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**Population genomics identifies genetic signatures of carrot domestication and improvement and uncovers the origin of high carotenoid orange carrots**

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300 word maximum.

**Abstract**

The selection of orange carrot (*Daucus carota* ssp. *sativus* L.) made this crop to become one of the richest sources of provitamin A carotenoids, and among 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 α- and β-carotene orange phenotype. The study highlighted that in carrot high α- and β-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.