Assessment of apple core collections constructed using phenotypic and genotypic data

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ABSTRACT. Several types of information can be used to select core collections, including passport data, agronomic data, and molecular data. However, little is known about the ability of core collections to retain the genetic diversity and structure of the whole collection for characters that were not considered during the selection, particularly when molecular markers are used. In this study, two core subsets were established for the apple (*Malus* spp) germplasm bank curated at the Apple Research Station, National Institute of Horticultural and Herbal Science, Korea, based upon genetic diversity estimated with 14 simple sequence repeat markers, and phenotypic diversity based on 23 traits. Comparisons between these two subsets and with the whole collection were used to determine the effect of the data used in the selection on phenotypic and genetic diversity, and population structure. The two subsets had a similar diversity and did not differ from the original collection, according to the Nei and Shannon diversity indices. Allele and class frequencies were also maintained in the two subsets. Overall, the type of data used to construct the core collection had little influence

on the phenotypic and genetic diversity retained. Therefore, in the case of apple collections, the use of molecular markers is preferable, because they allow rapid and reliable characterization.