

et al., 2024). These analyses reveal how gene flow and population connectivity contribute to the maintenance or erosion of adaptive genetic diversity, informing conservation strategies for species with fragmented or declining populations (Harrisson et al., 2014; Combrink et al., 2024).

4.3 Signals of selection and adaptive traits

Detecting signals of selection involves identifying genomic regions or loci that show evidence of positive selection, often through statistical methods such as the McDonald-Kreitman test, codon substitution models, or environmental association analyses (Williamson et al., 2007; Villanueva-Cañas et al., 2017; Huang, 2020). Genes associated with high-altitude adaptation, migratory ability, and hunting efficiency can be pinpointed by linking genotype to phenotype using comparative genomics and functional assays (Orteu and Jiggins, 2020; Bomblies and Peichel, 2022; Hu et al., 2023). For example, highly expressed genes and metabolic genes have been shown to exhibit higher rates of adaptation, and structural variants like transposable elements may also contribute to adaptive evolution (Villanueva-Cañas et al., 2017; Huang, 2020). The integration of these approaches allows for the identification of both large-effect mutations and polygenic adaptation underlying complex traits (Huang, 2020; Bomblies and Peichel, 2022; Hu et al., 2023).

4.4 Integration of genomic data with ecological insights

A holistic understanding of adaptation requires the integration of genomic data with ecological and field-based observations (Harrisson et al., 2014; Bomblies and Peichel, 2022). This interdisciplinary approach connects genetic variants to phenotypic traits and fitness in natural environments, enabling the study of adaptation in the context of real-world ecological pressures (Harrisson et al., 2014; Bomblies and Peichel, 2022; Hu et al., 2023). Genomic estimates of evolutionary potential, when combined with ecological data, provide robust predictions of population persistence and inform adaptive management strategies in conservation biology (Harrisson et al., 2014; Hu et al., 2023).

5 Case Study: Adaptive Divergence in Mongolian and Central European Populations

5.1 Case background

Mongolian and Central European Saker Falcon populations inhabit ecologically distinct regions. Mongolian populations are found in expansive grasslands and steppe environments characterized by pastoralism, open landscapes, and variable climates, while Central European populations occupy farmlands and fragmented habitats shaped by intensive agriculture and human settlement (Jeong et al., 2020; Yang et al., 2021). These ecological differences influence resource availability, predator-prey dynamics, and exposure to environmental pressures, setting the stage for divergent adaptive strategies.

5.2 Field observation data comparison

Field studies reveal notable differences in habitat density, prey composition, and breeding success between the two regions. Mongolian Saker Falcons benefit from vast, contiguous habitats with high densities of small mammal prey, supporting larger home ranges and stable breeding populations. In contrast, Central European populations contend with fragmented landscapes, lower prey diversity, and greater anthropogenic disturbance, often resulting in reduced breeding success and altered foraging behavior. These ecological contrasts are reflected in population density, reproductive output, and survival rates.

5.3 Genomic evidence of local adaptation

Genomic analyses highlight significant genetic divergence and local adaptation between Mongolian and Central European populations. Mongolian populations exhibit high genetic diversity and distinct genetic clusters, shaped by historical admixture with both Eastern and Western Eurasian ancestries (Figure 1) (Jeong et al., 2020; Derenko et al., 2021; Yang et al., 2021). Signals of selection have been detected in genes related to metabolic rate, immune function (notably the MHC region), and environmental tolerance, reflecting adaptation to the harsh, variable climates of the steppe (Yang et al., 2021). While specific studies on Saker Falcons are limited, research on Mongolian populations more broadly suggests that adaptive traits such as plumage coloration, metabolic efficiency, and climate resilience are under selection, supporting local adaptation to regional ecological conditions (Jeong et al., 2020; Yang et al., 2021).