

Genomics variation in yew (*Taxus baccata* L.): a study involving three populations from different Italian regions

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Figure 1. Sampling sites of the three populations

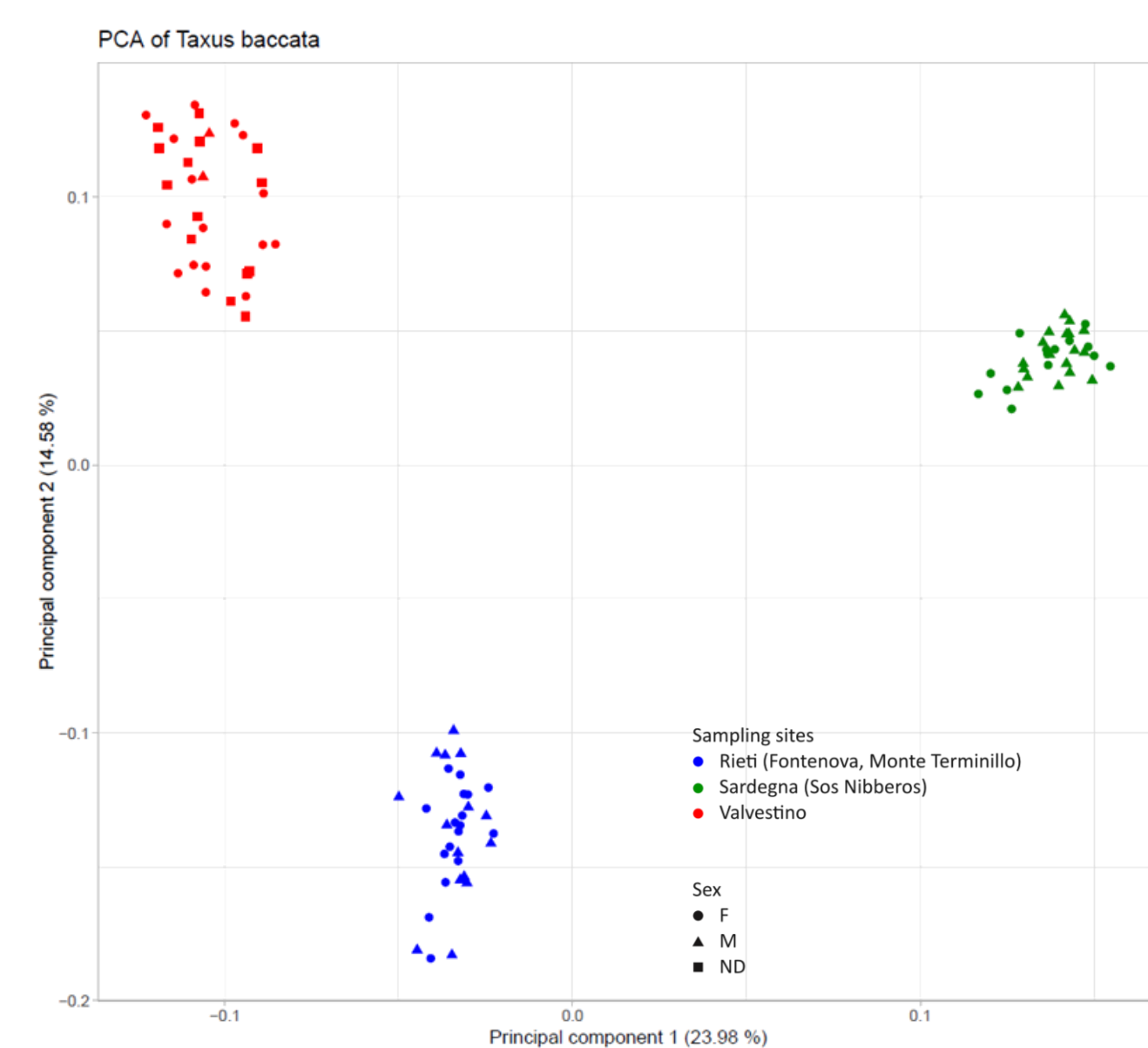


Figure 2. PCA analysis of the 96 plants of the three populations

