सिएमएस वंशक्रमों का उपयोग कर शीतोष्ण गाजर (डॉकस कैरोटा ली.) में अनुवंशिक अध्ययन

HETEROSIS STUDIES ON YIELD AND QUALITY TRAITS IN TEMPERATE CARROT (*Daucus carota* L.) USING CYTOPLASMIC MALE STERILE (CMS) LINES

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NEW DELHI – 110012

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HETEROSIS STUDIES ON YIELD AND QUALITY TRAITS IN TEMPERATE CARROT (*Daucus carota* L.) USING CYTOPLASMIC MALE STERILE (CMS) LINES

A Thesis
By

HEMANT GHEMERAY

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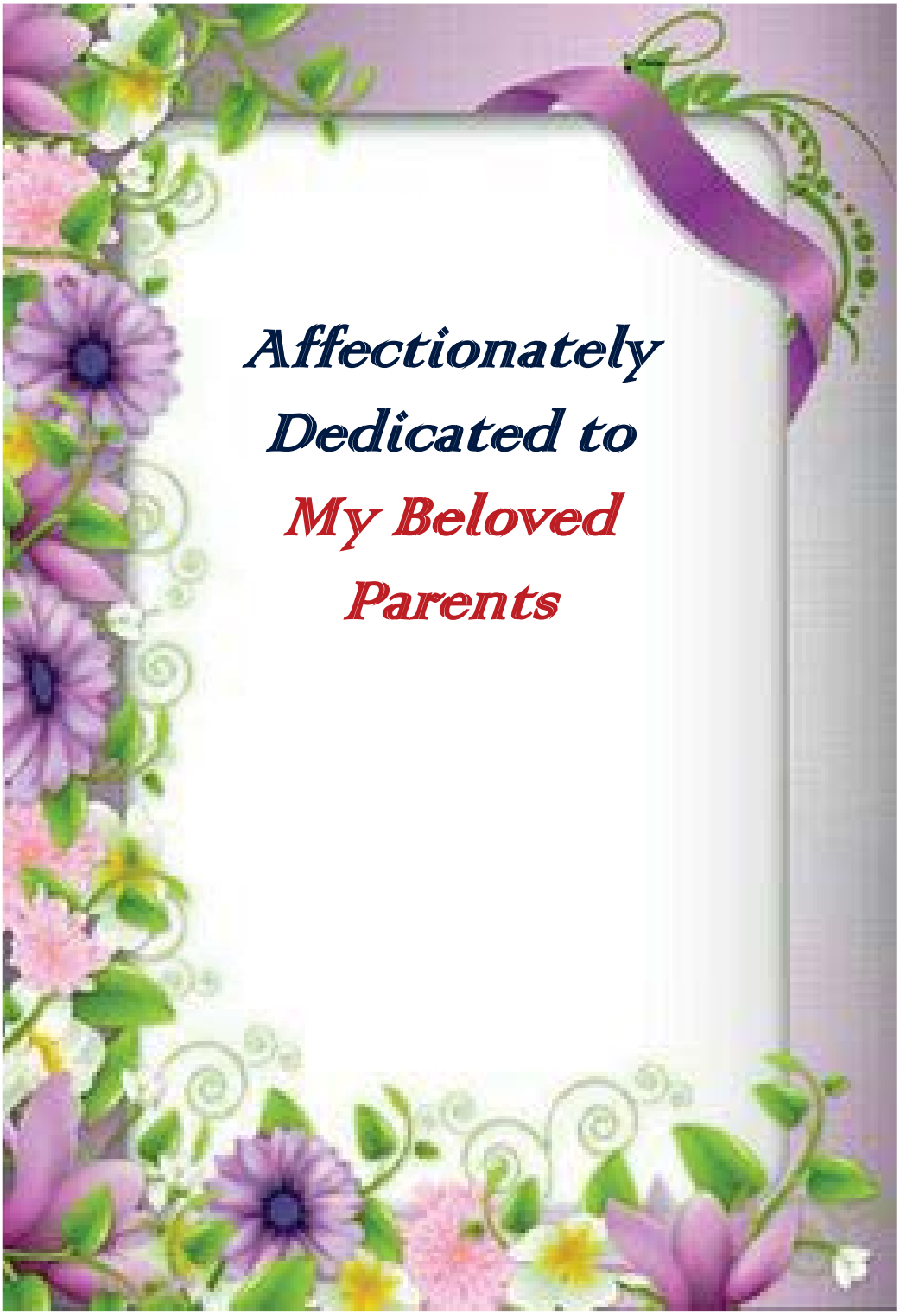
This is to certify that the thesis entitled "Heterosis Studies on Yield and Quality Traits in Temperate Carrot (*Daucus carota* L.) Using Cytoplasmic Male Sterile (CMS) Lines" submitted to the post graduate school, ICAR- Indian Agricultural Research Institute, New Delhi in partial fulfillment of the requirements for the tha award of DOCTOR OF PHILOSOPHY IN HORTICULTURE (VEGETABLE SCIENCE) embodies the results of bonafide research work carried out by Mr. HEMANT GHEMERAY Roll No. 10908 under my guidance and supervision. No part of the thesis has beeen submitted for any other degree or diploma award.

All the assistance and help received during the course of the investigaion have beeen duly acknowledge hy him.

Raj Kumar

Chairman, Advisory Committee


Affectionately
Dedicated to
My Beloved
Parents

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Place: New Delhi *Hemant Ghemeray*

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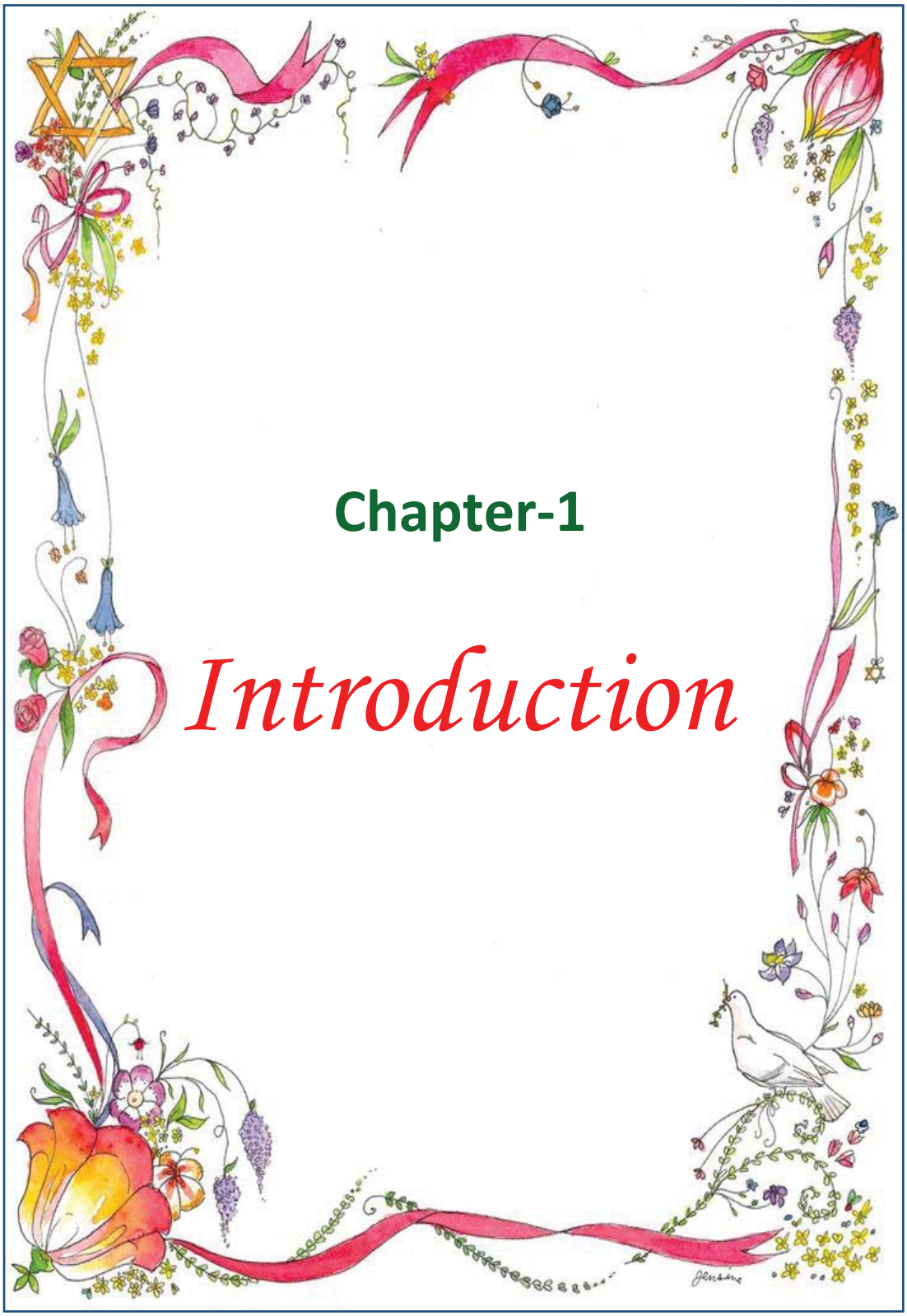
CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDIX



Chapter-1

Introduction

Chapter 1

Introduction

The eudicot plant family *Apiaceae* comprising 466 genera and 3820 species (Plunkett *et al*., 2018) contains numerous species of economic and nutritional importance. This aromatic family harbours species used as spices, vegetables, herbs, condiments and species having ethno medicinal value including some of the poisonous species (Plunkett *et al*.2018). The genus *Daucus* is one of the important genera belonging to this aromatic family, covering species from wide range of climatic regions across the world and exhibiting significant quantitative characters. The cultivated carrot (*Daucus carota* L. subsp. *sativus*, 2n = 2x = 18) is among the top ten most important vegetable crops with global distribution (Iorizzo *et al*. 2016). Because of wider adaptation , carrot serve as a significant source of nutrition and dietary vitamin A globally with major production areas of Europe, Asia and America including other tropical or subtropical regions (Que *et al.*2019). Carrot is a multi-nutritional dietary food source and has antioxidant, anticancer properties due to presence of carotenoids (α-carotene and β-carotene:$C_{40}H_{56}$), anthocyanins, lycopenes, phenolics, dietary fibres, minerals (Ca, Fe, P, Mg, etc.) and ascorbic acids (Sharma *et al*., 2012; Ahmad *et al*., 2019; Yoo *et al.,* 2020). Versatile colour variations are present in carrot with different bioactive compounds. The original carrots were purple and yellow in Central Asia, domesticated around 1,100 years ago (Rong *et al*. 2014; Iorizzo *et al*. 2016). These yellow or purple carrots are described as anthocyanin or eastern type carrots while the orange, red or yellow types are described as carotene or western type carrots (Rong *et al*., 2014). The western type carrots rich in carotenoids are profoundly utilized for human consumption. The origin of western type carrot is still obscure. Being rich source of carotenoids, carrots are considered vital for protection against cardiovascular disease (CVD), cataracts, jaundice and various types of cancers (Que *et al*., 2019). Due to this immense potential of carrots, the sequencing of carrot genome facilitated the determination of a key gene

DCAR_032551 regulating carotenoids accumulation in carrot roots. In addition to carotenoids, orange coloured carrots also consist of lutein, phytoene, lycopene and £-carotene (Arscott and Tanumihardjo,2010). Besides lycopene, red colour carrots commonly contain α-carotene and β-carotene. Anthocyanins are another class of ubiquitously present natural pigments imparting black, blue, purple colour to different fruits and vegetables (Singh *et al*., 2018a; Singh *et al*., 2018b). Anthocyanins have ROS scavenging activities and also include health benefits like protection from heart disease, different types of cancer and diabetes (Singh *et al*., 2018a; Que *et al.,* 2019). The importance of anthocyanins in health benefits facilitated the development of black carrot varieties across the world including India such as Pusa Asita, Kashi Krishna and Punjab Black Beauty. Lycopene is other important carotenoids prevalent in red colour carrots and having anticancer potential.

Recently, emphasis has been given to polyphenols in vegetable crops which renders colour, flavour, bitteness, odour and have radical scavenging activities (Leja *et al.,*2013). Phenolics acids and flavonoids are major class of polyphenols (Kamiloglu *et al.,* 2015). The phenolic constituents in carrots are of single aromatic ring (Arscott and Tanumihardjo, 2010). The study of ascorbic acid, cupric ion reducing antioxidant capacity (CUPRAC) and ferric reducing ability of plasma (FRAP) has been ascribe to be an effective method to find out antioxidant capacity of crops (Singh *et al.,* 2018). Besides having potential of carrots for functional food industry with multiple nutritional benefits, carrot is an important industrial crop for pigment industry as antioxidant and natural food colorants (Assous *et al*., 2014; Kumar *et al*., 2019). Carotenoids, anthocyanins, betalins, chlorophylls etc. are commonly utilized natural food pigments Cortez *et al.* (2016) and their consumption has been linked with decrease in different types of cancers, obesity and diabetes. The anthocyanin rich concentrates are prepared from processing of black carrots, and are considered as better choice for colouring soft drinks, fruit juices and jellies as healthy natural food colorant. Carrot fibre has excellent water retention

capacity which make it potential texturizing agent. Thus, carrot is considered as an affordable option in functional food and pigment industry with multiple nutritional and economic advantages. Attributed to above mentioned medicinal and natural food colorant properties of carrot, the development of nutrition rich hybrids has become the focus of carrot breeders worldwide. The cytoplasmic male sterility (CMS) based heterosis breeding has been proved instrumental in generation of high yielding and nutritionally rich hybrids across the vegetable crops (, Liu *et al*., 2019; Que *et al*., 2019). Among the CMS systems prevalent in carrots, the pt-cytoplasm based carrot resources exhibits replacement of stamens with petal like structures rendering failure of male reproductive function (Robison and Wolyn, 2006; Szklarczyk *et al*., 2014; Liu *et al.,* 2019). This phenomenon is regarded as maternally inherited petaloid type cytoplasmic male sterility. The mitochondrial *atp9* gene is associated with pt-CMS in carrot and (Szklarczyk *et al*.,2014) explained clearly the two functional carrot *atp-9* genes, *atp9-1* and *atp9-3*. They reported the overexpression of *atp9-1* relative to *atp9-3* in CMS plants, whilst reverse is true in fertile plants. Owing to a point mutation occurred at a stop codon (TAA) the open reading frame (*orf*) of *atp9-3* is 13 amino acid shorter than *atp9-1.* The petaloid type CMS system is quite stable and has been widely exploited for heterosis breeding in carrots (Morelock *et al*., 1996; Szklarczyk *et al*., 2014; Que *et al*., 2019). The quantity and composition of phytochemical profiling in carrots vary widely among different root colors, tissues, organs during plant growth and development, type of genotype genetic background and cultivars type (Sharma *et al.,* 2012; Ahmad *et al.,* 2019). Much progress has been made towards identification of carotenoid biosynthetic genes in carrot. About 44 and 24 genes have been well determined in carrots for isoprenoid biosynthetic pathway and carotenoid biosynthetic pathway, respectively (Iorizzo et al.,2016). Hence, breeding for nutrition rich hybrids is gaining impetus in carrots. In this context, petaloid type CMS system is conspicuous in carrot and the development, identification, maintenance of suitable inbred parents is basic requirement. The

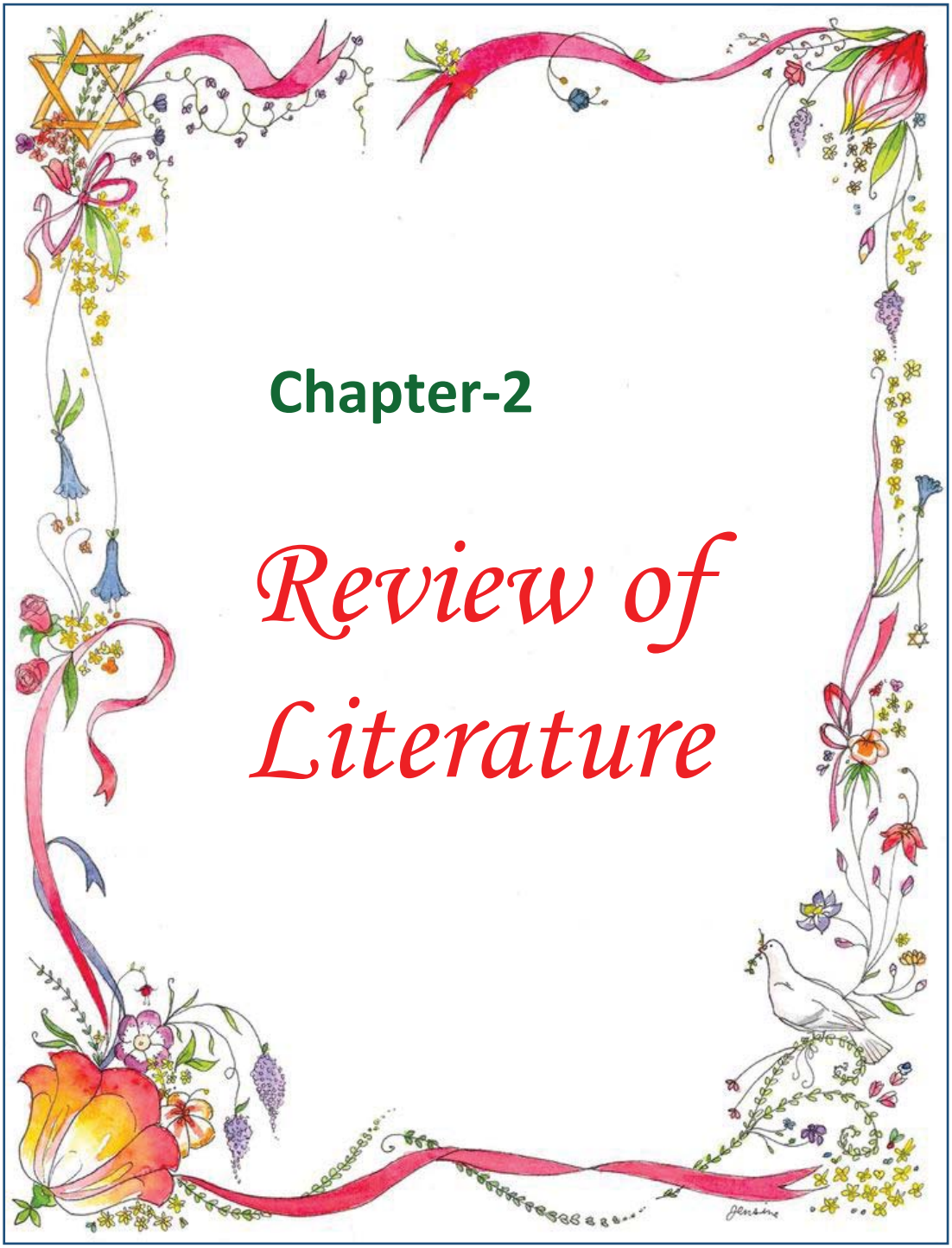
combining ability is pivotal for choosing the superior heterotic parents in carrot heterosis breeding. In order to develop heterotic hybrids, it is important to select proper parental pairs with corresponding quantitative characters traits and biological parameters. The value of parental forms is best outlined by their combining ability, which is established by trait inheritance in hybrids (Karkleliene *et al*.,2005). Hence, combining ability study is remain prerequisite for selecting of superior heterotic parents in carrot hybrid breeding. There are two types of combining ability, general combining ability and specific combining ability. The former refers to the average performance of a line and useful in the selection of parents for hybridization. Whereas, specific combining ability refers to the specific performance of a cross and useful in the selection of superior hybrids. For estimation of combining ability, crosses had to be made in line × tester fashion. For desirable selection and subsequent hybrid development both general combining ability (GCA) and specific combing ability (SCA) which characterise and related to the breeding value of either parent, its association with additive gene action, and other related to non-additive effects respectively are requisite for finding better parents and better population structure. Hitherto scanty details to be had against gene action, heterosis and combining ability in temperate CMS based hybrid carrot allied to antioxidants synthesis, concurrently no such details available concerning exploitation of CMS regime in carrot. Moreover, the farmer acceptance for F_1 hybrids is expanding because of its consistent uniformity, versatility, quality and tolerance to various stresses. For desirable selection and subsequent hybrid development both general combining ability (GCA) and specific combing ability (SCA) which determines additive and non-additive gene effects, respectively, are essential for population improvement (Singh *et al*., 2018a; Aditika *et al*., 2020). Basic knowledge of the heritability and combining ability of lines plays an important role in reducing the costs and time of carrot breeding (Jagosz *et al*., 2012). Knowledge about the trait inheritance and genetic basis of heterosis is not well known in tropical carrots, since limited work has been

carried out in tropical carrots. Very few public sector hybrids had been released so far in tropical carrot. Thus, the studies regarding combining ability and heterosis in tropical carrot had to be made in a greater extent, which would be helpful in the development of superior carrot hybrids and for future breeding programme. Hitherto, scanty knowledge is available for the study of combining ability, gene action and development of heterotic antioxidant rich carrot hybrids based on petaloid type CMS system. Then meagre information is available regarding exploring potential of petaloid CMS based heterotic hybrids of carrots for nutrition and natural food colorant industry. Therefore, the present investigation is first of its kind for accomplishing the objectives of hybrid breeding for various commercial horticultural traits and functional food industry. The current experimentation investigation giving an insight observation of heterosis and combining ability based on indigenously developed petaloid CMS lines in temperate carrots to realise the opportunity of developing horticultural and antioxidant rich hybrids carrot with industrial and nutritional standards. Estimation of genetic diversity and combining ability forms an integral part of heterosis breeding. Thus, the studies regarding combining ability and heterosis in temperate carrot had to be made in a greater extent, which would be helpful in the development of superior carrot hybrids and for future breeding programme. Keeping in mind the above circumstances, the present study "**Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus)* using Cytoplasmic male sterile (CMS) lines"** was carried out with the following objectives:

1. To characterize temperate CMS lines for important horticultural and quality traits

2. To study heterosis and combining ability for horticultural traits

3. To study gene action for yield and quality traits using CMS based F_1 hybrid population



Chapter-2

Review of Literature

Chapter 2

Review of Literature

A brief review of the research works conducted in a carrot for improvement of yield and yield-contributing traits has been made in this chapter. This would be greatly helpful for gaining a better understanding of the study. A basic outline of the works in carrot regarding combining ability using cytoplasmic male sterility (CMS) lines and heterosis breeding for several quantitative and qualitative traits had been presented below.

2.1 Quantitative characters and Qualitative characters Characterization of Parental Lines

Carrot is one of the most important dietary sources of pro-vitamin A across the world. It is an important nutritional crop and is a significant source of antioxidant compounds (Que *et al*., 2019). It is a potential component of functional food and natural pigment industry. Despite of its economic, dietary and industrial value, meagre efforts have been made for enhancing its productivity in the country like India. In this context, the present investigation highlights the potential of petaloid type CMS system of temperate carrots using indigenous germplasm for enhancing its nutritional and industrial value. The essence of any crop genetic improvement programme lies in crop genetic diversity and appropriate characterization of germplasm. Nowadays, the cytoplasmic male sterility (CMS) based heterosis breeding has been proved instrumental in generation of high yielding and nutritionally superior hybrids across the vegetable crops (Singh *et al*., 2019a; Singh *et al*., 2019b; Liu *et al*., 2019; Que *et al*., 2019).. The mitochondrial *atp9* gene is associated with pt-CMS in carrot and Szklarczyk et al. (2014) explained clearly the two functional carrot atp-9 genes, atp9-1 and atp9-3. They gave an account of the overexpression of ATP synthase gene viz., atp9-1 compare to atp9-3 in CMS

plants, while reverse is true in case of fertile plants. Due to a point mutation takes place at a stop codon, the open reading frame (ORF) of atp9-3 is 13 amino acid smaller than atp9-1. Since the estimation of the degree of variation among the superior breeding populations, inbred lines and varied plant genetic resources is of prime importance in population genetics and crop breeding methodology. Much progress has been made towards identification of carotenoid biosynthetic genes in carrot. About 44 and 24 genes have been well determined in carrots for isoprenoid biosynthetic pathway and carotenoid biosynthetic pathway, respectively (Iorizzo *et al.,*2016). Hence, breeding for nutritionally rich hybrids is gaining impetus in carrots. In this context, petaloid type CMS system is conspicuous in carrot and the development, identification, maintenance of suitable inbred parents is basic requirement. In another study, the 16 genotypes of *Daucus carota* L. were characterized for few quantitative characters traits by (Priya *et al.,*2015). The profound variability was observed for different quantitative characters traits and higher amount of variability was also reported for vegetative, pre-flowering and maturity traits in contrast to seedling traits. Out of total variation, the 87.24% of variation was explained by first 5 axis based on principal component analysis (PCA). (Koley *et al.,*2014) evaluated 16 Indian commercial carrot cultivars for β-carotene, total phenolics, total flavonoids, total monomeric anthocyanin and antioxidant activity. Antioxidant activity was measured using four *in vitro* assays viz. ferric reducing antioxidant power among carrot cultivars, significant differences were obtained with respect to antioxidant composition and antioxidant activity. Total phenols and total flavonoids varied from 7.98 to 291.48 mg/100 g fresh weight (FW) and 3.00 to 111.70 mg/100 g FW respectively. PCA revealed that the first two components represented 92.9% of the total variability in the total variation. Orange cultivars were found to be rich sources for β-carotene compared to red & black cultivars. Antioxidant compounds are widespread in the plant kingdom including fruits and vegetable crops, and they play a significant role in plants and human health. The discovery

and subsequently the isolation of vitamin C evoked the interest in antioxidant activity and their extraction from plants (Kasote *et al.,*2015). The major carotenoids determined in carrots were β-carotene (41.60–71.2 mg/kg FW). The total phenolic contents of carrots ranged from 114–306 mg catechin/kg FW. There was considerable variation in carotenoid contents between locations and years among cultivars. Significant differences were found between the two consecutive years in total phenolic contents and level of antioxidant activity in carrots varied significantly over the years (Bozalan and Karadeniz, 2011). However, the orange carrot possessed higher amount of carotenoids. The content of carotenoids negatively correlated with total phenolics, flavonoids and antioxidants activity. Hence, they concluded that broad genetic base and selection based on total antioxidant content could be significant component in the future carrot-breeding programme.

2.2 Analysis of genetic diversity and genetic structure based on molecular markers

The greater the genetic diversity among the parental lines, the greater the heterosis in hybrids. Molecular markers can best estimate the genetic diversity among the genotypes. In spite of its immense economic possibility in a hybrid breeding, the molecular fingerprinting behind this biological event are still limited (Lippman and Zamir 2007; Groszmann *et al.* 2013; Fujimoto *et al.* 2018; Li *et al.* 2018). The contemporary advancement in QTL and genomic study have helped in setting out the heterosis by describing exhaustive expression study of hybrid vigour in different crop plants at gene level (Groszmann *et al.* 2013; Fujimoto *et al*.,2018; Li et al., 2018; Lauss *et al*., 2018). (Niemann *et al.,*2001) initiated the identification of SSR loci in carrot for linkage mapping. In cross-pollinated crops like carrot, the molecular diversity was very high and non-structured. The study demonstrated that URPs can be used successfully in genetic diversity study of carrots. Likewise a study was conducted to understand the heterosis and genetic distances in carrot using RAPD and AFLP markers (Jagosz *et*

al.,2011). The experiment was conducted with 15 inbred lines and 34 hybrids. The correlation between heterosis in carrot hybrids and the genetic distances of their parents was estimated in this study. The traits taken for evaluation include yield traits *viz.* total yield and marketable yield and other quality traits *viz.* carotenes, dry matter, total sugar, monosaccharides and nitrates. Mid-parent and high-parent heterosis was also calculated. RAPD and AFLP techniques were used to calculate genetic distances. Heterosis for total and marketable yield was found to be significant. Thus, estimation of the genetic distances was found to contribute for carrot hybrid yield prediction. This work would be helpful for the reduction of costs and quicker identification of superior hybrids since it favours the possibility of heterosis prediction. In another similar study, molecular genetic diversity among parental lines, using 15 parents and 50 F_1 hybrids were studied. The hybrids showed 18% higher average root yield compared to parents. The genetic diversity study of parents using various informative molecular markers revels that ISSR markers were more instrumental for molecular characterisation study in carrot. For all the 15 carrot lines, the homogeneity study enumerates the genetic similarity ranged from 0.45 to 0.73 and the genetic distance out of these genotypes ranged from 0.27 to 0.55 suggesting high diversity among the genotypes (Kushalf *et al.,* 2011). Subsequently, simple-sequence repeats (SSRs) have become the most preferred marker for population genetic analyses. A set of SSR markers used to study gene dispersal in wild carrot populations (Rong *et al*.,2010). Even though carrot is economically most important member of Apiaceae family, the molecular resources in this species are relatively underdeveloped. The breeding of carrot will be facilitated by the availability of informative, polymorphic and robust PCR-based markers, such as microsatellites (or SSRs) (Cavagnaro *et al.* 2011). They reported on the development of 300 carrot SSR markers and their characterization at various levels, which will facilitate future studies and assist in breeding, genetic diversity analysis and genomic studies of carrot and other members of Apiaceae family. Recent results of (Clotault *et al.,*2010) indicated that SSR

markers were helpful in evaluation of genetic diversity in the cultivated carrot. For the assessment of genetic diversity of populations occurring in natural habitats and large gene bank collections, microsatellite or simple sequence repeat (SSR) markers proved to be useful. It is also useful in revealing relationships between crop plants and their wild relatives (Varshney *et al.,* 2010; Kalia *et al*.,2011). However, the development of SSRs is costly and time consuming. So, nowadays expressed sequence tags (ESTs) can serve as a potential source of SSRs, which can reveal polymorphism within and between the related taxa (Ellis and Burke, 2007). In addition, an entirely a new set of microsatellite markers, derived from the expressed sequence tags (ESTs) sequences of carrots, have been developed and utilized successfully. Here in our study using simple sequence repeat (SSR), polymorphism was assessed different Indian temperate carrot lines and landraces. Plants were grown in the field and characterized for various traits. Hence, it is believed that the Asian gene pool showed higher genetic diversity than the Western gene pool. The results of SSR analysis supported by quantitative characters characterization and in agreement with current knowledge on the history of carrot domestication and breeding (Baranski *et al*., 2012).

2.3 Heritability and gene action

Heritability is the most important component exploited by plant breeders and geneticists as a tool to quantify the precision of a field trial for single trait or series of characters. The success of any crop genetic improvement programmes to the great extent depends upon heritability of the traits, which denoted as the ratio of variances, i.e. proportion of variance due to the variation in additive genetic variation of genotypes (Visscher *et al*.,2008). The main role of heritability is to compute the response to the selection. Moreover, the heritability can be classify into two groups namely, broad sense heritability ($H^2_b = V_G/V_P$; $VG = V_A + V_D + V_I$), which represents the proportion of phenotypic variation and includes the dominance and epistatic effects, contrarily narrow sense heritability ($h^2_{ns} = V_A/V_P$; $V_P = V_G + V_E$) signifies the

proportion of phenotypic variance attributable to additive genetic effects (Visscher *et al.*,2008; Evans *et al*., 2018). The narrow-sense heritability holds a very significant position in crop improvement programme, as it amenable to artificial and natural selection depends on additive genetic variance (Visscher *et al*., 2008; Evans *et al.,* 2018). Moreover, crop diversity and creation of heritability are the essentials in crop improvement programme. Hence, it is the aggregation of interaction among the environment, genetic resources and management systems and practices, encompassing the variety and variability that are necessary for sustainable food production and food security (Renna *et al*., 2018). However, the genetic diversity based on quantitative characters data does not reliably depict true genetic variation as the majority of the quantitative characters traits are highly influenced by environmental conditions and are having polygenic inheritance (Zhang *et al*.,2015). Generally, the phenotypic characterisation exercised for varietal characterisation and then for formulating genetic analogy. Among 96 genotypes the significant variability and high heritability with higher genetic coefficient of variation (GCV) was observed. Yield parameters like root weight, vegetative weight, harvest index possessed higher values of GCV, heritability and genetic gain and suggested traits specific information can be applied in crop improvement. Correlation and path coefficient studies in carrot were studied by (Bhagchandani and Choudhury,1980). Examination of the parents and F_1 from a 6 × 6 diallel cross (with reciprocals) involving inbred lines indicated that root weight (yield) was positively correlated phenotypically with top length and weight, root length, and diameters of root and root core. Path coefficient analysis showed that root diameter had the highest direct effects on yield, followed by top weight and root length. Root diameter recommended as the most reliable selection criterion for improving yield. In another study, inheritance and expression of purple and yellow storage root colour in carrot studied. It has found that the purple and yellow root colours were conditioned by single dominant gene, P_1 and Y_2. Among these Y_2 conditioned low carotene content of the storage root xylem ("core") in high carotene

orange background whereas in lower carotene orange background the yellow appearance often spread into phloem. P_1 and Y_2 not linked to each other. P_1 showed differences in expressivity within storage roots and throughout the plant. Purple root and flower pigmentation inherited together in derivatives of PI 173687, but PI 175719 purple-rooted derivatives had no purple flower pigmentation (Simon *et al.,*1996). Studies regarding genetic variability, heritability and genetic advance for various quality characters were conducted and considerable amount of genetic variability were present. In which, highest value of genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as percentage of mean was observed for carotenoid content. Thus, it was clear that the carotenoid content could improve through selection (Kaur *et al.,*2005). Heritability and genotypic correlation among leaf and root traits in carrot, cultivar Brasilia progenies were studied by (Alves *et al.,*2006). The objective of this work was to estimate genetic parameters associated with traits of importance to carrot breeding, including: number of leaves per plant (NL), root length (RL), root weight (RW), root diameter (RD), and xylem diameter (XD). The experiment consisted of 69 half-sib families derived from cultivar Brasília. The broad-sense heritability (h_a^2) values ranged from 29.9% (for RD) to 77.6% (for LL). Genotypic, phenotypic, and environmental correlations showed a large variation in magnitude with the highest genotypic correlation (0.85) being observed between the traits RW and RD. Negative genotypic correlation was observed between RL and XD, which indicates that the development of new cultivars suitable for processing the baby-carrots is feasible using populations derived from cultivar Brasilia. High negative environmental correlation values were obtained between the traits RW and XD, as well as RD and XD. This information would be of extreme importance aiming to optimize the selection process when using segregating populations derived from the tropical-adapted cultivar Brasilia. Another study was conducted to determine the extent of genetic variability to find the inter relationship of different traits and its direct and indirect effects on yield in which twenty seven

F_1 hybrids were evaluated at IARI regional station, Karnal to determine the genetic variability, correlation and path coefficient for eleven traits. Top length, gross weight/plant and net root weight/plant showed high heritability with high genetic advance as percentage of mean, which revealed that these traits are governed by additive gene action and selection will be more effective for these traits. Path analysis studies for net marketable root weight/plot indicates that gross marketable weight/plot founds to be the most important yield contributing traits, that is followed by other traits like net root weight/plot, top length, root girth, root to shoot ratio and percentage of unmarketable root. Hence, while selecting the genotypes for increasing the yield, importance should be given to the above-mentioned traits. Characterization of European carrot genotypes through principal components and regression analyses was studied by (Kumar *et al*.,2011). The effect and contribution of each character on root yield was measured. The genotypes were characterized into four principal components based on their total variation (83.86%). A combination of characters like root diameter root weight, marketable root yield, core diameter, flesh thickness, shoulder thickness, and days to marketable maturity forms the first principal component accounted for more than 39% of the total variation. Multiple linear regression models were developed to quantify the importance of each variable in predicting average root weight and marketable root yield. Based on model I it is found that the average root weight can be predicted on the basis of leaf length, shoulder thickness, crown diameter, marketable root yield per plot, forking, and cracking percentage. While marketable root yield can be best predicted by shoulder thickness, crown diameter, root weight, and cracking percentage as on model II. It is clear that for the estimation of total yield including marketable and nonmarketable roots, model I is suitable for and for the estimation of marketable yield model II is best. Genetic analysis of root yield and its contributing traits in tropical carrot was studied by (Selvakumar *et al*.,2017). Determining the gene action involved in the inheritance of economic traits of three carrot hybrids by using six generation mean analysis (P_1, P_2, F_1, F_2,

B_1 and B_2) was the objective of this study. Gene actions involved in the inheritance of economic traits, *viz*., root length, root weight, shoulder diameter, root diameter, flesh thickness, core diameter and root to top ratio were analyzed using three crosses of carrot. In the all white pale crosses the genetics of root weight, root to top ratio and root diameter were complementary type of gene interaction. Based on the results obtained they concluded that the improvement of tropical carrot for these traits can be done through biparental mating followed by mass and cyclic recurrent selection in advanced generation. (Chaitra A. *et al* 2017) studied diverse carrot genotypes under tropical conditions for their genetic variability parameters, reported higher heritability for shoulder length and shoulder width and all the other characters showed low to moderate heritability indicating the influence of environment on these traits. Hence provides useful information about the genetic variation available in carrot for the root traits, which helps us to plan a suitable strategy for the crop improvement of carrot to tropical region. Heritability in a broad sense presented a higher environmental influence for yield than the quality characters of carrot roots. Selection of inbred parents and identification of suitable heterotic combinations is decisive to expedite any breeding programme.

2.4 Combining ability

2.4.1 Quantitative characters Traits

(Sincik *et al*., 2014) estimated the combining ability in turnip rape through diallel analysis involving five diverse genotypes. A 5 x 5 full diallel crosses study, including the reciprocals, with turnip rape (*Brassica rapa* L.) was performed to determine both the magnitude of gene action and heterotic performance of the crosses for seed yield and important yield components. All 20 F1 hybrids and their parents were sown in a randomized complete block design with 3 replicates. During both years, the mean squares of the general combining ability (GCA), specific combining ability (SCA) and reciprocal combining ability (RCA) were statistically significant for all traits evaluated. The parent Malvira was a good general combiner because

this parent had the highest significant positive GCA effects for all the characteristics evaluated. In addition, Lenox proved to be a good general combiner for plant height. The significant positive mid-parent and high-parent heterosis values were obtained with several crosses in important yield components. In conclusion, the parents used in this study exhibited positive GCA effects for seed yield. Therefore, they could be considered as promising parents in the production of F1 hybrids and in further breeding studies. (Barbara Jagosz *et al*., 2012) investigated the combining ability of inbred lines in terms of traits important for the development of hybrid carrot cultivars with high yields and better root quality. The experimental plant material consisted of 15 inbred lines that were crossed in an incomplete diallel design to produce 34 hybrids. It was observed that the variation of general combining ability (GCA), specific combining ability (SCA) and reciprocal effects (RE) were significant for most of the tested characters. Among the tested lines, the RFO had the most positive GCA for the yield.Most of the crosses based on the RFO and 2163 lines yielded well. The ratio of GCA: SCA indicated that additive gene effects mainly affected the quality traits, but non-additive gene effects controlled the yield more. The units of general combining ability (GCA) and specific combining ability (SCA) is imperative for determination of any parental genotypes and inbreed lines in crossing programme (Kaushik *et al.,*2018). The assessment of SCA correlated with non-additive effects i.e. dominance effects; additive × dominant and the dominant × dominant interactions. Since, line x tester analysis emerges as an ideal biometrical technique for evaluating combining ability effects of lines and testers and bringing knowledge with respect to nature of gene actions (Kempthorne 1957; Esposito *et al.*, 2014; Dey *et al*., 2014). The parental GCA estimates in desirable direction also indicates potentiality of parents in generating promising breeding populations.

2.4.2 Quality traits

Carrot is an important nutritional crop and is a significant source of antioxidant compounds (Que *et al.,* 2019). It is a potential component of functional food and natural pigment industry. Despite of its economic, dietary and industrial value, meagre efforts have been made for enhancing its productivity in the country like India. Study on carotenoid content of carrot varieties and (Harper and Zscheile, 1945) made lines. In which, carotenoid content of 16 commercial varieties and 18 superior lines of carrots were measured with a photoelectric spectrophotometer and chromatography. Based on its relative position on the adsorption column and colour, lycopene and γ- and ζ-carotene were identified. For improving the quality of carrot, the carotenoid content has to be improved, since it is the most beneficiary compound in carrot. To examine the differences in carotenoid, antioxidant, vitamin content, total phenolic acids level and mineral contents between several genotypes of carrot, Nicolle et al. (2004) conducted a study. They observed a large variation in the content of carotenoids ranging from 0.32-17 mg/100g of fresh weight. In yellow and purple carrots, lutein represents nearly half of the total carotenoids. In contrast, in orange carrots, beta carotene is the major carotenoid (65%). It was found that among various coloured carrots, dark-orange carrots exhibited highest values for all the components. Thus, purple and dark-orange carrots should be preferred to usual carrot varieties to benefit from the various micronutrients while white carrots are rich in Vitamin C content. (Antonio *et al.,*2006) estimated the heritability and minimum gene number for production of total carotenoids. They reported that the broad sense heritability for all carotenes ranged from 28-48% except lycopene and phytoene (44-89%). The gene number estimates for carotenoids showed that the inheritance of *α*-carotene, β-carotene and total carotenoids in the orange × dark orange cross was continuous while for β-carotene and total carotenoids in the orange × white cross was discrete inheritance. (Baranski *et al.,* 2012) studied tissue specific accumulation of carotenoids in carrot roots.. The level of β-carotene was heterogeneous

across root sections of orange, yellow, red and purple roots, and in the secondary phloem increased gradually from periderm towards the core, but declined fast in cells close to the vascular cambium. (Kaur *et al.,*2009) studied genetic variability, heritability and genetic advance for quality traits in carrot. The experimental material comprised of 38 Asiatic and European carrot genotypes of diverse geographical origin. All the varieties differed significantly with respect to different characters studied. They reported wide range of variation for different traits viz., carotene content from 0.78 mg/100g (Hisar Local-10) to 6.01 mg/100g (Alipur Collection), juice yield from 440 ml/kg (PC32) to 559.5 ml/kg (Hisar Local-10) and total sugars from 2.92% (HC-116) to 4.91% (Pusa Kesar). GCV ranged from 5.39% (juice yield) to 50.14% (carotene content). This showed that the carotene content having higher range of variation and have a better scope of improvement through selection. However, accurate results obtained, when heritability studied in conjugation with genetic advance. The genetic advance revealed that carotene content (103.18) had high genetic advance. Though characters such as juice yield had high heritability value, their GCV was comparatively less resulting in less genetic advance. In order to improve the quality traits of tropical carrot, (Kushlaf and Kalia, 2012) conducted experiment to develop bio fortified carrots with five CMS lines crossed with ten fertile inbred lines in a line × tester fashion during 2008-2009. The 15 parental genotypes and their resulting cross combinations evaluated in RBD with three replications. At optimal marketable stage, ten plants taken at random for recording the horticultural and quality traits. The 10 parental genotypes of IPC series remains found be suitable parents with higher heterotic ability for many characters. Similarly, the hybrids like IPC 11 × IPC 13, IPC 11 × IPC 104 and IPC 126 × IPC 76 could be useful for specific traits, whereas IPC 126 × IPC 104 as multi-nutrient rich including anthocyanins for carrot breeding programmes. Recently, Koley et al. (2019) carried out profiling of antioxidant activity of *in vitro* assays viz. ferric reducing antioxidant power (FRAP), cupric reducing antioxidant power (CUPRAC). Among carrot

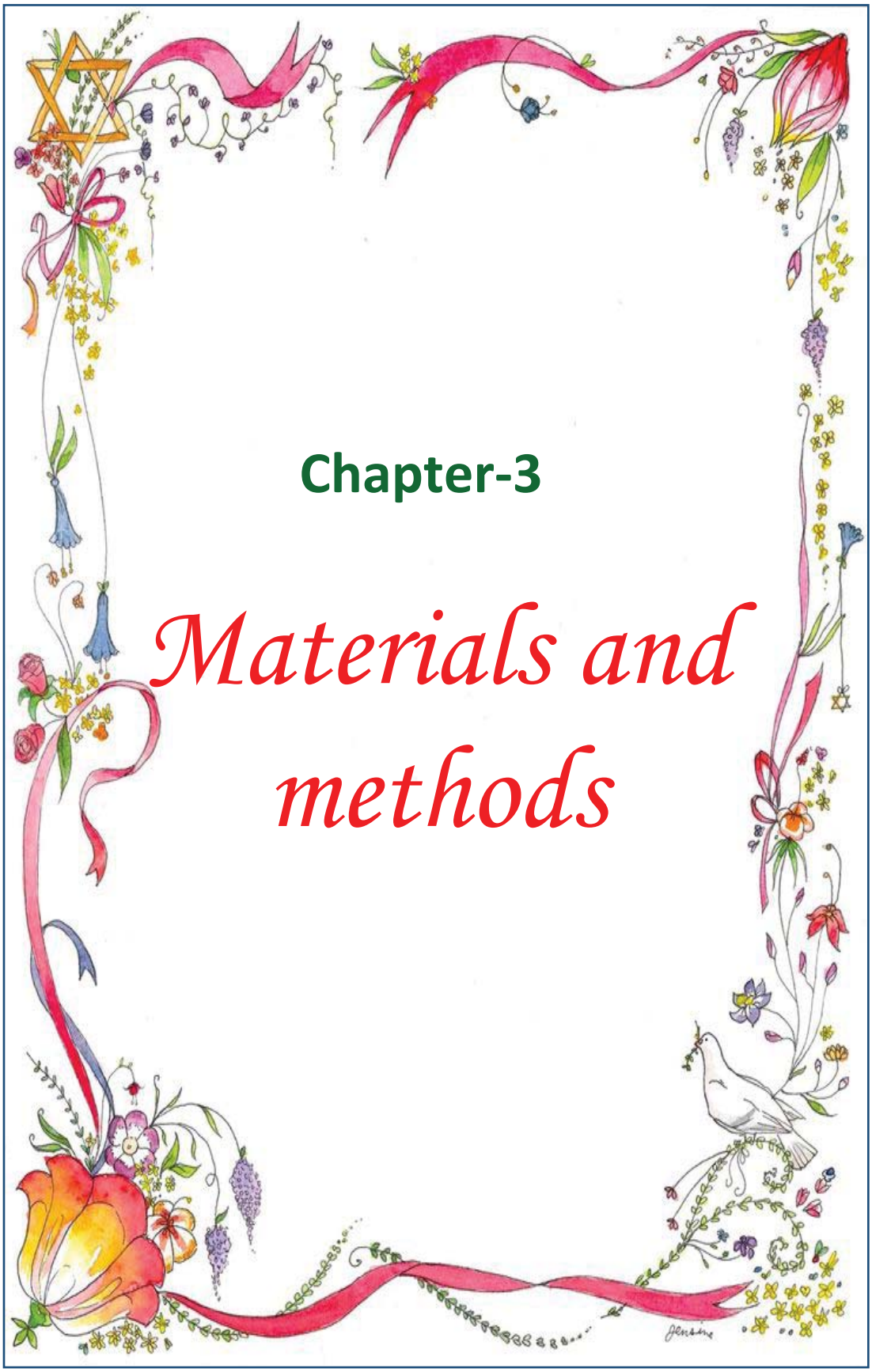
genotypes, significant difference ($p<0.05$) was observed with respect to antioxidant composition and antioxidant activity. Total phenols and total flavonoids varied from 12.59 to 290.18 mg GAE/100 g fresh weight (FW) and 4.91 to 109.2 mg CE/100 g FW respectively. High positive correlation between phenolics and antioxidant activity suggested that phenolics might be predominant antioxidant in carrot.

