

336 Assessing Genetic Variability of *Pelargonium* Species Using PCR-based TRAP Markers

Wai-Foong Hong¹, Chang-Qing Bai², Michael Broe³, Jinguo Hu⁴, Charles Krause⁵, David Tay^{*6}, Guo-Liang Wang⁷

¹The Ohio State Univ., Dept. of Plant Pathology, Columbus, OH 43210; ²The Ohio State Univ., Ornamental Plant Germplasm Center, Columbus, OH 43210; ³The Ohio State Univ., Ornamental Plant Germplasm Center, Columbus, OH 43210; ⁴USDA-ARS Northern Crop Science Laboratory, Sunflower Research Unit, Fargo, ND 58105; ⁵USDA-ARS, Application Technology Research Unit, Wooster, OH 44691; ⁶The Ohio State Univ., Ornamental Plant Germplasm Center, Columbus, OH 43210; ⁷The Ohio State Univ., Dept. of Plant Pathology, Columbus, OH 43210

Pelargonium is one of the important flower crops in USA. It is a priority genus for conservation at the USDA Ornamental Plant Germplasm Center (OPGC). It belongs to *Geraniaceae* family and comprises of about 280 species. To understand the genetic variation of the *Pelargonium* collection at OPGC, the PCR-based TRAP (target region amplified polymorphism) marker system which was newly developed in sunflower was used in this study. Twelve sets of primers were used to fingerprint 46 accessions representing 21 commercial *P. hortorum*, 17 scented geraniums and 8 other unidentified *Pelargonium* taxa. About 150 DNA bands could be detected in each primer and accession combination. Cluster analysis showed that molecular data was highly correlated with the phenotypes. Cultivars with similar morphological

traits were clustered together. These results demonstrated that the TRAP system is a useful technique for the characterization and classification of *Pelargonium* collections.