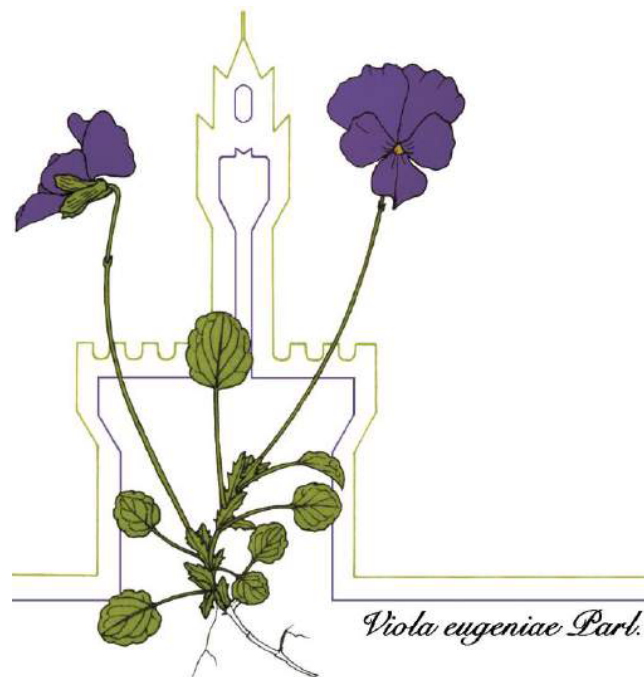


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## ABSTRACTS

KEYNOTE LECTURES, COMMUNICATIONS, POSTERS

### 3.5 = Genetic diversity in the threatened *Bellevalia webbiana* (Asparagaceae) parallels functional and reproductive traits

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Amongst the numerous Italian narrow endemic plants, the Webb's hyacinth (*Bellevalia webbiana* Parl., Asparagaceae; 1, 2, 3) is one of the most evolutionarily relevant, and threatened. According to (4), the range of this bulbous perennial herb is restricted to an area of pre-Apennines (100–700 m a.s.l.) in Tuscany, and Emilia-Romagna (Central Italy), with two disjunct population groups. Typical habitats for Webb's hyacinth are open fields, and meadows, wood margins, olive groves, and vineyards. During the last century, Webb's hyacinth disappeared from several historical localities due to the development of human settlements (4). For these reasons, this species is currently listed in The IUCN Red List of Threatened Species as Endangered (EN A2c) (5). Despite contributions providing important information on the species' reproductive (6), and functional (7) traits, no population genetic information was available so far.

In this study, a DNA fingerprinting approach was applied to study the five richest populations of this species (each with  $N > 50$  individuals): three in Tuscany (Pratolino, Uccellatoio, Tavarnuzze), and two in Emilia-Romagna (Casola Valsenio and Faenza). For each population, we sampled leaf tissues in silicagel from 15 individuals. The primers selected for the ISSR analysis were (Hex)ISSR4, (Fam)CT8 and (Tet)ISSR8. A total of 108 loci were detected (100% polymorphic) in the 75 individual profiles. AMOVA highlighted that 71.2% of genetic variation is within populations, and 28.8% among populations, with an average  $F_{ST} = 0.29$  (a value only slightly below the mean found in plants using ISSR, see 8). Average gene diversity over loci ranges from 0.083 (Uccellatoio) to 0.116 (Pratolino) in Tuscan populations, while it is slightly higher in the populations from Emilia-Romagna (0.129 for Faenza and 0.131 for Casola Valsenio). Despite the low genetic variability among populations, the individuals from Faenza are neatly differentiated from the others, showing 11 specific loci. Indeed, they group separately both in PCoA and NeighborNet analyses of the molecular binary matrix. The optimum number of genetic clusters (9) inferred from the STRUCTURE analysis (burn-in period of 50,000 and a posterior number of 100,000 MCMC permutations, 15 replicates for each value from  $K = 1$  to  $K = 10$ ) is  $K = 2$ . The individuals from Pratolino, Uccellatoio, Tavarnuzze, and Casola Valsenio either belong to the first  $K$  group (33 out of 60 individuals showing a proportion of membership above 80%) or are a genetic admixture among the two  $K$  groups (27 out of 60 individuals). On the contrary, the proportion of membership to the second  $K$  group is above 80% in all the 15 individuals from Faenza.

Interestingly, the population from Faenza is the only one statistically different as far as CSR strategy is concerned, being more 'competitor' and less 'stress-tolerant' compared to the other four populations (7). As far as reproductive features (6), the same population shows the tallest inflorescences, with the highest number of flowers, and the highest fruit set. This population is also the only actively conserved by the owners of "Apicoltura Lombardi" in their property. In this framework, our idea is that this 'protected' population is allowed to express its competitive potential, by maintaining a number of genetic traits otherwise lost in the other, disturbed (6, 7), populations. Indeed, disturbance may have caused germplasm selection, and genetic drift, in Pratolino, Uccellatoio, Tavarnuzze, and Casola Valsenio. The peculiar, genetically differentiated, population from Faenza may be seen as an Evolutionarily Significant Unit (ESU; 10), deserving special conservation attention, in order to guarantee the survival of this species. Finally, Emilia-Romagna may represent the centre of origin for *B. webbiana*, by considering that the two populations from this region hold the highest levels of intrapopulation variability, and that Faenza population shows the highest levels of specific loci, but it also shares rare fragments with other populations.

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