2.5 Heterosis

Shull (1914) first coined the term heterosis. Heterosis is the phenomenon where offspring manifests better qualitative, quantitative attribute compare to either of its parents, and it is generally termed as F_1 hybrids in crop plants. The F_1 hybrids display heterosis and uniformity for various qualitative and quantitative traits compared to open pollinated varieties (OPV). Heterosis or hybrid vigour, resulting in concentration of favourable parental genetic makeup and exhibit outstanding traits of hybrid offspring relative to the average of their genetically diverse parents (Lauss *et al*., 2018; Fujimoto *et al*., 2018). So far, different hypothesis and genetic mechanisms have been put forward to elucidate this complex phenomenon viz., dominance model, over-dominance model and epistasis model (Groszmann *et al*., 2013; Fujimoto *et al*., 2018; Li *et al.*, 2018). Various theories have been put forth to explain the genetic basis of heterosis; expression of hetrozygosity and accumulation studies of favourable dominant alleles in the F1 contributed by both male and female parents. It has found more pronounced in cross-pollinated species. The production of heterotic F_1 hybrids involves the series of stages i.e., identification and characterisation of CMS lines, production of maternal CMS lines, then development of fertile parental inbreed lines with significant traits with high general combining ability (GCA) in desirable directions. Finally, selection best heterotic crosses and testing of F1 progeny remain most critical production of hybrid seed (Kvasnikov and Zhidkova, 1980). The method of has greatly contributed to the increase in crop productivity. A one of the major component that exploits heterosis in crops is the cytoplasmic

male sterility (CMS). Cytoplasmic male sterility CMS is a maternally inherited trait facilitating efficient hybrid seed production as it is a maternally inherited trait that often associated with open frames (ORFs) found in mitochondrial genome (Chase *et al* 2007). Cytoplasmic male sterility has been transferred/ introgressed into improved carrot genetic background (Kalia *et al*.,2004). The petaloid type CMS system is quite stable and has been widely exploited for heterosis breeding in carrots (Morelock *et al.* 1996; Szklarczyk *et al.* 2014; Que *et al.,* 2019). It is regulated by Sp cytoplasm with two independent genes (M1M2). Among the CMS systems prevalent in carrots, the Sp-cytoplasm based carrot resources exhibits replacement of stamens with petal like structures rendering failure of male reproductive function (Robison and Wolyn, 2006; Szklarczyk *et al*., 2014; Liu *et al.,* 2019). This phenomenon is regarded as maternally inherited petaloid type cytoplasmic male sterility. The biological phenomenon of heterosis long been proved to be instrumental in enhancing horticultural productivity in carrot. Heterosis for marketable yield measured at 25 to 30 % over open pollination cultivars. Most cultivars are two or three way hybrids and produced by cytoplasmic male sterility. The aim of carrot breeding depends on the production method and the intended breeding objective. An increase in productivity is always one of the main goals of any crop-breeding program including carrot however; importance in increase in yield potentials of horticultural and quality traits is major objective. Since, carrots contain different combinations and concentration of macronutrients and nutrients. Moreover, carotenoids remains the main determining factor, which can be indicative of nutritional value and consumer acceptability. It has been reported significant heterosis for quantitative and yield traits carrot. Which increase and manifested the genetics of heterosis in quantitative characters characters viz., root yield, uniformity in root maturity, root shape, size and nutritive value (Kvasnikov and Zhidkova,1980). Therefore, new technologies put impetus to accelerate crop improvement through improving phenotyping and genotyping methods and by increasing the available

genetic diversity in breeding germplasm (Tester *et al.,* 2010). Following the report of cytoplasmic male sterility (CMS), the generation of CMS based hybrids in carrot become prominent. Since as per many report CMS can appears following spontaneous mutation as a product of distant hybridisation and interchanging of nuclear and cytoplasmic genes. Hence, these very breeding tools successfully used for a longer time. As per many reports important horticultural traits for carrot like root characters, quality traits and composition of phytochemical profiling in carrots vary widely among different root colors, tissues, organs during plant growth and development, type of genotype genetic background and cultivars type (Sharma *et al.,* 2012; Ahmad *et al.,* 2019). Hetrosis in carrot has been for various quantitative traits viz., root length, root yield, core diameter, root diameter and most carotenoid content. This phenomenon has been much developed in both temperate and tropical carrot as it can sustainably lowering the cost of hybrid seed production. However, the intensity of use of principle procedure much less frequently used in recent past in temperate carrot. Therefore, it is necessary to harness it in temperate carrot enabling present breeding prospects. (Verma *et al.*, 2002) evaluated heterosis for many quantitative characters traits in some of the prospecting CMS lines of carrot viz., 28 and 240607 as female lines. Similarly, four CMS lines viz., 1060, 1061, Autumn king and Shin Kuroda identified as male sterile parent and their crosses recorded significant heterosis. Litvinova *et al.*, (1979) successfully identified few CMS lines viz., Nantes-14, Chanteny-2461 in F1 hybrid production of temperate carrot and reported a heterosis of 20-22% higher than other commercial check. Subsequently tester of significant carotenoid content made crossed with superior CMS lines followed by practicing standard backcrossing procedures. As results, significant relationship detected between the petaloid CMS type and high carotene content lines.



Chapter-3

Materials and methods

Chapter 3

Materials and Methods

The representation of materials and methodology taken during the course of experimentation entitled "Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus)* using Cytoplasmic male sterile (CMS) lines" has been presented in this chapter.

3.1 Experimental Location and Plant Materials

The field experiment under the present investigation was carried out during 2016-2017 and 2017 -2018 at Naggar Experimental Farm of ICAR-IARI, Regional Station, Katrain, and Himachal Pradesh, India, located along the left bank of river Beas. The Naggar research farm is located at the geographical latitude and longitudes of 32.12N and 77.13E, respectively, and at 1,800 m altitude above mean sea level (AMSL). The experimental site received annual rainfall and snowfall of 950-1000 mm and 1000-1100 mm, respectively. The large numbers of cytoplasmic male sterile (CMS) lines of temperate carrot have been developed at ICAR-IARI, Regional Station, Katrain, following repeated backcrossing for more than ten generations and even some of the CMS lines are at BC_{14} stage. In the current study, the plant materials constitute a set of 10 CMS lines of temperate carrot (used as female parent) having promising quantitative characters and floral characteristics (Table 3.1). A large number of superior lines of temperate carrot were developed at this station. The experimental plant material also included single commercial CMS based carrot F_1 hybrids from ICAR-IARI Regional Station Katrain as standard checks (Table 3.1).The parental CMS and pollen parents used in the present study were selected among already developed CMS and fertile pollen lines at ICAR-IARI, Regional Station, Katrain.

3.2 Crop Raising and Mating Design

For raising healthy crops, the seeds of 10 CMS and 10-pollen parent were sown in the beds of standard size 3m × 1m × 0.15m (Figure 3.1) with inter-and intra-row spacing of 45 cm and size of the plot was 3.0 x 3.0 m^2. The recommended package of practices, suggested for growing a healthy carrot crop at the Naggar Experimental Farm, were followed for better quantitative characters and phenotypic expression of crop (Sharma 2003). Then all the 10 CMS lines were crossed with each of 10 testers following line × tester mating design (Kempthorne 1957) at flowering stage to develop 100 test cross progenies during spring-summer season of 2017. All the CMS lines were covered under muslin cloth cage to prevent any type of natural cross pollination (Figure 3.1). For the pollination purpose, the fresh pollen was collected from the respective superior male fertile testers grown on separate field. Then fresh pollen collected from each of male fertile testers was used to pollinate each of the CMS lines manually for the hybrid seed production.

3.3 Experimental Design

The characterization of parental lines, study of heterosis and combining ability for different quantitative characters traits, qualitative characters traits was performed. The healthy seeds of all the parental lines (10 CMS and 10 male fertile tester lines) and their 100 F_1 hybrids and 1 commercial CMS based hybrids (Pusa Nayanjyoti) as standard checks were done by sowing crops for the two consecutive year i.e., on 5th September, 2016 and 23rd August, 2017 respectively . The bed size of 3m × 1m × 0.15m with inter-and intra-row spacing of 25 cm and size of the plot was 3.0 x 3.0 m^2. All the parental lines along with their 100 testcross progenies and 1 standard check were evaluated in randomized block experimental design with three replications. For data recording of quantitative characters and quantitative characters traits, ten randomly selected well established plants were tag-labelled in each plot/block of all the three replications. For the analysis of qualitative characters traits, the roots of 10 randomly selected

well established plants of each genotype in all the three replications in each plot/block was chopped at fresh marketable stage and homogenized for analysis of qualitative characters compounds.

Table 3.1. List of CMS and male fertile lines along with standard checks used in the current study

Code	Line	Role	Status	Developmental Stage
L1	KT-7A	Female Parent	CMS line	BC_{12}
L2	KT-10A	Female Parent	CMS line	BC_{9}
L3	KT-28A	Female Parent	CMS line	BC_{12}
L4	KT-39A	Female Parent	CMS line	BC_{9}
L5	KT-47A	Female Parent	CMS line	BC_{13}
L6	KT-62A	Female Parent	CMS line	BC_{9}
L7	KT-80A	Female Parent	CMS line	BC_{12}
L8	KT-95A	Female Parent	CMS line	BC_{9}
L9	KT-98A	Female Parent	CMS line	BC_{12}
L10	KT-8542A	Female Parent	CMS line	BC_{12}
T1	KS -20	Male Parent	Tester line	Completely homozygous
T2	KS -21	Male Parent	Tester line	Completely homozygous
T3	KS -22	Male Parent	Tester line	Completely homozygous
T4	KS -50	Male Parent	Tester line	Completely homozygous
T5	KS -59	Male Parent	Tester line	Completely homozygous
T6	NK-1	Male Parent	Tester line	Completely homozygous
T7	PY-1 (Katrain local sel.8)	Male Parent	Tester line	Completely homozygous
T8	PN-1(Katrain local sel.11)	Male Parent	Tester line	Completely homozygous
T9	New Kuroda	Male Parent	Tester line	Completely homozygous

T10	KS -73	Male Parent	Tester line	Completely homozygous
C1	Pusa Nayanjyoti (CHECK)	Standard check	CMS hybrid	Commercially cultivated

*Where, L: lines, T: testers, C: commercial checks

Figure 3.1 General view of field during crossing programme

3.4 Evaluation of testcross progenies

A total of 100 test-cross progenies of temperate carrots along with 20 parental genotypes (10 pt-CMS and 10 inbreds) and one commercial CMS based temperate carrot hybrid as standard check were evaluated for different quantitative and qualitative traits. The crop was raised following all the recommended good agricultural practices by ICAR-IARI, Regional Station guidelines for growing of healthy carrot crop with better expression of data. The plot size was 10 × 1.5 m^2 and inter-and intra-row spacing was 25 cm × 10 cm. All the 20 parental genotypes including 100 F_1 hybrids and 1 standard check were evaluated in randomised complete block design with three replications for two consecutive years 2016-17 and 2017-18. Then 10 randomly selected carrot plants were tag labelled for recording the observation and qualitative characters analysis per genotype per plot per replication. 10 roots of each genotype in replicated trail per genotype per plot was harvested at fresh marketable stage and homogenised for analysis of antioxidant compounds.

3.5 Quantitative characters traits

For the characterization of parental lines and their 100 F_1 hybrids along with standard checks, and for combining ability and heterosis analysis, the observations were recorded for the 13 quantitative characters traits on individual plant basis of five randomly selected well-established plants of each genotype of all the three replications at the appropriate commercial harvesting stage, and averages were computed. The pooled data was used for further statistical analysis. The observations were recorded for following quantitative characters traits:

3.5.1 Leaf length (cm): The leaf length was recorded with centimetres scale from top of root to tip of the leaf on the ten randomly plants in each genotype/plot/replication and average was calculated.

3.5.2 Net shoot weight (g): The net shoot weight was computed as weight of plant including the stalk and leaves at the time of harvesting on five selected plants of each genotype/plot/replication and average plant weight was calculated.

3.5.3 Root length (cm): The root length was recorded with centimetres scale from base of root to top of the root on the ten randomly plants in each genotype/plot/replication and average was calculated.

3.5.4 Plant weight : The plant weight was computed as weight of root including the stalk and leaves at the time of harvesting on five selected plants of each genotype/plot/replication and average plant weight was calculated.

3.5.5 Net root weight (g): The net root weight was calculated by taking the weight of marketable carrot roots completely devoid of leaves and stalk.

3.5.6 Root diameter (cm): This parameter was measured as the average equatorial length of the half cut root i.e. the maximum distance between the outermost bottoms on both sides of ten randomly selected well established roots of each of CMS and male fertile lines, 100 test cross progenies and one commercial standard checks of all the three replications.

3.5.7 Core diameter (mm): The core length of carrot root was measured with the help of Vernier Calipers and then average of core length of ten roots/genotype/replication was calculated.

3.5.8 Cortex thickness (mm): The Cortex thickness of carrot root was measured with the help of Vernier Calipers and then average of Cortex thickness of ten roots/genotype/replication was calculated.

3.5.9 Root shape (cm^2) : It was computed as the product of root length and root diameter of each root. The mean value of five root of each genotype/replication was calculated.

3.5.10 Root to shoot ratio : It was computed as the product of net root weight to gross root weight of each root. The mean value of five root of each genotype/replication was calculated.

3.5.11 Days to maturity (in days): The data recording for root maturity was carried out as the number of days taken from the date of seed sowing to the date by which the roots attains horticultural maturity of each genotype/plot are at root harvesting maturity stage.

3.5.12 Harvest index (%): The harvest index was expressed in percentage and was calculated as the ratio of marketable root weight (economic yield) to the gross weight of plant (biological yield).

3.5.13 Marketable root yield (t/ha): The root harvested from ten selected plants in each line were weighed separately and average weight of roots calculated. Then yield was calculated in t/ha by multiplying the average marketable root weight with plant population per hectare.

3.6 Qualitative Traits

The observations were also recorded for each of parental CMS and male fertile lines and their 100 F_1 hybrids along with one standard checks from the ten randomly selected well established roots of each genotype of all the three replications at respective plant growth stage for the following traits:

- Leaf division
- Leaf intensity of green colour: light/ medium/dark
- Root: Anthocyanin coloration of shoulder: Absent/ Present
- Root: Green colour of shoulder: Absent/ Present
- Root: Scars on surface: Absent or very weak/ Weak/ Medium/ Strong/ Very strong
- Root: External colour: White/ Yellow/ Orange/Dark orange/ Pinkish red/ Red/ Purple/ Others
- Root: Diameter of core relative to total diameter: Very small/ Small/ Medium/ Large/ Very large
- Colour of core: White/ Yellow/ Orange/ Pinkish red/ Red/ Purple/ Others

- Colour of cortex: White/ Yellow/ Orange/ Pinkish red/ Red/ Purple/ Others
- Root: Colour of core compared to cortex: Lighter/ Same/ Darker
- Root: Green coloration in interior (in longitudinal section): Absent/ Present
- Roots texture (Fine/Coarse)
- Cavity spot (Present/absent)
- Forking (Present/absent)
- Splitting (Present/absent)

3.7 Estimation of vitamins, bioactive and antioxidant compounds

The estimation of important bioactive and phytopigments determining potential of carrot as industrial crop was computed in all 20 parental genotypes, their 100 testcross progenies and commercial check in replication. The functional food and natural pigment industry potential of carrot was determined by estimation of phenolic compounds, vitamins (pro-vitamins; beta carotene, lycopenes, total carotenoids, ascorbic acid) and antioxidants (CUPRAC, FRAP, anthocyanins). For the extraction and analysis of qualitative characters traits the five randomly selected roots of each genotype from all the three replications were chopped at fresh marketable stage, then homogenized and pooled sample of ten roots of each genotype/replication was used for qualitative characters analysis.

3.7.1 Cupric ion reducing antioxidant capacity (CUPRAC) assay

To estimate the antioxidant capacity based on CUPRAC assay (µ mol trolox/g) the Apak et al. (2007) approach was utilized with slight modifications. At the fresh marketable root stage the pooled sample from 10 roots of each genotype/replication was chopped, homogenized for CUPRAC assay. A sample of 5g fresh weight (FW) was refrigerated and immediately stored until subjected to qualitative characters analysis. The preparation of ethanol extract was carried

out by crushing the 5g homogenized root sample in 15 ml of 100% ethanol using sterilized mortar pestle. This extract was centrifuged at 10,000 rpm for a period of 15 min at 4ºC followed by storage of supernatant at -20°C. After this, 100 µl of sample extract was blended with 4 ml of CUPRAC reagent comprising 1 ml neucuproine, 1 ml ammonium acetate, 1ml $CuCl_2$ and 1 ml of distilled water (pH 7.4). Then the absorbance was recorded at wave length of 450 nm using double beam UV-VIS spectrophotometer. For reducing the error while analysis, CUPRAC estimation was performed in triplicate for each extract of each genotype of carrot in all the replications.

3.7.2 Ferric reducing ability of plasma (FRAP) assay

For determination of antioxidant capacity based on FRAP assay (µ moltrolox/g), the approach followed by Benzie and Strain (1999) was exploited with minor modifications. The preparation of FRAP reagent was fulfilled by mixing of acetate buffer (300 mM, pH 3.6), a solution of 10 mM TPTZ in 40 mMHCl, and 20 mM $FeCl_3$ at 10:1:1 (*v*/*v*/*v*) ratio. The carrot root sample preparation was done by crushing the 5g homogenized sample in 15 ml of 100% ethanol using mortar pestle followed by its centrifugation at 10,000 rpm for 15 min at 4ºC and storage of supernatant at -20°C. Then 100 µl of this extract was thoroughly mixed with the FRAP reagent (3.0 ml) for FRAP assay. At the wavelength of 593 nm the optical density value was recorded using double beam UV-VIS spectrophotometer. For each of the carrot genotype of each replication the analysis was performed in triplicateAnalysis was performed in triplicate for each extract of each genotype of all the three replications.

3.7.3 Estimation of TPC (total phenolic content)

For the quantification of TPC (mg of gallic acid/100 g FW) in carrot parental genotypes and their testcross progenies, the Folin–Ciocalteu method (Ainsworth and Gillespie, 2007) with minor alterations was utilized. An amount of 5g homogenized root sample was crushed in 15 ml of 80% ethanol using mortar pestle for the preparation of extract to estimate TPC. Then it

was subjected to centrifugation 10,000 rpm for 15 min at 4ºC followed by -20°C storage of supernatant. Then 0.50 mL volume of extract was blended with 2.5 mL of 1:10 diluted Folin-Ciocalteu reagent. The neutralization of this mixture was doen with 2 mL of 20% sodium carbonate (Na_2CO_3) solution. The incubation of reaction mixture was accomplished at room temperature for 30 min. the optical density of resulting blue colour was estimated at 750 nm with the help of double beam UV-VIS spectrophotometer. For the calibration gallic acid was used. The calculation was performed as per formulae

TPC (mg of gallic acid/100 g FW) = [(O.D. at 750 nm + 0.022) × volume × dilution × 10]/0.016 × sample weight

3.7.4 Quantification of TAA (total ascorbic acid) content

The direct colorimetric method as elaborated by Ranganna (1979) was used for quantification of total ascorbic acid (mg/100g) content by using 2, 6-dichlorophenol indo-phenol solution (dye) which is decolourized by ascorbic acid in sample extracts. To prepare the ascorbic acid standard, 100 mg of L-ascorbic acid was dissolved in 3% HPO_3 (metaphosphoric acid) and made the final volume to 100 ml with 3% metaphosphoric acid followed by further dilution by taking 10 ml of 1 mg/ml ascorbic acid. The final volume was made up to 100 ml with 3% metaphosphoric acid. The dye solution was prepared by dissolving , 50 mg of the sodium salt of 2,6-dichlorophenol indo-phenol dye in 150 ml of hot glass distilled water containing 42 mg of $NaHCO_3$ (sodium bicarbonate). The final volume was made up to 200 ml followed by storage of dye in dark bottle at refrigerated conditions and was standardized for each day. The dye factor was determined as per the formula: Dye factor = 0.5/titer value. The 5g sample of fresh homogenized carrot roots of each genotype/replication was extracted with 4% oxalic acid and volume made to 100 ml and centrifugation was done. Then 5 ml of supernatant was pipette out and 10 ml of 4% oxalic acid was added to it. Then titration was carried out against 2, 6-

dichlorophenol indo-phenol dye. Titer value was recorded and used for calculation of total ascorbic acid content as per the given formula.

$$\text{Total ascorbic acid } \left(\frac{\text{mg}}{100\text{g}}\right) = \frac{titarte\ value * dye\ factor * sample\ volume\ made\ up * 100}{titrate\ volume * weight\ of\ sample}$$

3.7.5 Estimation of anthocyanin content

To determine the anthocyanin content (mg/100g), the procedure described by Ranganna (1979) was followed with slight modifications. The homogenized root sample of each carrot genotype per replication (2g) was crushed using mortal-pestle in 15 ml of ethanol–hydrochloric acid mixture (95% C_2H_5OH and 1.5 N HCl in the ratio of 85:15). After this, in a 50 ml volumetric flask the extraction mixture was transferred followed by overnight storage at 4°C. Then its filtration was done through Whatman No. 1. The absorbance of filtrate was recorded at 535 nm using a double beam UV-VIS spectrophotometer.

- Total anthocyanins content = OD × dilution factor × total volume made up × 100/sample weight × 98.2

3.7.6 Quantification of TCC (total carotenoid content), β-carotene and lycopene)

To quantify the concentration of carotenoids like TCC (total carotenoid content) (mg/100g), β-carotene (µg/100 ml) and lycopene (mg/100g), the protocol postulated by Rangana (1979) was followed with slight changes. The 5g of homogenized sample of carrot roots was mixed with 30 ml acetone till the residue ended up to a colorless solution. Then this extract was decanted into a funnel filled with 20 ml of petroleum ether (BP 60–80 ◦C). To remove the extra amount of water 5% sodium sulphate (Na_2SO_4) was added to the extract solution. The final volume was made up to 50 ml. Then at 503 nm and 452 nm the absorbance was recorded using double beam UV-VIS spectrophotometer. The carotenoids were estimated as per the formulae:

Lycopene (mg/100g) = [3.1206 × OD at 503 nm × volume made up × dilution factor × 100] / sample weight × 1000

Total carotenoid content (mg/100g) = [3.857 × OD at 452 nm × volume made up × dilution factor × 100] / sample weight × 1000

The β-carotene (μg/100 g) = [OD at 452 nm × 13.9 × 10^4 × 1000] / [sample weight × 560 × 1000]

3.8 Combining ability and Statistical analysis

The ANOVA (analysis of variance) analysis of all the resultant data of qualitative characters and antioxidant compounds computed in a randomised block design carried out by GLM procedure of SAS version 9.4 (statistical analysis system) software (SAS Institute, 2013). For heterosis analysis, combining ability assessment of bioactive compounds line × tester (Kempthorne, 1957) statistical analysis was performed using software Windostat Version 9.3 from Indosat Services, Hyderabad, India. The F test was utilized to analyse the significance at 5% and 1 % probability for combing ability of data. The heterosis of antioxidants compounds present in carrot was calculated as per Singh et al. (2018a) via formulae viz,

Heterosis over mid parent (MPH) % = ((F1-mid parent /mid-parent) X 100,

Heterosis over better parent (BPH) % = ((F1- better parent / better parent) X 100

The significance was tested at 5% and 1% level of significance. The estimate of narrow sense heritability (h^2ns) were computed by (Robinson 1966) and were grouped as high (>30%), medium (10-30%) and low (<10%).

Table 3.2 Line × Tester Analysis of Variance (ANOVA) for Combining Ability

SoV	Df	MS	EMS	F calculated
Replications	r-1	Mr	-	Mr/Me
Treatments	t-1	Mt	-	Mt/Me

Parents	p-1	Mp	-	Mp/Me
Parents (Lines)	f-1	Mf	$\sigma^2e + r\,\sigma^2fm + rm\,\sigma^2f$	Mf/Mfm
Parents (Testers)	m-1	Mm	$\sigma^2e + r\,\sigma^2fm + rf\,\sigma^2m$	Mm/Mfm
Parents vs Crosses	1	MpvsMc	-	MpvsMc/Me
Crosses	c-1	Mc	-	Mc/Me
Line × tester effect	(f-1) (m-1)	Mfm	$\sigma^2e + r\,\sigma^2fm$	Mfm/Me
Error	(r-1) (mf-1)	Me	σ^2e	-
Total	(fmr-1)		-	-

Where,

r: number of replications; t: number of treatments (total number of genotype); p: number of parents; f: number of female parents (number of lines); m: number of male parents (number of testers); c: total number of crosses; MS: mean squares; df: degree of freedom; SoV: source of variation; EMS: expected mean squares; Me: mean sum of squares due to error; Mf: mean sum of squares due to lines; Mm: mean sum of squares due to testers; Mfm: mean sum of squares due to line x tester; σ^2e: variance due to error; σ^2fm: variance due to female × male; σ^2m: variance due to males; σ^2f: variance due to females.

3.8.1 Estimation of genetic components of variance:

The general (σ^2gca line, σ^2gca tester) and specific combining ability (σ^2 sca) variances were tested against their respective error variances, derived from the analysis of variance of the different quantitative characters and qualitative characters traits as follows by subjecting to statistical software SAS version 9.4 (SAS Institute 2013):

Covariance of half-sib of line (Cov. Line HS) = $\frac{Mf-Mfm}{rm}$

Covariance of half-sib of tester (Cov. tester HS) = $\frac{Mm-Mfm}{rf}$

Covariance of full-sib (Cov. FS) =

$$\frac{(Mf-Me)+(Mm-Me)+(Mfm-Me)}{3r} + \frac{6rCOv.HS-r(f+m)Cov.HS}{3r}$$

Assuming no epistasis, the σ^2gca of parents and σ^2 sca of crosses were computed as follow:

σ^2gca = Cov. HS = [(1 + F)/4] σ^2A

σ^2sca = [(1 + F)/2]^2 σ^2D

Where, σ^2A and σ^2D are additive genetic variance and dominance genetic variance, respectively and F is the inbreeding coefficient.

The narrow-sense heritability (h^2ns = V_A/V_P; $V_P = V_G + V_E$) estimates were categorized into three classes viz., high (> 30%), medium (10-30%) and low (< 10%) Robinson et al. (1966).

The Genetic advance (GA) was calculated as = H^2_b x phenotypic standard deviation x K, where K value is 2.06, which is standardized selection differential constant at 5% selection intensity (Johnson et al. 1955).

Further, the ratio of additive to dominance variance (σ^2A/D) coupled with predictability ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was computed to estimate the relative proportions of additive versus non-additive type of genetic control of traits under study Verma and Srivastava (2004). The average degree of dominance (ā) was computed as per Dabholkar et al. (1999) with statistical software SAS v9.4 as:

ā = $\sqrt{2\sigma^2 D/\sigma^2 A}$, where σ^2A is additive variance and σ^2D is the dominance variance. As per Dabholkar (1999), is the value of ā was 0 then no dominance was considered in the action of genes; if value is > 0 but < 1, partial dominance was considered; if the value was = 1, complete dominance was considered and if value was > 1, over-dominance was considered in the action of genes.

3.8.2 Determination of combining ability (GCA and SCA) effects

The following linear model as per Kempthorne (1957) and Dabholkar (1999) was used to estimate gca and sca effects of lines, testers and their interactions:

$$X_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where, X_{ijk}: mean value of a trait measured on i × j cross combination in the k_{th} replication;

μ: overall general population mean;

g_i: gca effect of i_{th} parent (female parent);

g_j: gca effect of j_{th} parent (male parent; tester);

s_{ij}: sca effect of i × j_{th} cross;

r_k: it represents the replication effect

e_{ijk}: error associated with each trait [environmental effect specific to $(ijk)_{th}$ individuals]

gca effect of line was computed as: g_i (lines) = $\frac{Xi...}{rm} - \frac{X...}{rmf}$

gca effect of line was computed as: g_j (tester) = $\frac{Xj...}{rm} - \frac{X...}{rmf}$

sca effect of i × j_{th} cross combinations as: s_{ij} = $\frac{Xij...}{r} - \frac{Xi...}{rf} - \frac{Xj...}{rm} + \frac{X...}{rmf}$

Where, X..... is sum of all the hybrids (line × tester) across all the replications

X_i.... is total of i^{th}lines (female parent) over all the testers (male parents) and 'r' replications

Xj.....is total of j^{th} testers (male parent) over all the lines (female parent) and 'r' replications

Xij...is total of $(ij)_{th}$ cross combinations over all the r replications

3.8.3 Determination of standard errors:

The estimation of standard errors and testing of gca and sca significance was computed by subjecting the data to statistical software SAS v9.4 as per Dabholkar (1999), Kanfany et al. (2018):

SE (gca for lines) = $\sqrt{Me/rm}$

SE (gca for testers) = $\sqrt{Me/rf}$

SE (sca) = $\sqrt{Me/r}$

Critical difference (CD) = Standard Error (SE)×'t' tabulated values for error degrees of freedom.

The significance was tested by means of 't' test.

Where, '*Me'* is error mean sum of squares, '*r'* is number of replications, '*m'* is number of males (testers), SE is standard error and '*f*' is number of females (lines).

3.8.4 Heterosis Estimates

Heterosis estimates for different traits were computed as per Xie et al. (2018) by subjecting the data to SAS statistical software version 9.4 based on formulae viz,

MPH% (Mid parent heterosis) = [(F_1-MP)/MP] x 100,

BPH% (Better parent heterosis) = [(F_1-BP)/BP] x 100,

SCH% (standard check heterosis) = [[(F_1-SC)/SC] x 100

Where F_1 is mean performance of hybrid over all the three replications, MP is mid-parent and BP is better-parent performance, SC is standard check and testing of significance was done at probability of $p < 0.05$, $p < 0.01$ and $p < 0.01$ through *F* test.

3.9 Principal component and dendrogram analysis

The dendrogram and cluster analysis of parental genotypes was accomplished based on qualitative characters assessment by calculating Euclidian distance employing R statistical hclust package program (R Studio 2020). To demonstrate the variation, determining role of individual traits and genotypes in controlling variation and, to reduce the variable space components, the PCA (principal component analysis) analysis was carried out (Jolliffe and Cadima, 2016). The PCA-biplot analysis was performed using R statistical package 'ggbiplot' in R Studio (2020).

3.10 Genetic Diversity Analysis in Parental CMS and male fertile Lines Using Microsatellites

3.10.1 Plant Materials and DNA Isolation

All the parental CMS lines and male fertile testers (10 CMS + 10 male fertile) were grown in open field conditions. Genomic DNA extraction and purification was done from 100 mg fresh green young leaves of 20-25 days old using cetyltrimethyl ammonium bromide (CTAB) method with slight modifications (Murray and Thompson 1980). First, collected 100-200 mg of fresh young leaves of carrots plants and homogenized to fine powder form with liquid nitrogen by grinding in pre-chilled pestle and mortar. Immediately transferred the fine powder to 2 ml autoclaved micro-centrifuge tube (MCT) containing 700 µl of 2% pre-warmed CTAB extraction buffer (pre-warmed at 65 ºC) added with 100 µl of β-mercaptoethanol and closed the MCT cap tightly. Then mixed the above mixture vigorously simultaneously incubated the micro-centrifuge tubes in hot water bath at temperature of 65ºC for about one hour, with intermittent shaking after every 15 minutes. The after taking out from hot water bath, the sample temperature was brought down to normal room temperature followed by addition of 500 µl of freshly prepared chloroform: isoamyl alcohol (CI, 24:1) then mixed the CI and sample gently by inversion followed by centrifugation at 12,000 rpm for 10 min at room temperature. After this, three different layers appeared top layer of aqueous phase, middle layer containing debris and proteins, bottom layer of chloroform. Then aqueous phase supernatant was transferred immediately into a new 1.5 ml micro-centrifuge tube (MCT) and added equal volume of chilled isopropanol (about 500 µl) and then inverted gently for DNA to precipitate, stored at -20ºC for overnight. Then on the next day after letting the sample to room temperature for few minutes, centrifuged them at 10,000 rpm for 10 minutes at 4ºC for DNA pelleting. After centrifugation, decanted the supernatant, and drain inverted on a paper towel. Then

washing of DNA pellet was done with 400-500 µl of 70% (v/v) ethanol 2-3 times followed by air-drying of pellet to get rid of ethanol completely at room temperature. The DNA pellet was dissolved in 50-100 µl of nuclease free double distilled water (ddH_2O) or 1X TE buffer. Then samples were left for 5-10 min to cool down and 2-3 µl of RNase was added to remove the RNA from DNA extracted, it was mixed by gentle tapping or inverting micro-centrifuge tubes. Then incubated the tubes for about half an hour at 37°C hot water bath with gentle shaking for every 10 minutes. The completely dissolved DNA sample was stored at 4 °C for immediate use and at -20 °C or -80 °C freezer for long-term storage.

3.10.2 Agarose Gel electrophoresis and DNA quantification

The gel electrophoresis was carried out using 1% agarose gel (Sigma-Aldrich, USA) dissolved in100 ml of 1xTAE or TBE buffer and stained with added 5µl of ethidium bromide (EtBr) to track the DNA during gel run. The 1 µl of each of DNA sample mixed with 3 µl of 6x loading dye and 3 µl of nuclease free water was loaded on the DNA mix well of gel electrophoresis unit. The DNA concentration estimation was done by comparing fluorescent intensity with known concentration of uncut lambda (ƛ) DNA (100ng/ µl) into the side wells. The gel electrophoresis was run at 70 V for 1 and 1/2 hours. Then gel picture was captured under UV light in gel documentation unit connected with computer apparatus. Genomic DNA samples were adjusted to 25-50 ng DNA/µl and stored at -80 ºC for further analysis.

Table 3.3 List of CMS lines used for cytoplasmic diversity and tester lines

Sr. No	CMS line	Sr. no	Tester
1	KT-7A	11	KS -20
2	KT-10A	12	KS -21
3	KT-28A	13	KS -22

4	KT-39A	14	KS -50
5	KT-47A	15	KS -59
6	KT-62A	16	NK-1
7	KT-80A	17	PY-1 (Katrain local sel.8)
8	KT-95A	18	PN-1 (Katrain local sel.11)
9	KT-98A	19	New Kuroda
10	KT-8542A	20	KS -73

3.10.3 Microsatellite Markers and PCR Amplification

For the genetic diversity analysis of parental CMS and male fertile lines, the pairs of 100 microsatellite primers comprising genomic-SSRs distributed throughout the carrot genome (Appendix I) were used. Among them 80 microsatellite primers were found to be polymorphic and of which 64 pairs of genomic-SSRs displaying clear amplification and polymorphism were used for final molecular analysis of 10 CMS and 10 tester lines. Eppendorf Mastercycler Nexus GSX1 was used for PCR amplification in a reaction volume of 25µl. The PCR reaction mixture comprised of 1µl of each forward and reverse primers, 2µl of genomic DNA template (50 ng), 12.50µl of 2× PCR Green master mix (GoTaq DNA polymerase; Promega, USA) and 8.50µl nuclease free water. The PCR cycling programme was set up as follow: an initial denaturation of 94 ºC for 4 min followed by 35 cycles of denaturation at 94 ºC for 30s, annealing of primers at 50 to 60 ºC for 30s depending upon appropriate primer annealing temperatures and extension at 72 ºC for 1min, then after completion of 35 cycles, final extension of 72 ºC for 7min was followed.

3.10.4 Gel Electrophoresis of PCR Products

Amplified PCR products were separated by 1.0% agarose gel electrophoresis in 1X TBE buffer (pH 8.0) and gel was run at 80 mA voltage for 120 min. Ethidium bromide (EtBr) of 0.5 mg/ml

was used for gel staining and gel pictures were captured using one digital gel documentation unit (BioSpectrum® Imaging System™, UK). The determination of fragment sizes were done using Promega^{TM} 50 bp DNA step ladder. The scoring of each of PCR product amplified was carried out as molecular weight basis (in base pair) using the software available in BioSpectrum® Imaging System™, UK.

3.10.5 Molecular Diversity, Cluster and Genetic Structure Analysis

Out of 80 microsatellite markers, 67 polymorphic microsatellite (genomic-SSRs) loci depicting genetic diversity were used for cluster analysis, dendrogram construction based on simple matching (SM) coefficient using DARwin software version 6.0.017 Perrier and Jacquemoud-Collet (2006). For testing the reliability of NJ dendrogram, a bootstrap value of 1000 replicates was used. For the allelic diversity analysis estimating observed number of alleles (N) per loci, observed heterozygosity (H_o), expected heterozygosity (H_e) and polymorphism information content (PIC) were computed through software CERVUS version 3.0 Kalinowski et al. (2007). The PIC in genetic studies is utilized as a measure of informativeness of a marker locus for linkage analysis (Moges et al. 2016; El-Esawi et al. 2016) and it categorizes informative markers as highly informative (PIC ≥ 0.5), reasonably informative (0.5 < PIC >0.25) and slightly informative (PIC < 0.25) (Moges et al. 2016; El-Esawi et al. 2016).The estimation of PIC for each locus using CERVUS 3.0 was calculated according to formula; PIC = 1-Σ Pi^2, where P*i* represents the *i*th allele frequency in a locus for the genotypes *P* under study Makumbi et al. (2011).The genetic structure analysis of parental population of testcross progenies was studied with Bayesian model-based clustering approach implemented in STRUCTURE version 2.3.4 software Pritchard et al. (2000) to assign individuals to *k* clusters and sub-clusters. For the estimation of proportion of ancestral contribution in each parental line, all simulations were performed by parameter setting as: “admixture model” with “correlated allele frequencies”. The algorithm was implemented with 10,000 length of burn-in period followed by 100000

Markov Chain Monte Carlo (MCMC) repetitions and plausible range of putative k values was kept from k = 1 to k = 10 run independently with 15 iterations for each k. The optimum value of k for determining most likely number of subpopulations was predicted according to simulation method of DeltaK (*ΔK*) Evanno et al. (2005) with the help of web-based STRUCTURE HARVESTER version v0.6.94 Earl and vonHoldt (2012). The *ΔK was estimated as follow,* $\Delta K = m\,(|L(K+1) - 2L(K) + L(K-1)|)/s\,[L(K)]$, where 'm' represents the absolute value mean, the mean likelihood for all runs of each K returned by STRUCTURE is denoted by 'L(K)', $s\,[L(K)]$ represents the standard deviation of 'L(K)'.

3.10.6 Correlation of Genetic Distances, Combining Ability and Heterosis

The Euclidean distance (ED), hereafter referred as phenotypic distance (PD) was calculated based on thirteen quantitative characters traits Plant height (cm), Root length (cm), Leaf length (cm), Root diameter (mm) , Core diameter (mm) , Cortex thickness (mm) , Gross root weight (g), Net root weight (g), Shoot weight (g), Root to shoot ratio, Root size (cm^2), Harvest index (%), Yield (tonnes/ha.) using distance function of R software (Rstudio 2015). The ED was calculated as per formula ED = $ED = \sum_{i=1}^{16}[(\mathrm{Xi} - \mathrm{Yi})/\mathrm{s}]^2$(Shifriss and Sacks 1980), where, ED is the Euclidean distance, s is the standard deviation of i^{th} trait, Xi is the performance of X parent for i^{th} trait, Yi is the performance of Y parent for i^{th} trait. The SM dissimilarity coefficient (hereafter referred as genetic distance: GD) was computed based on SSRs data analysis using DARwin software version 6.0.017. The association among GD, PD, MPH, BPH, SCA was computed by Pearson's correlation coefficients (r) (pearson product moment correlation coefficient: PPMCC) by using R software pakages version 3.5.1 in Rstudio 1.1.456 (RStudio 2015) and testing of significance at $p < 0.05$ and $p < 0.01$. The corrplot displaying correlation among distances, heterosis and combining ability was demonstrated via Rcorrplot package in Rstudio (Wei and Simko 2017).

3.11 Characterization of CMS lines for Floral Traits

The field experiment under the present investigation was carried out during 2017-2018 at Naggar Experimental Farm of IARI, Regional Station, Katrain, Himachal Pradesh, India, situated along the river Beas. All the CMS lines along with their maintainers were evaluated in RBD design with three replications. Data were recorded from 10 randomly selected plants of each genotype, 12 flowers were taken for recording the observations for floral traits, and average data was used for further statistical analysis.

Floral Traits

i. **Petal colour**: The observation was recorded at full flowering stage during early morning hours in 12 flowers per genotype in all the replications.

ii. **Petal size (mm)** - The data on petal length and petal width was taken at full flowering stage in 12 flowers per genotype in all the replications with the help of microscope.

iii. **Petaloid shape (µm)** - The sepal length and width was measured at full flowering stage in 12 flowers per genotype in all the replications with the help of microscope

iv. **Petaloid length (l x w) (µm)** - The stigma shape was observed at full flowering stage in 12 flowers per genotype in all the replications.

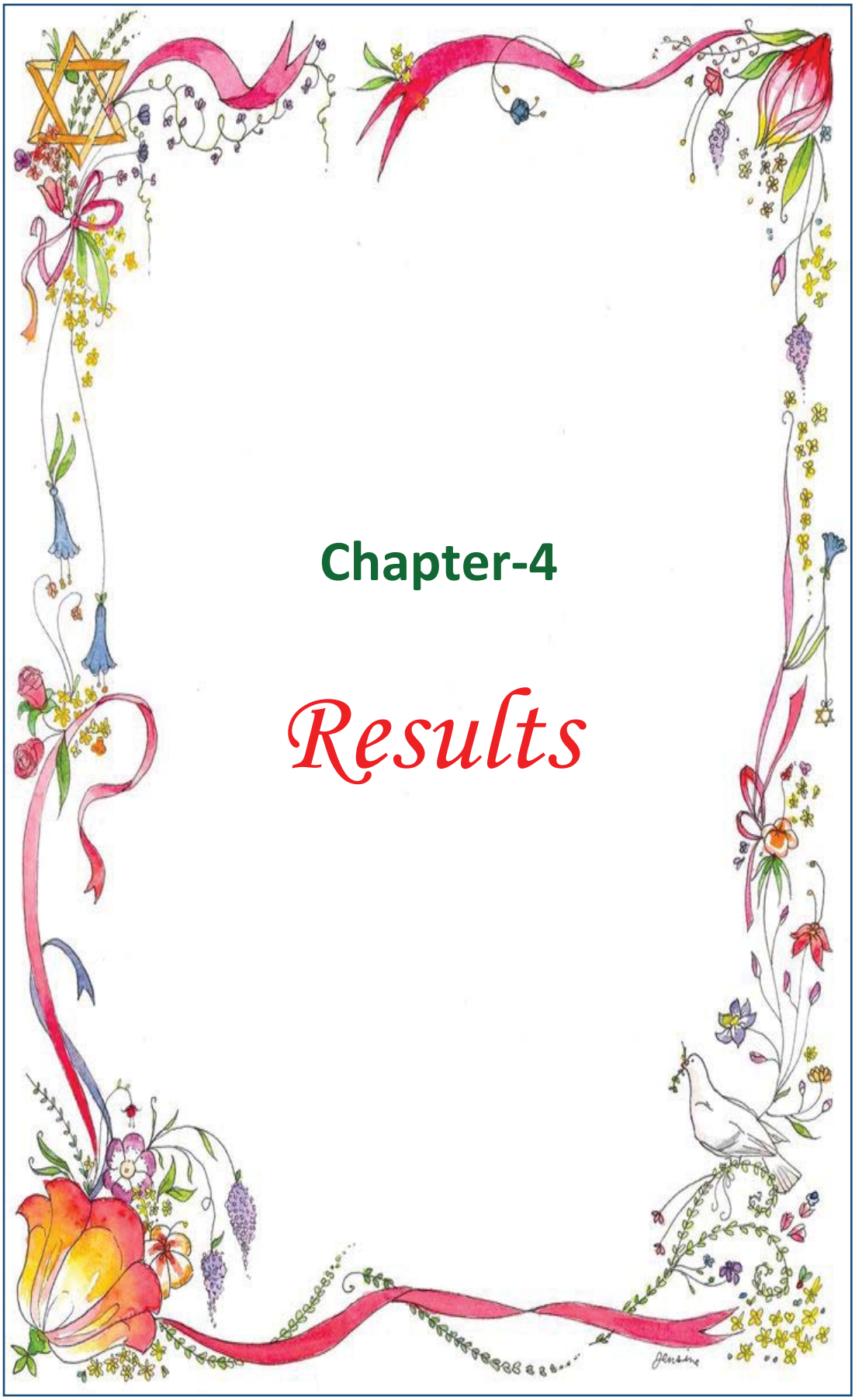
v. **Style length (µm) -** The style length was measured at full flowering stage in 12 flowers per genotype in all the replications with the help of of microscope.

vi. **Style diameter (µm) -** The Style diameter was measured at full flowering stage in 12 flowers per genotype in all the replications with the help of of microscope.

vii. **Anther size (µm) -** The Anther size was measured at full flowering stage in 12 flowers per genotype in all the replications with the help of of microscope.

viii. **Presence of floral nectarines-** The presence of floral nectarines was observed at full flowering stage in 12 flowers per genotype in all the replications.

ix. **Presence of viable pollen-** The pollen viability was estimated on the basis of staining pollen with 2% acetocarmine and viewing under light microscope at 10 X and 40x magnification. The observation was recorded at full flowering stage in 12 flowers per genotype in all the replications.



Chapter-4

Results

Chapter 4

Results

The present experiment entitled "Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus)* using Cytoplasmic male sterile (CMS) lines" was carried out during 2016-2017 and 2017 -2018 at Naggar Experimental Farm of ICAR-IARI, Himachal Pradesh, India, located along the left bank of river Beas. The results obtained in the current study were subjected to appropriate statistical analysis and have been presented in this chapter under the following heads:

4.1 Qualitative traits of parents

All the 10 CMS lines and 10 testers along with one commercial standard checks were evaluated for different qualitative traits. The results are presented in Table 4.1. All the parental genotypes were free from physiological disorders of forking, cavity spot, splitting and found free from green and anthocyanin coloration in its roots shoulder at harvesting stage. All the lines and testers were having fine and smooth fine root texture and no secondary roots observed at root harvesting stage in any of these genotypes. Majorly of the genotypes have orange coloured roots with cylindrical shape except New Kuroda, which had conical roots. In majority of the genotypes, the leaf attitude was erect for all CMS line, except CMS lines KT-7A, KT-28A, KT-47A, KT-80A, KT-95A and KT-98A, which had semi-erect leaf division. Likewise, in all the fertile testers were having completely erect leaf attitude except KS-21. All the lines and testers were having fine and smooth fine root texture and no secondary roots observed at root harvesting stage in any of these genotypes.

4.2 Quantitative characters traits

4.2.1 Characterization of lines and testers for quantitative characters traits

The mean performance of lines and tester is presented in Table 4.2. The mean value for leaf length among the lines ranged from 13.50 cm (KT-7A) to 27.50 cm (KT-8542A). Similarly, among the testers the mean value ranged from 15.5 cm (KS -22) to 25.5 cm (NK-1). The CMS lines, KT-8542A, KT-98A, KT-39A, KT-80A, KT-62A, KT-47A and testers NK-1, KS -73, New Kuroda, KS -50, KS -59, KS -21, PN-1 performed better for leaf length as compared to best check (Pusa Nayan Jyoti). However, the mean value for root length among the CMS lines ranged from 17.50 cm (KT-98A) to 25.50cm (KT-7A). Among the parental CMS lines, the lines KT-7A, KT-80A, KT-10A and among the testers, KS -20 had the highest root length among the rest of genotypes and best check (Pusa Nayan Jyoti). While, the CMS lines KT-98A, KT-39A and KT-8542A had less root length in contrast to other parental lines. The mean value for root diameter and root to shoot ratio of the CMS lines ranged from 35.00 mm (KT-62A) to 46.67 mm (KT-28A) and 1.97 (KT-95A) to 11.82 (KT-39A), respectively. Among the CMS lines, KT-28A, KT-47A and KT-98A, and among the testers KS -21, KS -59 had higher root diameter than rest of the lines and testers, respectively and also with respect to best check (Pusa Nayan Jyoti). Similarly, for the root to shoot ratio, CMS lines KT-7A, KT-10A, KT-28A, KT-39A, KT-98A and KT-8542A and testers KS -21, KS -22, KS -59, KS -73, New Kuroda, NK-1, PN-1, and PY-1 performed better as compared to best check (Pusa Nayan Jyoti). Similarly, among the CMS lines the mean value for core diameter, cortex thickness and root size ranged from 8.00 mm (KT-62A) to 15.00 mm (KT-80A), 22.67 mm (KT-39A) to 35.67 mm (KT-28A), and 68.25 (KT-62A) to 100.32 (KT-28A), respectively. Among the parental CMS lines, the lines KT-47A, KT-28A, KT-98A, KT-95A, KT-10A and tester KS -20 had the higher cortex thickness and root size, respectively. The mean value for gross root weight among the CMS lines ranged from 78.60 g (KT-47A) to 104.39g (KT-28A).

Only one CMS line, KT-28A had lesser gross root weight than best check (Pusa Nayan Jyoti). While, the CMS lines KT-98A, KT-39A and KT-8542A had less gross root weight as compared to other parental lines. The mean value for gross root weight and shoot weight among the lines ranged from 78.60 g (KT-47A) to 104.39 g (KT-28A). Only one CMS line, KT-28A had lesser gross root weight than best check (Pusa Nayan Jyoti). While, the CMS lines KT-98A, KT-39A and KT-8542A had less gross root weight as compared to other parental lines. The mean value for gross root weight and shoot weight among the lines ranged from 78.60 g (KT-47A) to 104.39 g (KT-28A). Similarly, among the testers the mean value ranged from 77.50 g (PY-1) to 123.06 g (KS -73). The CMS line, KT-28A and testers KS -73, KS -20 performed better for gross root weight as compared to the check (Pusa Nayan Jyoti). For shoot weight of the CMS lines, KT-95A, KT-80A and testers KS -50, KS -20 was higher as compared to Pusa Nayan Jyoti. The mean value for yield and harvest index among the lines ranged from 23.22 tonnes /ha (KT-47A) to 36.30 tonnes /ha (KT-28A) and 66.33 % (KT-95A) to 92.01 % (KT-39A), respectively. Similarly, among the testers the mean value for yield ranged from 24.78 tonnes /ha (KS -50) to 43.80 tonnes /ha (KS -73) and harvest index ranged from 58.67 % (KS -50) to 94.34 % (KS -59) respectively. The mean value for yield and harvest index in the CMS line KT-28A, KT-7A, KT-39A, KT-98A, KT-10A and KT-39A, KT-28A, KT-7A, KT-10A, KT-98A, KT-8542A was better as compared to the check (Pusa Nayan Jyoti).

