Target Region Amplification Polymorphism (TRAP) as a Tool for Detecting Genetic Variation in the Genus *Pelargonium*

The *Pelargonium* species are some of the most popular flowers in the world. In 2004, the combined wholesale value for all flats, hanging baskets, and pots of *Pelargonium* in the United States was over $206 million. Some *Pelargonium* species produce compounds that may be used in both agriculture and medicine. Oils produced by *Pelargonium* species have been used as perfumes, food flavoring, and have also shown an inhibitory effect on bacteria, nematodes, and insects. Additionally, some *Pelargonium* varieties are resistant to arthropods, attributed to the anacardic acid composition of glandular exudates from their leaves.

Ornamental plants are often selected for their aesthetic qualities, rather than their ability to survive in a given environment. Interest in breeding for ornamental purposes has lead to many improved or novel cultivars. Efforts have been made to improve cultivars through traditional breeding and genetic transformation. As a result, the genetic basis of most modern flower cultivars risk the loss of important traits. Gene banks serve an important function by maintaining examples of plants with traits that could be otherwise lost before anyone understood their importance. To keep a diverse collection of *Pelargonium* examples, it is important to be able to determine genetic similarities between them.

The use of target region amplification polymorphism (TRAP) to determine genetic similarities among accessions was examined. TRAP is a technique

Figure 1.Sample Trap image generated by the primer combination w3a-700. Most of the samples on the left half of this image are from *P. xhortorum*, while the right have represents different species. The LI-COR DNA size standard is loaded in the last lane of the right.

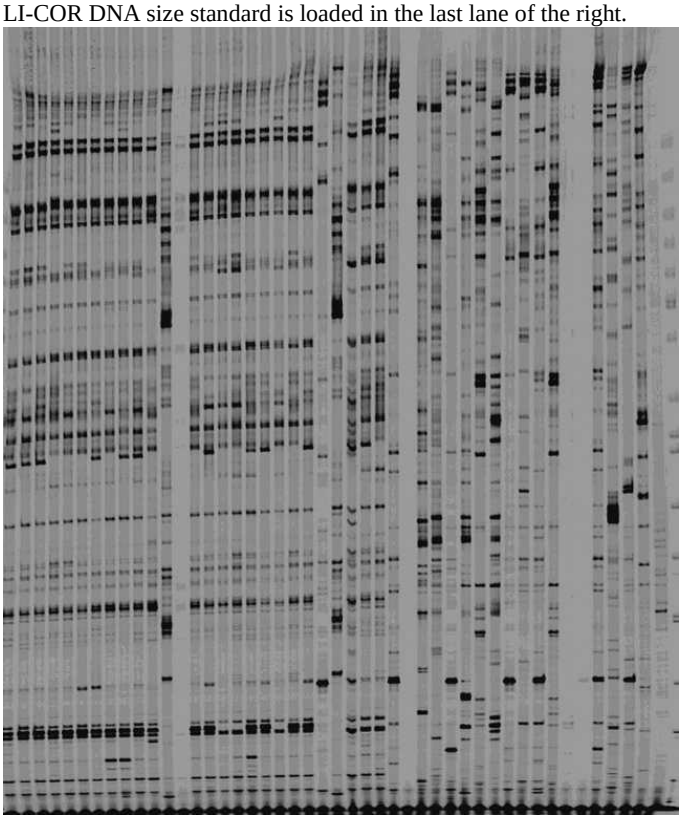
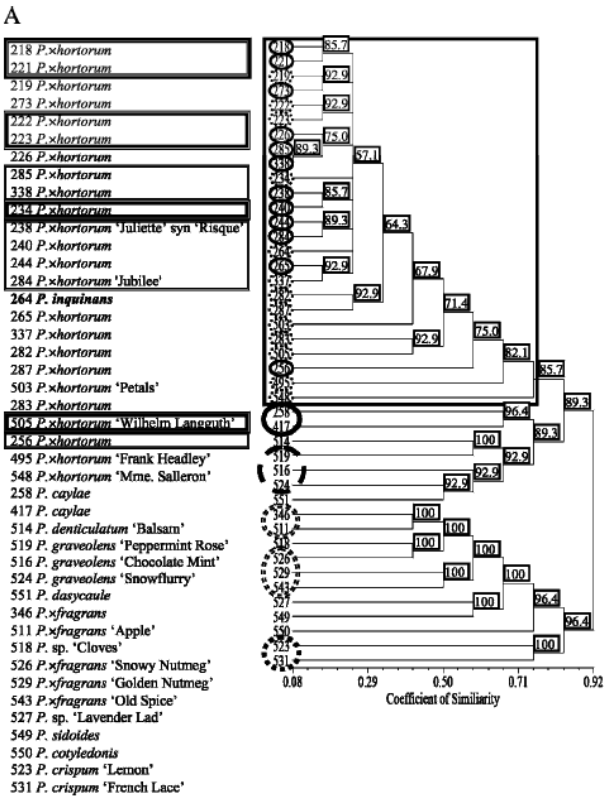


Figure 2.Sample Dendogram from w3a-700 primer set.



that combines the AT- and GC- rich regions of DNA with a third "fixed" primer that matches a gene of interest. The advantages of TRAP are that there is no need for extensive treatment of the DNA samples, many samples can be amplified in a single laboratory reaction, and that previously reported genetic information has the potential to be used as the target DNA.

To evaluate TRAP's potential, two issues needed to be considered. The first was isolation of high-quality of DNA for TRAP reactions. The second issue was whether or not TRAP markers could distinguish *Pelargonium* accessions and group them according to phenotypes. Gel images (Figure 1) of 46 species of *Pelargonium* were used to create two dendograms (Figure 2) from separate data sets. These dendograms placed *P. x hortorum* with related plant material and formed a separate group including scented species and cultivars. The results demonstrated that most of the *Pelargonium* accessions could be differentiated from each other using TRAP markers and that groups formed based on similar result from the TRAP were consistent with what was previously known about the accessions. This information will be used to identify unique plant examples within the *Pelargonium* collection at the Ornamental Plant Germplasm Center in Columbus, OH.

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