

Integrating Ecology and Genomics to Understand Population Dynamics and Adaptive Evolution in the Saker Falcon

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Abstract This study systematically integrates the latest findings from field-based ecological surveys and genomic research to analyze the population dynamics and adaptive evolution of the Saker Falcon at both global and regional scales. The research encompasses ecological characteristics such as geographic distribution, breeding biology, diet composition, and migration patterns, as well as genomic findings on genetic structure, gene flow, signals of selection, and local adaptation. A case study comparing Mongolian and Central European populations reveals adaptive divergence shaped by distinct ecological environments and discusses its implications for conservation strategy development. The study aims to guide future Saker Falcon conservation research in optimizing monitoring frameworks, applying genomic technologies, and advancing adaptive management.

Keywords Saker Falcon; Population dynamics; Adaptive evolution; Genomics; Conservation biology

1 Introduction

The Saker Falcon (*Falco cherrug*) is a large, wide-ranging raptor distributed across Eurasia, from Central Europe to East Asia, and is recognized for its ecological role as a top predator in grassland and steppe ecosystems (Streetsky et al., 2018). Despite its broad range, the species has experienced dramatic population declines over recent decades, primarily due to habitat loss, prey depletion, electrocution, and unsustainable trapping for the global falconry trade, leading to its current classification as Endangered by the IUCN (Streetsky et al., 2018; Karyakin et al., 2023; Kovacs et al., 2023). Conservation efforts have been implemented in several countries, including artificial nest provision, habitat management, and legal protections, with varying degrees of success (Bagyura et al., 2023; Hohenegger, 2023; Zhang et al., 2024). Understanding the population dynamics and adaptive evolution of the Saker Falcon is crucial for effective conservation, as these processes underpin the species' resilience to environmental change and anthropogenic pressures (Zhan et al., 2013; Zinevich et al., 2023).

Integrating ecological field data with genomic analyses offers a comprehensive approach to raptor conservation. Field observations provide essential information on population size, breeding success, migration routes, and threats such as electrocution and poaching (Dixon et al., 2020; Karyakin et al., 2023; Zhang et al., 2024). Genomic data, including whole-genome sequencing and population genetic studies, reveal patterns of genetic diversity, population structure, hybridization, and adaptive traits that are not detectable through fieldwork alone (Nittinger et al., 2007; Zhan et al., 2013; Zinevich et al., 2023; Petrov et al., 2024). For the Saker Falcon, genomic studies have clarified taxonomic uncertainties, identified distinct lineages and ecotypes, and uncovered signatures of rapid evolution related to predatory adaptations and environmental stressors (Zhan et al., 2013; Zinevich et al., 2023; Petrov et al., 2024; Al-Ajli et al., 2025). The complementary use of these data sources enhances our understanding of migration, gene flow, and local adaptation, informing targeted management and reintroduction strategies (Zhan et al., 2013; Petrov et al., 2023; Zinevich et al., 2023; Petrov et al., 2024; Zhang et al., 2024).

This study aims to integrate the latest findings from field-based ecological research and genomic studies to assess global and regional population trends and the drivers of decline or recovery, analyze the genetic structure, diversity, and adaptive traits within and among populations, and propose an adaptive management framework to provide evidence-based support for the long-term conservation of the Saker Falcon.