

## OMICS APPROACH TO UNCOVER THE ORIGIN OF HIGH CAROTENOID ORANGE CARROTS

COE K.\*, BOSTAN H.\*, ROLLING W.\*\* , TURNER-HISSONG S.\*\*\* ,  
MACKO-PODGÓRNI A.\*\*\*\* , SENALIK D.\*\* , SETH R.\* , LIU S.\* , CURABA J.\* ,  
MENGIST MOLLA F.\* , GRZEBELUS D.\*\*\*\* , VAN DEYNZE A.\*\*\*\*\* , DAWSON J.\*\*\*\*\* ,  
ELLISON S.\*\*\*\*\* , SIMON P.\*\*\*\*\* , IORIZZO M.\*\*\*\*\*

\*) Plants for Human Health Institute, North Carolina State University,  
Kannapolis, North Carolina, USA

\*\*) US Department of Agriculture (USDA)–Agricultural Research Service,  
Vegetable Crops Research Unit, Madison, Wisconsin, USA

\*\*\*) Bayer Crop Science, Chesterfield, Missouri, USA

\*\*\*\*) Department of Plant Biology and Biotechnology, Faculty of  
Biotechnology and Horticulture, University of Agriculture in Krakow, Poland

\*\*\*\*\*) Seed Biotechnology Center, University of California–Davis,  
California, USA

\*\*\*\*\*) Department of Horticulture, University of Wisconsin–Madison,  
Wisconsin, USA

\*\*\*\*\*) Department of Horticultural Science, North Carolina State  
University, Raleigh, North Carolina

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The selection of orange roots in carrot (*Daucus carota* ssp. *sativus* L.) resulted in one of the richest sources of provitamin A carotenoids in one of the most popular vegetables worldwide. However, the origin of orange carrot is still debated, and the roles of genomic loci controlling carotenoid accumulation and other important domestication and improvement traits remain largely uncovered. Here we leveraged an improved carrot reference genome and resequencing of 630 carrot accessions to study carrot domestication and improvement. The study demonstrated that carrot was domesticated during the Early Middle Ages in the region spanning Western Asia to Central Asia, and orange carrot was selected during the early Renaissance period in Europe, likely in the Netherlands. A progressive reduction of genetic diversity accompanied this process. Genes controlling

vernalization/flowering, plant development and morphology, carotenoid biosynthesis, and photosynthesis/light response were under selection during domestication and improvement. Three recessive genes, at the *REC*, *Or*, and *Y2* QTLs, were essential to select for the high  $\alpha$ - and  $\beta$ -carotene orange phenotype. The study highlighted that in carrot high  $\alpha$ - and  $\beta$ -carotene biosynthesis is controlled through molecular mechanisms that regulate the interaction between the carotenoid biosynthetic pathway, the photosynthetic systems and chloroplast biogenesis. Overall this study elucidated the history of carrot domestication and breeding and uncovered the genetic mechanisms that established the basis for modern day orange carrot.