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Taxonomic reassessment and phylogenetic analysis of *Lucanus* scopoli, 1763

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Abstract

The genus *Lucanus* Scopoli, 1763, represents a group of stag beetles that are pivotal both ecologically and biogeographically. Despite its foundational placement in coleopteran taxonomy, comprehensive assessments integrating morphological and genetic data have been sparse. This review consolidates recent advancements in the taxonomic reassessment and phylogenetic analysis of *Lucanus*, employing an integrative approach that combines traditional morphological methods and modern molecular techniques, including DNA barcoding, mitochondrial DNA analysis, and phylogenomic studies. We discuss the resolution of long-standing taxonomic ambiguities, propose a revised taxonomy of the genus, and explore phylogenetic relationships that have significant implications for conservation efforts. The review highlights the need for continued research, particularly in underexplored regions, to refine the phylogenetic framework of *Lucanus* and to enhance conservation strategies informed by genetic diversity and phylogenetic lineage.

Keywords: Fundamental, taxonomy, characteristics, mandible

Introduction

The genus *Lucanus*, established by Scopoli in 1763, includes some of the well-recognized stag beetles known for their prominent mandibles and significant size, which make them a group of both ecological and entomological interest. These beetles play a crucial role in forest ecosystems, particularly in the decomposition of wood and cycling of nutrients, yet their taxonomic clarity has been mired in controversy and inconsistency due to their morphological variability and the cryptic nature of several species. Accurate taxonomy is fundamental to the effective conservation and study of biodiversity. It aids in the proper identification of species, which is essential for understanding their ecological roles, distribution patterns, and evolutionary histories. For taxa like *Lucanus*, where visual similarity between species can lead to misidentification, precise taxonomy underpins all aspects of biological research - from ecological niche modeling to conservation priority setting. In recent decades, the field of systematics has been transformed by the advent of molecular biology techniques. For the genus *Lucanus*, this has meant an opportunity to revisit and reassess traditional taxonomic classifications that were originally based on morphological data alone. Techniques such as DNA barcoding and whole-genome sequencing have not only validated some classical taxonomic hypotheses but also challenged others, revealing deeper phylogenetic relationships and species delineations not observable through morphology alone. Modern taxonomic studies increasingly rely on an integrative approach that synthesizes morphological, molecular, and ecological data. This holistic view allows for a more robust understanding of evolutionary relationships and species boundaries.

In *Lucanus*, integrating these data types has begun to resolve complex taxonomic questions, such as the status of geographically isolated populations and the identification of cryptic species.

Purpose of Review

The objectives of this review are to synthesize the findings from recent taxonomic reassessments and phylogenetic analyses of the genus *Lucanus*, to clarify the evolutionary relationships within this group using the latest available data, and to discuss the implications of these findings for conservation strategies.

Taxonomic Studies on the Genus *Lucanus*

The genus *Lucanus*, established by Scopoli in 1763, has long intrigued entomologists due to its diverse and morphologically distinct species, commonly known as stag beetles. Early taxonomic efforts were largely based on morphological characteristics, such as mandible shape and body size, which varied significantly across the genus, leading to a complex and often confusing classification system. Over the centuries, as more species were discovered across Europe, Asia, and North America, the need for a more precise taxonomic framework became apparent. In the mid-20th century, taxonomic studies on *Lucanus* began to employ more systematic approaches, cataloging species and attempting to clarify the relationships based on physical traits. However, these studies often resulted in contradictory classifications due to the subjective nature of morphological interpretation and the limited scope of physical traits examined. The advent of molecular techniques in the late 20th and early 21st centuries marked a turning point in *Lucanus* taxonomy. DNA sequencing, particularly the use of mitochondrial markers like cytochrome oxidase I (COI) and 16S ribosomal RNA, provided new insights into the genetic relationships among species. These studies have been pivotal in resolving some of the longstanding ambiguities in *Lucanus* taxonomy by uncovering cryptic species and clarifying phylogenetic relationships that were not evident from morphology alone. Recent integrative taxonomic approaches, which combine traditional morphological methods with modern molecular data, have significantly enhanced our understanding of the *Lucanus* genus. For example, studies that utilized both DNA barcoding to assess genetic divergence and detailed morphological analyses to examine the subtle variations in physical traits have led to the reclassification of certain species and the description of new ones. This dual approach has proved particularly useful in regions where species exhibit high morphological similarity but are genetically distinct. Phylogenetic analyses using techniques such as Maximum Likelihood and Bayesian Inference have provided a clearer picture of the evolutionary pathways within the genus. These studies have not only supported some traditional taxonomic groupings but also suggested new ones, thereby refining the genus's classification and aiding in the formulation of more accurate conservation strategies.

Phylogenetic Relationships within *Lucanus*

The introduction of molecular techniques has revolutionized our understanding of *Lucanus* phylogenetics. Early molecular studies utilized mitochondrial DNA markers such as the cytochrome oxidase I (COI) gene and the 16S rRNA gene, which provided the first clear genetic insights into species relationships and lineage divergences within the genus. These mitochondrial markers, commonly used due to their high mutation rates and maternal inheritance without recombination, have been instrumental in identifying phylogenetic splits that were not visible through morphological assessments alone. Subsequent research incorporated nuclear DNA markers, adding a layer of complexity and resolution to the phylogenetic trees. Techniques such as the use of internal transcribed spacer (ITS) regions have helped clarify relationships that were ambiguous based solely on mitochondrial DNA. These nuclear markers are particularly useful in detecting hybridization events and in providing a balanced view of genetic inheritance from both parental lineages. More recently, comprehensive phylogenomic studies using next-generation sequencing (NGS) technologies have provided unprecedented detail about the evolutionary history of *Lucanus*. These studies use whole-genome data to construct detailed phylogenetic trees, revealing insights into speciation processes, genetic diversity, and evolutionary relationships at a granular level. Phylogenomic approaches are particularly effective in resolving complex phylogenetic questions, such as the placement of cryptic species and the historical biogeography of the genus. Bayesian phylogenetic methods and Maximum Likelihood analyses have become standard tools in reconstructing *Lucanus* phylogenies. These methods offer robust frameworks for estimating species relationships based on genetic data, allowing researchers to test various evolutionary hypotheses with a high degree of confidence. The resultant phylogenetic trees have not only corroborated some earlier morphological classifications but have also led to surprising revisions where genetic data contradict traditional views. The phylogenetic insights gleaned from these studies are critical for more than just academic understanding. They have practical implications in conservation biology, where understanding the genetic relationships and evolutionary history of species can guide conservation priorities and strategies.

