Genetic structure detected in Acacia tortilis trees along the Arava valley in Israel and Jordan

Yael Rodger*1,2, Shiri Bar-David1, Gidon Winters2
1 Mitrani Department of Desert Ecology, Ben-Gurion University of the Negev
2 The Dead Sea-Arava Science Center, Tamar Regional Council
*yael.roder@gmail.com

Introduction
Genetic diversity is essential for potential adaptation to environmental changes and therefore long-term survival of a species. Our aim was to contribute to the conservation and effective spatial management of Acacia tortilis, a keystone species in the arid Arava valley, Israel1.

Research Objectives
1) Quantify levels of genetic diversity within and among the different subpopulations
2) Combine landscape ecology and population genetics to explore features that might explain the population structure

Methods
I collected leaf samples from trees in 14 subpopulations (Fig. 1), extracted DNA and amplified it using 6 microsatellite primers. Each sample was genotyped by allele size.

![Figure 1. Subpopulation sampling sites in Israel (brown trees) and Jordan (purple) with sample sizes. Inset: 2 sites from the species’ central distribution in Sudan and Egypt (black).](image1)

Results
Average allelic richness across loci ranged from 4.74 (Peres) to 6.38 (Tala Bay), an average of 5.55±0.51. Average observed heterozygosity was high (0.75±0.012) compared to sites from the central distribution (0.60±0.04). Significant genetic structure was detected by three measures: F-statistics (Fig. 2), Bayesian clustering (Fig. 3), and population graphs (Fig. 4).

![Figure 2. Analysis of Molecular Variance. Fst = 0.039, p<0.001.](image2)

Discussion
High genetic diversity and significant genetic structure was found in the sampled population over a small geographic distance. Geographic distance is a significant factor affecting connectivity within the population. Northern and southern subpopulations are highly differentiated but there is evidence for gene flow between central subpopulations in a stepping-stone model (Fig. 3). Management plans should consider the population’s genetic structure to maintain genetic diversity along the entire distribution of A. tortilis.

References
3 Newman (2005) Social Networks. 27: 39-54

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