Table 4.1 Qualitative traits of parental CMS and tester lines

Parental lines/testers/ checks	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-7A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10A	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39A	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62A	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98A	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542A	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Contd. Table 4.1 Qualitative traits of parental CMS and tester lines

KS -20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KS -21	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KS -22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KS -50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KS -59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
PY-1 (Katrain local sel.8)	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
PN-1 (Katrain local sel.11)	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
New Kuroda	orange	Conical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
Pusa Nayanjyoti (CHECK)	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Parents/Traits	Leaf length (cm)	Root length (cm)	Root Diameter (mm)	Core diameter (mm)	Cortex thickness (mm)	Plant Weight (g)	Root weight (g)
KT-7A	13.50±0.20	25.50±0.11	38.33±1.07	14.00±0.08	24.33±0.99	95.00±2.37	82.00±0.72
KT-10A	18.49±2.16	22.50±0.58	41.67±1.47	12.00±0.22	29.67±1.67	94.00±2.78	78.50±0.81
KT-28A	15.49±0.81	21.50±0.33	46.67±0.92	11.00±0.01	35.67±0.93	104.39±3.38	90.77±0.87
KT-39A	26±1.72	19.00±0.31	36.67±1.21	14.00±0.12	22.67±1.15	86.40±0.76	79.50±1.17
KT-47A	22.5±1.46	20.50±0.26	45.00±0.46	9.00±0.15	36.00±0.40	78.60±2.83	58.07±0.18
KT-62A	22.50±0.55	19.50±0.47	35.00±0.97	8.00±0.02	27.00±0.97	87.53±0.98	67.50±1.59
KT-80A	24.00±1.32	24.00±0.78	38.33±0.64	15.00±0.20	23.33±0.83	95.20±1.40	67.50±1.09
KT-95A	16.09±0.22	21.90±0.21	43.33±0.13	13.00±0.05	30.33±0.08	98.69±2.24	65.46±1.11
KT-98A	26.5±2.04	17.50±0.57	45.00±1.03	11.00±0.34	34.00±1.09	94.39±2.01	78.50±1.38
KT-8542A	27.5±0.97	19.50±0.03	38.33±0.28	11.00±0.01	27.33±0.29	93.00±1.95	75.50±1.11
KS -20	23.5±1.56	24.50±0.35	43.33±0.54	12.00±0.08	31.33±0.58	101.79±0.90	79.12±2.56
KS -21	21±1.16	18.00±0.58	46.67±0.58	11.00±0.38	35.67±0.84	105.4±1.06	85.50±1.64
KS -22	15.5±1.49	17.50±0.50	35.00±1.00	13.00±0.44	22.00±0.64	105.26±2.65	88.70±2.87
KS -50	22.49±0.48	18.50±0.26	41.67±1.35	12.00±0.28	29.67±1.6	105.6±0.61	61.95±1.82
KS -59	16.49±2.30	20.50±0.65	45.00±1.25	14.00±0.31	31.00±0.94	83.2±0.55	78.50±2.78
NK-1	29.5±1.21	14.50±0.09	40.00±0.82	11.00±0.28	29.00±0.59	93±1.09	78.50±0.81
PY-1 (Katrain local sel.8)	21.50±0.43	18.50±0.01	36.67±1.29	14±0.40	22.67±0.95	77.5±0.91	61.40±0.86
PN-1 (Katrain local sel.11)	20.5±1.02	19.50±0.55	40±0.44	14±0.09	26±0.53	93.8±2.09	78.38±1.65
New Kuroda	22.5±0.97	20.50±0.44	43.33±0.09	15±0.42	28.33±0.51	87.80±3.16	75.12±0.61

KS -73	28.5±0.28	21.50±0.41	38.30±0.87	17±0.01	21.33±0.87	123.06±1.65	109.50±1.29
Pusa Nayan Jyoti(CHECK)	19.43±1.38	21.73±0.56	43.50±1.25	14.67±0.62	29.17±1.64	99.33±2.24	77.50±2.16
CD (5%)	3.44	0.28	0.56	0.02	0.27	0.13	0.04
CD (1%)	4.6	0.37	0.61	0.03	0.37	0.18	0.05

Table 4.2 Characterization of parental CMS lines and tester of temperate carrots including commercial checks for 13 quantitative characters traits

Parents/Traits	Shoot weight (g)	Root to shoot ratio	Root to shoot ratio	Days to harvesting (in days)	Harvest index (%)	Yield (tonnes /ha.)
KT-7A	13±2.11	6.47±1.02	6.47±1.02	92.67 ± 0.58	86.36±1.89	32.79±0.28
KT-10A	15.5±3.59	5.40±1.49	5.40±1.49	92.00 ± 1.00	83.61±3.38	31.40±0.32
KT-28A	13.63±3.03	6.95±1.32	6.95±1.32	90.67 ± 1.53	87.02±2.45	36.30±0.34
KT-39A	6.90±1.03	11.82±2.00	11.82±2.00	85.33 ± 1.53	92.01±1.17	31.8±0.47
KT-47A	20.53±2.75	2.87±0.35	2.87±0.35	90.33 ± 1.53	73.97±2.51	23.22±0.07
KT-62A	20.03±1.39	3.39±0.31	3.39±0.31	92.00 ± 1.00	77.11±1.56	26.99±.63
KT-80A	27.7±.67	2.44±0.06	2.44±0.06	92.00 ± 1.01	70.90±0.53	26.99±0.43

KT-95A	33.23±1.43	1.97±0.07	1.97±0.07	92.00 ± 1.02	66.33±0.81	26.18±0.44
KT-98A	15.9±2.96	5.11±0.96	5.11±0.96	89.00 ± 1.00	83.20±2.80	31.40333±0.55
KT-8542A	17.5±0.84	4.32±0.14	4.32±0.14	90.00 ± 1.00	81.19±0.50	30.2±0.44
KS -20	22.68±2.75	3.55±0.55	3.55±0.55	97.67 ± 1.53	77.72±2.65	31.65±1.02
KS -21	19.9±1.43	4.32±0.39	4.32±0.39	92.00 ± 1.00	81.12±1.35	34.2±0.65
KS -22	16.56±1.42	5.40±0.58	5.40±0.58	93.00 ± 1.00	84.26±1.35	35.48±1.14
KS -50	43.64±1.94	1.42±0.10	1.42±0.10	91.33 ± 1.53	58.67±1.77	24.78±0.73
KS -59	4.70±2.54	25.09±16.68	25.09±16.68	92.00 ± 1.00	94.34±3.08	31.4±1.11
NK-1	14.5±0.98	5.43±0.37	5.43±0.37	91.67 ± 1.53	84.41±0.92	31.4±0.32
PY-1(Katrain local sel.8)	16.09±0.42	3.81±0.11	3.81±0.11	90.67 ± 1.53	79.22±0.51	30.99±0.36
PN-1(Katrain local sel.11)	15.41±3.64	5.42±1.454	5.42±1.454	91.00 ± 1.00	83.64±3.54	31.35±0.66
New Kuroda	12.67±3.77	6.64±2.43	6.64±2.43	91.33 ± 1.53	85.7±3.85	30.05±0.24
KS -73	13.56±2.45	8.40±1.82	8.40±1.82	89.33 ± 1.53	88.99±1.88	43.80±0.51
Pusa Nayan Jyoti(CHECK)	21.83±2.89	3.62±0.56	3.62±0.56	90.67 ± 1.53	78.05±2.64	31±0.86
CD (5%)	0.14	0.09	0.09	3.09	0.2	0.79
CD (1%)	0.19	0.12	0.12	4.72	0.27	1.06

Contd. Table 4.2 Characterization of parental CMS lines and tester of temperate carrots including commercial checks for 13 quantitative characters traits

4. 2. 2. Analysis of variance for quantitative characters traits

The measure of mean square for various quantitative characters traits in randomized block experimental design (RBD) unfold notable variation among different treatments in the study for all the characters except cortex thickness at 0.01% probability (Table 4.3). Besides, in each replication a non- significant block effects were found for all the quantitative characters traits studied except root to shoot ratio and leaf length at the probability of 0.01% (Table 4.3). The analysis of variance (ANOVA) for combining ability signifies high and significant differences ($P < 0.001$) among the treatments and parents for all the quantitative characters and horticultural traits (Table 4.3) except cortex thickness, plant height and core diameter. Similarly, measure of CMS lines were found significant for all the characters at 0.1% except for leaf length, core diameter, cortex thickness, shoot weight. The non-significant estimate of mean squares found for testers viz., plant height, core diameter, cortex thickness and yield and they were significant for rest of the traits (Table 4.3). The significant differences was recorded in lines x testers for the most of traits except plant height, root diameter, core diameter, cortex thickness, shoot weight, yield, harvest index, root to shoot ratio index. However the estimate of mean squares of parents x crosses were significant for almost all characters except core diameter, cortex thickness, gross root weight, net root weight (Table 4.3). The variance for combining ability study also revealed significant variations for 100-testcross combination in 13 traits, except for cortex thickness at 0.1% probability. However, non-significant variation observed for three replications for most of the characters except for root shoot ratio and leaf length, hence propounding existence of genetic difference in all cross combination. The line versus tester interaction effects found significant for all the 13 quantitative characters and horticultural traits except for cortex thickness. The significant difference for mean square estimates found in treatments versus environment for almost all traits excluding plant height and cortex thickness at 0.01% probability (Table 4.3). A line versus tester study was carried

out in two diverse environments in the year 2017 and 2018 by generating 100 F_1hybrids each year using 20 diverse parents. Analysis of variance revealed significant differences among the genotypes together with significant G × E interaction for most of the traits under study. Significant variation observed for almost all character except diameter, core diameter and cortex thickness on pooled data over environments indicating that the parents were diverse for most of the traits resulting in substantial genetic variability and heterosis in the F_1 hybrids.

Table 4.3 Line versus Tester Analysis of variance for combining ability for various quantitative traits in carrot

Source of variation	DF	Leaf length (cm)	Root length(cm)	Root diameter (mm)	Core diameter (mm)	Cortex thickness (mm)	Gross root weight (g)	Net root weight (g)
Replicates	2	3759.75*	26.68	135.78	40.77	2230.24	2953.98	432.19
Environments	1	4131.61***	6.06	25469.10***	5688.39**	33324.90***	4375.37***	93.16*
Treatments	119	332.53 ***	16.58***	162.12***	3046.83***	1034.61	2133.64***	1137.67 ***
Parents	19	91.14 ***	18.85***	42.27***	18.58	70.86	469.54***	726.20 ***
Parents (Line)	9	105.29***	9.13***	47.71***	20.85	78.03	232.76 *	624.65 ***
Parents(Testers)	9	80.24 ***	23.17***	41.34***	13.12	69.10	685.29***	774.47 ***
Parents (L vs T)	1	62.02 ***	67.36***	1.74	47.32	22.13	658.75 *	1205.67***
Parent vs Crosses	1	1648.42***	64.45***	2306.46***	51.20	817.46	23229.21***	15.39
Crosses	99	365.56 ***	15.66***	163.46***	3658.27***	1221.77	2239.92***	1227.98***
Line effect	9	648.82	43.80***	178.78	4793.37	1418.35	2918.67	1018.02
Tester effect	9	388.51 *	32.62**	264.50	3469.76	922.39	2670.32	1423.88
Line x Tester effect	81	331.54***	10.65***	150.53***	3553.09***	1233.19	2116.68***	1229.54***
Env x Treat	119	141.55***	14.70***	8.42*	3044.29***	837.19	191.54 ***	79.98***
Env x Parents	19	26.70***	12.75***	8.35	2.67	10.28	60.62	68.08 ***
Env x Parents (L)	9	26.29***	15.90***	9.27	2.83	11.24	47.97	70.75***

Env x Parents (T)	9	29.07***	10.72***	7.80	2.62	9.71	79.82	69.65 ***
Env x Crosses	99	63.79 ***	15.22	6.24	3658.71***	1003.55	139.63*	79.10***
Env x Line effect	9	307.86	19.81	23.26***	4589.62	1238.39	457.90 ***	196.79**
Env x Tester effect	9	35.93 *	11.76	9.60*	3565.61	1034.37	25.26	123.22 *
Env x L * T effect	81	39.77 ***	15.09***	3.98	3565.61***	974.04	116.98	61.12 ***
Error	476	109.11	2.81	6.12	724.84	2801.26	106.83	21.63
Total	719	**176.54**	7.21	68.58	1496.13	2222.62	478.65	218.27

*, **, significant at 5%, 1% probability respectively through F test

Contd. Table 4.3 Line versus Tester Analysis of variance for combining ability for various quantitative traits in carrot

Source of variation	DF	Shoot weight (g)	Root size (cm^2)	Root to shoot ratio	Days to maturity (in days)	Harvest index(%)	Yield (t/ha)
Replicates	2	4246.66	637.27	411.01*	0.25	1131.42	192.80
Environments	1	4172.05***	70212***	93864***	12.42**	36895***	121145.8***
Treatments	119	884.85 ***	484.42***	187.23***	6.08**	357.74 ***	71.69***
Parents	19	272.20*	313.61***	140.94***	13.56**	163.14 ***	35.52**
Parents (Line)	9	204.31	297.36***	145.35***	15.96**	174.80 ***	42.91**
Parents(Testers)	9	367.41 **	333.71***	150.87***	7.98**	164.52 ***	27.89
Parents (L vs T)	1	26.32	278.89***	11.82	5.47**	45.79	37.66
Parent vs Crosses	1	980.26**	7907***	237.19**	29.56**	7641.99***	357.67***
Crosses	99	1001.46***	442.22***	195.61***	4.65**	321.51 ***	75.744**
Line effect	9	1518.69	470.31	100.51	5.53	483.90	133.44
Tester effect	9	1707.24	867.86*	241.84	5.06	215.86	37.28
Line x Tester effect	81	865.58***	391.81***	201.04***	4021**	315.23 ***	73.60***

Env x Treat	119	184.49 *	385.43***	115.59***	25.05*	474.43 ***	63.36***
Env x Parents	19	62.49*	339.62***	85.98***	3.54	124.85 ***	46.04***
Env x Parents (L)	9	50.95*	338.92***	76.82*	2.88*	84.12	32.82*
Env x Parents (T)	9	74.86*	334.06***	99.49***	5.64	151.973***	55.19***
Env x Crosses	99	146.56*	396.05***	113.69***	10.55**	408.94 ***	59.66***
Env x Line effect	9	552.12 ***	551.77	92.16	3.32	465.715	93
Env x Tester effect	9	84.34	762.97*	155.05	36.25	716.925	72.50
Env x L x T effect	81	108.41	337.98***	111.49***	8.55	368.42***	54.53***
Error	476	140.31	27.86	31.44	290	44.414	16.69
Total	**719**	**298.87**	**1142.65**	**1378.88**	**2.82**	**224.518**	**202.95**

*, **, significant at various probability viz., 5%, 1% through F test

4.2.3. Genetic components of variance with respect to quantitative characters traits

The measure of genetic components of variance and gene action study represented in Table 4.4. The GCA variance (σ^2_{gca}) of lines and testers founds lower in compare to SCA variance (σ^2_{sca}) for most of the traits quantitative characters traits. The measure of dominance variance (σ^2D) relatively higher to additive component of variance (σ^2A) for all the traits. The value of degree of dominance recorded higher than unity for all the characters indicating potent nature of various traits. Further, the ratio of additive to dominance variance (σ^2A/D) in associate with predictability ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) observed less than unity for all the traits suggesting prevalence of non-additive gene action. The estimate of variance due to environment (σ^2E) was relatively lesser than additive component of variance (σ^2A) and dominance variance (σ^2D) except plant height and cortex thickness. The measures of heritability correlated with selection efficiency. In this experimentation, the lowest value of narrow-sense heritability (h^2ns) was observed for harvest index (4.95%) and highest h^2_{ns} value recorded for shoot weight (23.07%). Generally, low level of h^2_{ns} measures found for all characters except for root diameter, shoot weight and leaf length for which moderate h^2_{ns}. The lower value of genetic advance (GA) at 5% selection recorded for all traits.

4.2.4. General combining ability (GCA) effects of lines and testers

The measures of combining ability found be suitable for preselection of parental lines and identifying promising hybrid combination. The values of GCA parental CMS lines and testers represented in Table 4.5. The GCA measures confirm that the CMS lines, KT-10A, KT-28A and KT-80A and tester KS-21, KS-22, KS-50 and New Kuroda had significant GCA effects in useful direction with respect to root diameter at root harvesting stage.

Table 4.4 Measures of genetic components of variance, heritability, genetic advance and predictability ratio for thirteen various horticultural traits (Pooled data).

Variance Components	Leaf length(cm)	Root length (cm)	Root dia. (mm)	Core dia. (mm)	Cortex thickness (mm)	Gross root weight (g)	Net root weight (g)	Shoot weight (g)	Root size (cm^2)	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
σ^2_{gca} Line	10.08	0.70	2.93	65.63	-32.28	47.57	16.69	24.02	7.53	1.48	0.24	7.45	2.03
σ^2_{gca} Tester	5.74	0.51	4.36	43.57	-40.55	43.43	23.46	27.16	14.15	3.83	0.06	2.98	0.42
σ^2L x t (SCA)	47.97	1.51	24.61	449.64	-353.75	342.08	202.24	131.37	62.24	31.58	0.10	46.39	10.34
σ^2Env	0.76	0.01	54.08	10.37	71.20	1.46	-0.04	1.76	1650.15	2232.20	0.97	45.22	300.60
σ^2Env x Line	8.80	0.60	0.68	124.48	-70.57	13.12	6.02	15.82	17.78	2.68	0.21	14.29	2.71
σ^2Env x Testers	-0.25	0.34	0.22	90.34	-77.37	-1.29	3.57	0.23	24.82	4.78	0.97	22.66	2.03
σ^2Env. x GCA	4.27	0.47	0.45	107.41	-73.97	5.91	4.79	8.02	21.30	3.73	0.22	18.48	2.37
σ^2 E	7.28	0.26	0.47	142.54	559.28	10.69	2.68	12.89	3.06	1.92	2.15	6.14	1.92
σ^2A	15.83	1.22	7.29	109.21	-72.84	91.01	40.16	51.18	21.69	5.32	13.31	10.43	2.46
σ^2D	47.97	1.51	24.61	449.64	-353.75	342.08	202.24	131.37	62.24	31.58	0.34	46.39	10.34
σ^2 A /σ^2D	0.33	0.80	0.29	0.24	0.20	0.26	0.19	0.39	0.34	0.16	0.18	0.22	0.23
Degree of Dominance	1.74	1.11	1.83	2.02	2.20	1.93	2.24	1.60	1.69	2.43	0.24	2.10	2.05
Heritability (NS) %	20.21	14.44	21.66	6.00	9.00	19.23	14.89	23.07	9.18	6.68	0.06	4.95	7.27
Genetic Advance 5 %	3.68	0.86	2.58	5.27	5.27	8.61	5.03	7.07	2.90	1.22	0.10	1.48	0.87
Predictability Ratio	0.24	0.22	0.19	0.17	0.25	0.21	0.16	0.28	0.25	0.14	0.97	0.18	0.19

σ^2A = additive genetic variance, σ^2D = dominance genetic variance, σ^2_{gca} = estimate of GCA variance, σ^2_{sca} = estimate of SCA variance

Table 4.5 Estimates of general combining ability (GCA) effects of lines and testers (Pooled data).

Lines/testers	Leaf length (cm)	Root length (cm)	Root diameter(mm)	Core diameter (mm)	cortex thickness (mm)	Gross root weight (g)	Net root weight(g)	Shoot weight(g)	Root size (cm2)	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/Ha)
KT-7A	0.81	0.01	-1.04***	-2.37	-0.18	-3.57***	-4.01***	-1.63	-2.42***	-0.31	0.73**	0.71	-1.01*
KT-10A	0.21	0.21	3.48***	-3.97	5.93*	0.28*	1.58**	-3.37**	4.54***	1.78***	0.62*	4.67***	0.10*
KT-28A	0.69	0.54***	1.00***	-2.47	1.96	6.87***	3.31***	1.33	3.18***	-0.36	-0.60*	1.53	0.59
KT-39A	-0.58	0.017	-1.33***	-3.37	0.52	-1.75	1.13*	-4.96***	0.01	1.62***	-0.49	0.87	-0.30
KT-47A	-5.80***	-1.05***	0.56**	-1.67	0.72	-9.47***	-6.17	-5.38***	-1.56**	0.82	0.17**	-0.19	-1.52***
KT-62A	2.29***	-0.35*	0.12	-4.17	2.78	-0.20	-1.89***	-0.39	0.12	-0.24	-0.71**	-0.44	-0.61
KT-80A	-3.28***	0.11	1.73***	-2.17	2.38	-0.25	-0.01	-2.32*	3.38***	0.51	-0.16	2.91***	-0.75
KT-95A	-1.58	-1.08***	-1.76***	-2.36	-0.91	-3.10**	-4.61***	-0.57	-3.4***	-0.40	-0.27	-4.89***	-1.18**
KT-98A	0.66	-0.33*	-1.91***	-2.77	-0.65	15.90***	6.27***	7.54***	-2.61***	-2.70***	0.06	-1.85*	1.15**
KT-8542A	6.56***	1.92***	-0.84***	25.33***	-12.57	-4.69***	4.40***	9.77***	-1.23*	-0.72	-0.44	-3.31***	3.54***
KS -20	-1.10	0.84***	-2.20***	-3.07	-0.64	-4.90***	-0.11	-7.01***	-2.06***	2.59***	0.56*	3.55***	0.14
KS -21	-2.30	1.02***	0.83***	-3.41	3.10	-8.13***	-6.11***	-2.11	2.64***	0.50	0.68**	0.29	-1.29**
KS -22	2.11*	0.61***	1.79***	-1.62	2.30	9.44***	3.95***	6.45***	4.03***	-1.72***	0.120	1.34	0.40
KS -50	0.43	-0.04	3.86***	-2.17	5.06	4.78***	1.06*	4.95***	6.91***	-1.46***	0.56*	-0.22	0.36
KS -59	0.64	-1.34***	-0.55*	-1.70	0.09	-0.63	2.59***	-3.27**	-2.27***	1.04*	0.56*	-1.84*	0.40
NK-1	4.79***	-0.58***	0.30	-1.89	1.14	2.72	-4.12***	7.21***	-2.68***	-2.42***	0.96	-1.46	-0.64
PY-1(Katrain local sel.8)	-3.72***	-0.65***	-3.16***	-2.60	-1.77	-4.16	-0.43	-3.63**	-4.30***	1.77***	-0.05	-2.37**	-0.19
PN-1(Katrain local sel.11)	-1.79*	0.18	-1.04***	-2.67	0.50	-7.80	-1.03*	-6.99***	-1.40*	2.49***	-1.10***	1.38	0.13
New kuroda	2.22**	-0.31	1.57***	21.58***	-9.62	10.43	10.02***	1.34	2.84***	-0.01	-0.10	1.14	1.50***
KS -73	-1.28	0.26	-1.40***	-2.41	-0.17	-1.74	-5.81***	3.08**	-3.71***	-2.8***	-0.71**	-1.82*	-0.82
CD (5%)	1.67	0.31	0.42	7.42	14.70	2.03	1.018	2.23	1.08	0.86	0.51	1.54	0.86
CD (1%)	1.67	0.318	0.42	7.42	14.70	2.03	1.018	2.23	1.08	0.86	0.28	1.541	0.86

*, **, Significance variation at various probability viz., $P \leq 0.05$, $P \leq 0.01$ through F test, CD: critical difference

Besides, the CMS lines, KT-8542 and KT-28 and tester KS-20, KS-21 and KS- 22, exhibited significantly high GCA effects for root length. The cytoplasmic male sterile line, KT-7A was poor general combining ability for almost all characters except for root length, plant height, and harvest index and leaf length. For the core diameter, the significantly high GCA in desirable negative direction observed in all CMS lines except for KT-8542A. For the cortex thickness, leaf length, gross plant weight, found high GCA observed in KT-10A, KT- 8542A, KT -28A CMS lines, respectively. Similarly, for days to maturity KT-7 has showed considerable GCA. For marketable net root weight, CMS lines KT -100A, KT-28A, KT-98A and KT- 8542A showed considerable high GCA. Similarly, CMS lines, KT-10A, KT-98A and KT-8542A had significantly high GCA for marketable yield.

4.2.5. Specific combining ability (SCA) effects of crosses

The results obtaining for specific combining ability 100 heterotic crosses are summarised in Table 4.6. Hence, in 100 cross combination 19, 27 and 41 has exhibited high SCA effects for all quantitative characters root traits namely, root length, root to shoot ratio and root diameter, respectively (Table 4.6). The effective SCA effective was observed in desirable negative direction for core diameter was recorded in hybrid KT-8542 × KS -22 (good general combiner × poor combiner) followed by KT-8542 × KS -20 (good general combiner × poor combiner) and KT-39 × New Kuroda (poor general combiner x good combiner). Among the 100-cross combination, 31 and 18 crosses shows high SCA effects in positive direction for plant height and leaf length (Table 4.6). The greater SCA effect for plant height was recorded in the cross, KT-8542 × KS -21 (good general combiner × poor combiner) followed by KT-10 × KS -50 (good general combiner × good combiner), and KT-47 × PY-1 (poorer combiner with non-significant effect × poor combiner). The commercially important horticultural characters viz. gross root weight (GRW), root size (RS), net root weight (NRW), 27,22 and 33 crosses showed greater SCA effects (Table 4.6). Regarding some of important quantitative characters

traits 100 cross combination, 18 and 23 crosses exhibited high positive SCA effects for leaf length (LL), leaf weight (LW), respectively. As far as the days to maturity (in days) and harvest index (HI%) and total marketable yield (TMY) is concerned, in 100 hybrids, in which 28, 22 and 20 hybrids exhibited considerable SCA effects (Table 4.6). The heterotic cross, KT-98 × NK-1 (significant good general combiner × good combiner) exhibited highest positive significant SCA effect for gross plant weight followed by KT-98 × PN-1 (good general combiner × poor combiner) and KT-80 × KS -73 (non-significant poor combiner × non-significant GCA). For the marketable net root weight, the hybrid, KT-98 × PN-1 (significant general good combiner × non-significant poor combiner) showed highest positive significant SCA effects followed by KT-98 × New Kuroda (significant general good combiner × significant good combiner) and KT-95 × KS -73 (poor combiner × poor combiner). As far as the root length is concern, the greater SCA effect recorded in the hybrid cross of KT-47 × KS -21 (non-significant GCA × significant good GCA) followed by KT-8542 × PN-1 (significant GCA × good general combiner) and KT-62 × KS -50 (poor combiner × non-significant GCA). The crosses, KT-8542 × NK-1 (poor combiner × significant poor combiner) followed by KT-62 × KS -73 (poor combiner × significant poor combiner) and KT-39 × KS -73 (significant GCA × significant poor combiner) displayed highest significant positive SCA effect for Root to shoot ratio. Similarly, for root diameter, the highest positive significant SCA estimate was observed in the hybrid KT-10 × New Kuroda (significant GCA × poor combiner) followed by KT-47 × KS -22 (significant GCA × significant GCA) and KT-98 × PN-1 (significantly poor combiner × significantly poor combiner). Similarly, for harvest index, the higher SCA effect observed in cross combination KT-10 × New Kuroda (significant GCA × good combiner) followed by KT-8542 × NK-1 (significantly poor combiner × poor combiner) and KT-98 × PN-1 (significantly below par combiner × good combiner). Finally for the yield, the cross KT-98 × PN-1 (significant GCA × poor combiner) exhibited highest significant positive SCA

effect. After that, the cross combination KT-10 × NK-1 (poor combiner × poor combiner) followed by KT-8542 × New Kuroda (significant poor combiner × significant GCA) and KT-47 × KS -59 (significant poor combiner × good combiner) exhibited significant positive SCA effects for yield character (Table 4.6).

4.2.6 Qualitative traits of crosses

The observations regarding qualitative traits of 100 crosses are presented in Table 4.7. The anthocyanin colouration of shoulder and green colour of shoulder at root maturity was absent in all the crosses and all the hybrids were also free from physiological disorders like cavity spot, forking, splitting, etc. All the crosses had fine root texture. The majorly all of the crosses had dark orange smooth roots. In majority of the crosses the leaf attitude were erect, except for the cross combination KT-10 × KS -73, KT-10 × KS-21, KT-10 × KS-22, KT-10 × KS-50, KT-10 × New Kuroda, KT-10 × NK-1, KT-10 × PN-1, KT-28 × KS-59, KT-28 × NK-1, KT-39 × New Kuroda, KT-8542 × KS-20, KT-8542× KS-21, KT-8542 × KS-22, KT-95 × New Kuroda, KT-95 × PN-1 with semi erect leaf attitude. Among the 100 crosses, all roots were cylindrical shaped roots with orange root colour.

Table 4.6 Estimates of specific combining ability (SCA) effects of 100 crosses for quantitative characters traits. (Pooled Data)

Crosses	Leaf length (cm)	Root Length (cm)	Root Diameter (mm)	Core Diameter (mm)	Cortex thickness (mm)	Root Weight (g)
KT-10 x KS -22	-2.59	0.68	-5.87***	3.72	-8.48**	16.98***
KT-10 x PN-1	-1.17	-2.38***	-4.49***	0.77	-11.21**	-13.97***
KT-10 x PY-1	0.13	0.95	-3.83***	1.70	-6.23**	-24.39***
KT-10 x KS -20	2.93	0.70	-3.33***	2.17	-5.99***	-4.28
KT-10 x KS -21	-11.37	-0.72	-2.04**	2.51	-5.86**	-21.81***
KT-10 x KS -50	10.43	-2.15***	-3.57***	2.27	-5.77***	-32.14***
KT-10 x KS -59	-12.19	-1.85***	-2.06**	1.80	-5.18**	-1.30
KT-10 x KS -73	-5.63	0.53	0.23	3.51	-5.06*	-25.09***
KT-10 x New Kuroda	19.77	0.86	26.42***	-21.49	-5.00**	-6.21
KT-10 x NK-1	-0.29	3.38***	-1.46*	2.99	-4.97**	18.61***
KT-28 x KS -22	-2.40	0.11	-4.85***	0.29	-4.92**	-22.96***
KT-28 x PN-1	-6.97	0.28	-2.01**	3.28	-4.87	-11.05***
KT-28 x PY-1	9.33	0.62	4.47***	5.20	-4.77	-5.06
+KT-28 x KS -20	-3.87	-0.36	-3.77***	2.67	-4.74	0.38
KT-28 x KS -21	-10.18	-2.54***	0.47	-1.98	-4.69	1.38
KT-28 x S -50	0.63	-0.48	-1.09	3.76	-4.58	21.05***
KT-28 x KS -59	-6.99	-0.43	3.32***	4.30	-4.32	-13.50***
KT-28 x KS -73	3.56	0.96	1.25	3.01	-4.25	2.92
KT-28 x New Kuroda	5.98	0.78	-0.26	-21.98	-4.17	-0.95
KT-28 x NK-1	10.90	1.05*	2.47***	1.49	-4.14	7.13*
KT-39 x KS -22	-7.59	1.38**	-3.97***	3.12	-4.10	-30.92***
KT-39 x PN-1	-8.17	-2.18***	3.23***	4.10	-3.99	-22.97***
KT-39 x PY-1	-0.87	1.15*	2.44*	-0.891	-3.96	10.08**
KT-39 x KS -20	1.93	1.65**	4.39***	2.57	-3.89	12.14***
KT-39 x KS -21	-6.38	-0.02	1.35	2.91	-3.52**	-19.66***

Crosses	Leaf length (cm)	Root Length (cm)	Root Diameter (mm)	Core Diameter (mm)	Cortex thickness (mm)	Root Weight (g)
KT-39 x KS -50	2.43	0.04	-7.51***	4.66	-3.47*	-22.11***
KT-39 x KS -59	8.80	0.33	2.74***	1.20	-3.41*	11.76***
KT-39 x KS -73	-6.63	-2.25***	2.12**	2.91	-3.37*	-5.56
KT-39 x New Kuroda	7.77	-1.68**	-3.76***	- 4.00	-3.36	-3.73
KT-39 x NK-1	8.70	1.58**	-1.03	3.39	-3.36	-18.66***
KT-47 x KS -22	3.70	0.46	11.62***	4.42	-2.93	24.68***
KT-47 x PN-1	1.12	0.88	-1.57	2.48	-2.93	-20.10***
KT-47 x PY-1	13.43	0.22	-2.382**	1.40	-2.89	5.15
KT-47 x KS -20	-0.76	-0.76	-3.33***	2.87	-2.83	27.51***
KT-47 x KS -21	-9.08	2.30***	5.28***	3.21	-2.82	26.16***
KT-47 x KS -50	-3.26	-1.63**	-2.11**	0.96	-2.60	8.96**
KT-47 x KS -59	0.10	0.91	0.85	4.50	-2.56	2.45
KT-47 x KS -73	-3.33	-0.18	-1.22	0.21	-2.32	-32.94***
KT-47 x New Kuroda	7.08	-1.36**	-8.50***	-21.78	-2.26	-12.59
KT-47 x NK-1	-8.99	-0.84	1.45*	1.69	-2.12	1.04
KT-62 x KS -22	7.90	1.26*	0.39	1.92	-2.11	-3.10
KT-62 x PN-1	-1.67	-0.06	1.77**	2.97	-2.09	-5.05
KT-62 x PY-1	1.63	-1.22*	-6.31***	-0.09	-1.70	-1.07
KT-62 x KS -20	-3.57	-1.96***	0.02	4.37	-1.67	5.18
KT-62 x KS -21	4.11	0.34	2.80***	2.71	-0.99	33.41***
KT-62 x KS -50	-10.06	2.16***	1.23	4.47	-0.88	-7.15*
KT-62 x KS -59	-4.69	0.96	-0.17	3.05	-0.86	6.87*
KT-62 x KS -73	2.86	-0.88	-2.24**	-0.28	-0.76	-0.63
KT-62 x New Kuroda	7.28	-0.31	-2.30***	-23.28	-0.56	0.67
KT-62 x NK-1	-3.79	-0.29	4.80***	4.19	-0.41	12.50***
KT-7 x KS -22	4.00	-1.11*	-1.35*	3.12	-0.41	19.56***

Crosses	Leaf length (cm)	Root Length (cm)	Root Diameter (mm)	Core Diameter (mm)	Cortex thickness (mm)	Root Weight (g)
KT-7* x PN-1	-1.57	0.56	-5.80***	1.17	-0.29	-4.34
KT-7 x PY-1	2.72	0.65	5.05***	3.10	-0.24	-14.86***
KT-7 x KS -20	-10.46	-1.84***	4.10***	2.57	-0.07	17.01***
KT-7 x KS -21	-1.78	-0.77	1.05	3.91	0.07	-4.86
KT-7 x KS -50	0.03	0.54	-1.90**	0.67	0.18	-3.23
KT-7 x KS -59	2.40	-1.40**	2.45***	1.20	0.31	-19.52***
KT-7 x KS -73	-1.03	1.24*	-2.53***	2.91	0.40	-8.49**
KT-7 x New Kuroda	8.38	1.31*	3.23***	-20.08	0.48	18.49***
KT-7 x NK-1	-2.69	0.83	-4.24***	1.39	0.72	49.28***
KT-80 x KS -22	-12.99	-0.21	-2.66***	1.92	0.73	-8.23*
KT-80 x PN-1	2.42	-0.28	0.17	0.97	0.80	-16.63***
KT-80 x PY-1	7.73	-1.44**	5.21***	4.90	1.24	-3.64
KT-80 x KS -20	-1.47	1.55**	5.70***	0.37	1.51	0.03
KT-80 x KS -21	4.22	0.87	-3.16***	2.71	1.65	-22.11***
KT-80 x KS -50	-5.96	1.44**	-0.36	1.47	1.84	38.26***
KT-80 x KS -59	1.40	0.74	-3.23***	3.00	2.02	4.80
KT-80 x KS -73	-2.03	0.13	0.52	2.71	2.29	6.41
KT-80 x New Kuroda	13.38	-0.78	0.46	-21.27	2.58	0.49
KT-80 x NK-1	-6.69	-2.01***	-2.63***	3.19	2.82	20.44***
KT-8542 x KS -22	5.32	-1.33**	-0.94	-24.15 *	3.04	-3.11
KT-8542* x PN-1	19.51	2.36***	-0.25	-20.61	3.10	-9.45**
KT-8542 x PY-1	5.28	-0.17	-1.75*	-21.94	3.22	24.82***
KT-8542 x KS -20	10.57	-0.99	3.91***	-24.13 *	3.33	4.26
KT-8542 x KS -21	22.36	2.15***	-0.78	-21.21	3.48	12.66***
KT-8542 x KS -50	10.03	0.05	1.70*	-21.03	3.61	-14.32
KT-8542 x KS -59	6.71	0.11	-0.19	-21.84	4.20	24.26***

Crosses	Leaf length (cm)	Root Length (cm)	Root Diameter (mm)	Core Diameter (mm)	Cortex thickness (mm)	Root Weight (g)
KT-8542 x KS -73	6.67	-0.73	-0.50	-20.24	4.54	27.52***
KT-8542 x New Kuroda	-89.07 ***	0.36	-5.77***	196.73 ***	6.09	5.11
KT-8542 x NK-1	2.59	-1.81***	4.60***	-21.54	6.74	41.71***
KT-95 x KS -22	0.50	-0.51	3.75***	4.13	6.80	-14.62***
KT-95 x PN-1	-9.07	1.41**	0.75	2.18	6.85	26.66***
KT-95 x PY-1	8.22	-0.75	-0.04	4.10	8.31	-3.36
KT-95 x KS -20	3.02	1.75***	-3.91***	2.57	8.37	-20.22***
KT-95 x KS -21	6.72	-0.92	-1.12	2.91	9.12	-13.28***
KT-95 x KS -50	-6.46	-0.86	7.50***	1.67	9.23	-13.08***
KT-95 x KS -59	3.90	-0.06	0.26	2.20	9.93	-9.29**
KT-95 x KS -73	-2.53	1.33**	2.56***	1.91	10.16	5.02
KT-95 x New Kuroda	3.87	-0.08	-3.32***	-22.03	10.25	4.12
KT-95 x NK-1	-8.19	-1.31*	-6.42***	0.39	10.59	-19.92***
KT-98 x KS -22	4.15	-0.75	3.89***	1.52	11.33	-3.10
KT-98 x PN-1	5.57	-0.58	8.19***	2.57	11.36	-19.36***
KT-98 x PY-1	-47.62 ***	-0.003	-2.81***	2.50	12.19	-10.11**
KT-98 x KS -20	1.68	0.25	-3.77***	3.96	12.23	14.37***
KT-98 x KS -21	1.37	-0.67	-3.90***	2.31	12.93	18.54***
KT-98 x KS -50	2.18	0.89	6.19***	1.07	13.14	-2.64
KT-98 x KS -59	0.55	0.69	-3.96***	0.60	13.99	25.98***
KT-98 x KS -73	8.11	-0.15	-0.24	3.31	14.43	-4.99
KT-98 x New Kuroda	15.53	0.913	-6.10***	-20.68	16.70	-5.38
KT-98 x NK-1	8.45	-0.568	2.47***	2.79	37.52	-5.71

*, **, Significance variation at various probability viz., $P \leq 0.05$, $P \leq 0.01$ through F test, CD: critical difference

Contd.Table 4.6 Estimates of specific combining ability (SCA) effects of 100 crosses for quantitative characters traits. (Pooled data)

Crosses	Root weight (g)	Shoot weight (g)	Root size ($cm^{2)}$	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
KT-10 x KS -22	19.89***	-3.87	-5.41**	1.57	-1.08	2.38	4.12**
KT-39 x KS -50	-7.20***	-7.94*	-6.63***	-4.67***	0.00	-8.32***	-1.57
KT-98 x KS -20	-11.64***	-10.53**	-5.98***	0.33	-0.10	-2.30	-2.60
KT-39 x KS -22	-9.32***	4.07	-8.18***	-3.47*	-0.16	-1.99	-2.35
KT-7 x PN-1	-13.92***	-7.66*	-9.43***	-2.66	0.39	-0.50	-1.80
KT-95 x NK-1	-14.91***	-17.56***	-11.08***	-0.83	0.95	-6.83**	-1.90
KT-80 x KS -59	-0.50	-0.75	-2.31	-0.13	-0.64	-1.53	0.32
KT-98 x KS -21	-10.23***	-14.76***	-6.21***	3.87**	1.45*	-2.50	2.72
KT-62 x PY-1	-3.99*	-2.32	-10.72***	-1.55	1.01	-8.78***	-1.22
KT-95 x KS -20	18.72***	2.12	3.22	7.52***	-1.05	-1.37	3.56*
KT-28 x KS -20	-15.67***	-6.36	-5.54**	-2.34	0.16	-8.12**	1.61
KT-10 x KS -50	-9.81***	-2.47	-11.23***	3.75**	-0.94	-7.51**	-3.43*
KT-80 x NK-1	-2.82	-2.59	-6.24***	1.12	-0.08	-8.35***	-1.22
KT-80 x KS -21	4.16	-3.68	2.77	2.82*	-0.33	0.58	3.11*
KT-47 x KS -20	2.48	1.12	-9.54***	3.79**	-0.43	-1.39	0.79
KT-7 x NK-1	-2.12	22.82***	-3.17	-7.20***	-0.83	-12.01***	-2.19
KT-10 x PY-1	-9.11***	-4.48	0.94	5.07***	0.72	-4.42	-1.55
KT-7 x KS -73	-0.38	4.30	-1.337	-3.87**	0.95	-1.66	-1.46
KT-28 x PN-1	4.14*	-4.74	0.85	0.91	0.81	-0.35	1.78
KT-10 x PN-1	-2.91	10.27**	-10.57***	-4.04**	-5.44***	-11.76***	-2.22
KT-98 x PY-1	-15.14***	15.88***	-4.85**	-4.57**	1.79**	-1.21	-2.59
KT-10 x KS -20	-23.64***	2.89	-4.45*	-1.73	1.06	-9.26***	-5.80***
KT-28 x KS -22	5.76***	3.50	-9.37***	-1.64	1.61*	-0.64	0.37

Crosses	Root weight (g)	Shoot weight (g)	Root size ($cm^{2)}$	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
KT-28 x KS -50	-2.55	13.61***	-4.43*	2.86*	-0.30	-3.39	-1.98
KT-98 x KS -59	-11.32***	8.24*	-2.35	-4.90***	0.78	-3.90	-2.92*
KT-80 x KS -22	-7.80***	-15.26***	3.28	2.68	-1.65**	-1.93	-1.27
KT-10 x NK-1	15.17***	-3.76	8.77***	-0.51	-0.72	2.77	8.29***
KT-39 x NK-1	3.22*	2.34**	-3.41	8.72***	0.83	9.00***	0.75
KT-10 x KS -21	-5.82***	2.19	-2.46	-2.98*	1.06	-4.56	-2.16
KT-7 x KS -22	-3.79*	-15.83***	-3.89*	2.084	0.14	0.75	-0.08
KT-95 x PY-1	-7.82***	32.40***	-9.64***	-0.65	-0.11	-7.47**	-3.08*
KT-47 x PN-1	-22.55***	2.67	-2.90	-6.23***	0.46	-2.03	-5.37***
KT-95 x KS -21	6.30***	-1.05	-0.44	2.26	0.39	-2.53	0.38
KT-62 x KS -20	14.19***	15.54***	-5.42**	1.12	-0.73	-4.98*	1.64
KT-10 x KS -59	20.05	6.15	-1.18	1.49	-0.16	-6.77**	3.50*
KT-47 x KS -59	11.13***	-2.14	1.49	3.29*	0.25	7.48**	4.77***
KT-47 x PY-1	4.94**	-2.58	-8.20***	3.81**	-1.66**	5.61*	0.78
KT-98 x KS -73	-20.42***	11.53**	-9.07***	5.98***	0.90	6.14*	-4.89***
KT-62 x KS -50	-2.55	-11.23**	10.66***	-4.54**	0.84	5.22*	2.11
KT-62 x KS -59	-2.13	3.23	1.17	-6.55***	-0.61	-0.26	-1.17
KT-47 x KS -50	0.14	-4.47	-9.37***	-12.37***	0.29	-3.14	-0.85
KT-10 x KS -73	4.56**	-8.64*	-0.07	3.48*	-1.08	8.18**	1.52
KT-7 x KS -21	4.87**	-5.86	0.74	1.11	0.00	1.89	1.60
KT-7 x KS -50	6.69***	-2.73	-0.49	-5.59***	0.57	2.85	1.11
KT-80 x KS -73	16.04***	18.3***	0.39	-11.14***	0.17	-0.97	1.68
KT-95 x KS -59	0.42	-7.52*	-4.24*	3.89**	0.72	7.34**	0.76
KT-80 x KS -50	7.20***	-1.55	1.74	-2.31	-0.38	5.11*	0.90
KT-62 x KS -73	16.07***	-15.72***	0.34	10.50***	-0.25	2.75	4.52**
KT-28 x KS -73	-5.13**	6.94	2.35	5.03***	1.50*	0.70	-3.04*

Crosses	Root weight (g)	Shoot weight (g)	Root size ($cm^{2)}$	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
KT-39 x KS -21	1.94	10.65**	1.51	7.40***	0.07	-1.58	-0.58
KT-62 x KS -22	-9.78***	28.38***	2.44	6.46***	0.34	-7.52**	-2.94*
KT-95 x PN-1	-6.27***	2.15	7.04***	5.46***	0.55	0.31	-2.22
KT-47 x KS -73	-5.57***	-8.30*	2.11	3.38*	-2.21***	-4.53	0.45
KT-62 x PN-1	20.05***	-2.81	4.23*	3.34*	-0.58	6.58**	4.45**
KT-28 x KS -59	3.12	-7.79*	4.61**	4.57**	0.50	3.42	1.85
KT-39 x PN-1	-5.36**	2.36	-5.13**	-1.54	-0.93	2.52	-0.90
KT-80 x PN-1	-15.62***	-3.68	-3.30	-10.97***	1.00	0.98	-2.81*
KT-39 x KS -73	3.71*	-11.22**	1.10	-3.37*	-0.45	2.57	1.65
KT-28 x PY-1	18.34***	0.19	12.10***	3.03*	0.45	4.34	3.35*
KT-98 x NK-1	6.77***	42.13****	2.27	-10.36***	0.98	-3.62	-0.77
KT-95 x KS -22	0.73	-9.92**	-1.70	6.76***	0.39	8.90***	-0.05
KT-47 x NK-1	-14.76***	-2.23	0.03	1.36	-0.04	-4.43	-3.83**
KT-62 x KS -21	-19.55***	16.00***	-4.47	-0.69	-1.11	-2.16	-6.01***
KT-80 x PY-1	-0.62	0.55	-2.86	-1.70	-0.56	3.63	-0.06
KT-62 x NK-1	-2.94	-19.52***	5.19**	0.78	0.34	10.044**	-0.42
KT-95 x KS -73	21.40***	17.83***	13.11***	0.57	-0.14	-0.23	2.37
KT-28 x NK-1	-1.65	6.25	5.07**	-0.08	0.95	0.70	-2.39
KT-7 x KS -59	-12.15***	18.61***	-3.12	-3.92**	-0.15	-8.033**	-3.50*
KT-39 x KS -59	-0.398	0.94	4.75**	-0.88	0.11	2.19	0.32
KT-47 x New Kuroda	7.085***	12.43***	-9.77***	-2.19	0.33	-12.89***	1.06
KT-7 x KS -20	2.51	-3.41	0.77	5.30***	-1.10	1.90	1.24
KT-7 x PY-1	-2.72	-6.82	7.19***	-6.06***	0.42	7.52**	0.23
KT-47 x KS -21	18.92***	5.99	13.67***	3.24*	0.50	9.98***	2.96*
KT-39 x KS -20	6.74***	-0.26	12.92***	-3.08*	0.07	6.37*	1.50

Crosses	Root weight (g)	Shoot weight (g)	Root size ($cm^{2)}$	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
KT-98 x KS -22	0.453	11.24**	1.84	1.12	-1.00	-1.21	-1.38
KT-28 x KS -21	-5.36**	-8.72*	-6.27***	0.87	0.55	0.03	-0.97
KT-98 x New Kuroda	23.52***	-0.18	1.12	-0.66	-0.55	-4.08	4.29**
KT-39 x PY-1	20.53***	6.89	13.38***	-12.46***	-1.58*	-1.30	4.20**
KT-98 x KS -50	-11.81***	15.69***	5.82***	-0.96	0.50	2.09	-4.28**
KT-98 x PN-1	49.88***	7.95*	17.41***	12.70***	1.07	10.60***	12.44***
KT-95 x KS -50	-1.27	-14.57***	7.36***	3.36*	0.75	8.07**	4.19**
KT-80 x KS -20	20.14***	8.74*	10.48***	-3.39*	-0.83	8.74***	3.85**
KT-47 x KS -22	-1.84	-2.47	22.47***	-14.76***	1.07	5.36*	-0.77
KT-95 x New Kuroda	-17.28***	-3.86	-3.62	0.60	-0.33	-6.17*	-4.03**
KT-8542 x KS -73	-30.28***	8.01*	-8.92***	1.85	-0.78	-12.95***	-2.81*
KT-8542 x PY-1	-4.37**	-7.94*	2.65	5.71***	0.12	2.09	-0.04
KT-39 x New Kuroda	-13.87***	3.65	-10.30***	4.08**	-0.30	-9.47***	-3.00*
KT-8542 x KS -21	4.76**	-0.75	1.15	-3.52*	-0.89	0.86	-1.05
KT-8542 x PN-1	-7.42***	9.39**	1.79	-0.54	1.35*	-6.36*	-3.34*
KT-62 x New Kuroda	-9.30***	-11.54**	-3.44*	6.61***	0.61	-0.87	-0.91
KT-28 x New Kuroda	-1.00	-2.87	0.64	-3.52*	-0.84	3.30	-0.58
KT-80 x New Kuroda	-20.17***	-0.11	-3.96*	8.04***	0.06	-6.25*	-4.49
KT-8542 x KS -59	-8.18	-2.48	1.17	5.63	2.09**	0.06	-3.93
KT-8542 x New Kuroda	18.38***	4.17	-9.07***	3.10*	0.50	-1.82	5.06***
KT-7 x New Kuroda	21.02***	-3.40	12.73***	5.09***	-3.26***	7.28**	4.86***

Crosses	Root weight (g)	Shoot weight (g)	Root size ($cm^{2)}$	Root to shoot ratio	Days to maturity (in days)	Harvest index (%)	Yield (t/ha)
KT-8542 x KS -22	5.70***	0.16	-1.46	-7.46***	1.67**	-4.08	4.41**
KT-8542 x KS -50	21.22***	15.68***	6.56***	1.705	0.89***	-0.99	3.80**
KT-8542 x KS -20	-13.86***	-9.85**	3.54*	-1.91	-1.88**	10.45***	-5.80***
KT-8542 x NK-1	14.06***	-16.38***	2.56	2.48	0.09**	12.74***	3.71**
KT-10 x New Kuroda	-8.37***	1.73	25.68***	-13.16***	0.50	30.98***	-2.26

*, **, Significance variation at various probability viz., $P \leq 0.05$, $P \leq 0.01$ through F test, CD: critical difference

4.2.7 Evaluation of the hybrids for quantitative characters traits

The *per se* mean performance of 100 crosses for different quantitative characters traits is presented in Table 4.8. The mean value depicting the hybrid performance for different root traits such as root length, root diameter and core diameter ranged from 16.50 cm (KT-95 × PY-1) to 25.50 cm (KT-62 × KS -50), 33.33 mm (KT-62 × PY-1) to 80 cm (KT-10× New Kuroda) and 7.00 mm (KT-28 × KS -21) to 16.00 mm (KT-47 × KS -22), respectively. The maximum root length was found in the hybrid KT-62× KS -50 followed by KT-80 × KS -21 and KT-80 × KS -22. The maximum average value of root diameter was found in the hybrid KT-10X New Kuroda followed by KT-47 × KS -22. The minimum core diameter was observed in the hybrid KT-28 × KS -21 followed by KT-39 × PY-1 and KT -62 × KS -73 (Table 4.8). Among the 100 crosses, 33, 52 and 7 had root length, root diameter and core diameter higher compared to the check (Pusa Nayan Jyoti), respectively. For plant height, the mean value of hybrids ranged from 33.00 cm (KT-47 × KS -21) to 67.00 cm (KT-28 × NK-1) and 88 and 100 crosses performed better than the check (Pusa Nayan Jyoti) for plant height. The cross combinations, KT-28 × NK-1 followed by KT-39 × NK-1 and KT-62 × KS -22 possessed the maximum plant height. The mean value of hybrids for gross plant weight, shoot weight and net root weight ranged from 63.20 g (KT-47 × PN-1) to 155.40 g (KT-98× PN-1), 6.90 g (KT-7 × PN-1) to 55.40 g (KT-62 × KS -22) and 45.50g (KT -8542 × KS -73) to 135.50g (KT-98× PN-1), respectively. Among the 100 hybrids, 41, 44 and 41 hybrids performed better with respect to gross plant weight, shoot weight and net root weight, respectively as compared to the check (Pusa Nayan Jyoti). For gross plant weight, the hybrid combination, KT-98× PN-1 followed KT-98 × New Kuroda and KT-98 × NK-1 had the higher value for gross plant weight than rest of hybrids. Similarly, with respect to shoot weight, the hybrid KT-62 × KS -22 followed by KT-98 × NK-1 had highest mean value than rest of the crosses. The crosses KT-98× PN-1 followed by KT-98 × New Kuroda had highest net curd weight among 100 crosses.

