

## Development and Analysis of SSR and SNP Markers for a Carrot Mapping Population

Pimchanok Satapoomin<sup>1</sup>, Massimo Iorizzo<sup>1</sup>, and Philipp W. Simon<sup>1,2</sup>

<sup>1</sup>Plant Breeding and Plant Genetics Program, University of Wisconsin-Madison, Madison, WI, USA

<sup>2</sup>USDA-ARS Vegetable Crops Unit, Dept. of Horticulture, University of Wisconsin-Madison, Madison, WI, USA

Carotenoid pigments are important components of the human diet and carrots are the primary source of the vitamin A precursors  $\alpha$ - and  $\beta$ -carotene in the U.S. Carotenoids play crucial biological roles in plants, however the role of genes coding for the carotenoid biosynthesis pathway in controlling carotenoid accumulation are not well understood. Previous study has shown that there are two main genes, *Y* and *Y2* control the difference of carotene content between domesticated orange and white wild carrot. Besides these two genes, the function, map location, and inheritance of *y3*, a newly discovered carotene-accumulating gene is being considered. To gain more information about *y3*, development of simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers in  $F_4$  populations derived from a cross of domesticated orange B493 crossed with white wild QAL are under investigation. The potential usefulness of these markers will be evaluated for robustness, clarity of band pattern, PCR success rate and polymorphism. All evaluated markers derived from two different approaches will be placed as SSR and SNP markers on the genetic linkage map that includes AFLPs marking carotenoid accumulation QTL to serve as codominant anchor loci across carrot maps.