a valuable source of phylogenetic information, particularly at species, genus and family levels, when used in combination with sequence-based data.

## Mitochondrial Genome Fragmentation and Control Region Duplication

Although most insects possess a single circular mitochondrial genome, several lineages exhibit unusual structural modifications, including genome fragmentation and duplication of the control region. Mitochondrial genome fragmentation involves the division of the genome into multiple mini-chromosomes and has been reported primarily in parasitic lice and a few related taxa. This rare phenomenon is thought to be associated with mitochondrial recombination and relaxed selective constraints, leading to increased structural variability. In contrast, duplication of the control region, which plays a central role in replication and transcription, has been documented in certain insect groups and may influence replication dynamics and mutation rates. Both fragmentation and control region duplication appear to have evolved independently in different lineages and provide valuable systems for studying mitochondrial genome plasticity (Cameron, 2014). These atypical features highlight the dynamic nature of insect mitochondrial genomes and contribute to our understanding of mitochondrial evolution beyond the canonical circular genome model.

## Mitochondrial Phylogenomics in Insects

The use of complete mitochondrial genomes has substantially improved phylogenetic analyses in insects. Unlike single-gene approaches, mitogenome-based studies integrate information from multiple protein-coding genes, RNA genes and genome architecture, resulting in more stable phylogenetic hypotheses. This approach has been particularly effective for resolving relationships within insect orders and among closely related taxa. Nevertheless, mitochondrial phylogenomics is not without limitations. Biases in nucleotide composition, unequal substitution rates and restricted lineage sampling can affect tree topology, especially when addressing deep evolutionary divergences. As a result, mitochondrial phylogenomic data are increasingly interpreted alongside nuclear genomic evidence (Cameron, 2014). Such integrative strategies help reconcile conflicting signals and provide a more reliable framework for understanding insect evolutionary history.

## Applications in Phylogeny and Pest Management

Mitochondrial genomics has become an essential resource for addressing both theoretical and practical questions in insect biology. In phylogenetic studies, mitochondrial genome data are widely applied to reconstruct evolutionary relationships, assess lineage divergence and refine taxonomic classifications across multiple hierarchical levels. The use of complete mitogenomes allows the integration of sequence-based characters with structural features, improving confidence in phylogenetic inference, particularly among closely related species and within insect families.

From an applied perspective, mitochondrial genomes play a critical role in pest management and agricultural biosecurity. Mitogenomic markers enable rapid species identification, which is especially important for detecting morphologically similar or cryptic pest species. They are also valuable for tracing the geographic origin, migration pathways and population connectivity of invasive insects. Furthermore, mitochondrial data contribute to studies on population genetics and demographic history, supporting the development of targeted control strategies. Increasingly, mitochondrial variation is being explored to understand patterns of insecticide resistance and adaptation to environmental pressures. Together, these applications demonstrate the importance of insect mitochondrial genomics as a bridge between evolutionary research and sustainable pest management practices.

## Limitations and Challenges

Despite the extensive use of mitochondrial genomes in insect research, several limitations and challenges remain. One major concern is strong nucleotide compositional bias, which can distort phylogenetic inference and lead to misleading evolutionary relationships. In addition, evolutionary rates often vary substantially among mitochondrial genes and across lineages, complicating comparative analyses. Mitochondrial DNA is maternally inherited and represents a single, non-recombining locus, which limits its ability to capture the full evolutionary history of species. Hybridisation and mitochondrial introgression may further obscure species boundaries and produce discordance between mitochondrial and nuclear phylogenies. Technical issues, including uneven taxon sampling, incomplete genome coverage and errors in genome assembly or annotation, also affect data reliability. These challenges highlight the need for cautious interpretation of mitochondrial data and emphasise the importance of integrative approaches that combine mitochondrial and nuclear genomic information for robust evolutionary and applied conclusions.

## Future Perspectives

Advances in sequencing technologies and bioinformatics are expected to further expand insect mitochondrial genomics. Improved genome assembly and annotation, along with broader taxon sampling, will enhance the reliability of comparative and phylogenetic analyses. Future studies are likely to increasingly integrate mitochondrial and nuclear genomic data to overcome current limitations and achieve more robust evolutionary inference. In applied entomology, mitogenomics will play a growing role in rapid pest detection, monitoring of invasive species and understanding climate-driven range expansion. These developments will strengthen the contribution of mitochondrial genomics to both evolutionary research and sustainable pest management.

## CONCLUSIONS

Insect mitochondrial genomics has emerged as a powerful framework for understanding genome structure, evolutionary patterns and practical applications in entomology. The compact and conserved nature of insect mitochondrial genomes, coupled with increasing availability of complete mitogenomes, has greatly improved phylogenetic resolution and comparative analyses at multiple taxonomic levels. Despite challenges such as compositional bias and limited resolution at deep evolutionary scales, mitochondrial data remain highly valuable when interpreted using appropriate analytical methods and integrated with nuclear genomic evidence. Importantly, mitochondrial genomics provides essential tools for species identification, detection of cryptic taxa and monitoring of invasive and economically important pests. Continued advances in sequencing technologies, improved genome annotation and integrative genomic approaches will further enhance the contribution of insect mitochondrial genomics to evolutionary research and sustainable pest management.

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