

Genetic Diversity of Spiders (Araneae) Communities in the South Caucasus

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Abstract

The field of research, recognised as a global biodiversity hotspot, boasts a rich diversity of spider species, shaped by its complex geography and ecological variability. For the most part, the study presents a comprehensive assessment of both genetic and species diversity of spider communities over 12 regions in Georgia and Armenia. A total of 490 spider specimens representing 10 families were determined using mitochondrial Cytochrome c Oxidase subunit I (COI) barcoding. Community diversity was assessed using Simpson's and Shannon-Wiener indices to establish the formal species diversity. In contrast, genetic variety was surveyed through the Maximum Composite Likelihood-based distance calculation in MEGA XI.

The region's high species richness, as well as the sites of Kintrishi, Lagodekhi, and the Botanical Garden in Yerevan, were identified as biodiversity hotspots. A direct relation was discovered between species and genetic diversity for the total dataset and at the family level, although a few locations exposed more prominent genetic variation than expected. Spider families unveil genetic homogeneity across research areas, pointing to extensive dispersal capabilities. Only the Gnaphosidae family showed remarkable genotype structure, particularly in arid and isolated environments like Meghri and Vashlovani. This suggests limited dispersal and possible historical segregation.

No correlation was found between genetic and geographical distances, highlighting the impact of habitat category and ecological factors over spatial division. These findings promote the role of natural heterogeneity in forming spider groups and offer valuable insights into the evolutionary dynamics of arachnid communities within the area.

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