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SEQUENCE-BASED AMPLIFIED POLYMORPHISMS ARE USEFUL FOR STUDYING GENETIC DIVERSITY OF WINTER SQUASH

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Germplasm conservation facilities require an accurate understanding of the patterns of genetic diversity within and among accessions (unique populations) that comprise germplasm collections and the ecogeographical patterns of this diversity. This information facilitates the efficient management of germplasm collections and aids in identification of possible gaps in diversity that need to be addressed. The objectives of this investigation were to determine the reliability of sequence-based amplified polymorphisms (SBAPs) for use in estimating genetic polymorphism within winter squash (*Cucurbita maxima*) and to describe geographical variation of genetic diversity within this species using the tested SBAPs. Twenty accessions of *C. maxima*, four each from South America, North America, Europe, Asia, and Africa, two plants per accession, were used for genotyping by SBAPs. The sets of SBAP primer pairs (one AT-rich, one CG-rich) were designed to preferentially amplify coding regions in *C. maxima* (Ferriol et al. 2003). Banding patterns obtained with SBAP markers were highly reproducible. Polymorphism was observed for the SBAP markers used, both within and among accessions. Due to their high reproducibility and high levels of polymorphism, SBAPs appear to be promising markers for studying genetic diversity of *C. maxima*. This paper discusses genetic diversity within and among *C. maxima* accessions. Geographic patterns of genetic diversity are also discussed.