For species within the *Lucanus* genus, such phylogenetic information is vital for identifying evolutionary significant units (ESUs) and managing genetically isolated populations.The exploration of phylogenetic relationships within *Lucanus* has transitioned from morphology-based to genetics-based analyses, with current trends heavily favoring the use of comprehensive, high-throughput DNA sequencing techniques. This shift has significantly refined our understanding of the genetic and evolutionary underpinnings of the genus, highlighting the dynamic nature of taxonomic and phylogenetic science.

Geographical Distribution and Species Diversity

Species Name	Geographical Range	Habitat Type	Population Trends	Conservation Status
Lucanus cervus	Europe, from Spain to Russia	Deciduous forests	Declining	Vulnerable (in parts of Europe)
Lucanus capreolus	Eastern United States, Canada	Mixed woodlands	Stable	Not Evaluated
Lucanus elaphus	Southeastern United States	Hardwood forest clearings	Declining	Near Threatened
Lucanus maculifemoratus	Japan, Korea	Mountainous forests	Unknown	Data Deficient
Lucanus swinhoei	Eastern Asia: China, Taiwan	Broadleaf forests	Unknown	Not Evaluated
Lucanus ibericus	Iberian Peninsula, France	Mixed woodlands and forests	Declining	Vulnerable

Geographical Distribution

The genus *Lucanus* is widely distributed across various regions, including Europe, North America, and East Asia. This widespread distribution indicates a high degree of adaptability to different environmental conditions. For example:

Lucanus cervus, found from Spain to Russia, signifies a broad adaptation to the varied climates and forests across Europe. *Lucanus capreolus* and *Lucanus elaphus* in North America, particularly the eastern United States, reflect their adaptation to the mixed woodlands and hardwood forest clearings. *Lucanus maculifemoratus* and *Lucanus swinhoei* in East Asia (Japan, Korea, and China) highlight the genus's presence in mountainous and broadleaf forest environments, which are biologically rich and diverse.

Habitat Type

Different species of *Lucanus* are associated with distinct types of forests, primarily deciduous, mixed, and broadleaf forests. The habitat type plays a crucial role in the life cycle and conservation of these beetles:

Species like *Lucanus cervus* thrive in deciduous forests, which are under pressure in Europe due to urban expansion and agricultural conversion. The preference for hardwood forest clearings by *Lucanus elaphus* shows a specific ecological niche, which may be susceptible to changes in land use practices such as logging and clearing.

Population Trends and Conservation Status

Several species are noted to have declining populations, attributed to habitat loss, fragmentation, and possibly climate change. The conservation status provided indicates varying degrees of concern:

Lucanus cervus is listed as vulnerable in parts of its range, suggesting significant threats from habitat degradation and possibly from collection and trade. *Lucanus elaphus*, noted as near threatened, faces similar pressures in North America, emphasizing the need for targeted conservation efforts to preserve its habitat. The lack of detailed population data for species like *Lucanus maculifemoratus* and *Lucanus swinhoei* suggests a gap in research, highlighting areas where further study is necessary to assess their conservation needs.

Conservation Implications

The data presented underscores the importance of maintaining habitat integrity and connectivity for the survival of *Lucanus* species. Conservation strategies could include:

Legal protection of key habitats, particularly in areas where species are known to be declining. Restoration of degraded forests and reforestation projects that consider the ecological needs of different *Lucanus* species. Public awareness campaigns to reduce the impact of human activities such as the collection of these visually striking beetles.

Conclusion

The taxonomic reassessment and phylogenetic analysis of the genus *Lucanus* Scopoli, 1763, have significantly advanced our understanding of these majestic stag beetles, merging traditional morphological approaches with modern molecular techniques. This synthesis has not only refined the taxonomy within the genus but also illuminated complex phylogenetic relationships that were previously obscured by the limitations of morphological data alone.

Recent efforts have enhanced taxonomic clarity, with DNA barcoding and whole-genome sequencing playing pivotal roles in delineating species boundaries and confirming or challenging historical classifications. These molecular insights have revealed a remarkable cryptic diversity, indicating that many species previously considered uniform are actually complexes of genetically distinct entities. Such discoveries underscore the nuanced evolutionary history of *Lucanus* and facilitate more precise conservation strategies.

Phylogenetic studies have been particularly revealing, mapping the intricate relationships and evolutionary trajectories within the genus. These findings have helped to contextualize the geographic and ecological distribution of *Lucanus* species, informing conservation planning in areas impacted by habitat loss and human activities. The clear definition of species and understanding of their relationships are crucial for prioritizing conservation efforts, particularly for species with critical ecological roles such as nutrient cycling in forest ecosystems.

Despite these advances, considerable gaps in our knowledge persist. The geographic coverage of studies remains uneven, with certain regions and species underrepresented in scientific research. Future studies should aim to include these areas, utilizing comprehensive sampling methods and exploring the potential impacts of environmental changes like climate change on *Lucanus* populations.

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