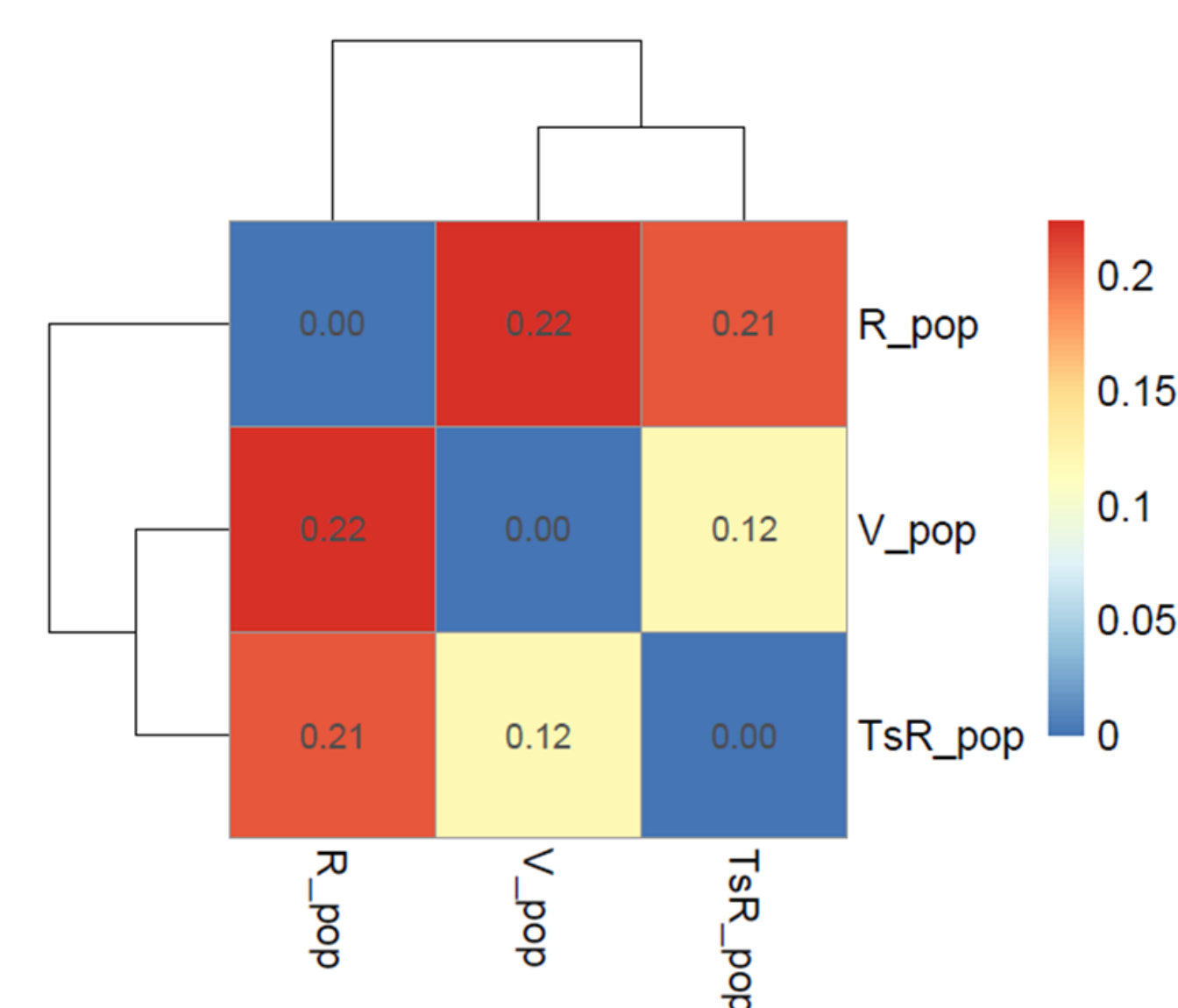


Figure 4. Fst measure of the genetic differentiation among the three populations

Pop	Het observed	Het expected	F _{is}	Area
V_pop	0,27	0,32	0,15	Lombardia
R_pop	0,29	0,31	0,06	Sardegna
TsR_pop	0,25	0,29	0,13	Lazio (Rieti)

Table 1. Observed and expected heterozygosity and inbreeding coefficient of the three populations.