The mean value of hybrids for leaf length was varied from 10.50 cm (KT-47 × KS -21) to 45.50 cm (KT-28 × NK-1). Similarly, the hybrid, KT-47 × KS -21 followed by KT-39 × NK-1 and KT-98 × NK-1 had maximum leaf length as compared to rest of hybrids (Table 4.8). The mean value for harvest index and total marketable yield among 100 hybrids ranged from 52.35% (KT -8542 × KS -73) to 92.07% (KT -39 × KS -73) and 18.2 t/ha (KT -8542 × KS -73) to 54.2 t/ha (KT-98× PN-1). The maximum percent harvest index was recorded in hybrid KT -39 × KS -73 followed by KT-39× KS -20 and KT-80 × KS -22. These three hybrids also performed better than best check (HVCF-16). Similarly, the highest average total marketable yield among 100 hybrids was recorded for hybrid KT-98× PN-1 followed by KT-98 × New Kuroda and KT-8542× KS -22. For the total marketable yield, 46 among 100 hybrids performed better than the check (Pusa Nayan Jyoti) (Table 4.8).

Table 4.7 Qualitative traits of 100 crosses of temperate carrot. (Pooled data)

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-10 x KS -73	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x KS-21	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x KS-22	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x KS-50	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x New Kuroda	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x NK-1	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x PN-1	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-10 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-28 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x KS-59	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x NK-1	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-28 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x New Kuroda	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-39 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-39 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-47 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Contd. Table 4.7 Qualitative traits of 100 crosses of temperate carrot. (Pooled data)

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-62 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-62 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-7 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-80 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Contd. Table 4.7 Qualitative traits of 100 crosses of temperate carrot. (Data pooled over environments)

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-80 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-80 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-80 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS - 73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS-20	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS-21	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS-22	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x New Kuroda	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-8542 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-8542 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x New Kuroda	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x PN-1	orange	cylindrical	Semi-erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-95 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x KS -73	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Crosses	Root Color	Root shape	Leaf attitude	Root Texture	Root: Green colour of shoulder	Root: Anthocyanin colouration of shoulder	Colour of core	Cavity spot	Forking	Splitting
KT-98 x KS-20	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x KS-21	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x KS-22	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x KS-50	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x KS-59	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x New Kuroda	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x NK-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x PN-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent
KT-98 x PY-1	orange	cylindrical	Erect	Fine	Absent	Absent	Orange	Absent	Absent	Absent

Table 4.8 Mean performance of 100 crosses for quantitative characters traits. (Pooled data)

Crosses	PH (cm)	LL (cm)	RL (cm)	RD (mm)	CD (mm)	CT (mm)	PW (g)	RW (g)	RS (cm^2)	RSR	DTM	HI (%)	Yield (t/Ha)
KT-7 X KS-20	42.00	23.00	19.00	45.00	12.00	33.00	89.00	77.53	85.50	7.57	90.67	87.19	31.01
KT-7 X KS -21	48.00	27.00	21.00	45.00	13.00	32.00	87.80	69.33	94.52	3.75	91.67	78.97	27.73
KT-7 X KS -22	58.00	37.50	20.50	43.33	14.00	29.33	87.80	74.33	88.89	5.62	91.00	84.66	29.73
KT-7 X KS -50	52.00	29.50	22.50	45.00	11.00	34.00	107.00	89.00	101.25	4.99	91.00	83.19	35.60
KT-7 X KS -59	53.00	34.50	18.50	45.00	12.00	33.00	102.80	68.50	83.25	2.01	92.00	66.63	27.40
KT-7 X NK-1	53.00	32.00	21.00	38.33	12.00	26.33	120.80	70.50	80.50	1.41	92.67	58.38	28.20
KT-7 X PY-1	48.00	26.50	21.50	45.00	13.00	32.00	83.40	73.50	96.72	8.73	91.00	88.25	29.40
KT-7 X PN-1	48.00	27.00	21.00	35.00	11.00	24.00	67.40	60.50	73.50	10.38	93.00	89.84	24.20
KT-7 X New Kuroda	50.00	27.50	22.50	48.33	14.00	34.33	126.00	108.50	108.72	6.23	92.00	86.11	43.40
KT -7 X KS -73	50.00	28.50	21.50	38.33	13.00	25.33	98.20	71.20	82.35	2.65	90.00	72.53	28.48
KT-10 X KS -20	55.00	32.00	23.00	41.67	10.00	31.67	73.00	53.50	95.83	2.81	91.67	73.34	21.40
KT-10 X KS -21	38.00	15.50	22.50	46.67	10.00	36.67	89.00	66.50	105.00	2.99	90.67	74.76	26.60
KT-10 X KS -22	51.00	30.50	20.50	43.33	13.00	30.33	127.30	105.50	88.84	5.11	90.33	82.91	42.20
KT-10 X KS -50	62.00	42.50	19.50	48.33	11.00	37.33	94.60	68.50	94.24	2.70	90.00	72.53	27.40
KT-10 X KS -59	38.00	19.50	18.50	45.00	11.00	34.00	126.40	99.50	83.23	3.77	89.33	78.78	39.80
KT-10 X NK-1	55.00	31.50	23.50	46.67	12.00	34.67	136.03	94.50	109.62	3.26	89.00	72.00	37.80
KT-10 X PY-1	45.00	20.50	24.50	40.00	10.00	30.00	83.20	71.50	98.00	6.29	91.00	85.97	28.60
KT-10 X PN-1	48.00	29.50	18.50	41.67	9.00	32.67	100.20	73.50	77.08	2.76	91.33	73.37	29.40
KT-10 X New Kuroda	61.00	41.50	19.50	80.00	11.00	69.00	105.60	79.50	156.00	3.07	91.33	75.32	31.80
KT -10 X KS -73	45.00	24.50	20.50	46.67	12.00	34.67	98.73	84.50	95.70	5.97	85.00	85.59	33.80
KT-28 X KS -20	49.00	25.50	23.50	38.33	12.00	26.33	87.83	70.71	90.07	6.18	91.67	80.70	35.13
KT-28 X KS -21	40.00	20.00	20.00	46.67	7.00	39.67	85.00	67.50	93.30	3.89	90.00	79.43	27.00
KT-28 X KS -22	52.00	32.00	20.00	41.67	11.00	30.67	127.00	93.50	83.33	2.83	91.00	73.63	37.40
KT-28 X KS -50	53.00	31.50	21.50	48.33	14.00	34.33	124.40	83.50	103.93	2.09	88.00	67.24	33.40

KT-28 X KS -59	44.00	23.50	20.50	48.33	15.00	33.33	104.13	86.50	99.08	4.93	89.00	83.05	34.60
KT-28 X NK-1	67.00	45.50	21.50	48.33	12.00	36.33	115.00	75.50	103.97	1.91	91.00	65.66	30.20
KT-28 X PY-1	55.00	32.50	22.50	46.67	15.00	31.67	121.80	98.50	105.04	4.29	91.33	80.93	39.40
KT-28 X PN-1	43.00	20.50	22.50	41.67	13.00	28.67	98.70	82.50	93.78	5.33	91.00	83.65	33.00
KT-28 X New Kuroda	48.00	26.50	21.50	46.67	12.00	34.67	114.80	90.50	100.32	3.82	90.67	78.89	36.20
KT -28 X KS -73	55.00	33.00	22.00	45.00	13.00	32.00	106.40	71.46	99.00	2.07	90.67	67.21	28.58
KT-39 X KS -20	53.00	28.50	24.50	45.00	11.00	34.00	93.20	85.18	110.22	11.70	90.67	91.38	34.07
KT-39 X KS -21	42.00	19.50	22.50	45.00	11.00	34.00	103.20	74.56	101.23	2.63	90.00	72.28	29.82
KT-39 X KS -22	45.00	23.50	21.50	40.00	13.00	27.00	104.00	75.56	85.97	2.68	90.67	72.66	30.22
KT-39 X KS -50	53.00	28.50	24.50	38.33	14.00	24.33	89.70	71.82	93.95	4.05	91.00	80.06	28.73
KT-39 X KS -59	58.00	36.50	21.50	45.00	11.00	34.00	98.70	84.50	96.75	6.27	89.00	85.71	33.80
KT-39 X NK-1	63.00	43.50	19.50	41.67	13.00	28.67	96.00	82.50	81.26	6.58	91.00	86.00	33.00
KT-39 X PY-1	43.00	18.50	24.50	41.67	8.00	33.67	122.20	100.50	102.02	4.77	91.00	82.28	40.20
KT-39 X PN-1	40.00	21.50	18.50	45.00	13.00	32.00	87.80	78.50	83.19	9.43	90.00	89.52	31.40
KT-39 X New Kuroda	48.00	28.50	19.50	40.00	9.00	31.00	99.98	75.27	78.00	3.06	91.00	75.30	30.11
KT -39 X KS -73	43.00	22.50	20.50	43.33	12.00	31.33	88.60	81.50	88.80	14.08	90.00	92.07	32.60
KT-47 X KS -20	44.00	26.50	17.50	38.33	13.00	25.33	87.60	74.44	67.13	5.66	91.00	84.98	29.78
KT-47 X KS -21	33.00	10.50	22.50	51.67	13.00	38.67	107.80	78.50	116.27	2.69	91.00	72.84	31.40
KT-47 X KS -22	50.00	26.00	24.00	60.00	16.00	44.00	97.20	75.50	144.00	3.60	90.67	77.75	30.20
KT-47 X KS -50	41.00	23.00	18.00	46.67	12.00	34.67	92.80	68.50	84.00	2.82	91.67	73.83	27.40
KT-47 X KS -59	43.00	24.50	18.50	45.00	16.00	29.00	95.50	83.40	83.26	7.71	90.67	87.40	38.20
KT-47 X NK-1	39.00	18.50	20.50	46.67	13.00	33.67	77.20	58.50	95.70	3.15	90.33	75.78	23.40
KT-47 X PY-1-1	51.00	34.50	16.50	38.33	12.00	26.33	84.40	73.50	63.25	6.98	92.00	87.10	29.40
KT-47 X PN-1	43.00	20.50	22.50	41.67	13.00	28.67	63.20	52.50	93.74	4.96	90.00	83.10	21.00
KT-47 X New Kuroda	41.00	21.50	19.50	36.67	13.00	23.67	122.00	91.50	71.52	3.10	90.33	75.07	36.60
KT -47 X KS -73	40.00	17.50	22.50	41.67	11.00	30.67	81.50	63.50	93.78	3.54	91.00	77.91	25.40
KT-62 X KS -20	50.00	32.50	17.50	41.67	12.00	29.67	123.00	91.92	72.91	2.99	90.00	74.78	36.77
KT-62 X KS -21	55.00	34.50	20.50	48.33	10.00	38.33	88.60	49.50	99.10	1.27	91.00	55.86	19.80
KT-62 * KS -22	63.00	39.50	23.50	46.67	11.00	35.67	129.40	74.00	109.63	1.34	88.00	57.21	29.60

KT-62 X KS -50	43.00	17.50	25.50	50.00	13.00	37.00	90.01	71.80	127.51	4.10	89.00	79.85	36.01
KT-62 * X KS -59	47.00	26.00	21.00	43.33	12.00	31.33	100.80	77.87	90.99	3.48	91.00	77.28	31.15
KT-62 X NK-1	53.00	32.50	20.50	50.00	13.00	37.00	81.00	73.50	102.49	10.65	91.33	90.74	29.40
KT-62 X PY-1	48.00	29.00	19.00	33.33	8.00	25.33	90.00	68.60	63.34	3.21	91.00	76.23	27.44
KT-62 X PN-1	49.00	28.50	20.50	45.00	11.00	34.00	109.60	98.50	92.26	9.02	90.67	89.89	39.40
KT-62 X New Kuroda	50.00	29.00	21.00	43.33	9.00	34.33	90.90	76.00	91.01	5.18	90.67	83.61	30.40
KT -62 X KS -73	55.00	34.50	20.50	40.00	8.00	32.00	98.00	86.37	82.00	7.94	90.67	88.16	34.55
KT-80 X KS -20	47.00	25.50	21.50	50.00	10.00	40.00	122.10	98.29	107.54	4.15	90.00	80.50	39.31
KT-80 X KS -21	50.00	24.50	25.50	43.33	12.00	31.33	88.50	76.65	110.50	6.74	90.67	86.67	35.40
KT-80 X KS -22	37.00	11.50	25.50	45.00	13.00	32.00	81.00	73.90	114.71	13.22	91.00	91.29	29.56
KT-80 X KS -50	42.00	19.50	22.50	50.00	12.00	38.00	112.00	86.15	112.60	3.40	89.00	76.99	34.46
KT-80 X KS -59	48.00	26.50	21.50	41.67	14.00	27.67	98.40	82.50	89.57	5.20	91.00	83.84	33.00
KT-80 X PY-1	45.00	25.50	19.50	43.33	14.00	29.33	98.00	73.50	84.54	3.01	91.00	75.01	29.40
KT-80 X PN-1	49.00	31.50	17.50	48.33	15.00	33.33	96.20	76.69	84.61	4.10	90.00	79.76	30.68
KT--80 X New Kuroda	48.00	26.50	21.50	45.00	11.00	34.00	73.00	63.50	96.73	8.41	91.00	87.10	25.40
KT-80 X NK-1	51.00	30.50	20.50	48.33	13.00	35.33	91.40	64.50	99.11	2.44	90.00	70.61	25.80
KT -80 X KS -73	45.00	25.50	19.50	45.00	13.00	32.00	132.00	87.97	87.78	2.03	91.00	66.71	35.19
KT-95 X KS -20	52.00	28.50	23.50	35.00	12.00	23.00	111.20	93.24	82.26	5.29	91.00	83.85	37.30
KT-95 X KS -21	53.00	31.50	21.50	41.67	12.00	29.67	94.50	69.50	89.58	2.83	90.67	73.63	27.80
KT-95 X KS -22	51.00	32.50	18.50	48.33	15.00	33.33	98.70	77.40	89.40	3.78	91.67	78.48	30.96
KT-95 X KS -50	42.00	20.50	21.50	55.00	12.00	43.00	95.50	79.80	118.18	5.14	90.67	83.59	38.20
KT-95 X KS -59	51.00	33.50	17.50	41.67	13.00	28.67	89.70	77.15	72.94	6.15	90.33	86.01	30.86
KT-95 X NK-1	44.00	24.50	19.50	35.00	11.00	24.00	75.73	57.50	68.25	3.23	92.00	76.00	23.00
KT-95 X PY-1	50.00	33.50	16.50	38.33	14.00	24.33	118.00	67.50	63.25	1.34	90.00	57.25	27.00
KT-95 X PN-1	37.00	12.50	24.50	41.67	12.00	29.67	84.17	68.50	102.08	4.67	90.33	81.52	27.40
KT-95 X New Kuroda	42.00	20.00	22.00	40.00	12.00	28.00	87.70	65.60	88.01	3.06	91.00	74.86	26.24
KT -95 X KS -73	45.00	22.00	23.00	43.33	12.00	31.33	134.00	89.50	99.67	2.01	88.33	66.79	35.80
KT-98 X KS -20	52.00	31.00	21.00	35.00	13.00	22.00	87.20	74.50	73.49	6.07	90.00	85.45	29.80
KT-98 X KS -21	49.00	26.50	22.50	38.33	11.00	27.33	91.83	74.70	86.22	4.56	91.00	81.52	36.73

KT-98 X KS -22	56.00	36.50	19.50	48.33	12.00	36.33	138.60	89.01	94.22	1.84	88.00	64.33	35.60
KT-98 X KS -50	52.00	30.50	21.50	53.33	11.00	42.33	126.40	75.50	114.67	1.49	89.00	59.76	30.20
KT-98 X KS -59	49.00	27.50	21.50	36.67	11.00	25.67	96.20	76.62	78.81	3.94	91.00	79.65	30.65
KT-98 X NK-1	62.00	43.50	18.50	45.00	13.00	32.00	143.00	89.50	83.26	1.69	91.33	62.66	35.80
KT-98 X PY-1	45.50	-25.00	20.50	35.00	12.00	23.00	81.40	68.04	71.75	5.10	91.00	83.58	27.21
KT-98 X PN-1	53.00	33.50	19.50	50.00	12.00	38.00	155.40	135.50	97.53	7.28	92.00	87.24	54.20
KT-98 X New Kuroda	55.00	33.50	21.50	36.67	13.00	23.67	151.20	118.50	78.88	3.66	90.00	78.38	47.40
KT -98 X KS -73	57.00	39.00	18.00	40.00	13.00	27.00	81.80	65.50	72.00	4.15	92.00	80.16	26.20
KT-8542X KS -20	47.00	25.00	22.00	45.00	13.00	32.00	86.00	75.50	99.00	7.20	91.00	87.79	30.20
KT-8542 X KS -21	63.00	39.50	23.50	45.00	12.00	33.00	98.90	76.77	105.75	3.50	92.00	77.66	30.71
KT-8542 X KS -22	47.00	26.50	20.50	46.67	10.00	36.67	109.50	74.00	95.69	2.08	92.67	67.58	43.80
KT-8542 X KS -50	49.00	26.50	22.50	53.33	12.00	41.33	142.40	95.00	119.93	2.01	92.00	66.71	38.00
KT-8542 X KS -59	45.00	23.50	21.50	45.00	13.00	32.00	92.80	73.77	96.68	4.12	91.00	79.57	29.51
KT-8542 X NK-1	45.00	26.50	18.50	51.67	12.00	39.67	102.00	92.17	95.55	11.40	90.00	90.48	40.80
KT-8542 X PY-1	38.00	13.50	24.50	38.33	13.00	25.33	88.90	74.50	93.90	5.18	91.00	83.79	29.80
KT-8542 X PN-1	60.00	36.50	23.50	43.33	14.00	29.33	98.70	68.79	101.86	2.30	92.00	69.70	27.52
KT-8542 X New Kuroda	58.00	38.00	20.00	40.00	11.50	28.50	134.00	108.50	79.94	4.33	91.00	81.01	43.40
KT -8542 X KS -73	47.00	26.00	21.00	41.67	15.00	26.67	87.00	45.50	87.50	1.10	92.00	52.36	18.20
Pusa Nayan Jyoti (CHECK)	41.17	19.43	21.73	43.83	14.67	29.17	99.33	77.50	95.33	3.62	90.33	78.05	31.00

PH=plant height, LL= leaf length, RL=root length, RD= root diameter, CD= core diameter, CT= cortex thickness, PW= Plant weight, RW=root weight, RSR= root to shoot ratio, RS= root size, DTM= days to maturity, HI= harvest index

4.2.8 Average heterosis for quantitative characters traits

The estimates of heterosis for various quantitative characters traits of 100 hybrids over mid parent are presented in Table 4.9. Among the 100 hybrids, very high and significant estimates of mid parent heterosis was observed in both the directions for all the 13 quantitative characters traits. For root length, the heterosis over mid parent ranged from -12.81 % to 33.76 %. The highest significant heterosis for root length in desirable direction was recorded in the hybrid KT-8542 × KS -21 (33.76 %) followed by KT-10× NK-1 (22.51%) and KT-47 × KS -21 (21.03%). Among the 100 crosses, 46 hybrids exhibited the significant heterosis for root length in desirable direction over mid parent (Table 4.9). The mid parent heterosis for root diameter ranged from -17.11% to 9.34%. Among 100 hybrids, 75 hybrids showed significantly higher heterosis in desirable direction over mid parent for root diameter The highest significant heterosis over mid parent in desirable direction for root diameter was observed in the hybrid KT-10 x New kuroda (100.68%) followed by KT-47 x KS -22 (59.38%) and KT-62 x NK-1 (39.24 %). For plant height, the heterosis over mid parent was ranged from -256.66 % to 85.66 %. Out of 100 crosses, 3 hybrids exhibited significant heterosis over mid parent in desirable direction for plant height. Highest heterosis for plant height was observed in the hybrid KT-62 x KS -22 (85.66%) followed by KT-98 x New kuroda (82.23 %) and KT-98 x PN-1 (75.25%). The average heterosis in desirable direction for gross plant weight and net root weight ranged from -21.45% to 96.97% and -48.63% to 61.14% respectively. The highest significant heterosis in desirable direction for gross plant weight was recorded in the hybrid KT-98 × NK-1 (96.97%) followed by KT-98 × New Kuroda (82.23%) and KT-98 × PN-1 (75.25%). Similarly, the highest significant heterosis in desirable positive direction for net root weight was observed in the hybrid KT-98 × PN-1 (61.14%) followed by KT-8542 × KS -50 (45.76%) and KT-98 × New Kuroda (44.85%).The significant mid parent heterosis for leaf length in desirable direction was ranged from 21.43% to 43.62%. The highest significant

heterosis over mid parent in desirable direction for leaf length was recorded in the hybrid KT-10 x KS -50 (43.62%) followed by KT-62 × KS -22 (39.52%) and KT-28 × NK-1 (38.97%). For leaf length among 8 crosses showed significant heterosis over mid parent in desirable direction. The heterosis over mid parent for root diameter and core diameter ranged from -12.31 % to 100.68 % and 15.79% to -53.52%, respectively. The highest significant heterosis in desirable direction for root diameter was recorded in the hybrid KT-47 × KS -22 (59.38%), followed by KT-62 × NK-1 (39.24%) and KT-95 × KS -50 (38.50%). Similarly, the greater heterosis was observed over mid parent in desirable negative direction for core diameter in the cross KT-28 x KS -21 (-53.52%) followed KT-39 × PY-1 (-50.78%) and KT-39× New Kuroda (-47.25%). For the root diameter and core diameter, the heterosis was observed in 74 and 87 crosses, respectively.

Table 4.9 Average heterosis of top 3 hybrids over the environments with their SCA value in parenthesis

Cross	Plant Height	Cross	Leaf Length	Cross	Root Length	Cross	Root Diameter	Cross	Core Diameter	Cross	Cortex Thickness
KT-62 x KS -22	85.66** (2.11**)	KT-10 x KS -50	43.62 ** (10.43)	KT-8542 x KS -21	33.76 ** (2.15**)	KT-10 x New kuroda	100.68 **(2.15 **)	KT-28 x KS -21	-53.52 (2.43**)	KT-10 x New kuroda	157.42 (-5.00*)
KT-98 x New kuroda	82.23 **(1.35**)	KT-62 x KS -22	39.52 ** (-6.7)	KT-8542 x PN-1	23.89 ** (2.36**)	KT-47 x KS -22	59.38 **(0.46)	KT-39 × PY-1	-50.78% (4.00)	KT-47 x KS -22	60.71(-2.93)
KT-98 x PN	75.25 **(2.56**)	KT-28 × NK-1	38.97* (10.9)	KT-10 x NK-1	22.51 ** (3.38** *)	KT-62 x NK-1	39.24 ** (-0.84)	KT-39× New Kuroda	-47.25 (-2.24**)	KT-39 x PY-1	56.68 (-3.96)

Cross	Plant weight	Cross	Root Weight	Cross	Root Size	Cross	Root to shoot ratio	Cross	Days to maturity	Cross	Harvesting Index	Cross	Yield
KT-98 x NK-1	96.97 ** (42.13** *)	KT-98 x PN-1	61.14 **(-19.36**)	KT-62 x KS -50	77.80 **(10.66**)	KT-95 x KS -50	43.95 ** (3.36**)	KT-80 x KS -73	-6.35** (0.17)	KT-10 x New kuroda	63.84 ** (30.98**)	KT-98 x PN-1	55.79 **(1244 **)
KT-98 x New kuroda	82.23 **(-0.18)	KT-8542 x KS -50	45.76 **(24.26 **)	KT-47 x KS -22	76.04 **(22.47**)	KT-80 x KS -22	37.82 **(2.68)	KT-95 x KS -73	-5.43**(0.95)	KT-80 x KS -20	44.96 **(8.74**)	KT-8542 x New kuroda	45.70 **(5.06 **)
KT-98 x PN-1	75.25 **(7.95 *)	KT-8542 x New kuroda	44.82 **(5.11)	KT-10 x New kuroda	67.92 **(25.68**)	KT-80 x KS -50	37.74 **(-2.31)	KT-39 x PY	-5.43**(-1.58*)	KT-95 x KS -50	42.11 **(8.07**)	KT-8542 x KS -50	37.03 **(3.80 **)

The mid parent heterosis for root size index, harvest index and total marketable yield ranged from -19.67 % to 77.80 %, -18.43% to 63.84% and -44.67% to 55.79%, respectively. For the root size index, the greater heterosis over mid parent suitably found in the cross combination KT-62 x KS -50 (77.80%) followed by KT-47 × KS -22 (76.04%) and KT-10 × New Kuroda (67.92%). The highest significant heterosis for earliness trait days to maturity in desirable negative direction was recorded in the hybrid KT-95 x KS -50 (-6.35%). Among the 100 crosses, 42 hybrids exhibited the significant heterosis for days to maturity in desirable direction over mid parent (Table 4.10). Similarly, the highest significant heterosis in desirable direction for harvest index was recorded in the hybrid KT-10 x New Kuroda (63.84%) followed by KT-80 × KS -50 (48.94%) and KT-80 × KS -20 (44.96%). Likewise, the highest significant heterosis in negative desirable direction for days to maturity was recorded in the hybrid KT-95 x KS-50 (-6.35%) followed by KT-39 × PY-1 (-5.43%) and KT-98 × KS -59 (-5.43%). The highest significant heterosis in desirable positive direction for total marketable yield over mid parent was recorded in the cross KT-98 × PN-1 (55.79%) followed by KT-8542 × New Kuroda (45.70%) and KT-8542 × KS -50 (37.03%). Among the 100 hybrids, the 69, 65 and 10 crosses showed significant heterosis over mid parent in desirable direction for root size index, harvest index and total marketable yield, respectively (Table 4.10).

Table 4.10 Average heterosis (MPH) for different quantitative characters traits in carrot. (Pooled data)

Crosses	PH (cm)	LL (cm)	RL (cm)	RD (mm)	CD (mm)	CT (mm)	PW (g)	RW (g)	RS (cm^2)	RSR	DTM(in days)	HI (%)	Yeild (T/Ha)
KT-7 X KS -20	7.19	-30.00 **	-12.81 **	16.16 **	-24.92	24.99	-0.66	-8.03 **	-8.04 *	16.28 **	-1.09	19.60 **	-6.77
KT-7 X KS -21	34.38	-14.09	4.51	12.91 **	-17.38	11.91	0.94	-12.31 **	7.09	9.36 *	-0.18	14.70 **	-13.77
KT-7 X KS -22	78.95	35.96 **	2.79	23.39 **	-11.46	29.42	-2.83	-15.45 **	12.63 **	14.13 **	-1.80*	13.98 **	-15.03
KT-7 X KS -50	43.67	5.38	3.74	19.12 **	-30.73	33.26	18.16 **	7.19 **	20.63 **	6.13	-1.44	28.10 **	-3.72
KT-7 X KS -59	52.58	16.89	-10.98 **	15.67 **	-29.07	25.10	27.36 **	-19.45 **	-9.35 **	-32.22 **	-1.78*	-6.01	-26.61 **
KT-7 X NK-1	42.01	-3.24	5.91	3.36	-21.89	2.67	41.10 **	-17.24 **	4.79	-30.97 **	1.09	-8.91	-26.82 **
KT-7 X PY-1	35.87	-11.05	1.40	26.43 **	-20.82	40.95	5.19	-6.11 *	17.39 **	14.26 **	-0.36	23.29 **	-11.76
KT-7 X PN-1	35.65	-11.55	1.73	-6.52 *	-33.73	-1.87	-21.52 **	-27.93 **	-14.04 **	17.17 **	1.64	9.53 *	-19.11 *
KT-7 X New Kuroda	35.65	-10.55	2.87	25.66 **	-18.75	35.33	51.73 **	29.57 **	27.20 **	4.00	-0.36	22.73 **	18.01 *
KT-7 X KS -73	27.28	-18.64	0.70	4.62	-26.45	11.38	0.8	-28.71 **	-6.71	-17.64 **	-2.17*	2.12	-34.45 **
KT-10 X KS -20	36.27	-0.54	1.27	3.80	-34.57	10.61	-16.36 **	-29.25 **	-1.50	6.98	-1.79*	8.48	-35.28 **
KT-10 X KS -21	3.00	-48.65 **	8.26 **	13.12 **	-33.48	20.53	5.11	-14.38 **	18.39 **	-0.71	-0.73	10.70 *	-25.75 **
KT-10 X KS -22	51.83	-0.28	15.56 **	18.66 **	-13.97	21.57	44.59 **	23.17 **	28.85 **	9.66 *	-0.37	22.18 **	11.49
KT-10 X KS -50	65.88	43.62 **	-6.17 *	23.37 **	-27.54	34.25	7.21	-1.98	18.99 **	17.03 **	-0.92	17.08 **	-20.19 *
KT-10 X KS -59	5.81	-34.91 **	-10.12 **	11.65 **	-32.16	18.74	61.21 **	33.90 **	10.10 **	-1.94	-2.55**	1.51	15.95
KT-10 X NK-1	42.86	-8.32	22.51 **	21.26 **	-18.16	25.38	38.49 **	16.03 **	48.92 **	20.82 **	-2.55**	19.28 **	32.38 **
KT-10 X PY-1	23.27	-25.05 *	6.26 *	8.13 **	-36.36	20.63	8.08	-2.08	24.42 **	14.47 **	-1.80*	10.56 *	-14.16

KT-10 X PN-1	31.27	-5.45	-9.10 **	7.27 **	-43.39	24.74	19.89 **	-3.26	0.61	0.08	0.74	-1.40	-14.55
KT-10 X New Kuroda	60.36	21.51 *	4.00	100.68 **	-33.42	157.42	30.81 **	5.49 *	67.92 **	0.27	-1.46	63.84 **	-10.71
KT-10 X KS -73	11.22	-33.90 **	0.58	22.67 **	-29.33	40.93	-1.1	-14.18 **	12.10 **	6.84	-0.55	22.02 **	-15.98 *
KT-28 X KS -20	24.79	-12.89	1.72	-8.56 **	-21.61	-17.06	-14.04 **	-25.40 **	-9.97 **	12.66 **	-4.69**	3.96	-8.60
KT-28 X KS -21	11.74	-34.87 **	5.15	8.45 **	-53.52	22.42	-5.55	-20.48 **	3.65	5.39	-3.26**	11.31 *	-27.45 **
KT-28 X KS -22	60.02	9.59	19.42 **	8.79 **	-27.33	12.89	36.03 **	-1.83	11.67 **	-9.81 *	-2.50**	11.32 *	-15.51 *
KT-28 X KS -50	46.10	12.25	8.18 *	18.01 **	-7.95	11.53	32.96 **	-1.63	22.39 **	-11.84 *	0.03	16.86 **	-21.49 **
KT-28 X KS -59	26.38	-17.22	2.91	14.84 **	-7.66	5.16	21.79 **	2.28	12.00 **	1.04	-0.36	10.36 *	-3.81
KT-28 X NK-1	79.12 *	38.97 **	17.31 **	20.04 **	-18.3	20.91	29.77 **	-13.00 **	30.45 **	-17.23 **	-0.91	9.82 *	-28.90 **
KT-28 X PY-1	55.34	11.96	10.85 **	20.35 **	-4.72	13.38	48.00 **	23.22 **	35.74 **	6.43	-1.81*	17.61 **	-0.82
KT-28 X PN-1	21.23	-28.18 *	9.63 **	2.57	-18.36	-2.55	11.03 *	-3.02	12.97 **	10.85 **	-1.45	9.22 *	-5.06
KT-28 X New Kuroda	29.95	-15.77	9.59 **	12.06 **	-27.5	15.44	33.41 **	5.18 *	15.06 **	-2.97	-3.57**	16.14 **	-12.10
KT-28 X KS -73	39.72	-3.35	8.16 **	13.01 **	-23.57	17.14	5.94	-29.64 **	8.20 *	-20.44 **	-0.73	5.11	-40.84 **
KT-39 X KS -20	28.36	-15.42	7.20 *	18.85 **	-30.46	32.89	13.59 **	6.41 **	32.06 **	18.45 **	-0.36	27.00 **	-3.82
KT-39 X KS -21	11.04	-42.17 **	13.91 **	15.46 **	-29.34	23.28	23.09 **	-6.82 **	30.66 **	-9.65 *	-2.73**	10.00 *	-22.37 **
KT-39 X KS -22	30.37	-29.10 **	21.53 **	16.82 **	-16.91	22.68	19.26 **	-13.38 **	28.95 **	-9.75 *	-1.44	10.43 *	-23.82 **
KT-39 X KS -50	38.37	-1.2	6.58 *	3.89	-10.93	-5.80	2.62	-0.92	33.76 **	21.70 **	-1.09	9.96	-15.41
KT-39 X KS -59	57.43	14.54	2.65	18.33 **	-34.36	33.02	27.23 **	4.78	25.06 **	-6.11	-3.36**	9.66 *	-5.45
KT-39 X NK-1	59.79	13.07	15.52 **	15.08 **	-14.46	14.82	16.41 **	-1.49	29.72 **	3.11	-2.47**	23.58 **	-10.33
KT-39 X PY-1	14.87	-36.40 **	9.20 **	20.02 **	-50.78	56.68	60.49 **	35.77 **	57.82 **	5.30	-5.43**	10.07 *	9.60

KT-39 X PN-1	6.69	-36.60 **	-6.66 *	23.07 **	-20.89	35.61	6.11	-8.56 **	14.35 **	3.33	-2.99**	14.57 **	-12.62
KT-39 X New Kuroda	23.18	-16.55	-6.71 *	6.42 *	-47.25	27.73	25.14 **	-3.90	6.96	-6.74	-5.37**	-1.80	-18.89 *
KT-39 X KS -73	3.89	-35.58 **	-10.90 **	21.17 **	-31.48	44.84	-6.02	-16.86 **	18.15 **	14.30 **	-2.30**	8.86 *	-19.32 **
KT-47 X KS -20	5.99	-29.07 **	-8.32 **	-7.11 **	-8.83	-21.40	5.31	3.28	-18.41 **	23.56 **	1.46	21.18 **	-0.14
KT-47 X KS -21	-13.27	-70.94 **	21.03 **	21.92 **	-7.20	15.86	33.79 **	17.80 **	39.07 **	13.48 **	0.55	34.38 **	1.71
KT-47 X KS -22	43.93	-3.3	11.58 **	59.38 **	13.56	60.71	15.79 **	-3.34	76.04 **	7.94	-1.44	27.92 **	-10.95
KT-47 X KS -50	6.43	-27.43 **	-6.89 *	15.79 **	-15.25	12.95	10.29 *	12.36 **	13.32 **	35.16 **	-2.17*	25.64 **	-5.23
KT-47 X KS -59	16.03	-26.87 **	0.62	8.62 **	5.28	-10.49	33.84 **	24.09 **	6.20	10.48 **	-2.50**	23.46 **	27.79 **
KT-47 X NK-1	-1.64	-41.80 **	-2.34	17.82 **	-4.68	10.39	-2.52	-24.90 **	21.21 **	-11.78 **	0.73	8.33	-29.44 **
KT-47 X PY-1	35.45	-3.85	-0.44	0.56	-18.35	-6.12	22.67 **	18.75 **	-3.56	24.29 **	-0.91	27.54 **	0.03
KT-47 X PN-1	14.02	-31.43 **	3.67	4.25	-12.58	-3.2	-20.48 **	-31.65 **	5.73	-0.41	0.07	13.16 **	-31.87 **
KT-47 X New Kuroda	4.63	-32.51 **	-9.94 **	-10.54 **	-16.16	-24.09	59.21 **	27.49 **	-3.74	-3.86	-2.69**	-2.50	9.16
KT-47 X KS -73	-3.87	-44.77 **	-5.77	6.39 **	-31.05	12.27	-18.14 **	-27.88 **	7.25	16.20 **	-1.98*	3.13	-20.48 *
KT-62 X KS -20	22.83	-7.23	-11.42 **	10.92 **	-9.57	7.98	47.98 **	24.06 **	2.06	-2.07	-2.66**	12.09 *	4.87
KT-62 X KS -21	47.7	1.27	13.34 **	24.96 **	-23.22	32.8	10.05 *	-30.18 **	23.17 **	-25.19 **	-2.00*	11.43 *	-44.67 **
KT-62 X KS -22	85.66**	39.52 **	18.29 **	37.49 **	-16.04	55.13	54.26 **	-8.96 **	59.03 **	-30.16 **	1.10	4.09	-21.41 *
KT-62 X KS -50	14.01	-33.36 **	14.90 **	36.60 **	-1.29	39.49	10.10 *	13.42 **	77.80 **	26.92 **	0.91	36.46 **	11.73
KT-62 X KS -59	29.63	-14.19	3.43	14.84 **	-15.55	14.53	35.77 **	9.93 **	22.35 **	-10.15 **	-1.09	8.14	-5.65
KT-62 X NK-1	36.44	-2.95	3.18	39.24 **	2.77	41.50	2.35	-3.33	56.23 **	17.20 **	-1.82*	28.12 **	-9.34

KT-62 X PY-1	30.26	-8.02	-5.24	-3.15	-41.64	8.75	23.60 **	10.29 **	8.49	13.04 **	-1.08	0.25	-10.42
KT-62 X PN-1	32.77	-9.23	1.43	24.09 **	-20.83	36.75	38.01 **	32.58 **	38.86 **	16.84 **	0.01	23.24 **	24.23 **
KT-62 X New Kuroda	30.27	-8.40	-2.26	16.21 **	-38.00	33.53	18.72 **	9.10 **	24.87 **	12.95 **	-1.46	13.47 **	-1.31
KT-62 X KS -73	34.79	-0.70	-6.64 *	12.79 **	-46.56	40.68	7.75	1.85	20.96 **	19.73 **	1.28	11.34 *	-0.61
KT-80 X KS -20	9.37	-28.57 **	1.40	29.51 **	-39.17	56.92	35.61 **	30.38 **	24.70 **	24.52 **	-0.73	44.96 **	5.05
KT-80 X KS -21	26.57	-17.2	11.80 **	9.11 **	-25.88	11.83	5.89	1.42	29.60 **	19.52 **	-0.18	26.22 **	-7.25
KT-80 X KS -22	2.22	-46.64 **	6.52 *	28.63 **	-20.09	45.82	-3.45	-6.96 **	48.86 **	37.82 **	-1.27	23.14 **	-21.14 **
KT-80 X KS -50	5.05	-35.88 **	7.33 *	32.83 **	-26.55	51.91	23.08 **	26.34 **	46.49 **	37.74 **	-2.68**	48.94 **	-5.67
KT-80 X KS -59	24.60	-11.85	-1.16	7.47 **	-19.41	4.52	21.24 **	11.04 **	9.37 *	7.70	0.55	15.94 **	-8.02
KT-80 X NK-1	9.46	-22.70 *	-8.87 **	17.28 **	-11.5	16.18	13.87 **	-3.84	19.85 **	7.04	022	8.75	-22.46 **
KT-80 X PY-1	25.28	-5.73	-9.30 **	36.31 **	-11.11	48.98	20.65 **	14.01 **	18.60 **	24.94 **	-0.92	31.63 **	-13.92
KT-80 X PN-1	22.52	-13.31	-2.86	20.63 **	-35.51	44.73	-15.44 **	-17.05 **	15.57 **	27.91 **	0.15	24.73 **	-24.67 **
KT-80 X New Kuroda	25.48	-5.40	-7.51 **	26.10 **	-26.46	42.81	9.49 *	-6.81 *	16.91 **	12.86 **	-0.36	14.93 **	-28.52 **
KT-80 X KS -73	4.48	-33.37 **	-4.80	23.27 **	-28.32	46.12	34.88 **	1.10	14.35 **	-3.06	-2.88**	15.28 **	-21.33 **
KT-95 X KS -20	32.97	-2.20	4.02	-13.95 **	-24.32	-22.84	22.70 **	19.77 **	-1.51	22.67 **	0.37	17.02 **	4.18
KT-95 X KS -21	48.73	10.47	5.12	-0.28	-23.11	-5.19	7.36	-3.95	8.34 *	14.67 **	1.28	9.70	-20.21 *
KT-95 X KS -22	57.74	17.80	7.31 *	30.45 **	-4.37	31.73	7.99	-4.04	21.07 **	19.29 **	-0.73	29.83 **	-15.39
KT-95 X KS -50	16.29	-16.9	-2.16	38.50 **	-23.82	53.53	-4.30	4.77	40.14 **	43.95 **	-6.35**	42.11 **	11.39
KT-95 X KS -59	47.17	14.18	-3.62	2.03	-22.60	-2.73	9.72 *	3.59	-8.76 *	11.26 **	-0.55	19.22 **	-5.49
KT-95 X NK-1	18.15	-17.58	-4.03	-10.29 **	-27.82	-15.47	-21.45 **	-27.88 **	-7.78	23.92 **	-2.33**	-0.27	-25.95 **

KT-95 X PY-1	41.85	8.28	-4.65	2.15	-14.08	-6.71	46.90 **	-5.65	-11.75 **	-22.52 **	-3.12**	0.70	-29.02 **
KT-95 X PN-1	4.79	-45.44 **	7.13 *	5.82 *	-27.15	10.00	-1.83	-12.65 **	19.10 **	7.03	0.04	12.66 *	-21.81 *
KT-95 X New Kuroda	14.18	-25.10 *	-2.88	-0.98	-29.83	-0.61	4.31	-11.15 **	2.43	6.41	0.18	3.73	-26.49 **
KT-95*KS -73	14.79	-27.77 **	2.19	12.35 **	-31.65	25.33	36.10 **	0.06	22.07 **	-8.67	-3.99**	5.46	-18.41 *
KT-98 X KS -20	23.47	-16.58	2.76	-15.95 **	-14.17	-30.54	-2.60	-12.89 **	-18.42 **	5.28	-1.82*	7.37	-19.46 *
KT-98 X KS -21	26.79	-22.16 *	13.12 **	-10.35 **	-26.14	-16.63	-4.21	-18.30 **	-4.33	0.79	-1.79*	2.27	-3.05
KT-98 X KS -22	58.44	9.53	12.81 **	27.11 **	-19.84	38	53.51 **	0.73	24.26 **	-20.24 **	1.10	5.23	-15.37 *
KT-98 X KS -50	32.91	-9.69	13.44 **	31.09 **	-26.84	44.02	39.68 **	-3.8	33.04 **	-20.96 **	-2.47**	20.07 **	-24.34 **
KT-98 X KS -59	30.09	-16.09	6.78 *	-12.31 **	-31.58	-16.84	19.27 **	-6.03 *	-7.63 *	-12.97 **	-5.43**	-5.39	-17.34 *
KT-98 X NK-1	54.01	12.9	6.59	12.53 **	-10.48	7.86	96.97 **	5.70 *	16.19 **	-45.98 **	-2.99**	-1.87	-13.71
KT-98 X PY-1	-111.77 **	-122.69 **	5.59	-9.09 **	-22.97	-16.04	2.75	-9.19 **	-4.85	9.26 *	-2.47**	3.62	-19.55 *
KT-98 X PN-1	75.25**	-5.09	3.27	23.92 **	-23.85	35.28	75.25 **	61.14 **	34.35 **	12.99 **	-5.43**	19.96 **	55.79 **
KT-98 X New Kuroda	82.23**	-6.59	8.33 **	-11.37 **	-20.66	-21.72	82.23 **	44.85 **	8.05 *	-6.74	-2.69**	0.07	19.37 *
KT-98 X KS -73	35.02	-6.17	0.85	1.15	-22.78	0.39	-15.98 **	-39.02 **	-19.67 **	-22.99 **	-1.98*	7.86	-42.61 **
KT-8542 X KS -20	9.67	-32.98 **	2.94	16.28 **	-11.67	15.07	-1.78	-12.75 **	9.98 **	1.83	-2.66**	29.35 **	-16.57
KT-8542 X KS -21	42.44	30.23 **	33.76 **	8.28 **	7.72	4.97	9.22	3.29	24.08 **	2.61	-2.00*	9.50 *	-1.77
KT-8542 X KS -22	19.92	10.49	16.07 **	25.49 **	-0.82	43.78	16.29 **	10.57 **	36.96 **	13.03 **	1.10	2.94	31.81 **

KT-8542 X KS -50	15.27	2.94	15.24 **	30.96 **	16.36	41.85	43.11 **	45.76 **	54.90 **	14.96 **	-1.46	17.81 **	37.03 **
KT-8542 X KS -59	7.43	-1.32	10.25 **	8.58 **	6.4	8.64	8.22	1.67	12.63 **	-8.57 *	-0.55	2.25	-2.75
KT-8542 X NK-1	3.06	-8.78	6.65 *	31.35 **	18.92	38.36	11.56 *	19.17 **	36.34 **	27.81 **	-1.46	25.35 **	29.07 **
KT-8542 X PY-1	-11.52	-23.56 *	11.07 **	5.28	3.36	1.60	1.81	9.39 **	27.22 **	15.75 **	-0.36	11.07 *	13.08
KT-8542 X PN-1	35.8	25.34 **	23.89 **	11.13 **	10.32	11.07	9.97 *	-4.61	22.59 **	-9.29 *	-2.76**	-2.89	-0.71
KT-8542 X New Kuroda	-256.66 **	21.43 *	11.68 **	-0.42	151.79 **	-584.00 **	49.03 **	44.82 **	4.1	-4.18	-1.44	5.42	45.70 **
KT-8542 X KS -73	-3.01	-32.62 **	4.27	11.68 **	6.9	10.01	-15.23 **	-48.63 **	-6.93	- 38.74 **	-1.09	-18.43 **	-18.58 *

*= significant at 5% probability, **= significant at 1% probability through F test, PH=plant height, LL= leaf length, RL=root length, RD= root diameter, CD= core diameter, CT= cortex thickness, PW= Plant weight, RW=Root weight, RSR= root to shoot ratio, RS= root size, DTM= days to maturity,HI=harvest index,yield=t/ha.

