



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

Yael Rodger^{*1,2}, Shirli Bar-David¹, Gidon Winters²

¹Mitrani Department of Desert Ecology, Ben-Gurion University of the Negev

²The Dead Sea-Arava Science Center, Tamar Regional Council

*yael.rodger@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.

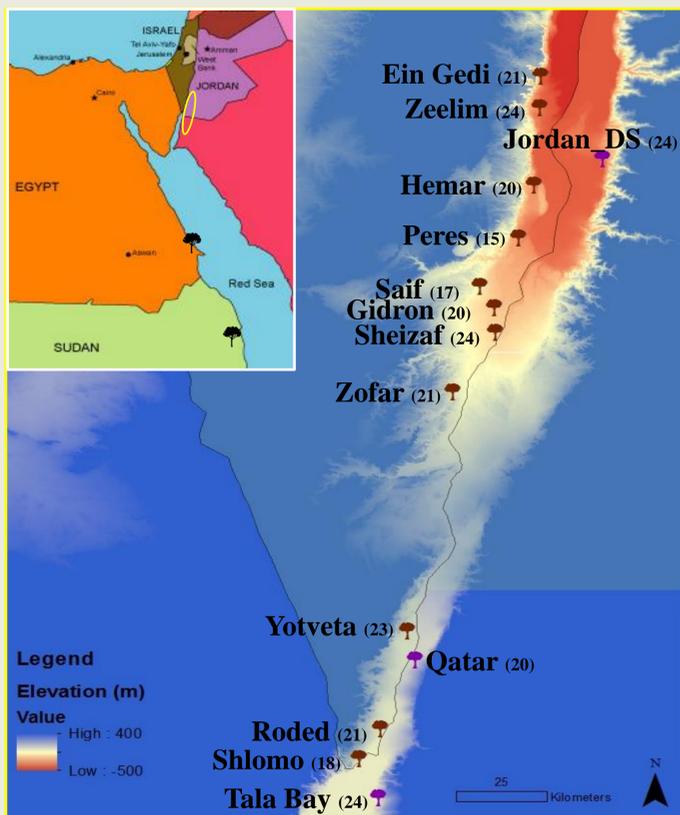


Figure 1. Subpopulation sampling sites in Israel (brown trees) and Jordan (purple) with sample sizes. Inset: 2 sites from the species' central distribution in Sudan and Egypt (black).

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).

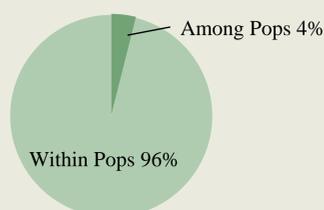


Figure 2. Analysis of Molecular Variance. $F_{st} = 0.039$, $p < 0.001$.

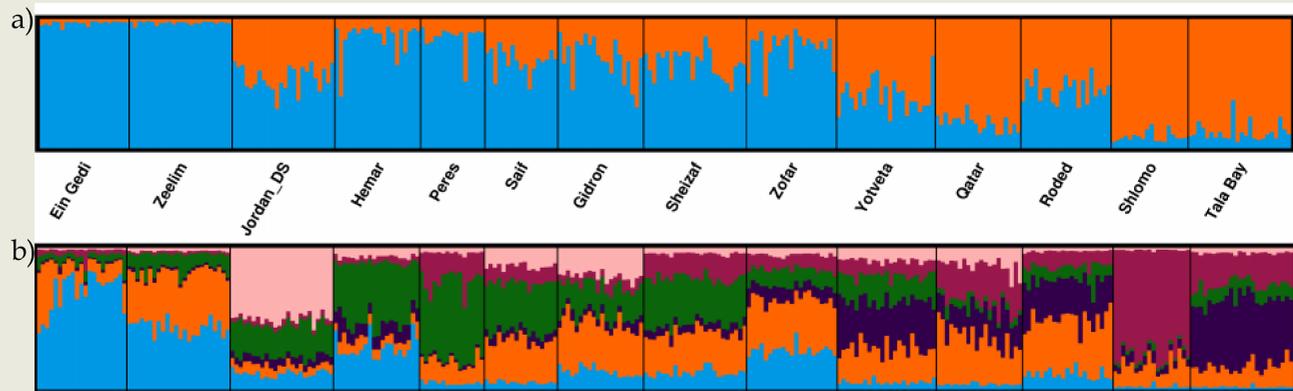


Figure 3. Structure results using Locprior for a) $K=2$ and further subclustering in b) $K=6$. Clustering may be related to delineation of drainage basins along the Arava valley.

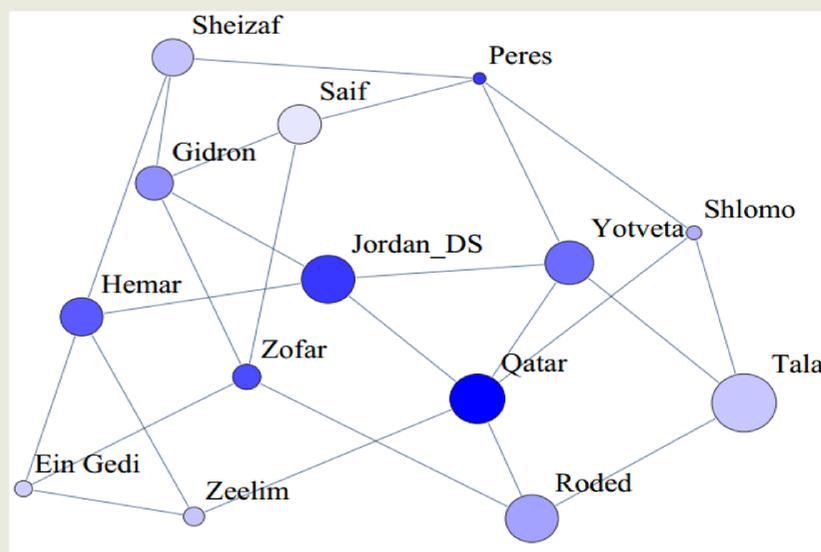


Figure 4. Population graph² with nodes representing sites, size scaled to allelic richness, and edges representing among-site variation, and color of nodes is scaled for Random Walk Betweenness Centrality³, indicating importance for gene flow of the entire network.

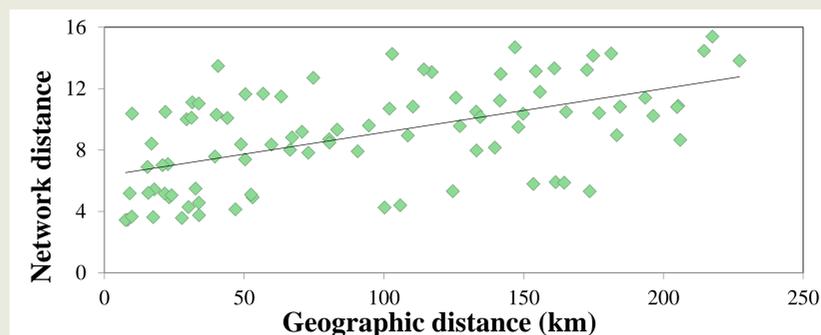


Figure 5. A Mantel test of network genetic distance and geographic distance between sites was significant ($R^2=0.31$; $p=0.01$), suggesting an effect of isolation by distance.

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

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