

Genomic Analysis Research and its Application for Breeding Carnation Cultivars

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Carnation (*Dianthus caryophyllus* L.) is one of the most popular flowers, not only in Japan but also worldwide. We bred carnation mainly for carnation bacterial wilt (CBW) resistance, and genomic analysis tools were constructed, including genetic linkage maps and whole genome sequences, to efficiently and quickly accelerate the breeding program.

CBW, caused by *Burkholderia caryophylli*, is one of the most damaging diseases that affects carnation production in Japan. To improve selection efficiency for breeding CBW-resistant carnations using *Dianthus capitatus* ssp. *andrzejowskianus*, we constructed the first molecular linkage map for carnation, and a quantitative trait locus (QTL) with a significant effect and two QTLs with small effects were detected [1]. We found that the STS-WG44 marker linked to the major QTL was useful for selecting the high resistant lines for breeding. In 2010, we produced the first CBW-resistant carnation cultivar 'Karen Rouge' by repeated crossing and selection via both conventional disease screening and marker assisted selection.

We also updated the genetic maps to improve their usefulness for breeding purposes and genetic research. We constructed an SSR (simple sequence repeats)-based reference genetic linkage map for carnation using SSR markers derived from a genomic library, expressed sequence tags, and RNA sequencing data [2]. We mapped QTLs for two traits (CBW resistance and anthocyanin pigmentation in the flower) and a phenotypic locus for flower-type. Recently, we constructed a higher density genetic linkage map using double-digest restriction site-associated DNA sequencing based on next generation sequence (NGS) technology.

Whole genome sequences are fundamental resources for genomic analysis. We determined the whole genome sequence of the 'Francesco' cultivar using multiple NGS platforms [3]. The total length of the non-redundant sequences was 569 Mb, which covered 91% of the estimated 622-Mb carnation genome, and 43,266 protein-coding genes were deduced in the genome. We also constructed a database for the genomic sequences (Carnation DB; <http://carnation.kazusa.or.jp/>).

The information and material resources that we have generated for carnation will help to enhance both fundamental and applied research on carnation and related plants.

References

- [1] Yagi, M. et al.: Construction of a genetic linkage map for the carnation by using RAPD and SSR markers and mapping quantitative trait loci (QTL) for resistance to bacterial wilt caused by *Burkholderia caryophylli*. J. Japan. Soc. Hort. Sci. 75: 166-172 (2006).
- [2] Yagi, M. et al.: Construction of a reference genetic linkage map for carnation (*Dianthus caryophyllus* L.). BMC Genomics 14: 734 (2013).
- [3] Yagi, M. et al.: Sequence analysis of the genome of carnation (*Dianthus caryophyllus* L.). DNA Res. 21: 231-241 (2014).