

Genetic diversity and differentiation of *Olea europaea* subsp. *cuspidata* in the Hajar Mountains, Sultanate of Oman

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INTRODUCTION

Olea europaea subsp. *cuspidata* (Wall. & G.Don) Cif. (wild olive) is one of the six subspecies important for the domestication of olive with valuable physiological and morphological traits. The distribution of wild olive stretches from South Africa over the Middle East and the Mediterranean region to China, mainly at mid to high altitudes with sufficient precipitation. Nowadays, wild olive populations are poorly connected, situated in fragile habitats, and are hence prone to additional stresses including erratic weather extremes and anthropogenic influences. This may result in further fragmentation of stands, shifts in demography, increased clonal growth, lower genetic diversity, and higher differentiation between olive stands due to genetic drift. Wild olive also grows in the Hajar Mountains, Sultanate of Oman (Figure 1), a habitat subjected to many anthropogenic disturbances. Therefore, the present condition of wild olive in the Hajar Mountains was studied

- to evaluate the vulnerability of the species based on dendrological and genetic data and
- to infer its population genetic structure, levels of genetic diversity and differentiation.



Figure 1 Wild olive tree in the Hajar Mountains (left). Sample location within the Hajar Mountain Range in the Sultanate of Oman (right)

RESULTS

- Underrepresented young age classes; small trees were heavily browsed (Figure 2)
- Expected heterozygosity was rather moderate ($H_e = 0.62-0.64$). However, EST-SSR markers alone generated much lower average heterozygosity levels ($H_e = 0.40$) than nSSR markers ($H_e = 0.87$); the youngest size classes contain relatively high level of genetic diversity
- Genetic differentiation was relatively low based on both tentatively selectively neutral nSSR and EST-SSR markers that could be under selection
- Suggested levels of genetic clusters was 8, but with no significant genetic structure (Figure 3)

METHODS AND MATERIALS

- Standard dendrological parameters of **362 individual trees** were taken (among those: diameter at breast height, diameter at base when tree smaller than 1.30m)
- **188 individuals** were chosen for genetic analyses; **12 polymorphic microsatellite markers** consisting of six nSSRs and six EST-SSRs from 26 published microsatellite markers were used for genetic analysis
- For comparative analyses, samples were grouped based either on their location (six groups, each including plateau and adjacent slope), plateau vs. slope site (two groups), or Akhdar vs. Shams mountain (two groups)

