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## **Genotyping apple (*Malus x domestica* Borkh.) heirloom germplasm collected and maintained by the Regional Administration of Friuli Venezia Giulia (Italy)**

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### **Abstract**

This paper reports the genetic diversity of apple germplasm collected in the Friuli Venezia Giulia region (northeastern Italy). The collection, maintained in three different locations, was represented by local cultivars which probably originated as chance seedlings together with cultivars introduced from neighbouring countries, the name and origin of most of which has been lost over time. A preliminary procedure described in the paper started with 469 molecular profiles analysed using 15 Simple Sequence Repeat (SSR) markers and allowed identification of the 'true-to-type' genotypes among those maintained in multiple locations. The set of the remaining 234 accessions was further reduced to 132 unique profiles by removing 102 synonyms, that is accessions with different name and the same molecular profile. Flow cytometry identified as many as 54 triploids (40.9%), whose status was confirmed by field observations on leaf size and the occurrence of triallelic profiles at several SSR markers. The remaining 78 diploid accessions were analysed for their genetic diversity, that is the number of alleles, observed and expected heterozygosity, polymorphism information content (PIC), the frequency of null alleles and the probability of identity for unrelated and full-sib genotypes. The paper provides a critical evaluation of the SSR markers adopted for the study, discusses the genetic diversity observed in the apple germplasm collection examined as well as its high frequency of triploids compared with other apple collections described in the literature.