4.2.9 Heterobeltiosis for quantitative characters traits

The estimates of heterosis for various quantitative characters traits of 100 hybrids over better parent are presented in Table 4.12. Among the 100 hybrids, very high and significant estimates of better parent heterosis were observed in both the directions for all the 13 quantitative characters traits.

With respect to traits like, root length , root diameter, leaf length and core diameter, cortex thickness, plant height, the significant heterosis over better parent in desirable direction among 100 crosses ranged from -19.95% to 24.42%, -17.72% to 43.61% and -121.09 % to 42.44%, similarly heterosis observed over better parent in desirable direction -53.82% to 34.75% and -32.99 to 55.84% , respectively. Out of 100 hybrids, 15, 60 and 5 crosses, respectively, exhibited significant heterosis over better parent in desirable direction for root length, root diameter and leaf length (Table 4.12). For the root length, the highest heterosis over better parent in desirable direction was observed in the cross KT-8542 × KS -21 (24.42%) followed by KT-8542 × PN-1 (21.41 %). Similarly, the highest significant better parent heterosis in desirable direction for root diameter was recorded in the cross KT-10 × New Kuroda (99.01%) followed by KT-47 × KS-22 (43.61%), KT-62 × KS-22 (35.75%)**.** For the leaf length, the highest heterosis over better parent in desirable direction was observed in the cross, KT-10 × KS -50 (42.44%) followed by KT-7 × KS-22 (33.01 %) and KT-62 x KS -22 (30.29%). For the core diameter, the highest heterosis over better parent in desirable negative direction was observed in the cross KT-62 x KS -73 (-57.56%) followed by KT-62 x PY-1 (-51.01 %). Similarly, the highest significant better parent heterosis in desirable direction for cortex thickness was recorded in the cross KT-10 × New Kuroda (152.24%) followed by KT-39 × PY-1 (55.84%), KT-95 × KS-50 (51.58%).The range of heterosis over better parent for plant weight, **shoot weight** and root weight, was -31.43% to 95.77%, -70.57% to 224.77 % and -56.39% to 57.79%, respectively. Among the 100 crosses, 48, 11, 20 hybrids depicted

significantly high heterosis over better parent in desirable direction for better parent for gross plant weight, net shoot weight net root weight, respectively. For plant weight, the hybrid KT-98 x NK-1 (95.77 %) followed by KT-98 x New Kuroda (75.67 %) and KT-98 x PN-1 (74.74 %) exhibited significantly high better parent heterosis in desirable direction. For the root weight, the hybrid KT-98 x PN-1 (57.79%) followed by KT-8542 x New Kuroda (41.45%) KT-8542 x KS -50 (40.22%) exhibited significantly high heterosis over better parent in the favourable direction.

Table 4.11. Heterobeltiosis of top 3 cross combinations over the environments along with their SCA effects (value in parenthesis)

Cross	Plant Height	Cross	Leaf Length	Cross	Root Length	Cross	Root Diameter	Cross	Core Diameter	Cross	Core Thickness
KT-28 x NK-1	79.12 *(12.66*8)	KT-10 × KS -50	42.44 (3.22)	KT-8542 x KS -21	24.42 **(2.15**)	KT-10 x New kuroda	99.01 *(26.42**)	KT-62 x KS -73	-57.56 (2.14**)	KT-10 x New kuroda	152.24(-5.06*)
KT-10 x KS -50	65.88(10.21**)	KT-7 × KS-22	33.0 (2.32*)	KT-8542 x PN-1	21.41 **(2.36**)	KT-47 x KS -22	43.61 **(11.62**)	KT-28 x KS -21	-53.82 (12.33**)	KT-39 x PY-1	55.84(-3.96)
KT-62 x KS -22	65.54(8.26**)	KT-62 x KS -22	30.29 (2.99)	KT-47 x KS -21	14.03 **(2.30**)	KT-62 x KS -22	35.75 **(0.39)	KT-62 x PY-1	-51.01(21.4**)	KT-95 x KS -50	51.58 (-2.11)

Cross	Plant Weight	Cross	Root Weight	Cross	Root Size	Cross	Root to shoot ratio	Cross	Days to Maturity	Cross	Harvesting Index	Cross	Yield
KT-98 x NK-1	95.77 ** (14.55**)	KT-98 x PN-1	57.79 ** (-19.92***)	KT-62 KS -50	68.50 **(10.66**)	KT-80 x KS -50	35.78 **(1.74)	KT-62 x PN-1	-7.85**(-0.58)	KT-10 x New kuroda	59.97 **(30.98***)	KT-98 x PN-1	45.94 **(12.44**)
KT-98 x New kuroda	75.67 **(10.44**)	KT-8542 x New kuroda	41.45 **(5.11)	KT-10 x New kuroda	66.28 **(25.68**)	KT-95 x KS -50	35.00 **(3.36*)	KT-8542 x KS-73	-7.19** (-0.78)	KT-80 x KS -50	39.92 **(5.11*)	KT-8542 x New kuroda	39.02 **(5.06*)
KT-98 x PN-1	74.74 **(8.57**)	KT-8542 x KS -50	40.22 **(-14.32)	KT-47 x KS -22	58.34 **(22.47***)	KT-8542 x NK-1	26.34 **(2.55**)	KT-62 x KS -73	-6.83**(-0.25)	KT-80 x KS -20	37.92 **(8.74**)	KT-8542 x KS-50	34.00 **(5.06*)

*: significant at 5% probability, **: significant at 1% probability, significant through F test

The range of heterosis over better parent for marketable yield, root size index, harvest index, days to maturity and root to shoot ratio was ranged from -50.50% to 45.94%, -24.49% to 68.50%, -20.57% to 59.97%,-2.15 to -7.85% and -49.75% to 35.00%, respectively. Among the 100 hybrids, 6, 37, 27 exhibited significantly high better parent heterosis in desirable direction for yield, harvest index, days to maturity and root to shoot ratio, respectively. For root to shoot ratio, the hybrid KT-80 x KS-50 (35.78 %) followed by KT-95 x KS-50 (35.00 %) and KT-8542 x NK-1 (26.34 %) exhibited significantly high better parent heterosis in desirable direction. Similarly, the cross KT-10x New Kuroda (59.97 %) followed by KT-80 x KS -50 (39.92 %) and KT-80 x KS -20 (37.92 %) depicted significantly high heterosis over better parent in desirable direction for harvest index. For days to maturity, the hybrid KT-80 x KS-20 (-7.85 %) followed by KT-8542 x KS-73 (-7.19 %) and KT-62 x New Kuroda (-6.83%) exhibited significantly high better parent heterosis in desirable direction. For the yield, the hybrid KT-98 x PN-1 (45.94%) followed by KT-8542 x New Kuroda (39.02%) and KT-8542 x KS -50 (34.00%) exhibited significantly high heterosis over better parent in the favourable direction.

Table 4.12 Heterobeltiosis (BPH) for different quantitative characters traits in carrot. (Pooled Data)

Crosses	PH (cm)	LL (cm)	RL (cm)	RD (mm)	CD (mm)	CT (mm)	PW (g)	RW (g)	RS (cm^2)	RSR	DTM (in days)	HI (%)	YEILD (t/ha)
KT-7 x KS -20	-3.12	-36.54 **	-13.95 **	10.42 **	-27.31	11.99	-4.29	-8.63 **	-9.82 *	11.04 *	-2.16*	15.72 **	-8.47
KT-7 x KS -21	31.80	-21.52	-6.11	4.7	-21.25	-5.04	0.04	-12.96 **	1.4	9.02	-1.08	10.92 *	-16.89
KT-7 x KS -22	65.64	33.01 *	-9.42 **	17.99 **	-15.19	23.53	-7.1	-19.22 **	-3.86	8.2	-1.80	10.79 *	-19.25 *
KT-7 x KS -50	39.13	2.72	-5.01	15.90 **	-33.37	22.16	12.73 **	-2.29	6.3	-10.16 *	-1.80	11.57 *	-4.51
KT-7 x KS -59	51.36	11.15	-19.37 **	9.54 **	-30.76	12.19	19.26 **	-22.83 **	-12.81 **	-37.07 **	-2.82**	-6.74	-27.47 **
KT-7 x NK-1	33.74	-15.18	-6.12	2.38	-27.31	-4.69	40.14 **	-18.91 **	-13.55 **	-33.36 **	0.00	-12.02 *	-27.45 **
KT-7 x PY-1	34.68	-16.97	-7.22 *	22.53 **	-21.25	36.23	-3.24	-15.24 **	0.59	9.20 *	-1.09	15.24 **	-11.78
KT-7 x PN-1	34.24	-15.76	-3.91	-8.27 **	-34.09	-4.91	-21.81 **	-29.23 **	-21.60 **	15.83 **	1.09	9.01	-20.31 *
KT-7 x New Kuroda	29.19	-18.64	-2.81	20.23 **	-22	26.03	46.17 **	25.34 **	21.09 **	3.87	-0.72	20.05 **	16.00
KT-7 x KS -73	14.81	-30.21 **	-0.58	4.37	-31.02	6.10	-9.62 *	-36.43 **	-12.25 **	-17.68 **	-2.17*	1.63	-42.67 **
KT-10 x KS -20	26.87	-6.97	-2.12	2.23	-35.31	8.23	-21.50 **	-32.14 **	-7.11	4.34	-3.17**	4.77	-37.16 **
KT-10 x KS -21	1.69	-51.59 **	-0.86	8.58 **	-33.81	11.02	1.4	-17.80 **	16.59 **	-2.55	-1.45	6.86	-29.21 **
KT-10 x KS -22	36.46	-5.59	3.75	9.62 **	-13.99	6.53	34.70 **	12.42 **	13.85 **	6.17	-0.37	18.55 **	4.83
KT-10 x KS -50	65.88	42.44 **	-12.39 **	22.27 **	-27.88	33.78	-0.32	-6.47 *	8.70 *	0.89	-1.10	1.81	-20.44 *
KT-10 x KS -59	1.68	-36.03 **	-16.99 **	9.54 **	-36.51	16.28	54.95 **	33.18 **	10.00 *	-10.76 **	-3.60**	0.53	15.88
KT-10 x NK-1	38.79	-17.19	10.67 **	18.06 **	-20.57	23.26	35.68 **	12.80 **	26.95 **	19.16 **	-3.26**	15.01 **	29.78 **
KT-10 x PY-1	20.41	-27.74 *	-0.85	1.2	-38.74	6.90	1.99	-7.52 *	10.38 *	11.74 *	-3.87**	3.17	-15.14

KT-10 x PN-1	28.43	-6.93	-12.38 **	5.41	-46.08	17.40	17.09 **	-6.14 *	-4.72	-0.95	0.74	-2.04	-14.87
KT-10 x New Kuroda	57.61	14.05	0.28	99.01 **	-38.68	152.24	29.45 **	3.89	66.28 **	-2	0.74	59.97 **	-13.19
KT-10 x KS -73	3.34	-41.64 **	-0.26	18.06 **	-36.34	23.26	-13.42 **	-26.63 **	9.62 *	4.58	-6.59**	21.67 **	-27.22 **
KT-28 x KS -20	13.02	-22.12 *	-5.35	-11.04 **	-22.37	-21.67	-14.40 **	-29.75 **	-10.90 **	5.73	-1.08	-0.9	-16.58 *
KT-28 x KS -21	9.84	-41.33 **	-0.05	8.31 **	-53.82	21.83	-7.83	-25.18 **	-2.71	3.17	-1.09	6.05	-32.63 **
KT-28 x KS -22	47.81	8.88	11.19 **	-3.3	-27.43	-7.44	34.37 **	-2.67	-5.41	-15.96 **	-2.82**	6.59	-20.46 **
KT-28 x KS -50	41.81	7.77	4.94	12.17 **	-8.23	2.87	31.07 **	-14.56 **	6.98	-26.48 **	0.00	0.45	-30.04 **
KT-28 x KS -59	25.08	-22.43	-1.31	12.17 **	-13.44	-0.77	10.58 *	-6.92 **	6.76	-4.56	1.47	7.83	-14.56
KT-28 x NK-1	69.06	20.21 *	9.94 **	12.17 **	-20.84	10.14	24.71 **	-19.13 **	6.83	-21.49 **	1.10	4.5	-35.68 **
KT-28 x PY-1	54.34	3.02	7.45 *	8.30 **	-8.14	-6.08	32.08 **	6.04 *	15.42 **	-0.04	-1.44	8.37	-10.95
KT-28 x PN-1	20.25	-32.60 **	9.33 **	-3.3	-22.11	-14.71	7.03	-9.68 **	2.17	7.63	-2.17*	7.05	-15.90 *
KT-28 x New Kuroda	24.03	-24.44 *	9.24 *	8.30 **	-33.12	4.84	24.49 **	-3.41	8.57 *	-4.60	-6.69**	11.90 *	-19.87 *
KT-28 x KS -73	26.29	-18.16	3.14	4.44	-31.05	-4.11	-2.07	-34.04 **	0.89	-21.91 **	1.47	3.99	-42.56 **
KT-39 x KS -20	22.25	-15.92	1.10	10.42 **	-32	16.08	5.6	3.85	12.83 **	11.86 **	-2.17*	23.24 **	-3.83
KT-39 x KS -21	7.06	-43.00 **	6.83	4.71	-32	2.17	17.58 **	-8.97 **	19.23 **	-10.97 *	-1.09	6.70	-23.80 **
KT-39 x KS -22	14.72	-37.30 **	11.68 **	14.37 **	-19.64	20.46	10.04 *	-19.64 **	26.31 **	-15.37 **	-5.04**	7.65	-26.29 **
KT-39 x KS -50	35.10	-8.79	1.97	-1.27	-13.48	-15.87	-5.49	-7.05 *	31.57 **	2.04	-3.26**	-3.98	-17.63
KT-39 x KS -59	47.85	8.30	-2.90	9.54 **	-36.55	16.28	23.52 **	3.48	12.45 **	-11.86 **	-3.87**	9.13	-8.26
KT-39 x NK-1	58.98	9.52	6.82	11.29 **	-19.64	3.80	12.91 *	-2.53	22.03 **	-1.57	-0.72	19.71 **	-11.22

KT-39 x PY-1	9.61	-38.73 **	4.39	19.13 **	-51.01	55.84	52.93 **	26.09 **	55.30 **	-0.48	-1.09	3.18	7.62
KT-39 x PN-1	1.97	-40.14 **	-7.73 *	17.94 **	-22.11	27.80	2.60	-9.71 **	8.33	0.98	-1.45	14.37 **	-15.48
KT-39 x New Kuroda	22.35	-17.35	-7.74 *	-0.49	-49.84	15.82	25.12 **	-4.15	-2.89	-7.71	-2.16*	-3.66	-19.01 *
KT-39 x KS -73	-1.26	-39.11 **	-13.86 **	18.55 **	-36.34	41.93	-18.45 **	-27.84 **	8.51	12.93 **	-1.45	8.02	-28.29 **
KT-47 x KS -20	1.49	-30.76 **	-13.94 **	-8.25 **	-15.9	-26.18	-5.8	-10.06 **	-24.49 **	19.25 **	-4.93**	17.16 **	-13.12
KT-47 x KS -21	-16.82	-71.40 **	14.03 **	20.22 **	-13.1	15.75	22.82 **	2.67	38.40 **	5.06	-1.45	29.99 **	-12.91
KT-47 x KS -22	26.04	-12.14	3.00	43.61 **	5.83	31.17	2.84	-19.45 **	58.34 **	4.94	-1.09	23.12 **	-24.67 **
KT-47 x KS -50	3.35	-31.07 **	-10.49 **	11.70 **	-21.34	3.61	-2.22	6.13	5.46	22.91 **	-3.26**	16.21 **	-15.61
KT-47 x KS -59	8.4	-28.80 *	-4.36	7.71 **	-7.69	-16.00	32.18 **	11.62 **	4	-4.69	-1.80	16.48 **	14.15
KT-47 x NK-1	-1.69	-45.24 **	-9.27 **	11.70 **	-8.57	0.02	-9.2	-33.81 **	5.11	-15.79 **	-1.09	4.92	-38.09 **
KT-47 x PY-1	28.56	-4.56	-4.36	-8.25 **	-26.53	-22.58	21.84 **	13.33 **	-12.90 **	19.85 **	-4.93**	27.29 **	-11.59
KT-47 x PN-1	8.39	-33.35 **	2.99	-0.27	-22.09	-15.7	-26.15 **	-39.87 **	2.08	-7.08	-1.09	6.45	-38.97 **
KT-47 x New Kuroda	3.35	-33.89 **	-10.50 **	-12.24 **	-27.57	-31.42	52.73 **	13.67 **	-4.73	-11.35 *	-0.74	-6.75	-4.92
KT-47 x KS -73	-8.15	-49.26 **	-9.33 **	-0.27	-41.64	-8.51	-31.43 **	-43.27 **	7.01	7.31	0.00	-3.84	-37.36 **
KT-62 x KS -20	15.33	-12.02	-16.09 **	2.24	-22.35	0.07	32.27 **	9.16 **	-15.49 **	-3.04	-1.80	11.14 *	-4.57
KT-62 x KS -21	44.51	-3.19	5.83	12.46 **	-33.16	16.28	0.95	-38.52 **	8.63	-27.66 **	-1.45	10.55	-50.50 **
KT-62 x KS -22	65.54	30.29 *	8.24 *	35.75 **	-27.22	43.01	36.91 **	-23.40 **	56.27 **	-31.37 **	-3.17**	2.73	-30.59 **
KT-62 x KS -50	12.98	-34.86 **	9.44 **	28.78 **	-14.76	32.38	-2.46	8.36 *	68.50 **	10.84 *	0.00	23.30 **	4.19
KT-62 x KS -59	23.49	-14.43	-2.59	5.47 *	-30.76	6.22	33.97 **	-0.05	6.39	-19.33 **	-0.37	4.57	-11.71

KT-62 x NK-1	33.74	-11.18	-4.99	33.54 **	-8.55	36.05	-4.74	-13.90 **	52.49 **	17.04 **	1.10	27.27 **	-16.76
KT-62 x PY-1	26.12	-10.05	-9.81 **	-3.27	-51.01	1.46	22.87 **	6.48	6.11	12.01 *	-2.88**	-2.46	-17.11
KT-62 x PN-1	28.75	-9.34	-0.19	17.94 **	-34.11	36.02	28.07 **	17.86 **	26.94 **	13.92 **	-1.81	18.81 **	16.60
KT-62 x New Kuroda	29.19	-12.83	-3.78	7.79 **	-49.84	28.81	13.80 *	-1.69	9.59 *	8.77	-6.83**	11.28 *	-10.09
KT-62 x KS -73	26.29	-11.19	-9.33 **	9.44 **	-57.56	29.43	-9.80 *	-19.16 **	7.33	15.48 **	-5.80**	6.36	-18.63 *
KT-80 x KS -20	8.41	-32.21 **	1.11	22.68 **	-42.6	38.08	31.30 **	18.58 **	14.29 **	11.07 *	-7.85**	37.92 **	4.64
KT-80 x KS -21	17.4	-20.79	-0.48	0.83	-31.12	-6.69	5.47	-7.68 **	27.63 **	2.64	-5.80**	20.14 **	-8.62
KT-80 x KS -22	-13.12	-50.21 **	-6.97 *	23.43 **	-25.38	42.00	-7.24	-19.24 **	35.17 **	23.75 **	-6.83**	16.63 **	-23.42 **
KT-**80** x **KS** -50	-1.39	-37.36 **	-2.65	28.78 **	-31.12	36.69	18.01 **	25.19 **	37.68 **	35.78 **	-5.80**	39.92 **	-8.48
KT-80 x KS -59	12.7	-12.03	-11.30 **	1.42	-19.62	-7.96	12.99 *	4.5	6.00	-13.23 **	0.72	7.69	-11.08
KT-80 x NK-1	5.66	-29.21 **	-19.95 **	15.74 **	-19.64	5.83	12.53 *	-11.43 **	4.87	-5.47	0.00	3.64	-23.51 *
KT-80 x PY-1	15.05	-7.74	-17.79 **	32.57 **	-13.90	46.94	10.46 *	13.82 **	8.14	11.36 *	-1.80	29.71 **	-15.80
KT-80 x PN-1	12.69	-13.35	-9.14 **	17.94 **	-36.86	37.49	-16.18 **	-23.74 **	12.74 **	10.64 *	-2.17*	15.51 **	-27.40 **
KT-80 x New Kuroda	19.75	-9.91	-13.46 **	20.23 **	-27.53	30.48	4.95	-13.11 **	14.50 **	-3.42	-3.87**	8.19	-28.89 **
KT-80 x KS -73	3.33	-40.37 **	-6.97 *	23.11 **	-31.03	42.00	21.49 **	-17.44 **	13.41 **	-16.93 **	0.00	5.83	-29.84 **
KT-95 x KS -20	19.94	-14.9	-3.18	-14.12 **	-26.19	-23.81	19.58 **	11.34 **	-7.51	14.69 **	-2.15*	9.83	1.93
KT-95 x KS -21	45.55	-3.18	-0.1	-3.05	-26.19	-11.92	7.06	-10.63 **	7.17	2.99	-1.08	3.01	-23.35 *
KT-95 x KS -22	46.32	14.95	-0.11	19.07 **	-7.74	14.51	4.43	-14.97 **	7.40	12.32 *	-2.87**	21.31 **	-19.86 *

KT-95 x KS -50	12.37	-22.54	-5.11	35.49 **	-26.19	51.58	-7.65	3.25	28.55 **	35.00 **	-2.51**	35.33 **	10.87
KT-95 x KS -59	46.32	3.96	-7.60 *	1.42	-24.99	-3.86	1.62	-0.26	-9.26 *	-6.64	-3.52**	9.28	-6.28
KT-95 x NK-1	11.04	-30.54 **	-10.09 **	-13.78 **	-32.36	-17.65	-22.89 **	-32.07 **	-21.08 **	14.64 **	-3.23**	-6.25	-26.85 **
KT-95 x PY-1	40.3	-3.14	-7.60 *	-5.57 *	-14.26	-18.00	33.68 **	-8.02 *	-21.40 **	-27.62 **	0.73	-2.16	-29.28 **
KT-95 x PN-1	3.47	-50.26 **	6.86	2.64	-28.08	2.63	-3.33	-17.90 **	13.27 **	-3.15	0.73	2.97	-22.71 *
KT-95 x New Kuroda	8.51	-34.62 **	-3.16	-1.46	-33.12	-3.49	-0.65	-15.27 **	1.89	-4.79	-1.80	-3.65	-27.99 **
KT-95 x KS -73	3.34	-40.36 **	-2.53	6.75 *	-36.34	8.75	23.34 **	-16.73 **	19.92 **	-18.17 **	-2.17*	-4.43	-28.87 **
KT-98 x KS -20	19.94	-20.09 *	-6.41 *	-17.72 **	-15.92	-32.99	-6.23	-13.70 **	-20.61 **	-3.08	-2.82**	2.16	-22.10 *
KT-98 x KS -21	19.87	-26.04 *	9.98 **	-10.81 **	-26.47	-18.83	-5.13	-19.13 **	-8.74 *	-3.3	-0.36	-2.74	-4.49
KT-98 x KS -22	36.99	-6.22	7.38	13.62 **	-20.61	15.17	46.65 **	-3.51	6.76	-27.07 **	-2.17*	0.58	-15.40
KT-98 x KS -50	27.21	-19.43	12.60 **	25.37 **	-27.85	35.6	33.18 **	-12.52 **	18.03 **	-35.16 **	0.00	3.04	-28.67 **
KT-98 x KS -59	19.86	-23.39 *	4.76	-13.81 **	-36.53	-19.85	11.77 *	-10.21 **	-10.49 *	-16.15 **	-0.72	-7.73	-22.33 *
KT-98 x NK-1	51.66	12.27	2.13	5.78 *	-12.32	0.27	95.77 **	3.28	-3.55	-49.75 **	0.73	-6.79	-17.32
KT-98 x PY-1	-111.02 **	-121.09 **	4.73	-17.72 **	-26.51	-29.19	-5.42	-18.22 **	-17.92 **	0.67	-1.09	-4.69	-23.54 **
KT-98 x PN-1	29.66	-13.48	0.63	17.54 **	-28.1	20.71	74.74 **	57.79 **	23.41 **	7.54	-0.72	17.36 **	45.94 **
KT-98 x New Kuroda	34.54	-10.84	5.52	-13.81 **	-27.55	-27.46	75.67 **	39.74 **	3.62	-10.15 *	-1.45	-3.76	15.30
KT-98 x KS -73	30.88	-8.02	-5.92	-5.97 *	-31.02	-16.36	-24.71 **	-45.49 **	-23.89 **	-25.92 **	-4.23**	6.51	-47.43 **
KT-8542 x KS -20	8.41	-35.68 **	-2.11	10.41 **	-15.9	7.9	-7.52	-16.99 **	-3.65	-0.47	0.00	27.89 **	-20.50 *

KT-8542 x KS -21	32.45	23.98 *	24.42 **	0.31	4.18	-7.08	5.71	-1.64	16.35 **	0.5	0.00	8.22	-8.05
KT-8542 x KS -22	2.16	-5.23	5.8	20.12 **	-4.55	31.01	8.66	0.15	30.37 **	9.66 *	-1.10	2.26	21.72 *
KT-8542 x KS -50	8.48	-7.99	9.33 **	27.28 **	11.5	36.26	33.46 **	40.22 **	52.91 **	-0.71	-1.08	4.59	34.00 **
KT-8542 x KS -59	-2.59	-9.75	3.43	2.72	-3.89	1.95	3.69	0.27	4.03	-16.96 **	-1.09	0.81	-4.56
KT-8542 x NK-1	-0.26	-9.1	-2.17	29.95 **	17.91	34.68	9.65	14.91 **	24.80 **	26.34 **	-4.93**	23.72 **	24.15 *
KT-8542 x PY-1	-18.54	-28.82 **	5.29	2.14	-4.08	-6.32	-4.23	4.15	21.64 **	13.24 **	0.37	6.02	9.67
KT-8542 x PN-1	25.22	14.46	21.41 **	8.93 **	1.35	9.1	7.75	-8.21 **	19.49 **	-10.42 *	1.10	-4.56	-2.24
KT-8542 x New Kuroda	-249.90 **	16.13	9.48 **	-4.82	340.75 **	-572.69 **	46.99 **	41.45 **	-2.9	-6.56	-0.73	5.41	39.02 **
KT-8542 x KS -73	-4.34	-34.07 **	1.68	11.54 **	-6.91	0.05	-25.58 **	-56.39 **	-12.15 **	-40.16 **	-7.19**	-20.57 **	-30.62 **

*= significant of variance at 5% probability, **= significant at 1% probability through F test, PH=plant height, LL= leaf length, RL=root length, RD= root diameter, CD= core diameter, CT= cortex thickness, PW= Plant weight, RW= root weight, RSR= root to shoot ratio, RS= root size, DTM= days to maturity, HI= harvest index, yield = t/ha.

4.2.9 Standard hetrosis for quantitative characters traits

The estimates of heterosis for various quantitative characters traits of 100 hybrids over commercial check are presented in Table 4.14. Among the 100 hybrids, very high and significant estimates of over commercial check heterosis were observed in both the directions for all the 13 quantitative characters traits. With respect to important quantitative traits like, root length , root diameter, leaf length and core diameter, cortex thickness, plant height, the significant heterosis over commercial check in desirable direction. Among 100 crosses, heterosis for root length , root diameter, leaf length and core diameter, cortex thickness and plant height ranged from 8.55% (KT-10 x NK-1) to 17.95% (KT-8542 x KS -21), 6.00% (KT-8542 x KS -22) to 92.67%, (KT-10 x New kuroda), 24.05% (KT-10 x New Kuroda) to 47.73% (KT-8542 x KS -21), -0.46% (KT-8542 x KS -50) to -59.02% (KT-28 x KS -21), 1.32% KT-80 x KS -59 to 166.16% and 1.37% (KT-95 x PN) to 83.56% (KT-28 x NK-1), respectively. Out of 100 hybrids, 3, 51 and 9 crosses, respectively, exhibited significant heterosis over commercial check in desirable direction for root length, root diameter and leaf length (Table 4.14). For the root length, the highest heterosis over commercial check in desirable direction was observed in the cross KT-8542 × KS -21 (17.95%) followed by KT-8542 × PN-1 (15.11 %). Similarly, the highest significant over commercial check in desirable direction for root diameter was recorded in the cross KT-10 × New Kuroda (92.67%) followed by KT-47 × KS-22 (44.50%), KT-95 x KS -50 (32.45 %)**.** For the leaf length, the highest heterosis over commercial check in desirable direction was observed in the cross KT-8542 x KS -21 (47.73 %) followed by KT-28 x NK-1 (42.22 %).). For days maturity, the highest hetrosis over commercial check in desirable direction was observed in the cross KT-10 x New Kuroda (-8.27%). For the core diameter, the highest heterosis over commercial check in desirable negative direction was observed in the cross KT-28 x KS -21 (-59.02%) followed by KT-62 x KS -73 (-53.17 %).

Table 4.13 Standard hetrosis 3 cross combinations over the environments along with their SCA effects (value in parenthesis)

Cross	Plant Height	Cross	Leaf Length	Cross	Root length	Cross	Root Diameter	Cross	Core Diameter	Cross	Cortex Thickness
KT-62 x KS -22	72.61 (22.03***)	KT-8542 x KS -21	47.73 **(22.36)	KT-8542 x KS -21	17.95 **(22.36)	KT-10 x New kuroda	92.67 **(26.42**)	KT-28 x KS -21	-59.02(-1.98)	KT-10 x New Kuroda	166.16 (-6.2)
KT-10*KS -50	65.88(5.21**)	KT-28 x NK-1	42.22 **(10.90)	KT-8542 x PN-1	15.11 **(5.32)	KT-47 x KS -22	44.50 **(11.62**)	KT-62 x KS -73	-53.17(-0.28)	KT-47 x KS -22	64.68 (-2.93)
KT-28*NK-1	69.06(12.33 **)	KT-8542 x New Kuroda	38.37 **(-89.07***)	KT-10 x NK-1	8.55 **(-0.29)	KT-95 x KS -50	(32.45 (7.50**)	KT-39 x PY-1	-53.17(-0.89)	KT-95 x KS -50	62.97(9.23)

Cross	Plant Weight	Cross	Root Weight	Cross	Root Size	Cross	Root to shoot ratio	Cross	Days to maturity	Cross	Harvesting index	Cross	Yield
1KT-98 x NK-1	80.54 **(12.03**)	KT-98 x PN-1	52.69 **(-19.36**)	KT-10 x New kuroda	57.86 **(25.68**)	KT-8542 x NK-1	38.59 **(2.84)	KT-10 x New Kuroda	-8.27(-1.08)	KT-10 x New kuroda	77.20 **(30.98***)	KT-98 x PN-1	51.07 **(12.44***)
KT-98 x New kuroda	62.00 **(5.44**)	KT-98 x New kuroda	35.22 **(-5.38)	KT-47 x KS -22	44.34 **(22.47***)	KT-98 x PN	33.89 **(12.70)	KT-39 x KS -22	-5.04(-0.16)	KT-80 x KS -20	42.32 **(8.74**)	KT-8542 x New kuroda	34.11 **(5.06***)
KT-98 x PN	61.14 **(10.55**)	KT-8542 x New kuroda	27.21 **(27.52***)	KT-62 x KS -50	32.29 **(10.66***)	KT-7 x PN-1	33.35 **(-2.66)	KT-28 x New kuroda	-4.68(-0.84)	KT-8542 x KS -22	35.01 **(-4.08)	KT-8542 x KS -22	25.93 **(4.41**)

*: significant at 5% probability, ** significant at 1% probability, significant through F test

Similarly, the highest significant standard hetrosis heterosis in desirable direction for cortex thickness was recorded in the cross KT-10 × New Kuroda (166.16%) followed by KT-47 x KS -22 (64.68%), KT-95 × KS-50 (62.97%). The range of heterosis over commercial check for plant weight, shoot weight and root weight was 10.03% to 80.54 %, 32.19 % to 147.90 % and 5.81 % to 52.69 %, respectively. Among the 100 crosses, 32, 11 and 14 hybrids depicted significantly high heterosis over commercial check in desirable direction for better parent for plant weight, shoot weight and root weight, respectively. For plant weight, the hybrid KT-98 x NK-1 (80.54 %) followed by KT-98 x New Kuroda (62.00 %) and KT-98 x PN-1 (61.14 %) exhibited significantly high standard heterosis in desirable direction. For the root weight, the hybrid KT-98 x PN-1 (52.69%) followed by KT-98 x New Kuroda (35.22%) and KT-8542 x New Kuroda (27.21%) exhibited significantly high heterosis over commercial check in the favourable direction. The range of heterosis over commercial check for marketable yield, root size index, harvest index and root to shoot ratio was ranged from 19.36 % to 51.07 %, 9.47 % to 57.86 %, 11.15% to 77.20 % and 11.16 % to 38.59 %, respectively. Among the 100 hybrids, 4, 72, 66 exhibited significantly high over commercial check in desirable direction for yield, harvest index and root to shoot ratio, respectively. For root to shoot ratio, the hybrid KT-8542 x NK-1 (38.59 %) followed by KT-98 x PN-1 (33.89 %) and KT-7 x PN-1 (33.35 %) exhibited significantly high standard heterosis in desirable direction. Similarly, the cross KT-10 x New Kuroda (77.20 %) followed by KT-80 x KS -20 (42.32 %) and KT-8542 x KS -22 (35.01 %) depicted significantly high heterosis over commercial check in desirable direction for harvest index. For the yield, the hybrid KT-98 x PN-1 (51.07 %) followed by KT-8542 x New Kuroda (34.11%) and KT-8542 x KS -22 (25.93%) exhibited significantly high heterosis over commercial check in the favourable direction.

Table 4.14 Standard hetrosis for different quantitative characters traits in carrot. (Pooled Data)

Cross	Plant Height	Leaf Length	Root length	Root diameter	Core diameter	Core thickness
KT-7 x KS -20	15.07	-30.47 *	-9.55 **	8.38 **	-29.76	23.50
KT-7x KS -21	31.50	-15.45	-3.89	8.37 **	-23.90	18.98
KT-7 x KS -22	58.90	18.51	-7.28 *	4.36	-18.05	7.90
KT-7 x KS -50	42.47	-3.61	-2.77	8.38 **	-35.61**	28.02
KT-7 x KS -59	45.21	9.82	-17.46 **	8.38 **	-29.76	23.49
KT-7 x NK-1	45.21	0.35	-3.90	-7.69 **	-29.76	-2.82
KT-7 x PY-1	31.50	-14.67	-5.03	8.38 **	-23.90	18.99**
KT-7 x PN-1	31.52	-17.05	-1.64	-15.71 **	-35.61	-11.47
KT-7 x New kuroda	36.99	-11.51	-0.51	16.40 **	-18.07	27.63
KT-7 x KS -73	36.99	-13.08	1.77	-7.68 **	-23.88**	-7.32
KT-10 x KS -20	50.69	1.93	2.89	0.34	-41.46	19.35
KT-10 x KS -21	4.12	-47.85 **	-2.77	12.39 **	-41.46	39.10**
KT-10 x KS -22	39.73	-9.93	1.76	4.36	-23.90	12.41
KT-10 x KS -50	69.85	35.90 **	-14.07 **	16.40 **	-35.61	41.17
KT-10 x KS -59	4.11	-36.79 **	-18.59 **	8.38 **	-35.59	28.00
KT-10 x NK-1	50.69	-2.03	8.55 **	12.39 **	-29.76	30.07**
KT-10 x PY-1	23.29	-25.74 *	-2.76	-3.67	-41.44	12.80
KT-10 x PN-1	31.51	-8.34	-14.06 **	0.34	-47.32	23.88
KT-10 x New kuroda	67.11	24.05 *	-1.64	92.67 **	-35.59**	166.16**

KT-10x KS -73	23.3	-27.31 *	-0.51	12.39 **	-29.76	30.07
KT-28 x KS -20	34.25	-14.67	-0.51	-7.68 **	-29.76	-2.81
KT-28 x KS -21	9.59	-36.79 **	-9.54 **	12.39 **	-59.02	52.63
KT-28 x KS -22	42.46	-5.97	0.63	0.34	-35.61	14.85
KT-28 x KS -50	45.21	1.14	-5.03	16.40 **	-18.07	27.63**
KT-28 x KS -59	20.55	-23.36	-10.68 **	16.40 **	-12.20	23.12
KT-28 x NK-1	83.56	42.22 **	-0.51	16.40 **	-29.76	36.65
KT-28 x PY-1	50.69	5.87	-2.76	12.38 **	-12.20	16.53
KT-28 x PN-1	17.81	-33.63 **	-0.51	0.35	-23.90	5.82**
KT-28 x New kuroda	31.52	-17.82	-0.51	12.39 **	-29.76	30.08
KT-28 x KS -73	50.68	1.92	2.89	8.38 **	-23.92	18.98
KT-39 x KS -20	45.21	-6.77	6.26	8.38 **	-35.61**	28.01
KT-39 x KS -21	15.07	-36.79 **	-0.5	8.38 **	-35.61	28.01
KT-39 x KS -22	23.3	-30.47 *	4.02	-3.67	-23.90	-0.76
KT-39 x KS -50	45.21	1.14	-5.03	-7.68 **	-18.07	-11.84
KT-39 x KS -59	58.9	20.09	-9.56 **	8.38 **	-35.63	28.00
KT-39 x NK-1	72.61	29.57 *	-0.51	0.35	-23.90	5.83
KT-39 x PY-1	17.81	-32.06 **	-2.77	0.34	-53.17**	28.38**
KT-39 x PN-1	9.60	-33.63 **	-14.06 **	8.38 **	-23.90	18.99
KT-39 x New kuroda	31.5	-8.35	-14.07 **	-3.67	-47.32	17.29
KT-39 x KS -73	17.81	-24.16 *	-14.06 **	4.36	-29.76	16.92

KT-47 x KS -20	20.55	-24.15 *	-9.54 **	-7.68 **	-23.90	-7.32
KT-47 x KS -21	-9.6	-69.19 **	5.16	24.43 **	-23.90	45.31
KT-47 x KS -22	36.99	-8.35	-5.02	44.50 **	-6.36	64.68
KT-47 x KS -50	12.33	-28.10 *	-17.46 **	12.39 **	-29.78	30.08
KT-47 x KS -59	17.82	-25.73 *	-11.81 **	8.38 **	-6.36	5.45**
KT-47 x NK-1	6.85	-35.21 **	-16.33 **	12.39 **	-23.90	25.57
KT-47 x PY-1	39.73	-0.45	-11.81 **	-7.68 **	-29.78	-2.81
KT-47 x PN-1	17.81	-30.47 *	-5.03	0.34	-23.88	5.83
KT-47 x New kuroda	12.33	-28.10 *	-17.46 **	-11.69 **	-23.92**	-13.91**
KT-47 x KS -73	9.59	-36.80 **	-9.55 **	0.35	-35.61	14.86
KT-62 x KS -20	36.99	-3.61	-11.80 **	0.35	-29.74	10.35
KT-62 x KS -21	50.68	4.29	-0.51	16.40 **	-41.46	45.68
KT-62 x KS -22	72.61	28.00 *	1.76	12.39 **	-35.61	34.59
KT-62 x KS -50	17.81	-36.00 **	2.89	20.41 **	-23.90**	38.72
KT-62 x KS -59	28.77	-15.45	-8.42 *	4.35	-29.76	16.92
KT-62 x NK-1	45.21	5.08	-10.68 **	20.41 **	-23.88	38.72
KT-62 x PY-1	31.51	-7.56	-15.20 **	-19.72 **	-53.17	-4.51
KT-62 x PN-1	34.26	-10.72	-6.17	8.38 **	-35.63	28.01
KT-62 x New kuroda	36.99	-5.19	-9.54 **	4.35	-47.32	30.45***
KT-62 x KS -73	50.68	10.61	-9.55 **	-3.67	-53.17**	21.81
KT-80 x KS -20	28.77	-25.73 *	6.28	20.41 **	-41.46	52.26

KT-80 x KS -21	36.99	-14.67	4.02	4.37	-29.76	16.9
KT-80 x KS -22	1.38	-51.01 **	-2.77	8.37 **	-23.90	18.98
KT-80 x KS -50	15.07	-38.37 **	1.76	20.41 **	-29.76	43.23
KT-80 x KS -59	31.51	-13.08	-7.29 *	0.34	-18.03	1.32
KT-80 x NK-1	23.29	-16.25	-16.33 **	4.36	-18.05**	7.90
KT-80 x PY-1	34.25	-5.19	-14.07 **	16.39 **	-12.20	23.12
KT-80 x PN-1	31.50	-14.66	-5.03	8.38 **	-35.61	28.01
KT-80 x New kuroda	39.74	-2.02	-9.55 **	16.40 **	-23.88	32.14
KT-80 x KS -73	23.29	-25.73 *	-2.77	8.37 **	-23.90	18.98
KT-95 x KS -20	42.47	-6.77	1.76	-15.71 **	-29.74	-15.98**
KT-95 x KS -21	45.21	4.30	-9.54 **	0.35	-29.74	10.35
KT-95 x KS -22	39.74	-2.02	-9.55 **	16.40 **	-12.18	23.11
KT-95 x KS -50	15.07	-27.31 *	-14.08 **	32.45 **	-29.74	62.97
KT-95 x KS -59	39.74	2.71	-16.33 **	0.34	-23.90	5.83
KT-95 x NK-1	20.56	-17.82	-18.59 **	-15.71 **	-35.61	-11.47
KT-95 x PY-1	36.99	-0.45	-16.33 **	-7.68 **	-18.05	-11.84
KT-95 x PN-1	1.37	-51.01 **	-2.75	0.34	-29.74	10.34
KT-95 x New kuroda	15.06	-28.89 *	-11.80 **	-3.67	-29.76	3.76
KT-95 x KS -73	23.30	-25.73 *	-2.77	4.36	-29.76	16.92
KT-98 x KS -20	42.47	-4.4	-1.63	-15.70 **	-23.92	-20.49
KT-98 x KS -21	34.26	-11.51	-5.04	-7.68 **	-35.61	1.69

KT-98 x KS -22	53.42	12.19	-7.28 *	16.40 **	-29.76	36.66
KT-98 x KS -50	42.47	-3.60	-2.77	28.44 **	-35.59	60.90
KT-98 x KS -59	34.25	-8.35	-9.54 **	-11.70 **	-35.61	-4.89
KT-98 x NK-1	69.85	34.32 **	-11.81 **	8.38 **	-23.90	18.98
KT-98 x PY-1	-112.34 *	-125.23 **	-9.57 **	-15.71 **	-29.76**	-15.98
KT-98 x PN-1	45.21	3.51	-8.42 *	20.42 **	-29.76	43.24**
KT-98 x New kuroda	50.68	6.67	-3.90	-11.70 **	-23.90	-13.92
KT-98 x KS -73	56.16	14.56	-6.15	-3.67	-23.88	-0.75
KT-8542 x KS -20	28.77	-23.36	2.89	8.37 **	-23.90	18.98
KT-8542 x KS -21	53.71	47.73 **	17.95 **	3.82	-8.77**	16.42
KT-8542 x KS -22	18.56	12.92	0.31	6.00 *	-15.55	26.47
KT-8542 x KS -50	25.9	9.63	3.66	19.01 **	-0.46	42.79
KT-8542 x KS -59	13.05	7.54	-1.94	1.63	-2.51	12.23**
KT-8542 x NK-1	15.75	8.31	-7.25 *	17.18 **	-1.86	37.32
KT-8542 x PY-1	-5.46	-15.19	-0.17	-9.86 **	-8.32	-9.56
KT-8542 x PN-1	45.32	36.39 **	15.11 **	0.10	-0.99	5.32
KT-8542 x New kuroda	-273.96 **	38.37 **	3.80	-7.85 **	1413.28 **	-578.69 **
KT-8542 x KS -73	14.14	-17.89	1.44	-1.56	2.71	-3.41

Cross	Root weight	Plant Weight	Root size	Root to shoot ratio	Days to maturity	Harvesting index	Yield
KT-7 x KS -20	-12.08 **	-4.64	-3.38	27.83 **	-2.16	27.70 **	-11.47
KT-7 x KS -21	-16.24 **	-5.93	4.43	25.51 **	-1.08	22.41 **	-16.51
KT-7 x KS -22	-14.65 **	-5.93	-0.99	24.56 **	-1.80	22.27 **	-16.45
KT-7 x KS -50	-5.97 *	14.64 **	9.47 *	3.43	-1.80	23.13 **	-11.01
KT-7 x KS -59	-25.74 **	10.14 *	-10.21 *	-15.46 **	-0.72	2.92	-32.41 **
KT-7 x NK-1	-21.97 **	29.43 **	-10.97 **	-23.28 **	-1.80	-2.9	-31.19 **
KT-7 x PY-1	-18.43 **	-10.64 *	3.6	25.71 **	0.36**	27.18 **	-17.75
KT-7 x PN-1	-31.90 **	-27.79 **	-19.26 **	33.35 **	-0.72	20.31 **	-25.74 **
KT-7 x New kuroda	20.61 **	35.00 **	24.70 **	19.88 **	-2.88	32.49 **	11.91
KT-7 x KS -73	-21.91 **	5.21	-9.63 *	-5.23	-1.08	13.23 *	-28.68 **
KT-10 x KS -20	-35.56 **	-21.79 **	-0.47	14.96 **	2.16**	16.06 **	-39.22 **
KT-10 x KS -21	-22.09 **	-4.64	10.69 **	11.49 *	-2.52	18.37 **	-28.89 **
KT-10 x KS -22	18.78 **	36.40 **	8.09	16.97 **	-2.88	31.32 **	8.46
KT-10 x KS -50	-18.43 **	1.36	3.19	11.16 *	-3.60	12.78 *	-27.06 **
KT-10 x KS -59	17.41 **	35.43 **	4.62	19.88 **	3.96**	11.36 *	5.57
KT-10 x NK-1	4.17	23.61 **	20.53 **	31.29 **	-1.80	27.40 **	23.08 *
KT-10 x PY-1	-19.35 **	-10.86 *	4.8	23.11 **	-1.44	14.28 *	-20.88 *
KT-10 x PN-1	-12.95 **	7.35	-9.55 *	11.42 *	-1.44	8.51	-22.45 *
KT-10 x New kuroda	-6.56 *	13.14 **	57.86 **	13.10 *	-8.27	77.20 **	-16.26
KT-10 x KS -73	-9.87 **	0.79	4.07	20.30 **	-1.08	35.55 **	-9.46