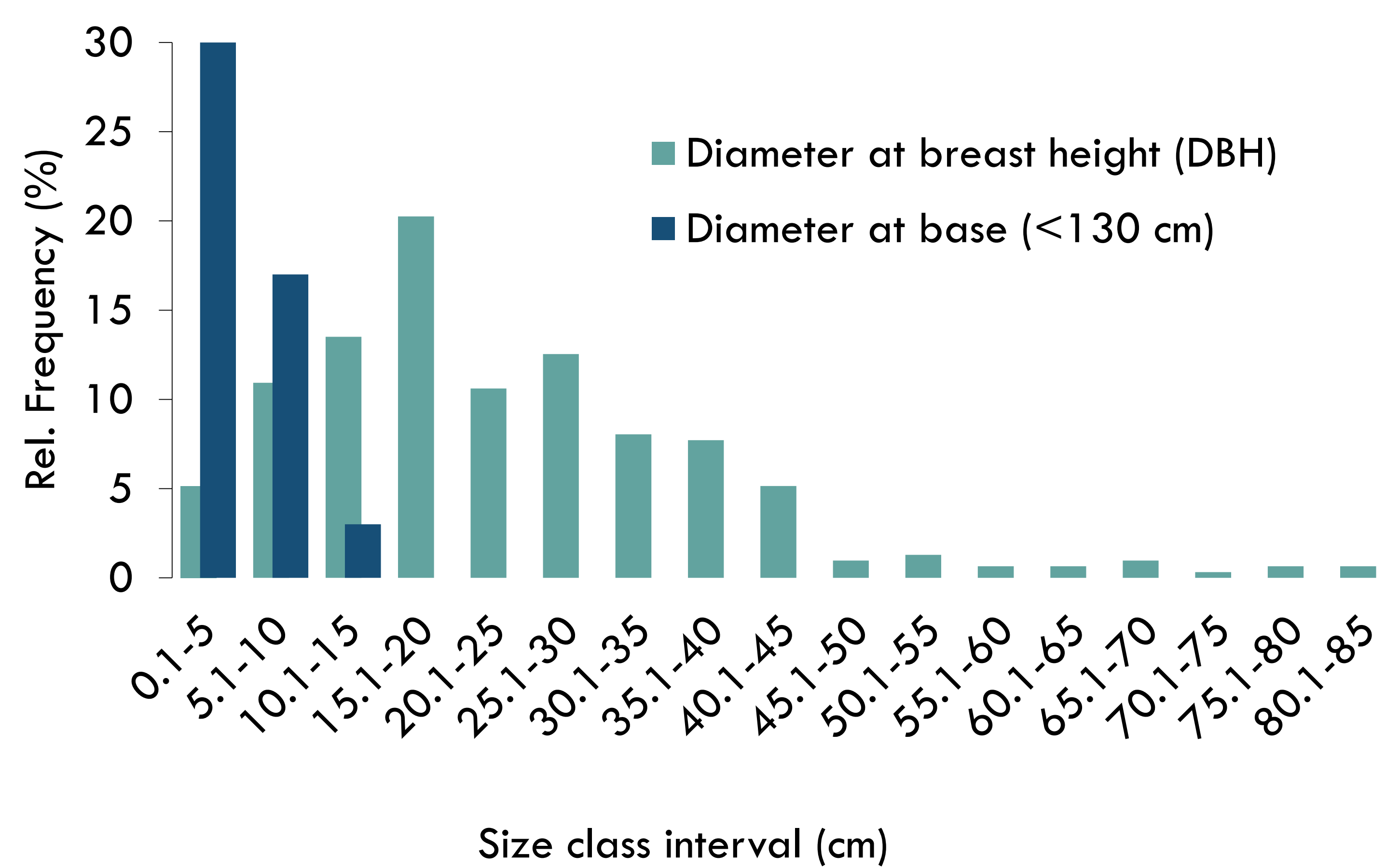


Figure 2 Distribution of the diameter at breast height (DBH) and diameter at base based on for 362 *Olea europaea* subsp. *cuspidata* trees in the Hajar Mountains range, Sultanate of Oman.

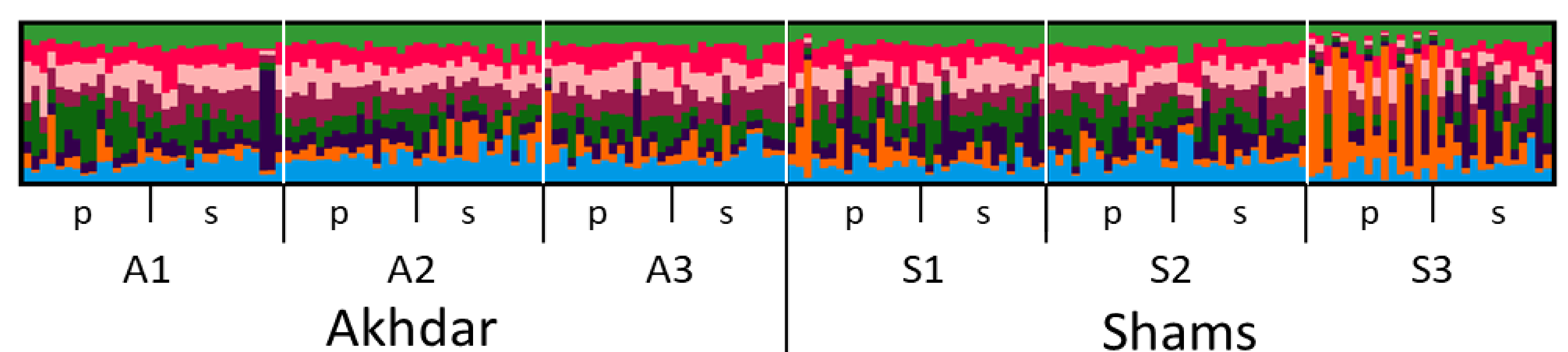


Figure 3 The STRUCTURE analysis for all 188 *Olea europaea* subsp. *cuspidata* individuals in the Hajar Mountains range, Sultanate of Oman. p = plateau, s = slope; A = Akhdar, S = Shams,

CONCLUSIONS

- Cumulative abiotic and biotic effects are the most plausible cause for demographic change.
- Comparatively high levels of genetic variation cannot preclude from being vulnerable, especially considering fragmentation, low or lack of regeneration, over-aging, and ongoing climate variations.
- Further studies of the next sibling generations are needed to better evaluate about the sustainability of this population.

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