Advances in Genetics and QTL Mapping In Carrot (Daucus Carota L.)

Selvakumar R1* and Pritam Kalia2

1Central Institute of Temperate Horticulture, India
2Indian Agricultural Research Institute, India

Submission: September 24, 2018; Published: February 27, 2019

*Corresponding author: Selva Kumar R, ICAR-Central Institute of Temperate Horticulture, Srinagar, Jammu and Kashmir, India

Mini Review

Carrot (Daucus carota L., 2n = 2X = 18; 1C= 473Mb) is a cool weather crop grown in temperate and subtropical regions for its edible storage tap roots both for fresh as well as processed vegetable throughout the world and is most important of all the root crops [1-3]. It has been classified as 'poor man's gingeng' due to its rich β-carotene and tocopherol with health promoting properties [4-5]. It led to increasing awareness to the consumer consumption and nutritional industry to make natural products rich in carotenoids and anthocyanins [6]. Carrot has naturally wide genetic diversity due to its natural single locus mutations, natural hybridization of its wild relatives and ancestors followed by human selection [7-8]. The natural allele collection of carrot includes dominant alleles such as A (α-carotene accumulation), io (intense orange xylem, which may be an allelic form of A), Lγ and Lγ (lycopene accumulation), O (orange xylem, which may also be an allelic form of A) as well as the recessives alleles y (yellow xylem) and rp (reduced pigmentation). The three dominant loci Y, Yγ and Y, control differential distribution of α and β-carotene in xylem/phloem tissue. The Y, mutant controls low carotene content of the storage root xylem ("core") in high carotene orange backgrounds [8]. Laferriere et al. [9] demonstrated that in yellow × white crosses, white colour was dominant over yellow which was controlled by a single dominant gene. Moreover, they reported that three dominant genes were responsible for the absence of pigmentation in white × orange crosses. Light orange colour has also been shown to be dominant to orange [10]. Kust [11] postulated three dominant alleles Y, Yγ and Y which prevented the formation of orange colour in root xylem tissue. Buish et al. [1979] characterized the effects of the series of Y alleles on carotenoid content in phloem and xylem. The Y and Yγ allele were governing white pigmentation of root which was dominant to orange (yy).

Laferriere et al. [9] hypothesized that single major gene was governing white:colour root of yellow × white crosses which three major genes were determining the white and orange. Further, research studies showed that two major genes in one cross and four major genes in orange × yellow cross. Simultaneously, Imam et al. [10] reported that lemon (light yellow) was dominant over light orange in lemon × light orange whereas light orange was dominant over orange in light orange × orange. Kust [11] described that dominant alleles of three genes (Y, Yγ and Y) control the orange colour in the xylem which was epistatic to two pigment enhancing genes (IO, O). The orange colour of phloem was governed by pigment enhancing genes (IO, O) in equal or higher number without dominant alleles (Y) and combination of these colour enhancing genes with three dominant allele (Y, Yγ and Y). Furthermore, he suggested that the genetic constitution of white was recessive at all loci (y, y, y, y, y, y, y, y, y, y, y, y, y, y, y, y). The genetic control of carotene synthesis is complex which includes several enhancer genes and inhibitor genes. Kust [11] postulated that the dominant (Y) locus controls the carotene accumulation in carrot xylem core whereas the recessive (y, y) locus conditioned the β, and γ-carotene rich orange xylem core. Furthermore, the dominant heterozygous (Yγ, γ) possess xanthophyll-rich yellow white core. Therefore, Y, y and Yγ loci were more influencing on the amount and distribution of α and β-carotene in which Y locus blocks the synthesis of α and β-carotene as well as xanthophylls whereas y and Yγ blocks synthesis of carotenes but not xanthophylls [12]. Umil et al. [13] studied in F1 populations of orange × red crosses that the inheritance of orange colour was governed by single dominant gene which is epistatic to red colour gene. Furthermore, on the basis biochemical analyses they proposed that ‘A’ gene for the accumulation of α-carotene were originated from orange parent and ‘L’ gene for lycopene formation were originated from the red parent.

Rhodes [14] in F1 populations of red × light yellow cross observed segregation of 15:1 ratio of yellow-orange to red colour. He suggested that two dominant genes conditioning the conversion of lycopene to α and β-carotene. The white or non-pigmentation of root were conditioned by recessive gene (rp) which controls the β-carotene synthesis. The mutant gene ‘rp’ had been identified and characterized, suggesting that it causes 93% reduction of to-
tal carotenoids [15]. Moreover, Koch et al. [11] postulated that ‘rp’ mutant produces more α-tocopherol which is provitamin-E.

The dominant gene of _P_ conveys the purple colour of root which shows only partial variation on roots and it is hypostatic to _P_ gene influencing pigmentation in aerial parts of petiole, leaf and floral corolla [8]. Anthocyanin accumulation in the carrot phloem is controlled by _P_ locus, with purple (_P_ ) dominant to non-purple (_p_ ). Although, _P_ and _Y_ loci were unlinked in _F_ progeny of two non-purple inbreds [9]. The sugar condition of carrot was governed by single dominant gene ‘G’, dominant to green ‘g’ [17]. Purple colour of root was governed by two complimentary loci in _F_ progeny of two non-purple inbreds [9]. The sugar condition of carrot was governed by single dominant gene (Rs). These genes express more reducing sugars of glucose and fructose in _Rs/-_ plants. In contrast, _rs/rs_ type plants produces more sucrose accumulation [18]. Broad sense heritability estimates have been determined for total dissolved solids 40-45% [19]. The _rs/rs_ mutant plants have carrot invertease enzyme which knockout the function enzyme [20]. The heritability of nematode resistance (_Meloidogyne javanica_) was evaluated using the open-pollinated cultivars Brasilia as resistant, and Kuronan as tolerant [21].

