Carrot Chromosomes and Linkage Groups

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The genome of carrot (*Daucus carota* L.) consists of ~480 Mb/1C organized in 9 chromosome pairs. The importance of carrots in human nutrition is triggering the development of genomic resources, including carrot linkage maps, a bacterial artificial chromosome (BAC) clone library and BAC end sequences (Cavagnaro et al., 2008). In contrast to these advances, the carrot genome is poorly characterized at chromosome level. While several linkage maps based on different types of molecular markers have been produced, there has been no effort to correlate the linkage groups with specific chromosomes. Carrot somatic metaphase chromosomes are 2–4 mm in length, thus they offer limited resolution for modern cytogenetic tools. On the other hand, preparation of meiotic chromosomes is technically challenging due to the flower bud size. In this work, we present our effort to establish a pachytene karyotype of carrot and to assign carrot linkage groups to pachytene bivalents. Carrot pachytene complements prepared from carrot line 2566B consisted of four metacentric and five subtelocentric chromosomes, and were up to ~8 times longer than their mitotic counterpart. Heterochromatin was mainly confined to the pericentromeric regions of each chromosome. Several BAC clones selected for genetically mapped DNA markers were mapped to specific chromosomes and linked markers were physically linked. Using two-color FISH, a probe cocktail composed by 11 BACs from eight linkage groups was sufficient to identify the 9 pachytene bivalents. Our work will be helpful to integrate the available linkage data with the chromosome morphology.