5.4 Implications for conservation strategies

The observed adaptive divergence underscores the need for region-specific conservation strategies. For Mongolian populations, maintaining large, connected habitats and supporting traditional pastoral land use are critical for preserving genetic diversity and adaptive potential. In Central Europe, conservation should focus on mitigating habitat fragmentation, enhancing prey availability, and reducing anthropogenic pressures. Genetic monitoring and the integration of genomic data into management plans will help safeguard locally adapted lineages and ensure the long-term viability of Saker Falcon populations across their range (Jeong et al., 2020; Derenko et al., 2021; Yang et al., 2021).

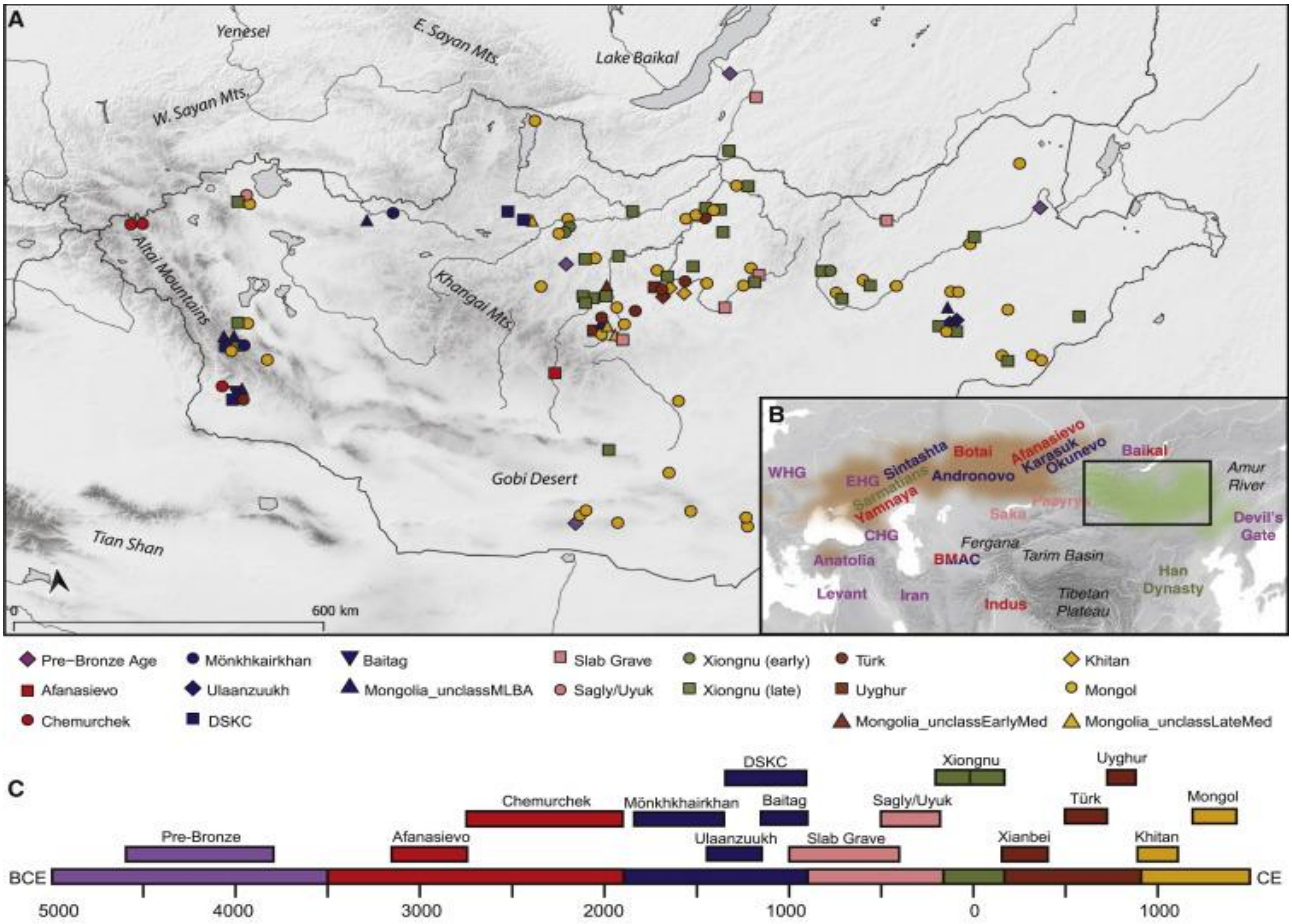

Figure 1 Overview of ancient populations and time periods (adopted from Jeong et al., 2020)

Image caption: (A) Distribution of sites with their associated culture and time period indicated by color: Pre-Bronze, purple; Early Bronze, red; Middle/Late Bronze, blue; Early Iron, pink; Xiongnu, green; Early Medieval, brown; Late Medieval, gold (see STAR Methods). See Figure S1A and Table S1B for site codes and labels; (B) Inset map of Eurasia indicating area of present study (box) and the locations of other ancient populations referenced in the text, colored by time period. The geographic extent of the Western/Central Steppe is indicated in light brown, and the Eastern Steppe is indicated in light green; (C) Timeline of major temporal periods and archaeological cultures in Mongolia. Site locations have been jittered to improve visibility of overlapping sites (Adopted from Jeong et al., 2020)

6 Integrative Analysis: Linking Ecology and Genomics

6.1 Correlating environmental variables with genetic markers

Ecological genomics leverages functional genomic approaches to identify genes and genomic regions associated with responses to specific environmental variables, such as temperature, habitat type, or resource availability (Ungerer et al., 2008; Katsikis et al., 2014). By analyzing correlations between environmental gradients and genetic markers, researchers can uncover the genetic basis of ecologically relevant phenotypic variation and adaptive traits (Ungerer et al., 2008; Katsikis et al., 2014). Statistical methods, such as multivariate analyses and environmental association studies, are commonly used to link environmental metadata with genomic data,