

## FROM GENETIC DIVERSITY ANALYSIS TO DETECTION OF SELECTIVE FORCES, VIA ASSOCIATION ANALYSIS: THE VALUE OF LANDRACE POPULATIONS

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Genetic diversity, population structure and the extent of linkage disequilibrium (LD) are investigated in 11 Sardinian populations of barley (*Hordeum vulgare* L.) landraces, through 134 SSAP markers. The structure of the multilocus association and the presence of outlier loci are also investigated, to determine which sources of diversification have shaped the genetic diversity of the Sardinian barley. Several datasets are used to test the consistency of the genetic diversity analysis results (e.g. datasets without rare alleles or without similar individuals, etc.). The UPGMA analysis shows a major clustering of the barley population landraces according to three main geographic areas of origin. The AMOVA analysis reveals that there is a greater genetic variance within than among the populations. Genetic structure analysis reveals the existence of four main genetic groups, in a genetic subdivision that is only partially explained by geographic patterns. The average LD within landrace populations is low; however, LD levels and the LD rate of decay are population dependent. The multilocus association and outlier detection analyses show that the genetic make-up of this Sardinian barley populations is at least partially determined by selection. Overall, these results demonstrate that these Sardinian barley landraces include valuable material for future breeding studies in Mediterranean environments, while also providing interesting implications with regard to association mapping studies.