GENETIC DIVERSITY AND POPULATION STRUCTURE OF *JUNIPERUS SERAVSCHANICA* KOM. IN CENTRAL ASIA REVEALED BY MICROSATELLITE MARKERS

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Juniperus seravschanica Kom. is a widely distributed and significant tree species in Central Asia, thriving in the mountain ranges from Oman to Uzbekistan, Kyrgyzstan, and Kazakhstan. It plays a vital role in forming shrub-forest massifs in mountainous regions, contributing to soil drainage and stabilization at medium to high altitudes. To gain a detailed understanding of the current status of *J. seravschanica* and to develop effective conservation strategies, a comprehensive study of the species' genetic diversity and population structure was conducted.

Leaf samples were collected from 15 *J. seravschanica* populations across Uzbekistan, Kyrgyzstan, and Kazakhstan to assess genetic diversity and population structure. Using 11 polymorphic simple sequence repeat (SSR) markers, genetic diversity parameters such as the number of alleles, the number of effective alleles, the percentage of polymorphic loci, and Nei's genetic diversity index were evaluated. Nei's genetic diversity index for *J. seravschanica* populations averaged 0.450, ranging from 0.407 to 0.566. The AMOVA revealed that 90.3% of the total genetic variation was within populations, indicating a high level of genetic diversity within each population. Gene flow, calculated using alleles from all populations, was estimated at 4.654. Population structure analysis showed weak clustering among the studied populations, supporting the AMOVA findings.

This study provides valuable insights into the genetic diversity and population structure of *J. seravschanica* in Central Asia. The high genetic diversity within populations suggests a strong adaptive capacity to environmental changes. These findings can be effectively utilized to develop conservation strategies for *J. seravschanica*, ensuring the long-term sustainability of this important tree species in Central Asia.

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