KT-28 x KS -20	-24.48 **	-14.71 **	-4.54	26.28 **	-1.80	12.82 *	-2.25
KT-28 x KS -21	-19.58 **	-8.93	2.08	23.23 **	-0.72	20.73 **	-21.05 *
KT-28 x KS -22	4.63	36.07 **	-0.75	0.38	-2.16	21.35 **	-6.79
KT-28 x KS -50	-8.16 **	33.29 **	12.25 **	-12.19 *	-0.72	14.36 *	-18.02
KT-28 x KS -59	0.06	9.25	12.02 **	28.20 **	-0.72	22.75 **	0.12
KT-28 x NK-1	-13.07 **	23.21 **	12.10 **	-6.22	-1.44	18.97 **	-24.62 **
KT-28 x PY-1	13.99 **	30.50 **	21.11 **	19.39 **	-2.88	23.37 **	4.35
KT-28 x PN-1	-2.91	5.75	7.2	28.55 **	-4.68	21.87 **	-1.45
KT-28 x New kuroda	3.83	23.00 **	13.92 **	13.94 **	-0.72	27.39 **	-6.10
KT-28 x KS -73	-18.97 **	14.00 **	5.86	-6.72	-2.88	18.39 **	-28.54 **
KT-39 x KS -20	-1.38	5.21	20.89 **	31.84 **	-1.80	35.18 **	-6.95
KT-39 x KS -21	-13.72 **	10.57 *	9.74 *	4.93	5.04**	17.04 **	-23.46 *
KT-39 x KS -22	-15.09 **	11.43 *	-4.08	-0.26	-5.04**	18.08 **	-23.74 **
KT-39 x KS -50	-15.97 **	-3.89	3.29	20.26 **	-1.80	5.33	-20.31 *
KT-39 x KS -59	-6.45 *	5.75	6.95	18.39 **	-1.44	19.71 **	-11.24
KT-39 x NK-1	-9.99 **	2.86	-7.33	16.01 **	-1.80	31.32 **	-14.10
KT-39 x PY-1	13.99 **	30.93 **	17.93 **	17.30 **	-2.16	13.18 *	4.12
KT-39 x PN-1	-16.26 **	-5.93	-8.06	19.01 **	-2.16	25.46 **	-18.23 *
KT-39 x New kuroda	-13.35 **	7.12	-9.61 *	8.77	-2.16	5.68	-21.64 *
KT-39 x KS -73	-11.36 **	-5.07	-1.53	33.10 **	2.88**	20.35 **	-10.78
KT-47 x KS -20	-14.59 **	-6.15	-19.10 **	24.90 **	-2.16	20.90 **	-15.97
KT-47 x KS -21	-2.68	15.50 **	27.39 **	20.20 **	-1.80	34.01 **	-12.51
KT-47 x KS -22	-14.89 **	4.14	44.34 **	8.26	3.96***	28.26 **	-22.06 *
KT-47 x KS -50	-15.92 **	-0.57	-3.86	19.75 **	-1.80	11.97 *	-22.64 *
KT-47 x KS -59	-1.59	6.55	-1.09	28.03 **	1.80**	26.53 **	3.88
KT-47 x NK-1	-38.87 **	-17.28 **	-4.18	-9.75	2.88***	7.89	-41.28 **
KT-47 x PY-1	-12.15 **	-4.21	-20.59 **	25.76 **	-1.80	22.64 **	-17.57
KT-47 x PN-1	-44.23 **	-32.29 **	-6.94	4.53	-2.88	16.37 **	-44.82 **

KT-47 x New kuroda	2.23	30.71 **	-11.32 **	2.32	-1.80	-1.58	-8.28
KT-47 x KS -73	-30.31 **	-20.18 **	-2.45	23.44 **	-1.80	7.13	-22.07 *
KT-62 x KS -20	3.67	31.79 **	-9.46 *	3.61	2.16***	14.69 **	-7.70
KT-62 x KS -21	-41.72 **	-5.07	-0.02	-17.23 **	-1.08	13.97 *	-50.27 **
KT-62 x KS -22	-19.06 **	38.64 **	13.81 **	-26.66 **	2.16***	7.02	-28.18 **
KT-62 x KS -50	-14.15 **	-0.81	32.29 **	18.44 **	2.52***	25.09 **	-4.48
KT-62* x S -59	-11.89 **	8.00	1.19	8.36	0.72**	13.59 *	-19.66 *
KT-62 x NK-1	-20.49 **	-13.22 **	7.20	25.42 **	-2.88	30.87 **	-21.06 *
KT-62 x PY-1	-17.46 **	-3.57	-21.99 **	19.70 **	2.52***	-1.04	-22.71 *
KT-62 x PN-1	9.31 **	17.43 **	7.73	28.14 **	-1.80	29.88 **	5.43
KT-62 x New kuroda	-11.58 **	-2.61	2.01	25.53 **	-4.68	17.44 **	-13.26
KT-62 x KS -73	-0.70	5.00	-2.60	32.84 **	-1.80	18.50 **	1.24
KT-80 x KS -20	12.61 **	30.82 **	22.45 **	16.33 **	-0.72	42.32 **	2.00
KT-80 x KS -21	-12.50 **	-0.81	17.48 **	17.43 **	-2.88	23.85 **	-8.21
KT-80 x KS -22	-14.66 **	-6.07	20.63 **	27.67 **	-0.72	21.50 **	-20.77 *
KT-80 x KS -50	-0.82	20.00 **	22.87 **	11.49 *	-1.80	30.35 **	-10.78
KT-80 x KS -59	-7.87 **	5.43	0.81	16.55 **	-0.72	16.98 **	-13.32
KT-80 x NK-1	-18.20 **	5.00	-6.41	1.30	-0.72	6.57	-25.44 **
KT-80 x PY-1	-11.47 **	3.07	-3.49	16.84 **	-1.80	24.47 **	-17.92
KT-80 x PN-1	-29.28 **	-21.79 **	0.61	24.45 **	2.88***	26.27 **	-29.23 **
KT-80 x New kuroda	-21.86 **	-2.07	6.58	11.46 *	-1.80	14.18 *	-30.68 **
KT-80 x KS -73	1.41	41.43 **	2.92	-4.44	-0.72	17.91 **	-12.72
KT-95 x KS -20	5.74 *	19.14 **	-0.91	20.12 **	-1.80	13.34 *	-1.41
KT-95 x KS -21	-15.29 **	1.25	0.82	17.83 **	-0.72	6.19	-23.01 *
KT-95 x KS -22	-10.15 **	5.75	1.03	15.87 **	-2.52	26.38 **	-17.08
KT-95 x KS -50	-15.75 **	-6.09	20.93 **	22.99 **	-2.16	22.50 **	2.60
KT-95 x KS -59	-12.07 **	-3.89	-13.70 **	25.40 **	1.44***	18.71 **	-13.27
KT-95 x NK-1	-37.27 **	-27.07 **	-25.76 **	22.85 **	2.88**	-3.59	-30.63 **
KT-95 x PY	-24.94 **	26.43 **	-26.06 **	-24.06 **	0.72**	-6.11	-34.06 **

KT-95 x PN	-23.85 **	-8.57	6.56	8.95	0.72**	12.57 *	-28.47 **
KT-95 x New kuroda	-23.80 **	-6.04	-4.15	9.88	-1.80	1.69	-30.53 **
KT-95 x KS -73	2.29	43.58 **	12.81 **	-5.87	-2.88	6.48	-11.50
KT-98 x KS -20	-16.49 **	-6.57	-14.94 **	20.68 **	0.72***	16.75 **	-19.36 *
KT-98 x KS -21	-21.75 **	-10.79 *	-7.47	20.40 **	1.80***	11.15 *	-1.13
KT-98 x KS -22	1.95	48.50 **	8.24 *	-9.2	-2.88	14.95 **	-12.42
KT-98 x KS -50	-15.35 **	35.43 **	19.67 **	-19.27 **	-0.72	17.76 **	-26.16 **
KT-98 x KS -59	-13.11 **	3.07	-9.25 *	12.63 *	-0.72	5.45	-19.60 *
KT-98 x NK-1	-0.06	80.54 **	-2.22	-37.43 **	-1.80	6.52	-14.42
KT-98 x PY-1	-20.87 **	-12.78 *	-16.79 **	25.34 **	-1.80	8.92	-20.86 *
KT-98 x PN-1	52.69 **	61.14 **	25.11 **	33.89 **	0.72**	34.12 **	51.07 **
KT-98 x New kuroda	35.22 **	62.00 **	5.06	11.87 *	0.36**	9.99	19.36 *
KT-98 x KS -73	-33.04 **	-12.36 *	-22.83 **	-7.77	2.16***	21.72 **	-34.60 **
KT-8542 x KS -20	-21.17 **	-7.86	3.23	9.17	0.72***	35.01 **	-23.10 *
KT-8542 x KS -21	-6.77 *	-0.59	7.09	14.98 **	-2.16	14.25 *	-7.63
KT-8542 x KS -22	5.81 *	10.03 *	5.05	20.29 **	-2.16	7.95	25.93 **
KT-8542 x KS -50	20.23 **	35.72 **	23.21 **	8.91	-1.08	10.42	22.84 *
KT-8542 x KS -59	-11.60 **	-8.77	-1.06	11.55 *	-2.16***	9.50	-13.15
KT-8542 x NK-1	6.12 *	-0.11	0.56	38.59 **	-2.88	30.61 **	17.75
KT-8542 x PY-1	-10.70 **	-15.74 **	-1.98	24.21 **	1.02**	11.92 *	2.26
KT-8542 x PN-1	-14.87 **	-1.21	1.41	0.76	-1.11	4.34	-11.61
KT-8542 x New kuroda	27.21 **	29.33 **	-9.61 *	7.85	-0.08	11.27 *	34.11 **
KT-8542 x KS -73	-46.43 **	-13.36 **	-20.27 **	-31.16 **	-2.10	-11.50 *	-13.68

*= significant of variance at 5% probability, **= significant at 1% probability through F test

4.3 Antioxidant and qualitative characters traits

4.3.1 Evaluation of parents for antioxidant traits

The measure of mean value of parental CMS lines and testers with commercial checks is summarised in Table 4.15. The mean estimates of antioxidant capacity related traits CUPRAC and FRAP among the CMS lines were ranged from 0.33 µ moltrolox/g (KT-98A) to 0.56 µ moltrolox/g (KT-8542A) and 0.05 µ moltrolox/g (KT-47A) to 0.34 µmoltrolox/g (KT-39), respectively. None of 10 parental lines performed better for CUPRAC content as compared to the check (Pusa Nayan Jyoti). Similarly no parental lines performed better than commercial check (Pusa Nayan Jyoti) rather one tester KS-20 having more FRAP content than check (Pusa Nayan Jyoti). The mean value for ascorbic acid content among the parental CMS lines ranged from 2.44 mg/100g (KT-95A) to 10.23 mg/100g (KT-62A). Among the testers, PY-1 had highest ascorbic acid content (7.98 mg/100g). One line, KT-62A had more average ascorbic acid content than the check, Pusa Nayan Jyoti. The four tester PY-1, KS-59, KS-21 and NK-1 had more average ascorbic acid content. The mean value of total phenolic content and anthocyanin content among the CMS lines was ranged from 185.63 mg of gallic acid/100 g FW (KT-62A) to 622.53 mg of gallic acid/100 g FW (KT-10) and 0.05 mg/100g (KT-95A) to 0.29 mg/100g (KT-10A), respectively. Among the ten testers, KS-73 had highest mean value for both total phenolic and anthocyanin content. The lines, KT-10A, KT-28 and KT-39 gave higher mean value of total phenolic content and none of the ten lines had more mean value of anthocyanin content as compared to the check (Pusa Nayan Jyoti). Similarly, the tester KS-73 and New Kuroda performed better with respect to these two compounds as compared to best check (Pusa Nayan Jyoti). The mean value of parental lines for lycopene, beta-carotene and total carotenoid content was ranged from 0.17mg/100g (KT-47A) to 1.35 mg/100g (KT-39A), 1.69 µg/100 ml (KT-95A) to 3.92µg/100 ml (KT-47A) and 0.13 mg/100g (KT-8542A) to 4.34 mg/100g (KT-62A). Among the testers, KS-73(1.26 µg/100 ml), PY-1 (1.06 µg/100

ml); KS-20 (3.49 µg/100 ml), PN-1 (3.40 µg/100 ml) and New Kuroda (3.20 µg/100 ml), KS-20(2.33) had highest lycopene, beta-carotene and total carotenoid content. The 3 CMS lines viz., KT-62A, KT-80A and KT-28A had more mean value for total carotenoid content as compared to Pusa Nayan Jyoti. For beta-carotene and lycopene content, 2 lines KT-47A, KT-8542A and KT-39 performed better than the check (Pusa Nayan Jyoti), respectively.

4.3.2 Analysis of variance for antioxidant and biochemic traits

The measure of mean squares estimates for 8 antioxidant and qualitative characters traits in RBD design are represented in Table 4.16. The variance analysis (ANOVA) for combining ability of different bioactive and antioxidant compounds in temperate orange coloured carrots depicted substantial genetic variation among all the treatments comprising parents, testcross progenies and commercial checks among 8 qualitative characters traits under observation significant at 0.1% probability (Table 4.16). The estimates of mean squares for environments found significant for only carotenoids content. The measure of means squares of CMS lines and testers recorded significant for all the studied antioxidant traits. The mean squares of parents x testcross progenies were also significant for all the traits except for anthocyanin content. The line × tester (crosses) mean squares were also significant for all the antioxidant traits. The genotype × environment (G × E) and environment × parent versus crosses mean square were found significant for the carotenoid content (total carotenoid and β-carotene) at p = 0.001 (Table 4.16). While for the antioxidant traits the variance analysis of G × E interaction was non-significant. The results indicated the true presence of inherent variation among all the parents and their 100 crosses.

Table 4.15. Characterization of parental CMS and tester lines including commercial checks for 8 antioxidants traits

Character	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocynin
KT-7	1.37±0.01	3.36±0.15	0.69±0.03	0.43±0.016	0.07±0.001	3.44±0.11	446.25±13.27	0.14±0.003
KT-10	1.26±0.07	2.99±0.12	1.04±0.05	0.42±0.012	0.09±0.003	5.33±0.12	622.5312.91	0.29±0.005
KT-28	2.33±0.07	3.00±0.02	0.56±0.05	0.45±0.001	0.07±0.002	6.78±0.13	568.98±9.23	0.20±0.006
KT-39	1.09±0.05	1.75±0.06	1.35±0.02	0.52±0.022	0.34±0.007	5.33±0.16	541.88±2.93	0.24±0.002
KT-47	1.01±0.04	3.92±0.10	0.17±0.03	0.41±0.005	0.05±0.001	3.98±0.15	226.88±5.52	0.14±0.003
KT-62	4.34±0.09	2.60±0.11	0.68±0.05	0.40±0.014	0.06±0.001	10.23±0.02	185.63±3.68	0.07±0.001
KT-80	2.49±0.11	2.60±0.09	1.17±0.06	0.54±0.013	0.14±0.003	6.43±0.14	230.62±5.20	0.16±0.002
KT-95	1.98±0.07	1.69±0.04	0.99±0.02	0.39±0.017	0.28±0.012	2.44±0.09	289.33±10.95	0.05±0.002
KT-98	1.32±0.04	2.07±0.04	0.44±0.00	0.33±0.002	0.18±0.000	4.66±0.20	289.33±2.61	0.13±0.004
KT-8542	0.13±0.00	3.77±0.16	0.69±0.10	0.56±0.017	0.11±0.002	6.43±0.23	302.34±9.81	0.17±0.004
KS-20	2.17±0.07	3.49±0.11	0.42±0.11	0.55±0.023	0.52±0.015	5.44±0.12	334.89±12.68	0.10±0.002
KS-22	1.27±0.01	2.59±0.06	0.81±0.11	0.58±0.024	0.16±0.005	6.44±0.00	367.34±3.31	0.10±0.001
KS-21	1.45±0.02	2.11±0.00	0.36±0.08	0.39±0.003	0.17±0.006	7.45±0.05	298.34±0.32	0.16±0.006
KS-50	1.40±0.01	2.52±0.10	0.65±0.09	0.71±0.029	0.08±0.003	5.22±0.10	385.22±2.78	0.25±0.011
PN-1	1.86±0.06	3.40±0.01	0.23±0.08	0.55±0.023	0.48±0.009	5.34±0.19	308.33±8.34	0.49±0.019
NK-1	1.41±0.03	3.49±0.12	0.36±0.01	0.42±0.015	0.45±0.017	7.44±0.07	384.44±3.47	0.49±0.011
KS-59	1.11±0.05	2.14±0.01	0.38±0.05	0.61±0.005	0.03±0.001	7.89±0.30	334.34±10.85	0.39±0.015
PY-1	1.06±0.04	1.64±0.01	1.06±0.04	0.40±0.011	0.37±0.007	7.98±0.34	245.43±1.33	0.29±0.001
KS -73	1.33±0.01	2.14±0.07	1.26±0.01	0.63±0.001	0.43±0.001	6.44±0.04	936.22±3.38	0.52±0.002
New Kuroda	3.2±0.07	2.44±0.00	0.29±0.10	0.41±0.004	0.15±0.001	4.33±0.10	467.33±6.32	0.51±0.018
Pusa Nayan Jyoti (check)	2.33±0.02	3.45±0.12	1.34±0.10	0.79±0.017	0.52±0.013	6.91±0.01	453.06±11.43	0.5±0.003
C.D. 5%	0.68	0.68	0.08	0.09	0.05	0.47	70.71	0.03
C.D. 1%	0.89	0.90	0.10	0.12	0.07	0.61	93.03	0.05

Table 4.16 Analysis of variance (ANOVA) of combining ability for various antioxidant compounds. (Pooled data)

Source of Variation	DF	Total Carotenoid	β-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
Replicates	2.00	0.02	0.02	0.03 **	0.00	0.00	0.60*	15703.57	0.00
Environments	1.00	25.8	26.88	0	0.00	0.00	0.00	0.00	0.00
Treatments	119.00	23.04 ***	20.16***	1.82 ***	2.02***	0.12***	18.94***	255322.28***	0.34***
Parents	19.00	4.93 ***	3.00 ***	0.78 ***	0.06***	0.16***	19.27***	183478.71***	0.14***
Parents (Line)	9.00	7.87 ***	3.69 ***	0.77 ***	0.03***	0.06***	28.28***	153475.90***	0.03***
Parents(Testers)	9.00	2.51 ***	2.55 ***	0.74 ***	0.07***	0.20***	9.74***	229593.00***	0.18***
Parents (L vs T)	1.00	0.33 ***	0.96 ***	1.18 ***	0.19***	0.63***	23.92***	38475.68***	0.88***
Parent vs Crosses	1.00	257.82 ***	107.92 ***	0.77 ***	0.03**	0.02***	10.11***	71286.82***	0.00
Crosses	99.00	24.15 ***	22.57 ***	2.03 ***	2.42***	0.11***	18.97***	270969.38***	0.38***
Line effect	9.00	145.88 ***	142.77 ***	2.68	1.72	0.19*	32.58	258762.00***	0.39
Tester effect	9.00	11.09	9.15	2.58	3.12	0.18	21.69	112451.23***	0.15
Line x Tester effect	81.00	12.07 ***	10.71 ***	1.90 ***	2.42***	0.09***	17.16***	289938.87***	0.41***
Env x Treat (g x e)	119.00	1.69	1.74	0	0.01				
Env x Parents	19.00	0.00	0.01	0	0.1		0.00	0.00	0.00
Env x Parents (L)	9.00	0.00	0.01	0	0.06		0.00	0.00	0.00
Env x Parents (T)	9.00	0.00	0.01	0	0.16				
Env x Crosses	99.00	1.98	2.03	0		0.00			0.00
Env x Line effect	9.00	15.00	16.37						
Env x Tester effect	9.00	0.51	0.54						
Env x L x T effect	81.00	0.70	0.61	0		0.00			0.00
Error	476.00	0.03	0.02	0.01	0.00	0.00	0.19	4541.90	0.00
Total	719.00	4.15	3.68	0.31	0.34	0.02	3.26	45308.35	0.06

*= significant at 5% probability, **= significant at 1% probability through F test, df = degree of freedom, L= lines, T = Tester

4.3.3 Genetic components of variance for antioxidant traits

The pooled appraisal of genetic variance components, predictability ratio, heritability, and gene action for 8 different bioactive compounds in temperate carrots over the two years is presented in Table 4.18. The pooled analysis results revealed that the magnitude of specific combining ability variance (σ^2_{sca}) variance for both lines and testers were higher than general combining ability variance (σ^2_{gca}) for all the bioactive compounds except for total carotenoid content (TCC) and β-carotene. The magnitude of σ^2_{gca} for FRAP, CUPRAC, lycopene, ascorbic acid and anthocyanin was less than unity. The estimates environmental variance (σ^2Env) were significantly non-zero for carotenoids and β-carotene content, while no contribution of residual variance was found for all other antioxidant traits. The effects of σ^2Env × lines, σ^2Env × testers, σ^2Env × GCA and σ^2Env × crosses were significant and less than unity for TCC and β-carotene. The genetic architecture analysis gives out that the measure of dominance variance (σ^2D) was higher than additive variance (σ^2A) for all the bioactive compounds except for TCC and β-carotene, however, the value of both σ^2D and σ^2A was less than unity for FRAP, CUPRAC, lycopene and anthocyanin content. The degree of dominance for all the antioxidant and qualitative characters traits was greater than unity except TCC and β-carotene indicating role of over-dominance for the expression of majority of traits. The ratio of additive to dominance variance (σ^2A/ σ^2D) was higher than unity for TCC and β-carotene, while it was less than unity for all other traits. It is accompanied with the results of predictability ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) exhibiting less than unity estimates for all the traits indicating the influence of non-additive gene action. To determine the efficiency in response to selection the heritability magnitude is computed for different traits. The pooled heritability analysis across the environments revealed the moderate estimates of heritability in narrow sense (h^2_{ns}) for all the traits except for TCC and β-carotene for which high h^2_{ns} was observed. Considerable genetic advance value GA) at 5%, selection intensity for total phenolic content accompanied with moderate h^2ns indicated

high selection efficiency for this trait. The low estimates of genetic advance value at 5 % selection intensity were computed for all other traits.

4.3.4 General combining ability (GCA) effects of parents for antioxidant traits

The pooled analysed results over the two years for general combining ability (GCA) effects of lines and testers are summarized in Table 4.18. The estimates of GCA effects revealed that the petaloid type CMS line KT-28A was good general combiner for TCC, β-carotene and anthocyanin content at $P < 0.0.001$, while it was perform lower combining ability for all other antioxidant traits under study. The CMS line, KT- 80A exhibited significantly high GCA effects for TCC, β-carotene, FRAP and ascorbic acids content at 0.1 % level of significance. The line, KT-10A was recorded significantly poor general combiner for all the qualitative characters traits except for anthocyanin. Likewise, the CMS line, KT -98A recorded relatively high GCA effects at $P < 0.001$ for majority of the qualitative characters traits except TCC, ascorbic acid and anthocyanin content. The CMS line, KT-62A exhibited significant GCA effects in desirable direction for TCC, β-carotene, lycopene, ascorbic acid and anthocyanins at $P \leq 0.001$ while the line, KT-47A exhibited positive significant GCA effect for majority of antioxidant traits except for TCC, β-carotene and lycopene content. The CMS line, KT-39A observed good general combiner for only FRAP and ascorbic acid content at $P \leq 0.001$ and was poor general combiner for all other antioxidant compounds. The lines KT-7A exhibited significant GCA effects in desirable direction for lycopene, CUPRAC, FRAP and anthocyanin contents and was poor combiner for all other traits. The line, KT- 95A was found good general combiner for TCC, βcarotene, FRAP and ascorbic acid content and the CMS line KT-8542A showed significantly high GCA effects in positive direction for lycopene, ascorbic acid and total phenolic content. However, among the 10 testers, KS-20 recorded good general combiner for TCC, β-carotene and anthocyanin content but it was poor for remaining traits. The tester, KS-21 exhibited significantly poor GCA effects in negative direction for all the

traits except for TCC, βcarotene, FRAP and anthocyanin content. The KS-22 depicted significant variation of GCA effects in positive direction for TCC and lycopene concentration at probability of $P \leq 0.001$ and was remains non-significant for other traits. However , KS-50 recorded desirable GCA effects with significance at $P \leq 0.001$ for CUPRAC, ascorbic acid, total phenol and anthocyanin concentration. The tester, KS-59 performed significant GCA effects at $P \leq 0.001$ for β-carotene, lycopene, FRAP and ascorbic acid content and was poor combiner for rest of the traits. The tester, NK-1 was poor general combiner for all the traits except TCC, ascorbic acid and lycopene concentration. The PY-1 exhibited significant GCA effects in desirable direction for ascorbic acid and total phenols at $P \leq 0.001$ while it was poor combiner for all other traits. Whereas, the tester PN-1 exhibited positive GCA effects significant at $P \leq 0.001$ for FRAP and total phenol only. The New Kuroda a tester found to exhibit significant GCA effects at $P \leq 0.001$ for CUPRAC and anthocyanin contents while it was poor general combiner for most of the traits. Tester KS-73 was also good general combiner for only TCC and β-carotene content.

Table 4.17 Estimates of genetic components of variance for different antioxidant compounds. (Pooled Data)

Variance Components	TCC	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
σ^2gca Line	2.43	2.38	0.04	0.03	0.00	0.54	4222.58	0.01
σ^2gca Tester	0.18	0.15	0.04	0.05	0.00	0.36	1784.06	0.00
σ^2 Lx t(SCA)	2.01	1.78	0.32	0.40	0.02	2.82	47421.90	0.07
σ^2 Env	0.09	0.09	0.00	0.00	0.00	0.00	-15.02	0.00
σ2 Env x Line	0.50	0.55	0.00	0.00	0.00	-0.01	-180.25	0.00
σ² Env x Testers	0.02	0.02	0.00	0.00	0.00	-0.01	-180.25	0.00
σ ² Env.x GCA	0.26	0.28	0.00	0.00	0.00	-0.01	-180.25	0.00
σ ² Env x L x t(SCAL)	0.23	0.20	0.00	0.00	0.00	-0.07	-1802.49	0.00
σ^2 E	0.01	0.00	0.00	0.00	0.00	0.04	901.24	0.00
σ ²A	2.62	2.53	0.09	0.08	0.01	0.90	6006.64	0.01
σ² D	2.01	1.78	0.32	0.40	0.02	2.82	47421.90	0.07
σ² A/ σ² D	1.30	1.42	0.28	0.20	0.41	0.32	0.13	0.13
Degree of Dominance	0.88	0.84	1.90	2.24	1.56	1.77	2.81	2.76
Heritability (NS) %	48.71	49.87	21.80	16.71	29.98	24.45	11.51	11.67
Genetic Advance 5 %	2.33	2.31	0.28	0.24	0.09	0.96	54.18	0.07
Predictability Ratio	0.57	0.59	0.22	0.17	0.29	0.24	0.11	0.12

σ^2A = additive genetic variance, σ^2D = dominance genetic variance, σ^2_{gca} = estimate of GCA variance, σ^2_{sca} = estimate of SCA

Table 4.18 Estimates of general combining ability (GCA) effects of lines and testers. (Pooled Data)

Lines/Testers	TCC	β-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7	-0.99***	-0.59***	0.31***	0.04***	0.03***	-0.31***	-60.36***	0.17***
KT-10	-1.27***	-0.94***	-0.14***	-0.14***	-0.04***	-0.85***	-66.44***	0.03***
KT-28	2.84***	2.75***	-0.07	-0.07***	-0.04***	-0.64***	-8.38	0.05***
KT-39	-0.35***	-0.62***	-0.14***	-0.05***	0.03***	0.56***	-6.42	-0.07***
KT-47	-2.41***	-1.712***	-0.26***	0.01	0.03**	1.13***	32.62***	0.07***
KT-62	0.28***	0.56***	0.22***	-0.05***	-0.01	0.55***	-16.65	0.08***
KT-80	1.44***	1.91***	-0.02**	-0.02	0.08***	0.44***	-71.22***	-0.04***
KT-95	0.87***	0.71***	-0.25***	-0.14***	0.04***	0.56***	-18.16***	-0.09***
KT-98	-0.84***	0.11***	0.18***	0.45***	0.01	-0.92***	127.23	-0.01**
KT-8542	-1.26***	-2.18***	0.18***	-0.03***	-0.12***	0.61***	87.81***	-0.04***
KS-20	0.41***	0.51***	-0.17***	-0.01	-0.02**	-0.24***	-16.00	0.02***
KS-21	0.76***	0.40***	-0.14	-0.12	0.12***	-0.11	-72.37***	0.08***
KS-22	0.12***	-0.55***	0.19***	-0.13***	-0.07***	-0.84***	1.76	0.00
KS-50	-0.40***	-0.36***	-0.14***	0.63***	-0.04***	0.61***	60.90***	0.02***
KS-59	-0.35***	0.25***	0.47***	-0.14***	0.02**	0.56***	-11.62	-0.09***
NK-1	0.05**	-0.14***	0.13***	-0.01	0.004	0.38***	-32.75***	-0.03***
PY-1	-0.72***	-0.39***	-0.15***	-0.10***	0.004	0.75***	51.66***	-0.00
PN-1	-0.14***	-0.19***	-0.02	-0.09***	0.04***	0.10	44.73***	-0.02***
New Kuroda	0.01	0.03	-0.12***	0.034***	-0.02**	-0.23***	-39.97***	0.05***
KS -73	0.25***	0.46***	-0.05***	-0.07***	-0.045***	-1.00***	13.67	-0.03***
CD (5%)	0.04	0.04	0.02	0.02	0.01	0.12	18.66	0.01
CD (1%)	0.04	0.04	0.02	0.02	0.01	0.12	18.67	0.01

*= significant at 5% probability, **= significant at 1% probability through F test, CD = critical difference

4.3.5 Specific combining ability (SCA) effects 100 test crosses

The pooled specific combining (SCA) ability effects of 100 testcross progenies of temperate carrots over the environments (year 1 and year 2) are summarized in Table.4.19. Out of 100 hybrids, for the CUPRAC content, 45 crosses exhibited positive significant SCA effects in desirable direction. Similarly, for the FRAP concentration the significant SCA effects in desirable direction were recorded in 31 crosses among 100 testcross progenies. The 32, 32, 34, 40, 41 and 40 among 100 hybrids showed significantly higher SCA effects for ascorbic acid content, phenolic content, anthocyanin content, lycopene content, β-carotene and TCC content respectively. With respect to CUPRAC content, the highest significant SCA effects in desirable direction was observed in the cross combination KT-98A x KS-50 (poor × poor general combiner) followed by KT-47A x PN-1 (poor general combiner × poor general combiner) and KT-28A x KS-73 (poor general combiner × poor general combiner). Similarly, for the concentration of FRAP, the hybrids KT-39A x KS-20 (good general combiner × poor general combiner) followed by KT-47A x KS 21 (good general combining ability × good general combiner) and KT-62A x PY-1 (poor GCA × poor GCA) significantly depicted the highest measure of SCA effects in desirable direction. The higher significant SCA effects in positive direction for ascorbic acid content was observed in the cross combinations KT-47A x KS-20 (good general combiner × poor GCA), followed by KT-8542A x KS-59 (good general combiner × good general combiner) and KT-62A x KS-50 (good general combiner × good general combiner). The heterotic cross of KT-98A x PN-1 (good combiner × good general combiner) performed highest significant positive SCA effects for total phenolic content, followed by KT-98A x KS-50 (good combiner × good general combiner) and KT-80A x KS-73 (poor general combiner × good combiner). The significant SCA effect for anthocyanin content was recorded in the hybrid cross KT-62A x KS-21 (good general combiner × good general combiner) followed by KT-8542A x KS-50 (poor general combiner × good general

combiner) and KT-7A x KS-20 (good general combiner × good general combiner). The heterotic cross KT-7A x KS-59 (good general combiner × good general combiner) shows the significantly greater SCA effects for the lycopene content followed by the cross combination, KT-47A x KS -59 (poor general combiner × good general combiner) and KT-95A x NK-1 (poor general combiner x good general combiner). For the β-carotene content, the highest SCA effects was in the cross combination KT-62A x KS-21 (good general combiner × good general combiner) followed by KT-39A x PY-1 (poor general combiner × poor general combiner) and KT-10A x KS -73 (poor general combiner × good general combiner). Likewise, the cross combination KT-62A x KS-22 (good general combiner × good general combiner) displayed significant SCA effects for total carotenoid content followed by KT-80A x KS -73 (good combiner × good combiner) and KT-62A x NK-1 (good general combiner × good general combiner).

Table 4.19 Estimates of specific combining ability (SCA) effects of 100 crosses for antioxidant traits. (Pooled Data)

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS-20	0.17 *	0.71***	-0.69***	-0.01	-0.17***	-3.02***	-42.17	0.63***
KT-7 x KS-21	0.24 ***	0.85***	-0.35***	0.06*	0.10***	-1.11***	12.09	-0.21***
KT-7 x KS-22	-0.99	1.03***	0.97***	0.02	-0.01	1.83***	-99.97***	-0.03*
KT-7 x KS-50	0.61 ***	-0.45***	-0.37***	-0.71***	-0.04	0.46*	-128.82***	-0.07***
KT-7 x KS-59	-0.35 ***	-0.06	2.39***	0.19***	0.01	0.23	196.99***	-0.26***
KT-7 x NK-1	0.08	-1.69***	-0.74***	0.01	-0.05*	-0.37	-35.66	-0.22***
KT-7 x PY-1	0.08	-0.90***	-0.63***	0.05*	-0.05*	0.22	185.46***	0.42***
KT-7 x PN-1	0.13	-1.29***	0.41***	0.26***	0.12***	0.03	96.68***	-0.06***
KT-7 x New Kuroda	-0.90 ***	1.64***	-0.49***	0.13***	0.14***	1.45***	-69.05*	0.03
KT-7 x KS -73	0.94 ***	0.16**	-0.51***	0	-0.06**	0.27	-115.55***	-0.24***
KT-10 x KS-20	0.08	-0.37***	0.02	0.11***	0.14***	0.19	16.52	0.48***
KT-10 x KS-21	0.68 ***	-1.45***	-0.04	0.15***	0.04	-1.55***	44.3	-0.14***
KT-10 x KS-22	-0.64 ***	-0.65***	0.07*	0.09***	-0.02	-0.47*	-204.14***	-0.08***
KT-10 x KS-50	-0.22 **	0.51***	0.12***	-0.62***	-0.07***	0.2	-203.36***	-0.11***
KT-10 x KS-59	0.76 ***	0.23***	-0.52***	0.25***	-0.08***	0.28	11.74	-0.10***
KT-10 x NK-1	-0.76 ***	-0.02	-0.21***	0.15***	-0.06**	0.51**	152.89***	-0.07***
KT-10 x PY-1	1.15 ***	-0.47***	0.17***	-0.02	0.04*	0.57**	390.84***	0.02***
KT-10 x PN-1	-0.54 ***	-0.01	0.02	-0.08**	-0.02	-0.29	-138.76***	-0.11***
KT-10 x New Kuroda	-0.08	-0.69***	0.05	-0.06*	-0.08***	-0.86***	-26.22	0.16***
KT-10 x KS -73	-0.45 ***	2.91***	0.32***	0.04	0.11***	1.42***	-43.82	-0.05***
KT-28 x KS-20	-3.15 ***	0.24***	-0.04	-0.12***	0	-0.65***	-263.57***	-0.20***
KT-28 x KS-21	-0.62 ***	-1.52***	-0.11**	0.01	-0.14***	2.61***	168.73***	-0.20***
KT-28 x KS-22	-1.75 ***	1.41***	0.50***	0.11***	0.07***	0.11	-128.26***	0.11***

KT-28 x KS-50	0.61 ***	1.66***	0.03	-0.49***	0.08***	-1.25***	22.71	0.13***
KT-28 x KS-59	2.64 ***	-1.35***	-0.74***	0.17***	0.10***	-2.17***	-217.53***	0.10***
KT-28 x NK-1	-1.83 ***	-0.67***	0.40***	0.19***	0.03	3.10***	-115.44***	-0.09***
KT-28 x PY-1	-0.83 ***	0.35***	-0.06	-0.04	0	-2.40***	215.76***	-0.16***
KT-28 x PN-1	1.64 ***	1.05***	-0.01	0	-0.11***	-0.36	166.26***	0.20***
KT-28 x New Kuroda	2.25 ***	0.20***	0.08*	-0.12***	0.03	-0.1	78.75**	0.09***
KT-28 x KS -73	1.04 ***	-1.38***	-0.05	0.30***	-0.06**	1.12***	72.60*	0.03***
KT-39 x KS-20	2.24 ***	0.78***	0.21***	-0.02	0.31***	-0.57**	206.97***	-0.10***
KT-39 x KS-21	0.58 ***	-0.02	0.22***	0.04	-0.21***	-0.27	75.78*	-0.21***
KT-39 x KS-22	-1.31 ***	-0.81***	0.09**	0.09***	-0.07**	0.23	298.31***	0.36***
KT-39 x KS-50	-0.37 ***	-0.31***	0.23***	-0.41***	-0.02	-0.29	114.25***	-0.06***
KT-39 x KS-59	-0.92 ***	0.16**	-0.21***	-0.01	0.04	-1.08***	-70.68*	-0.01***
KT-39 x NK-1	0.54 ***	-0.61***	-0.04	-0.12***	-0.17***	0.99***	228.42***	0.08***
KT-39 x PY-1	-0.53 ***	3.00***	0.81***	-0.05	-0.05*	0.48*	-196.96***	0.04***
KT-39 x PN-1	2.24 ***	0.78***	-0.41***	0.05	-0.03	1.35***	-282.01***	0.01***
KT-39 x New Kuroda	-1.06 ***	-0.78***	-0.41***	0.25***	0.04	-0.29	-205.58***	-0.08***
KT-39 x KS -73	-1.40 ***	-2.19***	-0.50***	0.17***	0.15***	-0.55**	-168.52***	-0.02***
KT-47 x KS-20	-0.99 ***	-1.12***	-0.26***	-0.08***	-0.15***	5.50***	-173.49***	-0.04***
KT-47 x KS-21	-0.96 ***	-1.06***	-0.23***	-0.05	0.28***	2.35***	-247.50***	-0.21***
KT-47 x KS-22	0.60 ***	-0.07	-0.61***	0.02	-0.07**	-0.80***	34.9	0.08***
KT-47 x KS-50	0.53 ***	-0.29***	-0.32***	-0.63***	-0.09***	-2.99***	-5.16	-0.14***
KT-47 x KS-59	-0.14 *	-0.83***	1.43***	0.05	0.16***	-1.58***	-78.31***	0.09***
KT-47 x NK-1	-0.09	1.43***	-0.59***	0.19***	0.14***	1.45***	309.95***	0.06***
KT-47 x PY-1	0.63 ***	1.10***	-0.31***	0.19***	-0.10***	-1.13***	-122.07***	0.08***
KT-47 x PN-1	1.50 ***	-0.35***	0.23***	0.33***	0	-0.07	-231.12***	0.01***

KT-47 x New Kuroda	-0.58 ***	-0.26***	0.18***	0.09***	-0.09***	-0.68***	367.64***	0.07***
KT-47 x KS -73	-0.49 ***	1.46***	0.47***	-0.11***	-0.08***	-2.04***	145.16***	0
KT-62 x KS-20	-0.50 ***	-1.91***	0.23***	0.16***	0.13***	-1.87***	340.16***	-0.28***
KT-62 x KS-21	-1.44 ***	5.21***	-0.16***	0.10***	-0.05*	-0.18	106.05***	1.48***
KT-62 x KS-22	4.71 ***	-1.01***	-0.17***	0.04	-0.04	-0.57**	-60.16*	-0.26***
KT-62 x KS-50	-0.65 ***	-0.63***	-0.12***	-0.57***	-0.09***	3.37***	35.48	-0.28***
KT-62 x KS-59	-0.52 ***	2.86***	-1.10***	-0.14***	-0.17***	1.12***	-107.82***	-0.16***
KT-62 x NK-1	2.69 ***	0.19**	0.23***	0.07***	-0.08***	0.29	-203.16***	-0.15***
KT-62 x PY-1	-2.38 ***	-1.29***	0.56***	0.10***	0.26***	-2.19***	42.65	-0.12***
KT-62 x PN-1	-0.78 ***	-0.73***	-0.04***	-0.17***	-0.09***	-0.2	-188.24***	-0.07***
KT-62 x New Kuroda	0.37 ***	-2.07***	0.17***	0.30***	-0.02	-0.50**	16.78	-0.16***
KT-62 x KS -73	-1.50 ***	-0.63***	0.40***	0.12***	0.14***	0.74***	18.25	0
KT-80 x KS-20	-2.10 ***	0.79***	0.36***	-0.14***	-0.21***	2.44***	32.21	-0.16***
KT-80 x KS-21	0.74 ***	-2.39***	0.36***	0.07**	0.02	0.41**	50.49	-0.06***
KT-80 x KS-22	-1.37 ***	-0.51***	0.36***	0.07**	0.13***	1.13***	28.23	0.07***
KT-80 x KS-50	-0.73 ***	0.07	0.28***	-0.54***	0.25***	-0.06	-84.24***	-0.08***
KT-80 x KS-59	0.22 ***	0.47***	-0.37***	-0.02	-0.16***	0.37	-80.26	0.14***
KT-80 x NK-1	0.77 ***	-0.98***	0.63***	0.10***	0.13***	-2.62***	117.75***	0.28***
KT-80 x PY-1	-1.05 ***	-1.65***	0	0.13***	-0.04	2.67***	-156.77***	0.05***
KT-80 x PN-1	-1.65 ***	1.50***	-0.67***	0.05*	0.15***	-1.45***	-95.79***	-0.03
KT-80 x New Kuroda	1.90 ***	1.83***	-0.42***	0.11***	-0.19***	-0.1	-3.01	-0.21***
KT-80 x KS -73	3.27 ***	0.87***	-0.53***	0.18***	-0.09***	-2.79***	526.91***	-0.01
KT-95 x KS-20	2.63 ***	2.44***	-0.22***	0.18***	-0.02	-1.22***	136.93***	-0.11***
KT-95 x KS-21	2.53 ***	-0.48***	-0.11**	0.16***	0.16***	0.56**	347.14***	-0.16***
KT-95 x KS-22	-0.29 ***	-0.06	-0.56***	0.11***	-0.01	-0.41*	208.91***	-0.08***

KT-95 x KS-50	0.20 ***	-0.33***	-0.21***	-0.65***	0.03	-0.19	-108.72***	-0.05***
KT-95 x KS-59	-0.59 ***	-1.35***	-0.85***	0.02	-0.10***	-0.35	66.11*	0.05***
KT-95 x NK-1	-1.75 ***	0.05	-0.61***	0.03	0.13***	-1.67***	-254.00***	-0.04***
KT-95 x PY-1	0.26 ***	-0.71***	-0.30***	0.07**	-0.19***	0.88***	-73.55*	-0.08***
KT-95 x PN-1	-1.27 ***	-0.47***	0.86***	0.02	0.05*	0.96***	-255.50***	-0.05***
KT-95 x New Kuroda	-0.93 ***	0.14*	1.05***	0.04	0.09***	1.79***	29.29	0.41
KT-95 x KS -73	-0.79 ***	0.77***	0.96***	0.02***	-0.13***	-0.35	-96.62***	0.11***
KT-98 x KS-20	0.65 ***	-0.77***	0.44***	-0.37***	-0.02	-0.87***	-151.54***	-0.14***
KT-98 x KS-21	-0.90 ***	0.79***	0.09***	-0.61***	-0.07***	-1.57***	-345.36***	-0.13***
KT-98 x KS-22	0.99 ***	0.39***	-0.55***	-0.55***	-0.04	-2.23***	113.71***	-0.06***
KT-98 x KS-50	-0.14 *	-0.62***	0.46***	5.06***	-0.10***	2.60***	562.85***	-0.11***
KT-98 x KS-59	-1.05 ***	-0.61***	-0.02	-0.58***	0.25***	-0.80***	-174.00***	0.16***
KT-98 x NK-1	-0.36 ***	1.88***	0.23***	-0.63***	-0.05*	-2.07***	-132.74***	0.23***
KT-98 x PY-1	2.05 ***	0.07	-0.47***	-0.55***	0.16***	2.03***	-199.88***	-0.12***
KT-98 x PN-1	-0.86 ***	-0.57***	-0.18***	-0.51***	-0.09***	0.18	653.05***	0.26***
KT-98 x New Kuroda	-0.66 ***	0.58***	0.22***	-0.65***	-0.06**	0.53**	-113.91***	-0.20***
KT-98 x KS -73	0.29 ***	-1.14***	-0.22***	-0.61***	0.01	2.19***	-212.18***	0.11***
KT-8542 x KS-20	0.97 ***	-0.80***	-0.04	0.28***	0	0.07	-102.02***	-0.08***
KT-8542*KS-21	-0.86 ***	0.07	0.31***	0.06*	-0.12***	-1.24***	-211.72***	-0.18***
KT-8542 x KS-22	0.05	0.28***	-0.10**	0	0.05*	1.18***	-191.54***	-0.10***
KT-8542 x KS-50	0.17 *	0.39***	-0.12***	-0.44***	0.06*	-1.84***	-104.99***	0.77***
KT-8542 x KS-59	-0.04	0.47***	-0.02	0.07**	-0.05*	3.98***	453.75***	-0.01
KT-8542 x NK-1	0.72 ***	0.41***	0.70***	0.01	-0.03	0.37	167.49***	-0.08***
KT-8542 x PY-1	0.62 ***	0.50***	0.23***	0.12***	-0.04	-1.12***	-85.49**	-0.13***
KT-8542 x PN-1	-0.41 ***	0.1	-0.21***	0.06*	0.01	-0.14	275.44***	-0.15***

KT-8542 x New Kuroda	-0.31 ***	-0.60***	-0.42***	-0.08**	0.14***	-1.25***	-74.69*	-0.10***
KT-8542 x KS -73	-0.92 ***	-0.84***	-0.33***	-0.09***	0	-0.01	-126.23***	0.07***
CD 95% SCA	0.14	0.11	0.07	0.05	0.04	0.38	59.02	0.03

*= significant at 5% probability, **= significant at 1% probability through F test.