BACKGROUND

Yew (*Taxus baccata* L.) is a tertiary relict and a long-lived dioecious tree species found across a wide natural range of locations, and it has been a major component of forests for many years. In the middle age the species was on the verge of extinction in Europe and today, it remains a tree of great ecological and economic value that is widely used. In contrast to other gymnosperms, the species has limited gene flow and the genetic diversity is highly structured at the local and regional scale. This aspect, in combination with a slow migration rate, specific soil requirements, and limited potential to adapt to the anticipated climate change can threaten yew populations in the present days and future climate change scenarios. For this reason, in some areas, conservation management targets the protection of yew populations.

RESULTS

96 yew plants were sampled from three natural populations in Sardinia (Sos Nibberos, SS), Lazio (Fontenova, Monte Terminillo, RI) and Lombardy (Valvestino, BS) (Figure 1). These sites were characterised by differences in altitude, climate, geography, sun exposure, temperature, water availability and soil types and compositions. From each population, 32 random plants were collected considering, when possible, both male and female plants. DNA were analysed by using 11,120 SNP markers generated through the ddRAD approach.

Main results:

- Principal component analysis (PCA) confirmed a high level of genetic variability among populations that are clearly differentiated, with the first three components explaining 23.98% (PC1), 15.48% (PC2), and 6.5% (PC3) of the total variance, respectively (Figure 2).
- Admixture analysis (Figure 3) supports the PCA results highlighting the absence of mixed ancestry and the presence of three clearly different populations.
- The three populations present an observed heterozygosity lower than the expected one (Table 1).
- The Sardinian population is genetically more isolated than the other two populations (Figure 4).

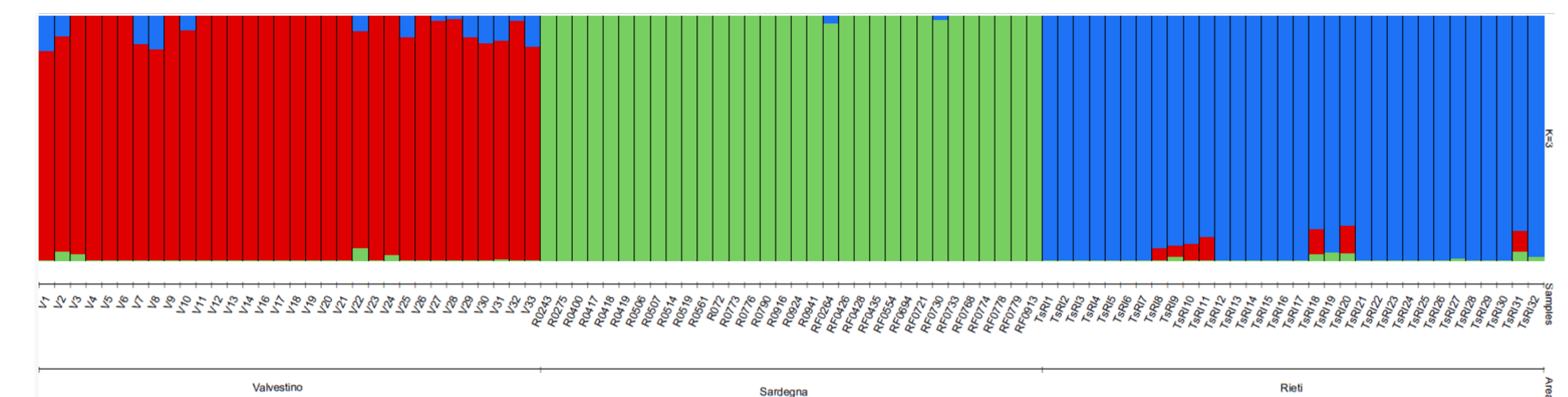


Figure 3. Population genetic structure at K = 3 of the 96 individuals from the 3 populations evaluated in the present study. Different colours correspond to different ancestral populations.



SUMMARY AND PROSPECTS

The three populations analysed are genetically different and the Sardinian population is genetically more isolated with respect to the other two populations. The population genetic structure confirms the absence of mixed ancestry in particular in the Sardinian population.

These results represent a preliminary report of a project, started in the frame of the National Biodiversity Future Centre, that aims to investigate the genetic diversity and structure of yew in different zones of Italy, in order to assess the conservation status of the population, to evaluate and develop suitable management strategies and to deal with the potential threats.