**Quantitative trait loci (QTL) mapping**

The recent development of molecular marker technologies and the use of these markers in detecting and mapping quantitative trait loci has become a powerful approach for studying the genetic and phenotypic basis of complex traits [22-25]. If individual genetic components associated with a complex trait can be identified, then research can focus on the function of each locus independently without the confounding effects of other segregating loci [25].

Bradeen et al. [26] identified six AFLP markers linked to _Y_ locus with distance of 2.8cM and 15.8cM from 103 _F_ populations of a cross 9304 × 7C7626 which segregated for core colour by using bulked segregate analysis [27]. Subsequently, Vivek et al. [28] identified a single AFLP marker from the _Y_ locus and assigned on linkage group B with size of 2.2cM by using these population. Moreover, they have identified horticulturally important QTLs through segregation analysis. Santos et al. [29] revealed that 287AFLP markers were mapped by using 160 _F_ population of Brasilia × HCM with character of medium orange and high carotene line, respectively. These markers were associated with _α_ and _β_-carotene, lycopene, and the precursor’s _ζ_-carotene and phytoene QTL conditioning each of the traits were measured. In total, 2, 3, 1, 4 and 5QTLs were detected for _α_-carotene, _β_-carotene, lycopene and the precursors _ζ_-carotene and phytoene accounting for 40%, 20%, 7.2%, 16.3% and 28%, respectively of total phenotypic variation whereas QTLs of Brasilia and HCM showed 3.7 to 13.2% total variation. Twenty major QTL have been identified for orange carrots which control carotenoids content [30]. Buish et al. [12] reported that these QTLs, two major genes (Y and _Y_) and clusters of genes were involved in common carotenoid biosynthetic pathway from the population of orange carrots (yyy_yy) and white carrots (YYY_Y_) with yellow and pale orange colour.

Santos et al. [29] identified that SNP based markers were closely linked to the _Y_ gene whereas as described by Bradeen and Simon (1998) also maps to this region. They considered _ZDS2_ and _ZEP_ as candidate gene for _Y_ QTL. Phenotype of yellow (santhophyll) and the orange (_α_- and _β_-carotene) were conditioned by _Y_ [12]. They revealed that _Y_ gene were derived from yellow segregates of _B493 × QAL_ population. Furthermore, since it maps to this important region, _Y_ may be responsible for at least some of the QTL effect observed by Santos et al. [31]. Santos et al. [29] identified quantitative trait loci (QTLs) for total carotenoids affecting the concentration of carotenoids in the ranges from 15.8, 21.7, 26.4, 37.7, and 44.2% of the total phenotypic variance for lycopene, _α_-carotene, _β_-carotene, _ζ_-carotene and phytoene, respectively. Just et al. [32] reported that 22 genes involved in the carotenoid biosynthesis and metabolism, provided gene-specific codominant polymorphisms for eight of the nine linkage groups. One major QTL has been identified for _β_-carotene, total carotene and lycopene accumulation in the _F_ population of _P50006_ and _HCM_ A.C. by using sequence related amplified polymorphism (SRAP) markers which showed 12.79%, 12.87%, and 14.61% of total phenotypic variations. The SRAP marker were tightly linked in 9 linkage groups in the size of 502.9cM with a mean interval of 5.5cM. The genetic variability of these three QTLs was due to additive genetic variance. In addition, a pair of epistasis QTL for _β_-carotene and lycopene accumulation showed 15.1% and 6.5% of total phenotypic variation, respectively. These SRAP markers linked to these QTLs could be used in selection or QTL pyramiding for high carotenoids and lycopene content in carrot breeding [33].

All five anthocyanin glycosides as well as root total pigment estimate (RTPE) differed quantitatively in the _F_ population. For the purpose of QTL analysis, a high resolution gene-derived SNP-based linkage map of carrot was constructed with 894 markers covering 635.1cM with a 1.3cM map resolution. A total of 15 significant QTL for all anthocyanin pigments and for RTPE mapped to six chromosomes. Eight QTL with the largest phenotypic effects mapped to two regions of chromosome 3 with co-localized QTL for several anthocyanin glycosides [34,35]. Ellison et al. [36] developed two closely linked codominant markers, 4135Apol, and 4144ApeKl, to more accurately select _y_y_ plants with increased _β_-carotene accumulation. These markers have been tested not only within the mapping population, but also in a group of unrelated genetic materials, and have proven to be very accurate in predicting orange and no orange phenotypes. Further they identified that the single large effect QTL on the distal arm of chromosome 7 overlapped with the previously identified _β_-carotene accumulation QTL _Y_. Fine mapping efforts reduced the genomic region of interest to 650kb including 72 genes [36].

This review briefly discussed about genetics and QTL mapping approaches in carrot for different carotenoids such as _α_-carotene,
β-carotene, γ-carotene, lutein and different anthocyanin pigments. It will help the carrot breeders to understand the genetic mechanism of different traits, application of molecular markers and to map the targeted nutritional content. Furthermore, recent development of genomic resources and genome sequence data will help the carrot improvement efforts and help to identify additional candidate genes underlying different carrot nutritional accumulation in carrots.

References