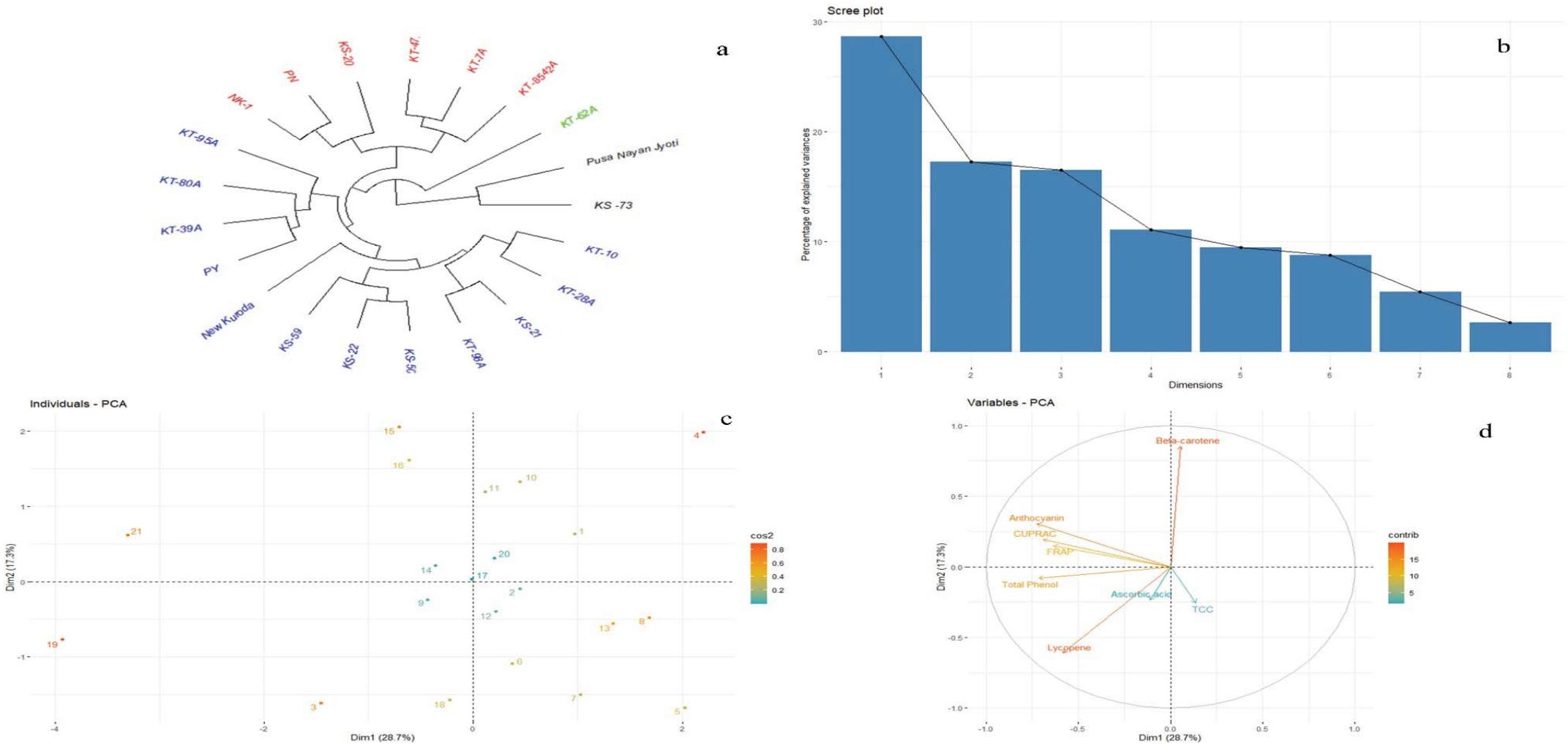


Figure 4.1: Dendrogram of 20 parental lines (10 CMS + 10 DH) based on 8 antioxidant and phytochemical traits using hierarchical cluster analysis

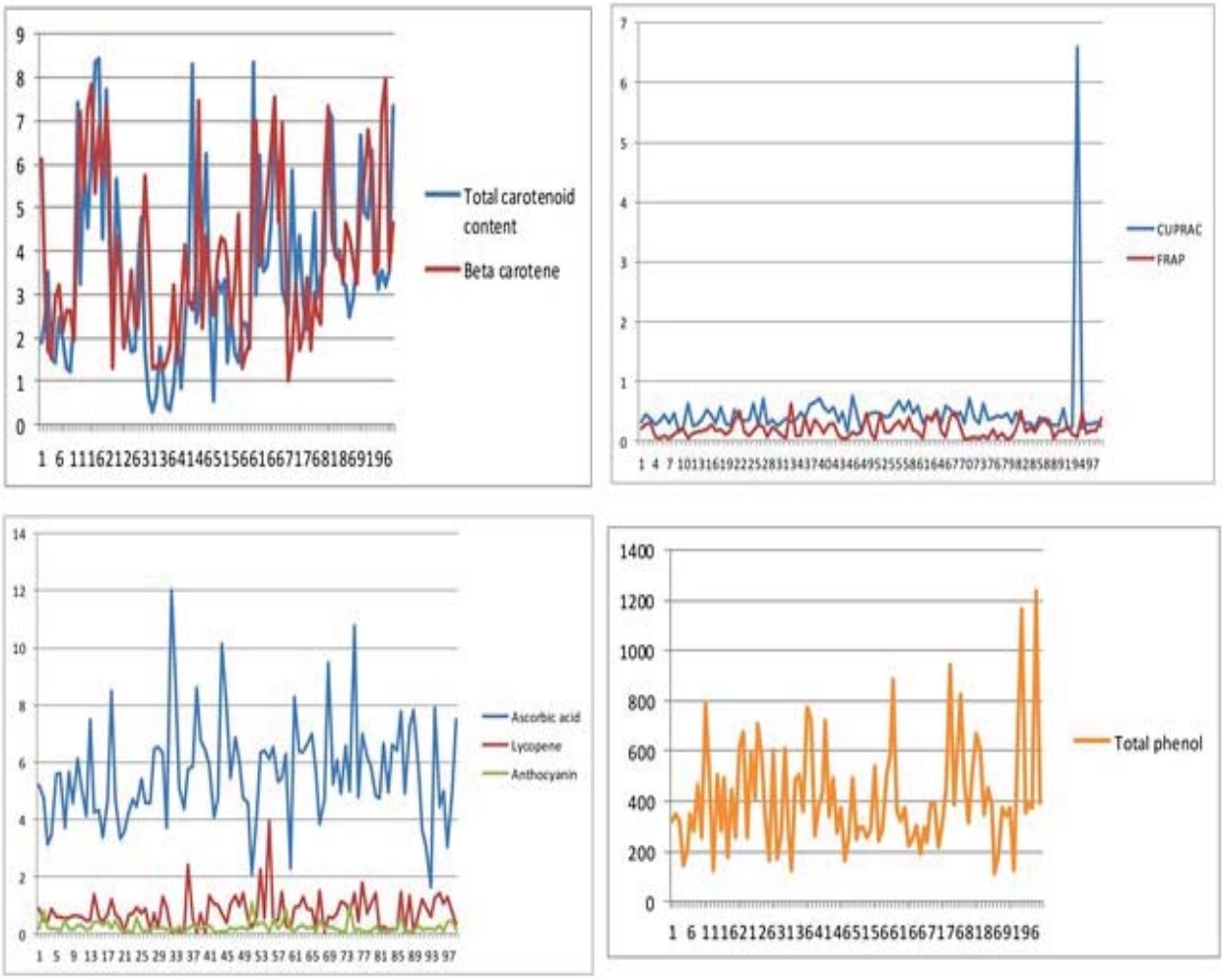


Figure 4.2 The analysis of results over the environments regarding *per se* performance of 100 testcross progenies of temperate carrot for different bioactive and antioxidant traits

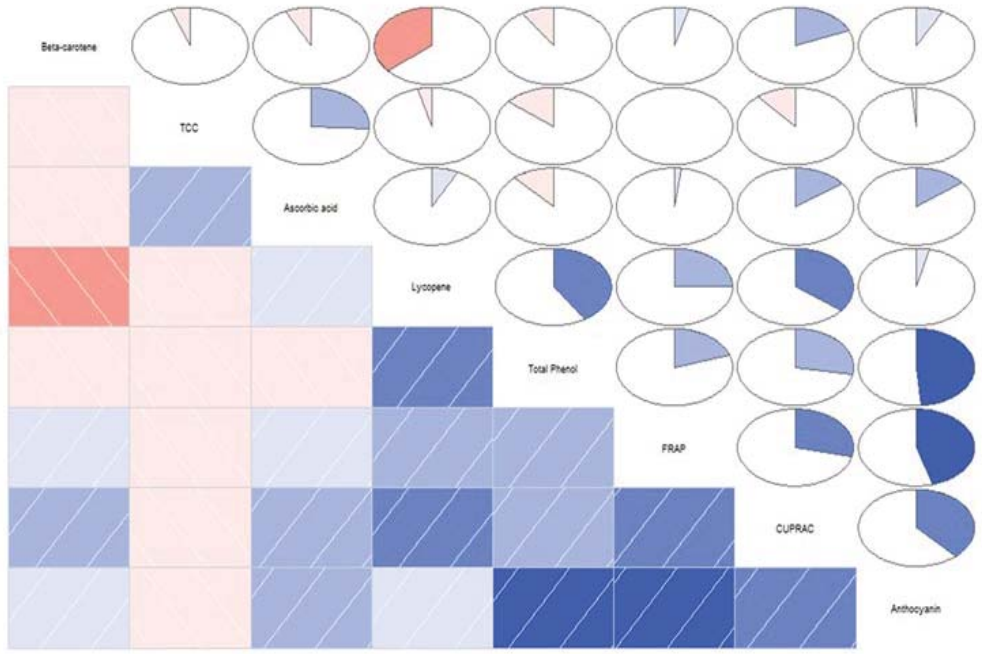


Figure 4.3 The interaction analysis among different antioxidant and bioactive compounds through pearson's correlation coefficient using "corrgram'' statistical package of R programming (R Studio, 2020).

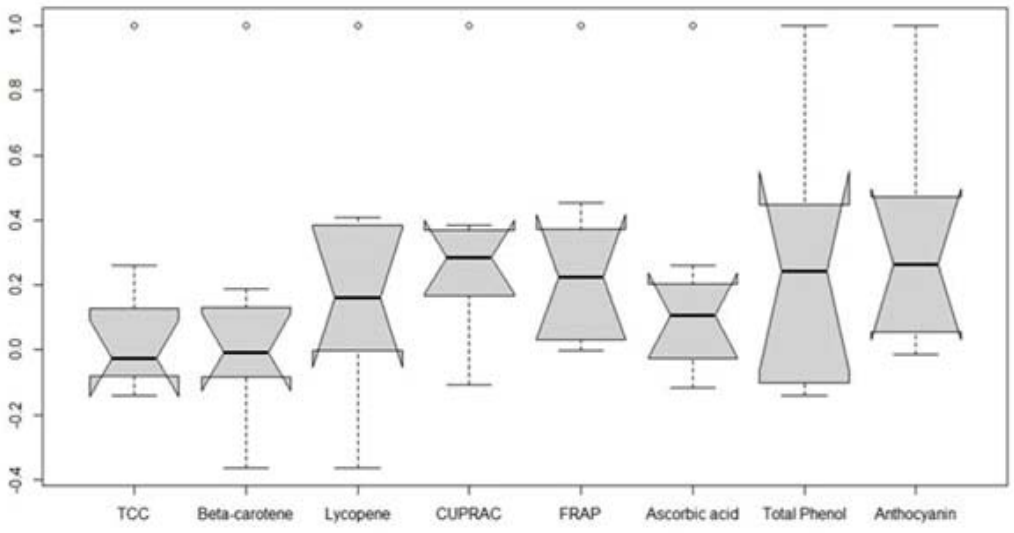


Figure 4.4 The boxplot distribution of antioxidant and bioactive compounds across the parental types.

4.3.6 *Per se* performance of 100 testcross progenies over the environments

The analysis of results over the environments regarding *per se* performance of 100 testcross progenies of temperate carrot for different bioactive and antioxidant traits is summarized in Table 4.23, Fig. 4.2. The mean value of 100 hybrids for traits related to antioxidant potential, CUPRAC and FRAP, ranged from 0.14µ moltrolox/g (KT-62A × KS-59) to 6.60 µ moltrolox/g (KT-98A × KS-50) and 0.03 µ moltrolox/g (KT-7A × KS-20) to 0.62 µ moltrolox/g (KT-47A × KS-21), respectively. For the CUPRAC content among 100 hybrids, 13 hybrids depicted high performance as compared to commercial check (Pusa Nayan Jyoti). The cross combination KT-98A × KS-50 followed by KT-62A × New Kuroda, KT-47A × PN-1 and KT-8542A × KS-20 exhibited the highest mean performance for the CUPRAC content over the years. Similarly, for the FRAP content, out of 100 crosses, 4 crosses (KT-47A × KS-21 followed by KT-95A × KS-21, KT-39A × KS-20 and KT-80A × KS-50) revealed higher performance than the best check (Pusa Nayan Jyoti) (Table 4.23). The mean *per se* performance of hybrids for ascorbic acid content and total phenolic content varied from 1.6272 mg/100g (KT-98A × KS-22) to 12.03 mg/100g (KT-47A × KS-20) and 110.07 mg of gallic acid/100 g FW (KT-95A × NK-1) to 1239.99 mg of gallic acid/100 g FW (KT-98A × PN-1), respectively (Table 4.17). Among the 100 testcross progenies, 49 and 14 crosses, outperformed for the ascorbic acid and total phenolic content, respectively, as compared to the check (Pusa Nayan Jyoti). The highest average ascorbic acid content was observed in the cross combination KT-47A × KS-20 followed by KT-8542A × KS-59 and KT-62A × KS-50 (Table 4.23). With respect to the total phenolic content the cross combination KT-98A × PN-1 followed by KT-98A × KS-50 depicted highest mean value. For the anthocyanin content, the *per se* performance of the 100 testcross progenies varied from 0.03mg/100g (KT-8542A × PN-1) to 1.0733 mg/100g (KT-7A × KS-20) (Table 4.20). Out of 100 hybrids, 6 hybrids had performed better than the check (Pusa Nayan Jyoti) for the anthocyanin content over the environments. Among

100 crosses, the mean value for lycopene, β-carotene and total carotenoid content varied from 0.03 mg/100g (KT-95A × NK-1) to 3.9467 mg/100g (KT-7A × KS-59), 1.00 µg/100 ml (KT-8542A × KS -73) to 7.98 µg/100 ml (KT-98A × NK-1) and 0.31 mg/100g (KT-47A × KS-20) to 8.43 mg/100g (KT-28A × New Kuroda), respectively. Of the 100 crosses, 15, 55 and 71 crosses outperformed for the lycopene content, β-carotene content and total carotenoid content respectively, when compared with the commercial check, Pusa Nayan Jyoti.

4.3.7 Heterosis analysis over the years for antioxidant traits

The results pertaining to average heterosis of cross combinations over the mid parent (MPH),better parent (Heterobeltiosis, BPH) and over the commercial check (standard hetrosis) for different antioxidant and bioactive compounds across the environments are presented in Table 4.24,Table 4.25 and Table 4.26. The data analysis over the years regarding average heterosis revealed that the 100-testcross progenies exhibited significant MPH, BPH and standard hetrosis for different antioxidant traits under study in both the directions. Firstly,for the antioxidant capacity related traits, CUPRAC and FRAP the estimates of MPH varied from 16.26% (KT-62A × NK-1) to 178.06% (KT-98A ×KS-50) and 19.07% (KT-39A × KS-20) to 908.33% (KT-47A × KS-59), respectively. Similarly, the estimates of heterobeltiosis varied from 17.83% (KT-7A × NK-1) to 832.24% (KT-98A × KS-50) for the CUPRAC content and 22.52 % (KT-62A × PY-1) to 706.67% (KT-47A × KS-59) for the FRAP content. For the antioxidant capacity related traits, CUPRAC and FRAP the estimates of standard hetrosis varied from -9.51% (KT-47 x PN) to 737.63% (KT-98 x KS -50) and -12.82% (KT-62 x PY-1) to -94.23% (KT-7*KS -20) respectively. For the CUPRAC content has greater significant heterosis over the mid parent, better parent and standard hetrosis observed in the cross combination KT-98A × KS-50 followed by KT-62A × New Kuroda, KT-7A × New Kuroda and KT-47A × NK-1. Among the 100 testcrosses, 18, 12 and none crosses exhibited significant heterosis in desirable direction for the CUPRAC content over the mid parent, better

Table 4.20. Average heterosis of top three hybrids over the environments with their SCA value in parenthesis

Cross	TCC	Cross	Beta-carotene	Cross	Lycopene	Cross	CUPRAC
KT-98 x PY	312.88**(2.05***)	KT-62 x KS-21	281.32**(5.21***)	KT-98 x KS-59	222.61** (-0.02)	KT-98 x KS-50	832.24**(5.06***)
KT-98 x KS-22	296.46**(0.99***)	KT-80 x New Kuroda	188.58**(1.83***)	KT-47 x PN-1	213.04**(0.23***)	KT-62 x New Kuroda	82.19** (0.30***)
KT-95 x KS-21	277.09**(2.53***)	KT-62 x KS-59	185.37**(2.86***)	KT-98 x NK-1	201.15** (0.23***)	KT-47 x NK-1	56.18** (0.19***)
Cross	**FRAP**	**Cross**	**Ascorbic acid**	**Cross**	**Total Phenol**	**Cross**	**Anthocyanin**
KT-47 x KS-59	706.67**(0.16***)	KT-95 x New Kuroda	79.37**(1.79***)	KT-98 x PN-1	302.17**(653.05***)	KT-62 x KS-21	1083.33** (1.48***)
KT-28 x KS-59	290.48**(0.10***)	KT-98 x KS-50	51.72**(2.60***)	KT-98 x KS-50	202.68**(562.85***)	KT-7 x KS-20	648.84**(0.63***)
KT-7 x KS-59	266.67**(0.01)	KT-7x New Kuroda	51.19**(1.45***)	KT-8542 x KS-59	182.62**(453.75***)	KT-8542x KS-50	301.35**(0.77***)

Table 4.21 Heterobeltiosis of top three cross combinations over the environments along with their SCA effects (value in parenthesis)

Cross	TCC	Cross	Beta-carotene	Cross	Lycopene	Cross	CUPRAC
KT-98 x PY-1	312.88**(2.05***)	KT-62 x KS-21	281.32**(5.21***)	KT-98 x KS-59	222.61** (-0.02)	KT-98 x KS-50	832.24**(5.06***)
KT-98 x KS-22	296.46**(0.99***)	KT-80 x New Kuroda	188.58**(1.83***)	KT-47 x PN-1	213.04**(0.23***)	KT-62 x New Kuroda	82.19** (0.30***)
KT-95 x KS-21	277.09**(2.53***)	KT-62 x KS-59	185.37**(2.86***)	KT-98 x NK-1	201.15** (0.23***)	KT-47 x NK-1	56.18** (0.19***)
Cross	**FRAP**	**Cross**	**Ascorbic acid**	**Cross**	**Total Phenol**	**Cross**	**Anthocyanin**
KT-47 x KS-59	706.67**(0.16***)	KT-95 x New Kuroda	79.37**(1.79***)	KT-98 x PN-1	302.17**(653.05***)	KT-62 x KS-21	1083.33** (1.48***)
KT-28 x KS-59	290.48**(0.10***)	KT-98 x KS-50	51.72**(2.60***)	KT-98 x KS-50	202.68**(562.85***)	KT-7 x KS-20	648.84**(0.63***)
KT-7 x KS-59	266.67**(0.01)	KT-7 x New Kuroda	51.19**(1.45***)	KT-8542 x KS-59	182.62**(453.75***)	KT-8542 x KS-50	301.35**(0.77***)

*: significant at 5% probability, **: significant at 1% probability, significant through F test

Table 4.22. Standard heterosis of top three cross combinations over the environments along with their SCA effects (value in parenthesis)

Cross	TCC	Cross	Beta-carotene	Cross	Lycopene	Cross	CUPRAC
KT-28 x KS-59	260.94** (0.10***)	KT-62 x KS-21	186.87 **(5.21***)	KT-7 x KS-59	194.16 **(2.39***)	KT-98 x KS-50	737.63 **(0.46**)
KT-28 x PN-1	227.47**(0.22**)	KT-28 x KS-50	125.16 **(1.66***)	KT-47 xKS-59	79.38 **(1.43)	KT-39 x KS-20	50.95 **(0.21***)
KT-28 x New Kuroda	259.80**(2.25***)	KT-80 x New Kuroda	117.09 **(1.83***)	KT-7 x KS-22	67.45 **(0.97)	KT-7 x KS-50	46.30 **(-0.71***)
Cross	**FRAP**	**Cross**	**Ascorbic acid**	**Cross**	**Total Phenol**	**Cross**	**Anthocyanin**
KT-47 x KS-21	19.23 **(0.28***)	KT-47 x KS-20	74.23 **(5.50***)	KT-98 x PN-1	173.69 **(113.56**)	KT-62*KS-21	278.67 **(1.48***)
KT-7 x KS-21	12.82 *(-0.10***)	KT-8542 x KS-59	56.18 **(3.98***)	KT-98 x KS-50	157.35) **(562.85***)	KT-7*KS-20	114.67 **(0.63***)
KT-98 x KS-59	8.33(-0.80***)	KT-62 x KS-50	47.15 **(3.37***)	KT-8542 x KS-59	108.56 **(453.75***)	KT-8542*KS-50	98.00 **(0.77***)

*: significant at 5% probability, **: significant at 1% probability, significant probability through F test

parent and over commercial check respectively. Similarly, for the FRAP content the measure of significant MPH, Heterobeltiosis and standard hetrosis was depicted in the heterotic cross KT-47A × KS-59 followed by KT-47A × KS-21 and KT-47A × KS-59. Likewise among the 100 hybrids, 27, 18 and none of the hybrids exhibited significantly high estimates of MPH and heterobeltiosis and standard hetrosis for the FRAP content. The measures of MPH heterobeltiosis and standard hetrosis for the ascorbic acid content among the 100 testcross progenies varied from 10.42% (KT-7A × PY-1) to 155.58% (KT-47A × KS-20) , 13.84% (KT-28A × NK-1) to 121.20% (KT-47A × KS-20), 8.45% (KT-28 x KS -21) to (74.23%) KT-47*KS -20 respectively. Amongst 100 testcross progenies, 27,17 and 12 hybrids exhibited significant high heterosis in desirable direction for the ascorbic acid content over the mid parent better parent and standard hetrosis respectively. The cross combinations, KT-47A × KS-20, KT-95A × New Kuroda and KT-47A × KS-20 depicted significantly highest positive heterosis for the ascorbic acid content in desirable direction. For the total phenolic content, the average and better parent heterosis and standard hetrosis varied from 25.01% (KT-80A × KS-22) to 314.95% (KT-98A × PN-1) and 18.46% (KT-28A × PY-1) to 302.17% (KT-98A × PN-1), 19.19% (KT-7 x KS -59) to 173.69% (KT-98 x PN-1) respectively. The significantly highest estimates of MPH, heterobeltiosis and standard hetrosis for the total phenolic content in desirable direction was revealed in the crosses KT-98A × PN-1 followed by KT-98A × KS-50 and KT-8542A × KS-59. A total of 37, 27 and 21 number of hybrid combinations exhibited significant heterosis over mid parent, better parent and standard hetrosis, respectively for the total phenolic content amongst 100 testcross progenies. The estimates of MPH, heterobeltiosis and standard hetrosis for the anthocyanin content varied from 15.38 % (KT-98A × KS-59) to 1546.38 % (KT-62A × KS-21) and 20.78 % (KT-95A × New Kuroda) to 1083.33 % (KT-62A × KS-21), 24.00% (KT-95 x New Kuroda) to 278.67% (KT-62 x KS -21) respectively. The hybrid combination KT-62A × KS-21 followed by KT-7A × KS-20 and KT-8542A × KS-50

exhibited significantly high estimates of heterosis for the anthocyanin content. Likewise, for the lycopene content the mid parent, better parent heterosis and standard hetrosis estimates varied from 15.72 % (KT-80A × KS-20) to 777.81% (KT-47A × KS-59), 10.51% (KT-80A × KS-22) to 222.61% (KT-98A × KS-59) and 7.58% (KT-95 x New kuroda) to 194.16% (KT-7 x KS -59) respectively. The cross combination KT-47A × KS-59 followed by KT-7A × KS-59 and KT-47A × PN-1 exhibited highest significantly highest estimates of MPH and standard hetrosis in desirable direction for lycopene content. Similarly, the cross combination KT-98A × KS-59 followed by KT-47A × PN-1 and KT-98A × NK-1 exhibited significantly highest estimates of heterobeltiosis for lycopene content. Among the 100 crosses, only 40,32 and 7 crosses over the mid parent better parent and standard hetrosis, respectively, showed significant heterosis for lycopene content.

For the β-carotene content the estimates of MPH, heterobeltiosis and standard hetrosis over the environments ranged from 6.15% (KT-10A × KS-50) to 185.66% (KT-95A × KS-20), 8.03 % (KT-39A × PN-1) to 281.32 % (KT-62A × KS-21) and 5.73% (KT-80 x KS -21) to 125.16% (KT-28 x KS -50) respectively. The hybrid combination KT-62A × KS-21, followed by KT-80A × New Kuroda and KT-62A × KS-59 exhibited significantly highest heterosis over the better parent and standard hetrosis in desirable direction for the β-carotene content. The MPH, BPH and standard hetrosis estimates varied from 6.76 % (KT-62A × KS-20) to 390.38% (KT-28A × KS-59) and 19.18% (KT-80A × PY-1) to 312.88 % (KT-98A × PY-1) and 5.87% (KT-95 x NK-1) to 260.94% (KT-28 x KS -59) respectively for the total carotenoid content (TCC). Among the 100 testcrosses, 79,73 and 24 crosses, respectively, exhibited significantly highest heterosis over the mid parent, better parent and standard hetrosis for the TCC. The significantly highest estimates of heterosis in desirable direction for the total carotenoid content was observed in the cross combinations KT-28A × KS-59, KT-98A × PY-1, KT-98A × KS-22 and KT-95 × KS-21.

Table 4.23 Mean performance of 100 crosses for antioxidant traits. (Pooled Data)

Crosses	Total carotenoid content	Beta carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total phenol	Anthocyanin
KT-10 x KS -73	1.89	6.11	0.88	0.31	0.22	5.19	318.39	0.19
KT-10 x KS-20	2.54	2.94	0.46	0.43	0.27	4.73	349.05	0.78
KT-10 x KS-21	3.51	1.73	0.43	0.37	0.31	3.11	320.46	0.22
KT-10 x KS-22	1.54	1.55	0.88	0.28	0.06	3.46	146.14	0.19
KT-10 x KS-50	1.43	2.91	0.59	0.34	0.04	5.59	206.07	0.19
KT-10 x KS-59	2.43	3.22	0.57	0.44	0.09	5.62	348.66	0.08
KT-10 x New Kuroda	1.99	2.13	0.55	0.30	0.05	3.69	282.34	0.48
KT-10 x NK-1	1.31	2.61	0.53	0.46	0.10	5.67	468.67	0.16
KT-10 x PN-1	1.22	2.62	0.62	0.15	0.18	4.58	254.51	0.14
KT-10 x PY-1	2.43	1.95	0.64	0.20	0.20	6.10	791.04	0.29
KT-28 x KS -73	7.43	5.44	0.59	0.63	0.05	5.10	492.86	0.29
KT-28 x KS-20	3.23	7.22	0.48	0.26	0.13	4.10	127.02	0.12
KT-28 x KS-21	6.00	5.33	0.45	0.28	0.14	7.49	502.95	0.18
KT-28 x KS-22	4.55	7.33	1.39	0.36	0.16	4.24	280.09	0.40
KT-28 x KS-50	6.33	7.85	0.58	0.52	0.19	4.34	490.20	0.44
KT-28 x KS-59	8.34	5.33	0.43	0.42	0.27	3.38	177.45	0.30
KT-28 x New Kuroda	8.43	6.88	0.66	0.30	0.17	4.66	445.37	0.43
KT-28 x NK-1	4.31	5.67	1.23	0.57	0.19	8.47	258.40	0.17
KT-28 x PN-1	7.69	7.33	0.67	0.29	0.10	4.72	617.58	0.47
KT-28 x PY-1	4.67	6.32	0.50	0.25	0.16	3.34	674.01	0.13
KT-39 x KS -73	1.78	1.33	0.06	0.53	0.33	3.53	253.71	0.12
KT-39 x KS-20	5.65	4.34	0.65	0.38	0.51	4.27	599.52	0.09
KT-39 x KS-21	4.23	3.55	0.70	0.34	0.14	4.69	411.96	0.05

KT-39 x KS-22	1.763	1.76	0.91	0.36	0.08	4.45	708.62	0.53
KT-39 x KS-50	2.23	2.44	0.70	0.63	0.16	5.39	583.70	0.14
KT-39 x KS-59	1.67	3.55	0.88	0.26	0.28	4.56	326.25	0.07
KT-39 x New Kuroda	1.75	2.30	0.09	0.70	0.24	4.57	163.00	0.15
KT-39 x NK-1	3.55	2.23	0.71	0.28	0.06	6.45	604.22	0.22
KT-39 x PN-1	4.77	3.66	0.19	0.36	0.24	6.52	171.28	0.16
KT-39 x PY-1	1.68	5.72	1.29	0.26	0.17	6.31	263.25	0.22
KT-47 x KS -73	0.65	3.99	0.91	0.31	0.09	3.72	606.44	0.13
KT-47 x KS-20	0.31	1.33	0.06	0.38	0.04	12.03	258.11	0.15
KT-47 x KS-21	0.64	1.33	0.13	0.31	0.62	9.00	127.73	0.05
KT-47 x KS-22	1.76	1.44	0.08	0.36	0.076	5.11	484.26	0.25
KT-47 x KS-50	0.97	1.33	0.03	0.47	0.09	4.38	503.34	0.06
KT-47 x KS-59	0.43	1.43	2.40	0.38	0.40	5.74	357.68	0.17
KT-47 x New Kuroda	0.32	1.78	0.56	0.60	0.11	5.86	775.28	0.29
KT-47 x NK-1	0.89	3.22	0.03	0.65	0.36	8.60	724.80	0.20
KT-47 x PN-1	2.14	1.44	0.72	0.71	0.26	6.78	261.22	0.16
KT-47 x PY-1	0.83	2.70	0.05	0.56	0.12	6.39	377.20	0.26
KT-62 x KS -73	2.34	4.11	1.34	0.48	0.28	5.92	430.24	0.29
KT-62 x KS-20	3.52	2.88	1.04	0.56	0.29	4.07	722.48	0.07
KT-62 x KS-22	8.31	2.66	1.02	0.31	0.08	4.76	339.92	0.06
KT-62 x KS-50	2.38	3.33	0.72	0.47	0.05	10.16	494.70	0.07
KT-62 x KS-59	2.65	7.44	0.36	0.14	0.04	7.87	278.89	0.07
KT-62 x New Kuroda	4.22	2.22	1.04	0.75	0.14	5.46	375.12	0.21
KT-62 x NK-1	6.23	4.35	1.34	0.47	0.11	6.86	162.41	0.14
KT-62 x PN-1	2.65	3.33	0.94	0.14	0.15	6.07	254.82	0.23
KT-62 x PY-1	0.54	2.55	1.40	0.41	0.45	4.75	492.63	0.21

KT-7 x KS -73	3.32	3.75	0.51	0.45	0.12	4.59	252.74	0.14
KT-7 x KS-20	3.08	4.29	0.21	0.48	0.03	2.07	296.43	1.07
KT-7 x KS-21	3.35	4.23	0.59	0.45	0.45	4.10	294.33	0.29
KT-7 x KS-22	1.42	3.76	2.24	0.39	0.15	6.31	256.40	0.38
KT-7 x KS-50	2.54	2.23	0.56	0.42	0.14	6.39	286.68	0.37
KT-7 x KS-59	1.64	3.22	3.94	0.55	0.25	6.12	539.99	0.06
KT- x New Kuroda	1.43	4.86	0.47	0.66	0.34	6.54	245.58	0.49
KT-7 x NK-1	2.34	1.32	0.47	0.50	0.18	5.34	286.20	0.16
KT-7 x PN-1	2.31	1.64	1.47	0.66	0.39	5.45	496.03	0.33
KT-7 x PY-1	1.78	1.84	0.30	0.45	0.18	6.30	591.73	0.84
KT-80 x KS -73	8.32	6.99	0.15	0.58	0.14	2.28	884.34	0.17
KT-80 x KS-20	2.98	6.99	0.92	0.30	0.04	8.27	359.96	0.07
KT-80 x KS-21	6.21	3.66	0.96	0.40	0.42	6.38	321.87	0.24
KT-80 x KS-22	3.54	4.55	1.29	0.38	0.34	6.36	373.74	0.28
KT-80 x KS-50	3.65	5.33	0.87	0.53	0.48	6.62	220.41	0.15
KT-80 x KS-59	4.65	6.36	0.84	0.29	0.14	7.00	251.88	0.25
KT-80 x New Kuroda	6.78	7.54	0.20	0.59	0.06	5.75	300.77	0.05
KT-80 x NK-1	5.56	4.66	1.49	0.53	0.41	3.84	193.25	0.46
KT-80 x PN-1	3.12	6.97	0.05	0.40	0.48	4.72	292.70	0.16
KT-80 x PY-1	2.78	3.76	0.59	0.48	0.24	9.50	238.64	0.26
KT-8542 x KS -73	2.54	1.00	0.56	0.29	0.03	5.23	390.23	0.23
KT-8542 x KS-20	5.87	1.67	0.73	0.70	0.05	6.08	384.76	0.14
KT-8542 x KS-21	3.22	3.25	1.12	0.38	0.07	4.89	218.69	0.10
KT-8542 x KS-22	4.32	1.75	1.05	0.29	0.05	6.57	313.01	0.10
KT-8542 x KS-50	2.76	2.10	0.68	0.62	0.09	5.01	458.69	0.99
KT-8542 x KS-59	2.18	3.38	1.40	0.36	0.04	10.78	944.92	0.1
KT-8542 x New Kuroda	3.28	1.75	0.41	0.38	0.19	4.77	388.12	0.15

KT-8542 x NK-1	4.87	3.03	1.78	0.42	0.04	7.00	637.53	0.08
KT-8542 x PN-1	2.89	2.52	0.72	0.39	0.13	6.19	822.96	0.03
KT-8542 x PY-1	3.43	2.34	1.03	0.45	0.03	5.87	468.96	0.07
KT-95 x KS -73	3.69	5.68	1.41	0.29	0.06	4.84	313.86	0.24
KT-95 x KS-20	7.23	7.33	0.11	0.49	0.19	4.74	517.74	0.07
KT-95 x KS-21	7.09	4.34	0.26	0.36	0.51	6.64	671.58	0.09
KT-95 x KS-22	3.98	3.88	0.14	0.29	0.15	4.93	607.48	0.08
KT-95 x KS-50	4.02	3.79	0.15	0.30	0.23	6.61	349.00	0.13
KT-95 x KS-59	3.24	3.33	0.13	0.20	0.15	6.41	451.31	0.12
KT-95 x New Kuroda	3.22	4.63	1.44	0.39	0.30	7.76	386.14	0.62
KT-95 x NK-1	2.48	4.33	0.03	0.34	0.37	4.91	110.07	0.08
KT-95 x PN-1	2.89	3.79	1.35	0.25	0.33	7.24	186.05	0.09
KT-95 x PY-1	3.78	3.24	0.06	0.28	0.05	7.82	374.93	0.09
KT-98 x KS -73	6.65	5.18	0.67	0.25	0.17	5.90	343.70	0.31
KT-98 x KS-20	4.89	5.66	1.21	0.54	0.16	3.60	374.66	0.11
KT-98 x KS-21	4.76	6.77	0.90	0.19	0.26	3.02	124.48	0.19
KT-98 x KS-22	6.31	5.76	0.59	0.23	0.10	1.62	657.68	0.17
KT-98 x KS-50	4.66	3.48	1.25	6.60	0.06	7.92	1165.96	0.14
KT-98 x KS-59	3.11	3.65	1.40	0.20	0.47	4.46	356.59	0.3
KT-98 x New Kuroda	3.56	7.25	1.05	0.30	0.13	5.01	388.33	0.08
KT-98 x NK-1	3.21	7.98	1.31	0.27	0.16	3.02	376.72	0.43
KT-98 x PN-1	3.52	3.64	0.75	0.31	0.16	4.98	1239.99	0.47
KT-98 x PY-1	7.32	4.62	0.33	0.26	0.37	7.49	393.99	0.12

Table 4.24 Average heterosis of 100 crosses for antioxidant traits. (Pooled Data)

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS-20	62.69 **	27.43**	-60.84**	-0.34	-89.77**	-53.38**	-24.10*	782.19**
KT-7 x KS-21	133.67 **	60.43**	12.03	9.76	277.78**	-24.70**	-20.94*	91.21**
KT-7 x KS-22	7.53 **	21.39**	200.56**	-22.64	30.43	27.69**	-36.97**	217.81**
KT-7 x KS-50	80.35 **	-21.18**	-15.21	-25.62	95.56**	47.58**	-31.04**	91.45**
KT-7 x KS-59	28.03 **	21.61**	638.85**	7.22	413.33**	8.03	38.35**	-76.25**
KT-7 x NK-1	75.02**	-62.00**	-10.33	19.45**	-30.77**	-1.84	-31.09**	-48.42**
KT-7 x PY-1	36.03**	-26.56**	-64.85**	9.60	-16.67	10.42*	71.10**	292.25**
KT-7 x PN-1	41.71**	-51.18**	220.29**	35.60**	44.24**	24.17	31.47**	4.71
KT-7 x New Kuroda	-38.75**	65.78**	-3.40	58.42**	217.58**	68.51**	-46.24**	50.25**
KT-7 x KS -73	158.36**	36.64**	-47.01**	-15.36**	-52.32**	-7.02	-63.44**	-56.00**
KT-10 x KS-20	46.08**	-9.50**	-36.00**	-11.03	-8.79	-12.16**	-27.09**	300.00**
KT-10 x KS-21	155.02**	-31.92**	-37.84**	-8.64	141.03**	-51.23**	-30.40**	-2.22
KT-10 x KS-22	18.04**	-43.55**	-4.33	-43.24**	-52.00*	-41.17**	-70.47**	-0.85
KT-10 x KS-50	4.34	6.15**	-29.71**	-39.14**	-52.94	5.97	-59.10**	-29.19**
KT-10 x KS-59	104.38**	2.75E+05	-19.72**	-13.78*	50	-14.93**	-27.12**	-74.51**
KT-10 x NK-1	-1.57	-19.42**	-23.33**	11.33	-62.96**	-11.20**	-6.91	-58.12**
KT-10 x PY-1	110.08**	-17.48**	-38.63**	-49.80**	-11.59	-8.32*	82.28**	2.89

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-10 x PN-1	-14.41*	-19.45**	-1.97	-68.33**	-35.67**	-14.12**	-45.32**	-64.26**
KT-10 x New Kuroda	-13.05**	-21.69**	-16.40**	-26.25**	-55.56*	-23.60**	-48.19**	19.50**
KT-10 x KS -73	39.99**	139.83**	-23.24**	-39.87**	-14.65	-11.70**	-59.15**	-53.28**
KT-28 x KS-20	51.13**	123.34**	-0.68	-46.22**	-55.68**	-32.88**	-71.89**	-20.00
KT-28 x KS-21	232.07**	110.05**	-2.88	-31.34**	19.44	5.30	15.98	1.85
KT-28 x KS-22	150.58**	162.45**	104.14**	-29.64**	39.13	-35.75**	-40.17**	168.89**
KT-28 x KS-50	240.53**	181.92**	-3.03	-8.67	157.78**	-27.59**	2.75	100.00**
KT-28 x KS-59	390.38**	110.06**	-7.96	-19.62**	446.67**	-53.91**	-60.71**	3.95
KT-28 x NK-1	133.59**	74.61**	166.91**	32.05**	-26.92	19.16**	-45.79**	-50.72**
KT-28 x PY-1	170.61**	177.20**	-38.21**	-40.28**	-25.76*	-54.72**	65.52**	-43.84**
KT-28 x PN-1	264.93**	129.00**	69.75**	-40.94**	-63.64**	-22.06**	40.79**	35.58**
KT-28 x New Kuroda	203.29**	146.94**	56.25**	-29.18**	54.55*	-16.03**	-14.05*	22.43**
KT-28 x KS -73	305.65**	116.48**	-34.55**	18.08**	-80.13**	-22.72**	-34.51**	-19.82**
KT-39 x KS-20	242.08**	67.87**	-25.73	-27.50**	19.07**	-20.68**	36.76**	-42.57**
KT-39 x KS-21	234.82**	80.16**	-17.59**	-25.27**	-43.79**	-26.48**	-1.94	-73.11**
KT-39 x KS-22	46.47**	-20.03**	-15.30**	-33.84**	-65.33**	-24.27**	55.87**	218.81**
KT-39 x KS-50	72.82**	13.24**	-29.27**	3.12	-20.63	2.28	25.92**	-39.31**
KT-39 x KS-59	49.96**	81.05**	2.12	-52.73**	54.95**	-31.00**	-25.53**	-76.60**

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-39 x NK-1	181.47**	-10.84**	-16.57**	-40.32**	-84.81**	1.15	30.46**	-39.45**
KT-39 x PY-1	55.11**	235.62**	7.2	-42.24**	-50.23**	-5.09	-33.12**	-13.38
KT-39 x PN-1	240.90**	42.60**	-75.13**	-31.98**	-39.84**	22.34**	-59.71**	-55.25**
KT-39 x New Kuroda	-13.03**	11.96**	-88.22**	50.98**	-2.04	-5.35	-67.70**	-59.11**
KT-39 x KS -73	46.57**	-29.79**	-94.89**	-8.09	-13.79	-39.94**	-65.67**	-66.67**
KT-47 x KS-20	-80.90**	-62.07**	-77.27**	-19.30**	-83.53**	155.58**	-8.11	27.78
KT-47 x KS-21	-44.31**	-55.21**	-50.00**	-21.83**	463.64**	57.58**	-51.36**	-64.44**
KT-47 x KS-22	40.47**	-57.42**	-82.22**	-27.27**	-26.98	-1.79	62.99**	113.89**
KT-47 x KS-50	-16.78**	-58.01**	-91.02**	-15.48**	38.46	-4.68	64.47**	-68.97**
KT-47 x KS-59	-64.17*	-52.52**	777.81**	-24.18**	908.33**	-3.15	27.47*	-34.59**
KT-47 x NK-1	-29.97**	-11.09**	-86.12**	57.43**	45.33**	50.66**	137.13**	-36.51**
KT-47 x PY-1	-24.19**	-2.69	-91.84**	39.06**	-39.68**	6.97	59.73**	21.88*
KT-47 x PN-1	56.58**	-60.15**	260.00**	48.61**	-0.63	45.64**	-2.39	-49.47**
KT-47 x New Kuroda	-85.67**	-43.91**	146.38**	47.37**	13.33	41.12**	123.36**	-9.18
KT-47 x KS -73	-45.01**	29.74**	28.21**	-39.39**	-61.38**	-28.45**	4.28	-58.79**
KT-62 x KS-20	6.76*	-4.80*	90.27**	19.51**	2.89	-48.01**	177.60**	-17.65
KT-62 x KS-21	-0.17	320.60**	33.55**	0.21	123.19**	-33.37**	78.53**	1546.38**
KT-62 x KS-22	199.29**	4.88	37.37**	-36.05**	-26.36	-42.86**	22.94	-25.49

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-62 x KS-50	-12.49**	28.53**	9.55	-15.32**	-19.05	31.56**	73.32**	-55.79**
KT-62*KS-59	-1.19	213.21**	-31.34**	-72.28**	-11.11	-13.13**	7.27	-68.12**
KT-62 x NK-1	119.66**	42.32**	159.39**	16.26*	-56.86**	-22.32**	-43.02**	-50.00**
KT-62 x PY-1	-82.84**	22.48**	61.77**	1.86	110.85**	-47.78**	128.57**	19.63
KT-62 x PN-1	-14.31**	11.83**	106.59**	-69.12**	-44.44**	-21.96**	3.18	-17.16**
KT-62 x New Kuroda	4.68**	-10.75**	115.81**	84.43**	36.51	-25.00**	14.90	-25.71**
KT-62 x KS -73	-18.27**	73.89**	38.49**	-7.25	13.51	-28.93**	-23.30**	-2.25
KT-80 x KS-20	30.76**	128.12**	15.72**	-44.79**	-87.82**	39.46**	27.30*	-41.03**
KT-80 x KS-21	216.46**	55.04**	24.95**	-12.54	170.97**	-8.07*	21.70	50.00**
KT-80 x KS-22	85.61**	76.03**	31.09**	-31.45**	126.67**	-1.14	25.01*	120.51**
KT-80 x KS-50	85.23**	108.74**	-4.03	-14.55**	342.42**	13.76**	-28.42*	-24.59**
KT-80 x KS-59	156.27**	168.83**	8.27	-49.49**	64.71	-2.14	-10.83	-6.67
KT-80 x NK-1	185.74**	47.96**	95.43**	11.30	40.11**	-44.58**	-37.16**	41.54**
KT-80 x PY-1	67.09**	68.87**	-46.45**	1.77	-3.27	31.88**	0.26	19.40*
KT-80 x PN-1	35.82**	131.00**	-92.87**	-25.88**	54.84**	-19.82**	8.62	-50.00**
KT-80 x New Kuroda	133.64**	197.45**	-72.67**	25.39**	-54.02**	7.00	-13.81	-84.16**
KT-80 x KS -73	332.30**	193.81**	-87.40**	-0.57	-51.16**	-64.47**	51.58**	-50.24**
KT-95 x KS-20	247.29**	185.66**	-84.34**	5.19	-51.46**	20.30**	65.88**	-4.55

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-95 x KS-21	334.77**	129.40**	-61.04**	-5.38	129.63**	34.34**	128.56**	-12.90
KT-95 x KS-22	145.81**	78.57**	-84.01**	-39.10**	-28.79*	11.14*	85.02**	9.09
KT-95 x KS-50	134.47**	77.63**	-81.65**	-44.51**	27.78	72.67**	3.48	-11.36
KT-95 x KS-59	108.86**	74.79**	-80.98**	-59.73**	1.08	24.17**	44.73**	-45.04**
KT-95 x NK-1	45.74**	67.60**	-95.54**	-14.52	1.37	-0.54	-67.33**	-70.19**
KT-95 x PY-1	143.77**	99.80**	-94.13**	-27.27**	-84.62**	50.27**	40.22**	-46.00**
KT-95 x PN-1	44.02**	48.00**	121.61**	-46.43**	-12.28	86.21**	-37.74**	-66.67**
KT-95 x New Kuroda	24.99**	123.09**	125.81**	-1.26	42.64**	129.44**	2.06	121.43**
KT-95 x KS -73	119.02**	195.64**	25.72**	-41.73**	-82.24**	9.08	-48.78**	-15.79*
KT-98 x KS-20	197.23**	29.29**	185.71**	24.67**	-52.15**	-28.71**	20.04	-4.35
KT-98 x KS-21	187.74**	140.99**	126.30**	-45.92**	48.57**	-50.06**	-57.63**	31.03*
KT-98 x KS-22	304.64**	57.92**	-4.84	-47.60**	-41.18**	-70.69**	100.31**	47.83**
KT-98 x KS-50	163.31**	24.44**	132.36**	1178.06**	-48.72*	60.32**	245.70**	-25.66**
KT-98 x KS-59	124.19**	66.14**	245.08**	-56.43**	353.97**	-28.86**	14.35	15.38*
KT-98 x NK-1	180.81**	100.78**	230.25**	-26.46**	-48.15**	-50.02**	11.83	38.71
KT-98 x PY-1	357.98**	89.13**	-55.26**	-26.50**	34.55**	18.54**	47.35**	-42.40**
KT-98 x PN-1	96.96**	12.46**	125.56**	-28.24**	-49.49**	-0.43	314.95**	50.80**
KT-98 x New Kuroda	53.65**	97.63**	190.57**	-16.74*	-21.21	11.61*	2.64	-75.13**

Crosses	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-98 x KS -73	252.14**	50.34**	-20.16**	-46.43**	-43.48**	6.31	-43.91**	-5.10
KT-8542 x KS-20	196.16**	-65.49**	32.33**	27.90**	-84.04**	2.41	20.76	3.70
KT-8542 x KS-21	142.27**	-31.63**	113.59**	-19.86**	-47.62*	-29.46**	-27.18*	-39.39**
KT-8542 x KS-22	212.99**	-60.31**	40.31**	-47.80**	-62.96**	2.05	-6.52	-25.93
KT-8542 x KS-50	133.37**	-50.34**	2.62	-1.58	-5.26	-14.02**	33.43**	375.20**
KT-8542 x KS-59	163.07**	-23.15**	162.93**	-37.14**	-33.33	50.62**	196.83**	-64.29**
KT-8542 x NK-1	263.60**	-50.39**	240.32**	-12.63*	-84.52**	0.91	85.66**	-75.76**
KT-8542 x PY-1	221.96**	-39.39**	18.77**	-5.03	-84.72**	-18.44**	71.23**	-69.34**
KT-8542 x PN-1	48.70**	-59.89**	57.69**	-28.92**	-55.93**	5.24	169.53**	-90.95**
KT-8542 x New Kuroda	3.35	-68.76**	-15.79	-20.27**	48.72*	-11.30*	0.85	-56.10**
KT-8542 x KS -73	85.21**	-61.07**	-41.93**	-5.13E+04	-88.96**	-18.69**	-36.99**	-31.73**

*= significant at 5% probability, **= significant at 1% probability through F test

Table 4.25 Heterobeltiosis of 100 crosses for antioxidant traits. (Pooled Data)

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS-20	32.64**	25.20**	-68.60**	-10.98	-94.19**	-61.95**	-33.57**	648.84**
KT-7 x KS-21	126**.83	30.57**	-14.49**	4.65	166.67**	-44.97**	-34.04**	81.25**
KT-7 x KS-22	3.53	7.43**	179.09**	-32.56**	-6.25	-2.07	-42.54**	169.77**

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS-50	78.52**	-31.12**	-17.87**	-40.24**	83.33*	22.41**	-35.76**	51.35**
KT-7 x KS-59	15.71*	-0.59	471.98**	-8.49	266.67**	-22.43**	21.01*	-83.76
KT-7 x NK-1	72.63**	-62.69**	-31.88**	17.83*	-60.00**	-28.23**	-35.86**	-66.67**
KT-7 x PY-1	20.71**	-45.34**	-70.93**	6.20	-50.45**	-20.98**	32.60**	194.19**
KT-7 x PN-1	23.07**	-51.47**	113.53**	20.97**	-17.36**	2.06	11.16	-32.43**
KT-7 x New Kuroda	-56.30**	43.06**	-31.40**	55.04**	132.89**	51.19**	-47.45**	-3.9
KT-7 x KS -73	155.05**	11.79**	-58.99**	-28.95**	-72.31**	-28.67**	-73.00**	-71.97**
KT-10 x KS-20	15.28**	-15.93**	-55.20**	-21.34**	-46.45**	-13.05**	-43.93**	168.97**
KT-10 x KS-21	137.61**	-41.92**	-58.08**	-11.9	84.31**	-58.17**	-48.52	-24.14**
KT-10 x KS-22	17.50**	-47.32**	-15.20**	-51.01**	-62.50**	-46.25**	-76.52**	-33.33**
KT-10 x KS-50	-0.95	-2.29	-43.04**	-51.53**	-55.56	4.88	-66.90**	-34.48**
KT-10 x KS-59	92.16**	9.31**	-45.28**	-27.12**	0.01	-28.73**	-43.99**	-77.78**
KT-10 x NK-1	-6.87	-25.18**	-48.48**	11.11	-77.78**	-23.79**	-24.71**	-66.67**
KT-10 x PY-1	93.76**	-36.06**	-39.02**	-50.79**	-45.05**	-23.53**	27.07**	2.3
KT-10 x PN-1	-28.28**	-24.34**	-40.16**	-72.04**	-61.81**	-14.22**	-59.12**	-71.62**
KT-10 x New Kuroda	-39.49**	-28.87**	-46.56**	-26.98**	-64.44**	-30.77**	-54.65**	-6.49
KT-10 x KS -73	35.87**	105.74**	-29.89**	-50.00**	-48.46**	-19.31**	-65.99**	-63.69**
KT-28 x KS-20	46.09**	107.75**	-13.61	-51.22**	-74.84**	-39.50**	-77.68**	-40.00**
KT-28 x KS-21	169.82**	78.99**	-20.12*	-35.58**	-15.69	0.54	-11.6	-8.33
KT-28 x KS-22	93.55**	144.58**	73.50**	-37.75**	0.00	-37.33**	-50.77**	101.67**
KT-28 x KS-50	172.54**	159.20**	-9.28**	-25.65**	141.67**	-35.91**	-13.85	81.08
KT-28 x S-59	261.72**	79.82**	-23.08**	-30.41**	290.48**	-57.16**	-68.81**	-21.37**
KT-28 x NK-1	87.46**	62.35**	118.34**	28.09**	-57.78**	13.84**	-54.58**	-65.31**
KT-2 x PY-1	96.99**	114.56**	-52.61**	-43.07**	-55.86**	-58.13**	18.46**	-52.33**
KT-28 x PN-1	228.17**	115.38**	19.53**	-46.50**	-79.17**	-30.30**	8.54	-4.73

