

GENETIC STRUCTURE OF ITALIAN ONION LANDRACES AND COMMERCIAL VARIETIES

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Onion (*Allium cepa* L.) is an outcrossing diploid species ($2n=2x=16$) of great economic importance, widely cultivated all over the world. The primary center of domestication and variability is identified with southwest Asia, although secondary centers of diversification have been recognized elsewhere (e.g. Mediterranean area). The privileged position of Italy in the Mediterranean area gave rise to a high onion biodiversity, established by commercial cultivars and local landraces. However, the Italian germplasm has been scarcely investigated from a genetic standpoint. In this study, we explored the genetic variation and parentage of 82 onion genotypes through KASP genotyping technology. SNP dataset inspection returned 375 polymorphic loci with a very low percentage of not calling (NC) (0.03%). Among 82 samples, 89% amplified all polymorphic loci and were considered for population structure analysis. The ΔK method suggested four clusters ($K=4$) as optimal. In particular, population 1 mainly included Spanish varieties, population 2 grouped varieties principally from USA. The other two populations, 3 and 4, grouped all wild species and the Italian germplasm, respectively. The SNP data were also used to investigate the presence of first- and second-degree relationships among the genotypes of our collection, but no relationships were found. In conclusion, the data generated in this work allowed distinguishing several genotypes coming from different molecular breeding programs (Spain, USA and Italy). Further researches on this onion collection are desirable to extend our knowledge into different variability levels (e.g. phenotypic, metabolic, etc). At the present day, this is the first report on genetic diversity assessment involving Italian onion landraces.