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-28 x New Kuroda	161.71**	124.01**	18.34**	-31.84**	13.33	-31.19**	-21.72**	-14.94**
KT-28 x KS -73	219.14**	85.49**	-52.65**	0.53	-88.46**	-24.64**	-47.36**	-44.59**
KT-39 x KS-20	157.22**	26.16**	-51.42**	-29.27**	-1.29	-21.51**	10.64	-59.15**
KT-39 x KS-21	193.35**	64.88**	-47.72**	-34.62**	-57.84**	-36.96**	-23.97**	-77.46**
KT-39 x KS-22	36.45**	-32.95**	-32.43**	-37.18**	-74.51**	-30.83**	30.77**	126.76**
KT-39 x KS-50	54.06**	-3.91	-47.72**	-10.59	-50.98**	1.25	7.72	-40.54**
KT-39 x KS-59	49.17**	64.87**	-34.65**	-56.16**	-15.69	-42.21**	-3.97E+10	-81.20**
KT-39 x NK-1	150.12**	-33.01**	-47.23**	-46.15**	-86.67**	-13.22**	11.51	-55.10**
KT-39 x PY-1	52.74**	225.10**	-4.56	-48.72**	-52.25**	-20.85**	-51.42**	-20.93**
KT-39 x PN-1	170.83**	8.03**	-85.45**	-33.74**	-48.61**	22.15**	-68.39**	-66.89**
KT-39 x New Kuroda	-41.68**	-3.82	-92.85**	35.26**	-29.41**	-14.21**	-69.92**	-70.13**
KT-39 x KS -73	33.37**	-36.14**	-95.07**	-16.32**	-23.08**	-45.13**	-72.90**	-75.80**
KT-47 x KS-20	-86.02**	-64.19**	-84.00**	-29.27**	-90.97**	121.20**	-22.93	9.52
KT-47 x KS-21	-52.87**	-65.55**	-63.30**	-23.89**	264.71**	20.85**	-57.19**	-66.67**
KT-47 x KS-22	26.05**	-64.66**	-89.23**	-37.75**	-52.08**	-20.59**	31.83**	83.33**
KT-47 x KS-50	-28.40**	-65.55**	-94.33**	-33.18**	12.50	-16.03**	30.66**	-75.68**
KT-47 x KS-59	-65.76**	-63.34**	536.12**	-36.44**	706.67**	-27.17**	6.98	-55.56**
KT-47 x NK-1	-39.93**	-16.02**	-89.77**	56.18**	-19.26**	15.59**	88.54**	-59.18**
KT-47 x PY-1	-26.10**	-30.97**	-95.26**	37.65**	-65.77**	-19.85**	53.69**	-9.30
KT-47 x PN-1	20.74**	-62.79**	213.04**	30.09**	-45.14**	27.01**	-15.28	-67.57**
KT-47 x New Kuroda	-90.58**	-54.50**	95.40**	47.37**	-24.44	35.37**	65.90**	-42.21**
KT-47 x KS -73	-51.75**	0.25	-27.25**	-50.00**	-78.46**	-42.13**	-35.22**	-73.89**
KT-62 x KS-20	-19.93**	-16.93**	53.43**	3.66	-42.58**	-60.18**	115.74**	-30.00
KT-62 x KS-21	-33.37**	281.32**	2.45	-1.24	50.98**	-42.42	44.80**	1083.33**
KT-62 x KS-22	93.32**	4.75	26.71**	-45.82**	-49.38*	-53.44**	-7.46	-36.67
KT-62 x KS-50	-42.17**	26.51**	6.86	-33.65**	-29.17	-0.65	28.42*	-71.62**

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-62 x KS-59	-38.02**	185.37**	-46.57**	-76.99**	-33.33	-23.07**	-16.58	-81.20**
KT-62 x NK-1	45.43**	24.13**	98.04**	13.94	-75.56**	-32.91**	-57.75**	-71.43**
KT-62 x PY-1	-89.32**	0.01	33.02**	1.65	22.52**	-53.54**	100.72**	-25.58**
KT-62 x PN-1	-38.82**	-1.42	38.24**	-73.25**	-68.75**	-40.6	-17.35	-52.70**
KT-62 x New Kuroda	-9.02**	-13.41**	53.92**	82.19**	-4.44	-46.63**	-19.73*	-57.79**
KT-62 x KS -73	-46.58**	58.60**	6.61	-24.21**	-35.38**	-42.10**	-54.04**	-44.59**
KT-80 x KS-20	22.47**	99.04**	-21.59**	-45.12**	-92.26**	28.72**	7.48	-52.08**
KT-80 x KS-21	150.77**	40.56**	-18.18**	-24.69**	147.06**	-14.36**	7.89	50.00**
KT-80 x KS-22	40.11**	75.80**	10.51**	-33.72**	112.50**	-1.24	1.74	79.17**
KT-80 x KS-50	44.67**	105.46**	-25.57**	-24.71**	247.62**	3.06	-42.78**	-37.84**
KT-80 x KS-59	85.11**	144.93**	-28.41**	-52.33**	0.01	-11.20**	-24.66	-34.19**
KT-80 x NK-1	123.74**	29.05**	27.56**	-1.23	-8.15	-48.34**	-49.73**	-6.12
KT-80 x PY-1	19.18**	37.87**	-49.15**	-11.11	-33.33**	19.10**	-2.76	-6.98
KT-80 x PN-1	18.65**	103.62**	-95.74**	-26.44**	0.01	-26.59**	-5.07	-66.89**
KT-80 x New Kuroda	107.44**	188.58**	-82.95**	10.49	-55.56**	-10.47*	-35.64**	-89.61**
KT-80 x KS -73	232.13**	167.97**	-87.83**	-7.89	-67.69**	-64.49**	-5.54	-67.52**
KT-95 x KS-20	231.95**	111.96**	-88.87**	-10.37	-62.58**	-12.87*	54.60**	-30.00
KT-95 x KS-21	277.09**	106.31**	-73.36**	-5.98	84.52**	-10.83**	125.11**	-43.75**
KT-95 x KS-22	101.60**	47.43**	-85.50**	-49.28**	-44.05**	-23.38**	65.37**	-20.00
KT-95 x KS-50	100.00**	48.38**	-84.82**	-57.18**	-17.86	26.69**	-9.40	-47.30**
KT-95 x KS-59	62.76**	56.44**	-86.85**	-67.12**	-44.05**	-18.72**	34.99**	-69.23**
KT-95 x NK-1	24.68**	24.32**	-96.96**	-17.93	-17.78*	-33.96**	-71.37**	-83.67**
KT-95 x PY-1	87.19**	97.23**	-94.31**	-28.93**	-86.49**	-1.88	29.59*	-68.60**
KT-95 x PN-1	39.60**	10.68**	36.59**	-54.41**	-30.56**	35.62**	-39.66**	-81.76**
KT-95 x New Kuroda	1.09	88.60**	46.04**	-4.45	9.52	79.37**	-17.37	20.78**
KT-95 x KS -73	83.32**	164.33**	12.17**	-53.16**	-85.38**	-24.79**	-66.48**	-54.14**

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-98 x KS-20	139.02**	3.01	179.69**	-0.61	-67.74**	-33.82**	11.88	-15.38
KT-98 x KS-21	174.54**	138.52**	107.66**	-50.43**	44.44*	-59.41**	-58.27**	18.75
KT-98 x KS-22	296.46**	42.02**	-26.71**	-59.08**	-44.44*	-74.75**	79.04**	30.77
KT-98 x KS-50	156.09**	13.39**	94.33**	832.24**	-62.96**	51.72**	202.68**	-43.24**
KT-98 x KS-59	105.93**	63.54**	222.61**	-66.58**	164.81**	-43.42**	6.66	-23.08**
KT-98 x NK-1	172.16**	59.91**	201.15**	-34.66**	-63.70**	-59.35**	-2.01	-12.24**
KT-98 x PY-1	312.88**	69.70**	-68.40**	-33.64**	0.01	-6.10	36.18*	-58.14**
KT-98 x PN-1	68.49**	-9.60**	72.41**	-42.86**	-65.28**	-6.80	302.17**	-4.73
KT-98 x New Kuroda	8.48**	82.53**	142.15**	-25.51**	-27.78	7.65	-16.9	-84.42**
KT-98 x KS -73	250.38**	47.82**	-46.30**	-59.47**	-60.00**	-8.39*	-63.29**	-40.76**
KT-8542 x KS-20	57.07**	-66.78**	6.02	26.57**	-90.32**	-5.49	14.89	-17.65**
KT-8542 x KS-21	32.11**	-46.66**	62.89**	-31.94**	-56.86**	-34.27**	-27.67*	-41.18**
KT-8542 x KS-22	72.76**	-66.52**	30.43**	-48.70**	-68.75**	1.97	-14.79	-41.18**
KT-8542 x KS-50	27.68**	-58.60**	-0.72	-12.00	-18.18	-22.12**	19.07	301.35**
KT-8542 x KS-59	47.21**	-39.81**	103.37**	-39.73**	-57.58*	36.71**	182.62**	-74.36**
KT-8542 x NK-1	98.82**	-52.23**	158.31**	-23.58**	-90.37**	-5.91	65.83**	-83.67**
KT-8542 x PY-1	80.97**	-56.48**	-1.68	-18.21**	-90.09**	-26.33**	55.11**	-75.58**
KT-8542 x PN-1	-20.38**	-61.83**	5.06	-29.55**	-72.92**	-3.68	166.91**	-93.92**
KT-8542 x New Kuroda	-46.20**	-74.26**	-40.24**	-30.75**	28.89	-25.80**	-16.95	-70.78**
KT-8542 x KS -73	1.75	-69.48**	-55.03**	-54.21**	-93.08**	-18.74**	-58.32**	-54.78**

*= significant at 5% probability, **= significant at 1% probability through F test

Table 4.26 Standard hetrosis of 100 crosses for antioxidant traits. (Pooled Data)

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS -20	23.53**	26.41 **	-83.85 **	-38.27 **	-94.23 **	-70.03 **	-34.57 **	114.67 **
KT-7 x KS -21	41.49**	27.23	-56.02 **	-42.92 **	-12.82 *	-40.64 **	-35.03 **	-42.00

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-7 x KS -22	5.32	4.68	67.45 **	-50.53 **	-71.15 **	-8.64 **	-43.41	-22.67 **
KT-7 x KS -50	7.01	-32.88 **	-57.76 **	-46.30 **	-71.79 **	-7.48	-36.72 **	-25.33 **
KT-7 x KS -59	-32.05**	-3.14	194.16 **	-29.39 **	-50.64 **	-11.39 **	19.19 *	-87.33 **
KT-7 x NK-1	4.22	-62.29 **	-64.97 **	-35.73 **	-65.38 **	-22.68 **	-36.83 **	-67.33 **
KT-7 x PY-1	-29.11**	-46.74	-77.14 **	-42.07 **	-64.74 **	-8.74 *	30.61 **	68.67 **
KT-7 x PN-1	-1.93	-52.15 **	9.81 **	-15.86 **	-23.72 **	-21.04 **	9.48	-33.33 **
KT-7 x New kuroda	-39.91**	39.40 **	-64.72 **	-15.43 **	-32.82 **	-5.21	-45.79 **	-1.33
KT-7 x KS -73	49.79**	8.93 **	-61.49	-42.92 **	-76.92 **	-33.49 **	-44.22 **	-70.67 **
KT-10 x KS -20	7.37	-15.11 **	-65.22 **	-45.45 **	-46.79 **	-31.52 **	-22.96 *	56.00
KT-10 x KS -21	48.21**	-49.69 **	-67.45 **	-53.07 **	-39.74 **	-54.87 **	-29.27 **	-56.00 **
KT-10 x KS -22	-36.12**	-54.37 **	-34.16 **	-64.06 **	-88.46 **	-49.86 **	-67.74 **	-61.33 **
KT-10 x KS -50	-40.63**	-15.35	-55.78 **	-56.45 **	-92.31 **	-19.06 **	-54.52 **	-62.00 **
KT-10 x KS -59	3.51	-5.31 *	-57.52 **	-43.76 **	-82.69 **	-18.58 **	-23.04 *	-82.67 **
KT-10 x NK-1	-43.78**	-24.38 **	-60.00 **	-40.80 **	-80.77 **	-17.91 **	3.44	-67.33 **
KT-10 x PY-1	4.36	-44.62 **	-52.05 **	-73.78 **	-60.90 **	-11.68 **	74.60 **	-40.67 **
KT-10 x PN-1	-42.85**	-25.40 **	-53.54 **	-80.55 **	-64.74 **	-33.64 **	-43.82 **	-72.00 **
KT-10 x New kuroda	-16.81**	-38.39 **	-58.51 **	-61.10 **	-89.74 **	-46.57 **	-37.68 **	-4.00
KT-10 x KS -73	-22.25**	78.22 **	-34.16 **	-59.83 **	-57.05 **	-24.76	-29.73 **	-62.00 **
KT-28 x KS -20	45.78**	109.75 **	-63.73	-66.17 **	-75.00 **	-40.64 **	-71.96 **	-76.00 **
KT-28 x KS -21	169.24**	55.48 **	-66.46 **	-63.64 **	-72.44 **	8.45 *	11.01	-63.33 **

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-28 x KS -22	93.13**	112.46 **	4.10	-54.33 **	-69.23 **	-38.51 **	-38.18 **	-19.33 **
KT-28 x KS -50	171.96**	125.16 **	-56.27 **	-33.19 **	-62.82 **	-37.11 **	8.20	-10.67 *
KT-28 x KS -59	260.94**	56.20 **	-67.70 **	-46.30 **	-47.44 **	-51.06	-60.83 **	-38.67 **
KT-28 x NK-1	87.05**	64.08 **	-8.32 *	-27.70 **	-63.46 **	22.64 **	-42.97 **	-66.00 **
KT-28 x PY-1	96.57**	86.38 **	-62.73 **	-67.86	-68.59 **	-51.64	48.77 **	-72.67
KT-28 x PN-1	227.47**	112.36 **	-49.81 **	-62.79	-80.77 **	-31.61 **	36.31 **	-6.00
KT-28 x New kuroda	259.80**	94.59	-50.31 **	-61.52 **	-67.31 **	-32.48 **	-1.70	-12.67 **
KT-28 x KS -73	218.45**	61.13 **	-55.53 **	-19.24 **	-90.38 **	-26.06 **	8.78	-42.00 **
KT-39 x KS -20	139.56**	27.38 **	-51.06 **	-50.95 **	-1.92	-38.18 **	32.33 **	-80.67 **
KT-39 x KS -21	82.98**	0.87	-47.33 **	-56.87 **	-72.44 **	-32.00 **	-9.07	-89.33 **
KT-39 x KS -22	-25.82**	-49.69 **	-31.93 **	-53.91 **	-83.33 **	-35.47 **	56.41 **	7.33
KT-39 x KS -50	-7.65	-29.99 **	-47.33 **	-19.66 **	-67.95 **	-21.91 **	28.83 **	-70.67 **
KT-39 x KS -59	-29.26**	1.98	-34.16 **	-66.17 **	-44.87 **	-33.98 **	-27.99 **	-85.33 **
KT-39 x NK-1	51.00**	-32.30 **	-46.83 **	-64.48 **	-88.46 **	-6.52	33.36 **	-56.00 **
KT-39 x PY-1	-28.33**	65.14 **	-3.85	-66.17 **	-66.03 **	-8.59 *	-41.89 **	-54.67 **
KT-39 x PN-1	115.81**	6.52 **	-85.34 **	-53.91 **	-52.56 **	-5.50	-62.19 **	-67.33 **
KT-39 x New kuroda	-19.81**	-31.97 **	-92.80 **	-10.78 *	-53.85 **	-33.83 **	-64.02 **	-69.33 **
KT-39 x KS -73	-23.68**	-60.41 **	-95.03 **	-32.77 **	-35.90 **	-48.84 **	-44.00 **	-74.67 **
KT-47 x KS -20	-86.98**	-59.30 **	-95.03 **	-50.95 **	-91.03 **	74.23 **	-43.03 **	-69.33 **
KT-47 x KS -21	-70.60**	-60.84 **	-90.06 **	-60.25 **	19.23 **	30.36 **	-71.81 **	-89.33 **

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-47 x KS -22	-31.47**	-59.83 **	-93.54 **	-54.33 **	-85.26 **	-25.92 **	6.89	-48.67 **
KT-47 x KS -50	-57.08**	-60.84 **	-97.27 **	-39.96	-82.69 **	-36.53 **	11.10	-88.00 **
KT-47 x KS -59	-83.76**	-58.33 **	79.38 **	-50.95 **	-22.44 **	-16.80 **	-21.05 *	-65.33 **
KT-47 x NK-1	-63.73**	-4.54	-97.27 **	-17.12 **	-30.13 **	24.52 **	59.98 **	-60.00 **
KT-47 x PY-1	-66.38**	-21.54 **	-96.27 **	-28.12 **	-75.64 **	-7.43	-16.74	-48.00 **
KT-47 x PN-1	-3.79	-57.70 **	-46.34 **	-9.51 **	-49.36 **	-1.74	-42.34 **	-68.00 **
KT-47 x New kuroda	-87.05**	-48.29 **	-57.76 **	-23.04 **	-78.21 **	-15.14 **	71.12 **	-40.67 **
KT-47 x KS -73	-72.39**	13.95 **	-31.68 **	-59.83 **	-82.05 **	-46.04 **	33.85 **	-72.67 **
KT-62 x KS -20	49.14	-16.13 **	-22.24 **	-28.12 **	-42.95 **	-41.02 **	59.47 **	-86.00 **
KT-62 x KS -21	24.11	186.87 **	-48.07 **	-49.68 **	-50.64 **	-14.72 **	-4.65	278.67 **
KT-62 x KS -22	260.09	-21.20 **	-23.98 **	-60.25 **	-84.42 **	-31.03 **	-24.97 **	-87.33 **
KT-62 x KS -50	7.73	-4.83	-45.84 **	-40.38 **	-89.10 **	47.15 **	9.19	-86.00 **
KT-62 x KS -59	15.45	114.68 **	-72.92 **	-82.24 **	-92.31	13.95 **	-38.44 **	-85.33 **
KT-62 x NK-1	170.89	25.45 **	0.37	-39.53 **	-78.85 **	-0.63	-64.15	-72.00 **
KT-62 x PY-1	-80.11	-24.77 **	4.60	-47.99 **	-12.82 *	-31.18 **	8.73	-57.33 **
KT-62 x PN-1	13.95	-2.80	-29.94 **	-81.40 **	-71.15 **	-12.02 **	-43.76 **	-53.33 **
KT-62 x New kuroda	69.46	-34.86 **	-21.99 **	-4.86	-72.44 **	-20.95 **	-17.20	-56.67 **
KT-62 x KS -73	-0.50	19.31 **	0.12	-39.11 **	-46.15 **	-14.24 **	-5.04	-42.00 **
KT-80 x KS -20	30.62	100.97 **	-31.43 **	-61.95 **	-92.31 **	19.84 **	-20.55 **	-84.67 **
KT-80 x KS -21	167.45	5.75 *	-28.45 **	-48.41 **	-19.23 **	-7.63	-28.96 **	-52.00 **

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-80 x KS -22	49.43	32.25 **	-3.35	-51.37 **	-34.62 **	-7.87 *	-17.51	-42.67 **
KT-80 x KS -50	54.29 **	54.56 **	-34.91 **	-32.35 **	-6.41	-4.05	-51.35 **	-69.33 **
KT-80 x KS -59	97.42	84.26 **	-37.39 **	-63.21 **	-73.08 **	1.45	-44.40 **	-48.67 **
KT-80 x NK-1	138.63	30.42 **	11.55 **	-32.35 **	-20.51 **	-44.35 **	-57.35 **	-8.00
KT-80 x PY-1	27.11	3.72	-55.53 **	-39.11 **	-52.56 **	37.55 **	-47.33 **	-46.67 **
KT-80 x PN-1	26.54	100.77 **	-96.27 **	-48.84 **	-7.69	-31.66 **	-35.40 **	-67.33 **
KT-80 x New kuroda	185.19	117.09 **	-85.09 **	-24.31 **	-87.18 **	-16.65 **	-33.61 **	-89.33 **
KT-80 x KS -73	254.22	101.59 **	-88.57 **	-26.00 **	-73.08 **	-66.89 **	95.19 **	-66.00 **
KT-95 x KS -20	209.16	114.00 **	-91.80 **	-37.84 **	-62.82 **	-31.37 **	14.28	-86.00 **
KT-95 x KS -21	220.17 **	26.22 **	-80.37 **	-53.49 **	-0.64	-3.81	48.23 **	-82.00 **
KT-95 x KS -22	71.17	10.62 **	-89.32 **	-62.79 **	-69.87 **	-28.52 **	34.08 **	-84.00 **
KT-95 x KS -50	69.81	8.11 **	-88.82	-61.52 **	-55.77 **	-4.25	-22.97 *	-74.00 **
KT-95 x KS -59	38.20	-3.24	-90.31 **	-74.63 **	-69.87 **	-7.14	-0.39	-76.00 **
KT-95 x NK-1	5.87 **	25.64 **	-97.76 **	-56.45 **	-28.85 **	-28.86 **	-75.71 **	-84.00 **
KT-95 x PY-1	58.94	-3.62	-95.53 **	-63.64 **	-90.38 **	13.32 **	-17.25	-82.00 **
KT-95 x PN-1	18.53 **	9.13 **	0.62	-68.29 **	-35.90 **	4.92	-58.94 **	-82.00 **
KT-95 x New kuroda	38.98	33.41 **	7.58 *	-50.11 **	-41.03 **	12.45 **	-14.77	24.00 **
KT-95 x KS -73	55.65 **	63.88 **	5.34	-62.37 **	-87.82 **	-29.87 **	-30.72 **	-52.00 **
KT-98 x KS -20	122.60	4.01	-9.32 **	-31.08 **	-67.95 **	-47.88 **	-17.30	-78.00 **
KT-98 x KS -21	71.24 **	45.92 **	-32.67 **	-75.48 **	-50.00 **	-56.22 **	-72.52 **	-62.00 **

Cross	Total Carotenoid Content	Beta-carotene	Lycopene	CUPRAC	FRAP	Ascorbic acid	Total Phenol	Anthocyanin
KT-98 x KS -22	124.61	6.57 **	-56.02 **	-69.98 **	-80.77 **	-76.44 **	45.16 **	-66.00 **
KT-98 x KS -50	53.51	-17.38 **	-6.34	737.63 **	-87.18 **	14.67 **	157.35 **	-72.00 **
KT-98 x KS -59	16.67	1.16	4.60	-74.21 **	-8.33	-35.37 **	-21.29 **	-40.00 **
KT-98 x NK-1	64.31	61.61 **	-2.36	-65.33 **	-68.59 **	-56.22 **	-16.85	-14.00
KT-98 x PY-1	133.91	1.69	-75.16 **	-66.05 **	-28.85 **	8.45 *	-13.04	-76.00 **
KT-98 x PN-1	34.26	-10.86 **	-44.10 **	-60.25 **	-67.95 **	-27.90 **	173.69 **	-6.00
KT-98 x New kuroda	49.14	29.12 **	-21.49 **	-61.10 **	-75.00 **	-27.36 **	-14.29	-84.00 **
KT-98 x KS -73	100.50	-8.35 **	-49.57 **	-67.44 **	-66.67 **	-14.58 **	-24.14 **	-38.00
KT-8542 x KS -20	46.28	-63.74 **	-45.34 **	-10.36 *	-90.38 **	-11.97 **	-15.07	-72.00 **
KT-8542 x KS -21	-17.60 **	-41.77 **	-16.02 **	-51.80 **	-85.90 **	-29.10 **	-51.73 **	-80.00 **
KT-8542 x KS -22	-6.08	-63.45 **	-21.74 **	-62.37 **	-90.38 **	-4.87	-30.91 **	-80.00 **
KT-8542 x KS -50	-23.46	-54.80 **	-48.82 **	-20.93 **	-82.69 **	-27.46 **	1.24	98.00 **
KT-8542 x KS -59	-30.19	-34.28 **	4.84	-53.49 **	-91.03 **	56.18 **	108.56 **	-80.00 **
KT-8542 x NK-1	20.03	-47.85 **	33.17 **	-45.88 **	-91.67 **	1.35	40.72 **	-84.00 **
KT-8542 x PY-1	-17.67 **	-52.49 **	-22.69 **	-42.07 **	-92.95 **	-14.91 **	3.51	-86.00 **
KT-8542 x PN-1	-36.55	-58.33 **	-45.84 **	-50.11 **	-75.00 **	-10.28 **	81.64 **	-94.00 **
KT-8542 x New kuroda	-26.04 **	-71.90	-69.19 **	-50.95 **	-62.82 **	-30.89 **	-14.33	-70.00 **
KT-8542 x KS -73	-41.77	-66.68	-57.76 **	-63.21 **	-94.23 **	-24.23 **	-13.87	-52.67 **

*= significant at 5% probability, **= significant at 1% probability through F test

4.3.8 Interaction analysis

The interaction analysis among different antioxidant and bioactive compounds was computed via pearson's correlation coefficient using "corrgram'' statistical package of R programming (R Studio, 2020). The association results pertaining to 8 different antioxidant traits are depicted in Fig.4.3. The total carotenoid content (TCC) exhibited the negative correlation with all the studied antioxidant traits except for ascorbic acid content. The non-significant positive association was found for β-carotene with CUPRAC, FRAP and anthocyanin concentration. The data analysis revealed positive interaction among lycopene, CUPRAC, FRAP, anthocyanin and total phenolic content (TPC). The analysis of interaction results also revealed positive association of FRAP with all the antioxidant traits except for TCC. The significant interaction was observed between FRAP and anthocyanin content at $P \leq 0.05$. The positive correlation was observed for ascorbic acid and all other bioactive compounds except for β-carotene and TPC. The interaction analysis results revealed significant positive association of TPC with anthocyanin content at $P \leq 0.05$. Likewise, anthocyanin exhibited significant positive interaction with TPC and FRAP content at $P \leq 0.05$.

4.4 Microsatellites based genetic diversity of parental lines

4.4.1 Allelic diversity

In the current experimentation, 100 pairs of genomic-SSR based primers were used to assess the molecular diversity of diverse parental lines of carrot studied. Out of 100 SSR primers, 67 pairs of primers exhibited explicit polymorphism and showed high allelic diversity (Table 4.27, Fig. 4.4.1 and 4.4.2). The observed heterozygosity (H_o) ranged from 0.03 (for the loci GSSR-91, GSSR-130, GSSR-145 and GSSR-155) to 0.19 (for the loci GSSR-70). The mean expected heterozygosity (H_e) was 0.70, with a range of 0.46 (GSSR-65) to 0.89 (GSSR-

130) and had higher mean value than H_o. The mean polymorphic information content (PIC) for 67 loci was 0.63. The PIC content ranged from 0.35 for the GSSR-65 to 0.86 for the GSSR-130 (Table 4.27).

Additionaly, the PCA and Neighbour joining (NJ) cluster analysis for 67 loci, showed distinct clusters and sub-clusters of parental CMS and tester based on their phylogeny (Fig.4.4.3; Fig. 4.4.4). The PCA results exhibited that first two major coordinate axis 1 and 2 (PC1 and PC2) described 61.41% of total existing variation among CMS and tester lines. The construct of dendrogram exhibited 3 main clusters of parental lines with internal sub-clusters indicating varied degree of diversity. As the less extent of variation explained by first two main coordinate axes (PC1 and PC2), the NJ clusters imparts clearer insights of clustering groups for decisive interpretation, the testers continue to exist in two different sub-clusters of two different main clusters. The CMS lines KT-10A, KT47A, KT- 80 A and KT-8542A placed different main cluster from rest of CMS lines and remained close affinity with tester line KS-20, KS-21and KS-22.The CMS lines KT-7A, KT-28A, KT-39A, KT-62A, KT-95A and KT-96A were remained in different main clusters and has no close affinity with any tester lines.

Table 4.27 Characteristics of 67 polymorphic SSR loci depicting diversity

Locus	H_o	H_e	N	PIC	Locus	H_o	H_e	N	PIC
GSSR-1	0.00	0.80	6	0.74	BSSR-1	0.00	0.77	5	0.71
GSSR-5	0.00	0.59	4	0.52	BSSR-5	0.00	0.75	5	0.69
GSSR-15	0.00	0.87	8	0.83	BSSR-10	0.00	0.75	5	0.69
GSSR-20	0.00	0.62	3	0.52	BSSR-15	0.00	0.66	5	0.59
GSSR25	0.00	0.84	9	0.80	BSSR-21	0.00	0.84	8	0.79
GSSR-30	0.00	0.65	3	0.56	BSSR-25	0.00	0.75	5	0.69
GSSR-35	0.00	0.63	4	0.54	BSSR-30	0.00	0.76	5	0.70
GSSR-40	0.00	0.64	4	0.55	BSSR-33	0.00	0.75	4	0.69
GSSR-45	0.00	0.73	6	0.67	BSSR-39	0.00	0.63	4	0.54
GSSR-51	0.00	0.70	4	0.62	BSSR-43	0.00	0.76	5	0.70
GSSR-55	0.00	0.60	4	0.50	BSSR-49	0.00	0.79	6	0.73

GSSR-60	0.00	0.76	6	0.71	BSSR-53	0.00	0.78	5	0.72
GSSR-65	0.00	0.46	2	0.35	BSSR-61	0.00	0.70	5	0.63
GSSR-70	0.19	0.66	4	0.58	BSSR-65	0.00	0.75	4	0.69
GSSR-75	0.00	0.72	4	0.65	BSSR-70	0.00	0.82	6	0.77
GSSR-80	0.00	0.68	4	0.60	BSSR-75	0.00	0.80	5	0.74
GSSR-84	0.00	0.72	5	0.65	BSSR-80	0.00	0.64	5	0.58
GSSR-91	0.03	0.76	5	0.70	BSSR-87	0.00	0.71	7	0.67
GSSR-96	0.00	0.75	4	0.68	BSSR-90	0.00	0.70	4	0.62
GSSR-101	0.00	0.76	6	0.71	BSSR-97	0.00	0.61	3	0.52
GSSR-105	0.00	0.73	4	0.66	BSSR-101	0.00	0.70	4	0.62
GSSR-109	0.04	0.73	4	0.66	BSSR-105	0.00	0.65	3	0.55
GSSR-115	0.00	0.70	6	0.65	BSSR-110	0.00	0.73	5	0.67
GSSR-20	0.07	0.65	4	0.57	BSSR-116	0.00	0.61	3	0.52
GSSR-125	0.00	0.75	4	0.68	BSSR-120	0.00	0.83	6	0.78
GSSR-130	0.03	0.89	12	0.86	BSSR-125	0.00	0.78	5	0.72
GSSR-135	0.00	0.67	4	0.59	BSSR-130	0.00	0.81	6	0.75
GSSR-140	0.00	0.63	3	0.54	BSSR-137	0.00	0.60	4	0.50
GSSR-145	0.03	0.52	3	0.46	BSSR-141	0.00	0.50	2	0.37
GSSR-151	0.00	0.67	5	0.60	BSSR-146	0.07	0.69	4	0.61
GSSR-155	0.03	0.75	4	0.68					

LG: linkage group, H_o: observed heterozygosity, H_e: expected heterozygosity, PIC: polymorphic information content

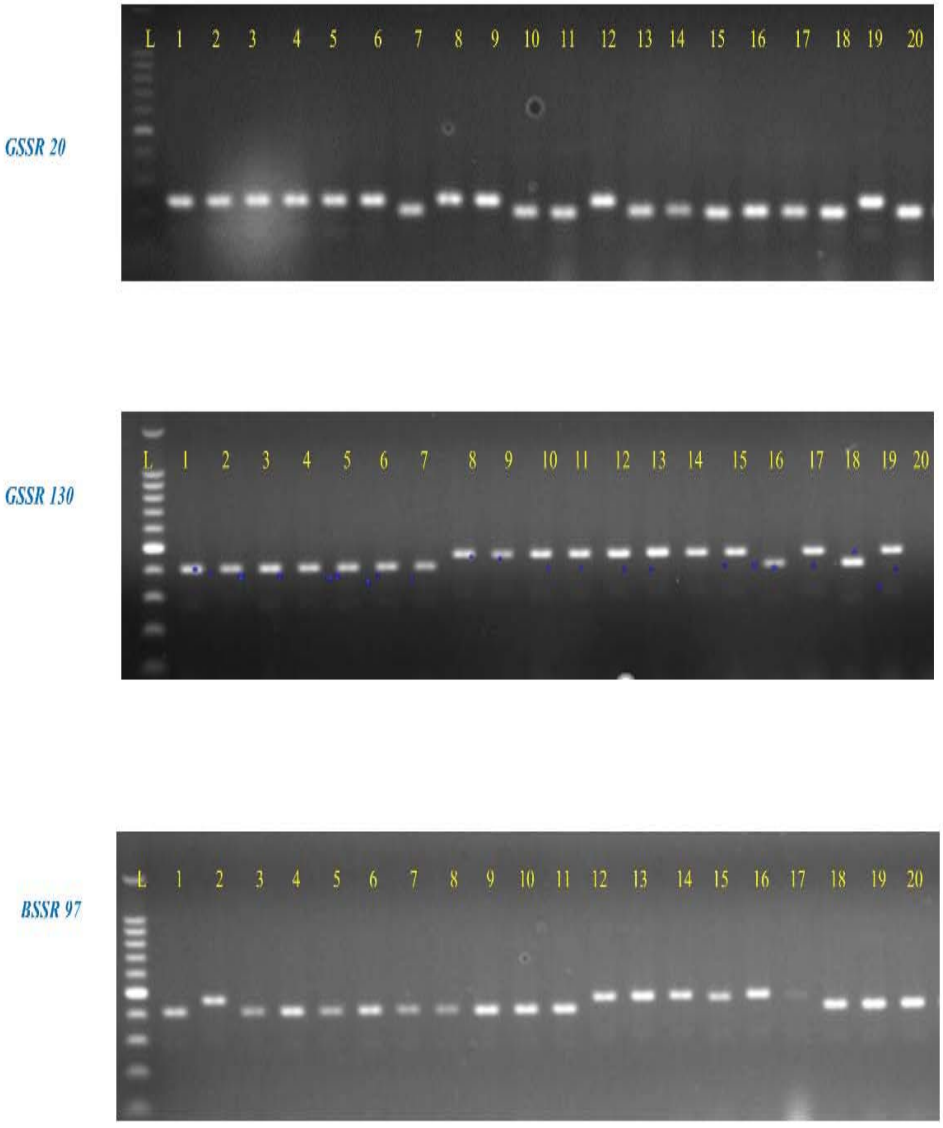


Figure 4.4.1 PCR amplification profile for 20 CMS and tester lines using SSR primers GSSR 20, GSSR 130 and BSSR 97; L is 50bp ladder

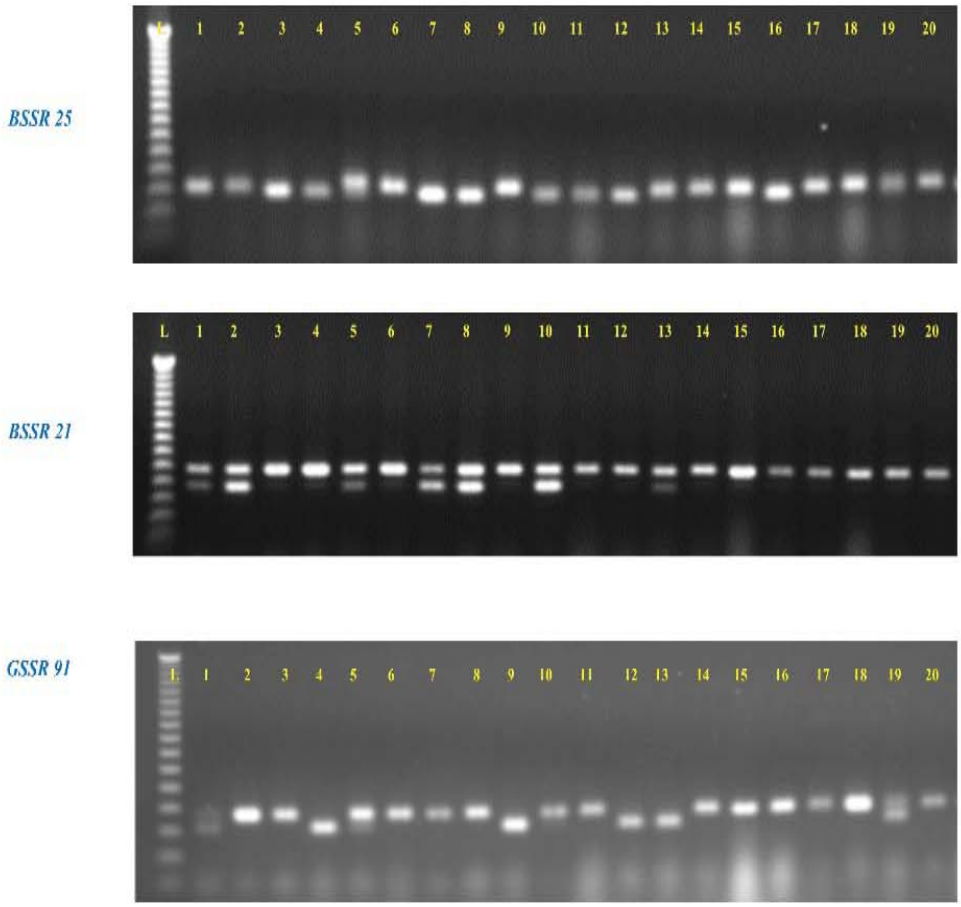


Figure 4.4.2 PCR amplification profile for 20 CMS and tester lines using SSR primers BSSR 25, BSSR 21 and GSSR 91; L is 50bp ladder

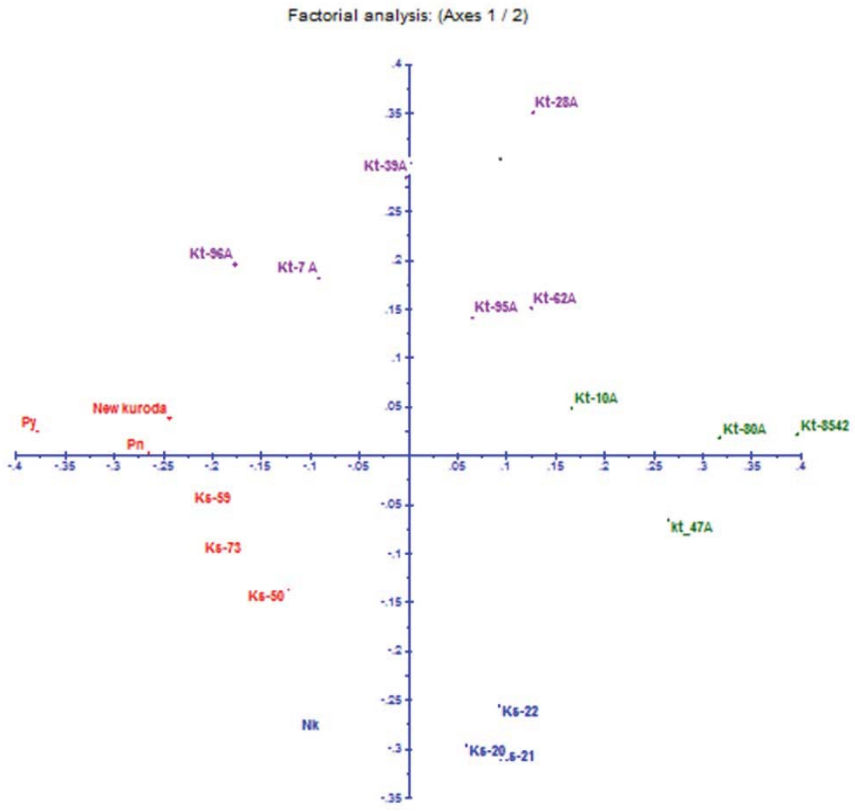


Figure 4.4.3 Classification of 20 parental CMS and tester inbred lines through PCA on the basis of SSR analysis (molecular data).

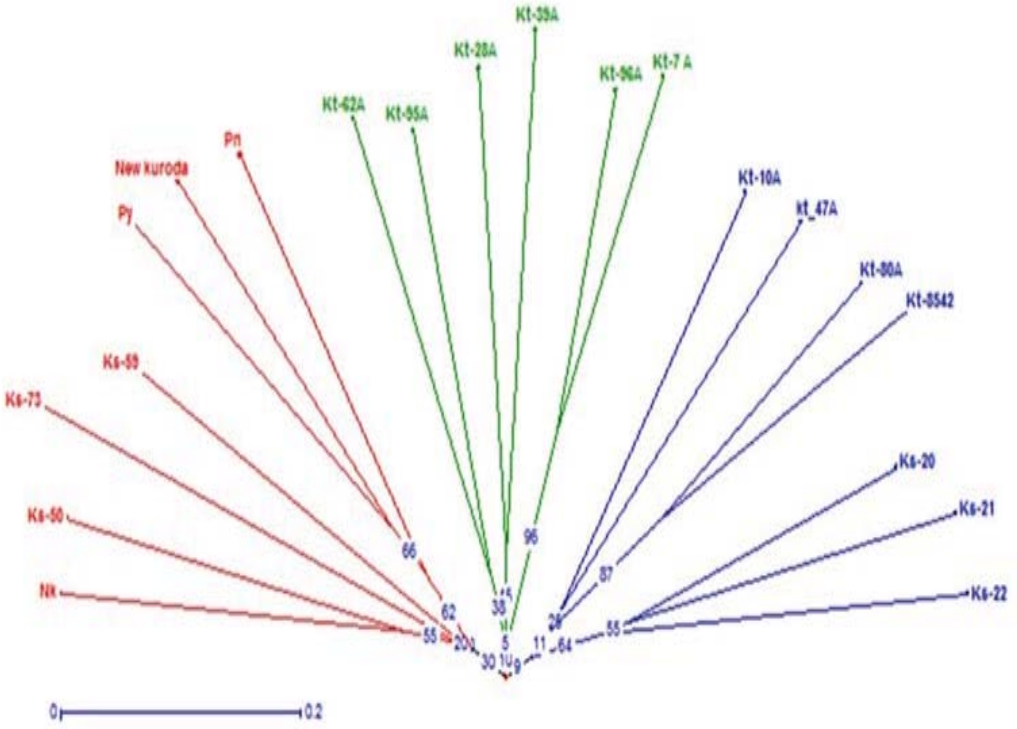


Figure 4.4.4 Dendrogram of parental lines through UPGMA cluster analysis illustrating the genetic relationships among them based on SSR analysis (molecular data).

4.5 Floral characterization of CMS lines

Different floral deformities have been observed in male sterile lines viz., reduction in floral size and petaloid anthers. In this regard the CMS lines were also characterized for different floral traits. The experimentation on floral characters in CMS and their tester are summarised in Table 4.28. It has been observed that Green petal colour and light green petaloid were majorly available in CMS lines. The existence of variation of light green/light green mid-rib in petaloid was also experience in the CMS lines. The CMS lines KT-7A had white petaloid while a range of white and greenish white petaloid colours were also seen in KT-28A, KT-39A and KT-10A, KT- 47A, KT-62A, KT-80A, KT-98A and KT-8542A, respectively. However, majorly at most 'petaloid' type CMS lines was recorded and not any of the CMS lines exhibited carpel-like structure (carpeloid). The CMS line petaloid shape was identical, as spoon type in all CMS lines; in spoon type, straight and curved petals observed extensively. The characteristic quantitative characters variation in petaloid shape and construct could may be due to influence of genetic background of the transformed CMS lines, however, it need further investigations. Nectary size and ovary development was shows perfect in all the observed CMS lines, indicating better prospects for seed setting. Interestingly, an enlarged size of ovary recorded in CMS lines as compared to their fertile counterpart (Table 4.28).

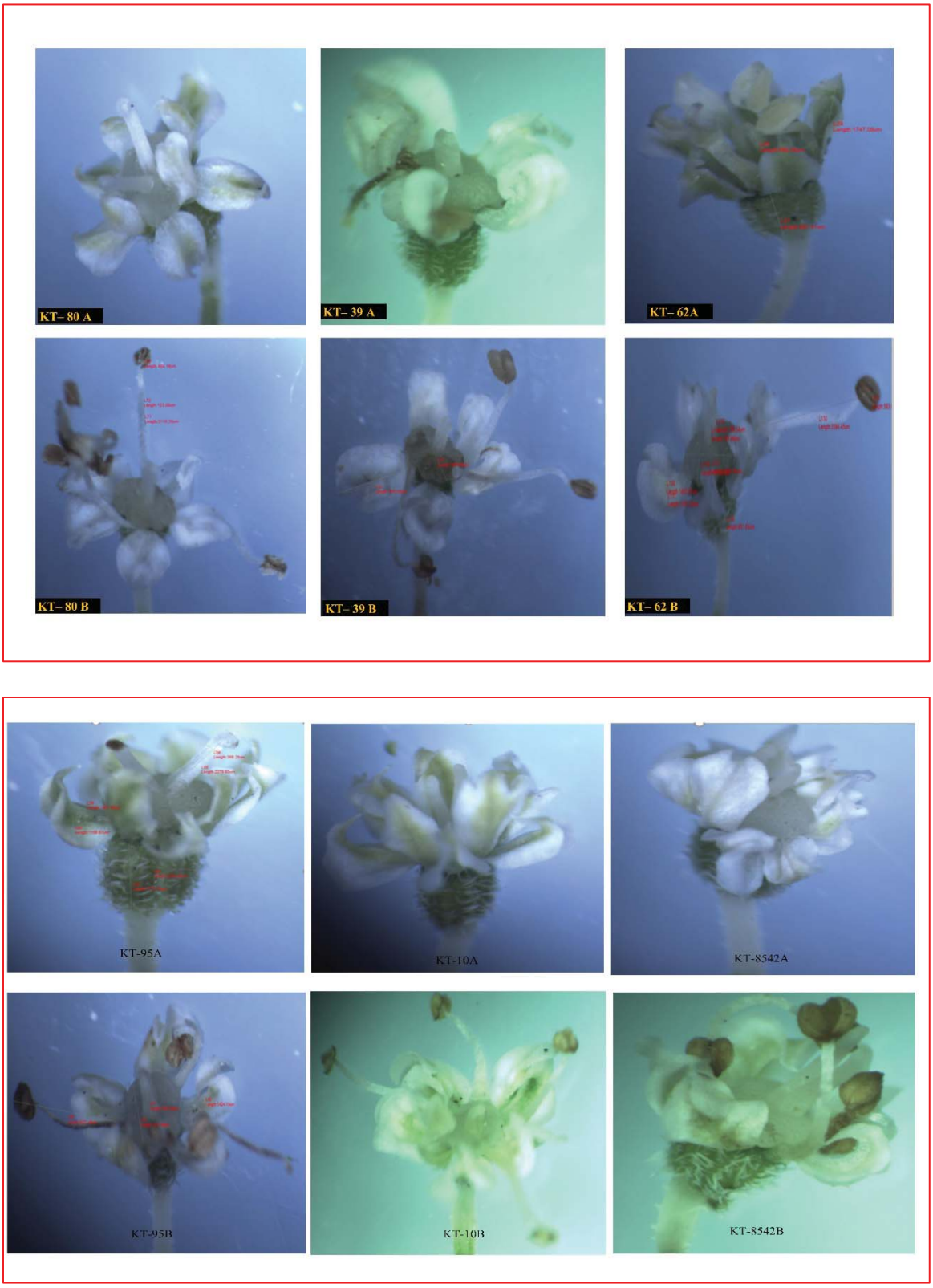


Figure 4.5.1 Flowers of some of the studied CMS lines and its maintainer lines showing petal color, stigma shape and sepal size etc.

Table 4.28 Floral characterization of CMS lines (A) and their respective maintainers (B) for qualitative traits.

CMS line/ maintainer	Petaloid colour/petal colour	Presence of floral nectaries	Presence of viable pollen	Petaloid shape	Type of ovary	Petaloid length size in lines (l x w)(µm)	Anther size of pollen parent (µm)	style length(µm)	style diameter(µm)
KT-7A	White	Present	Absent	spoon	Normal	1854.35 x 1248.80	-	1259.47	168.43
KT-7B	White	Present	Present	-	Normal	1568.89 x 1090.32	345.45 x 132.34	472.72	102.45
KT-10A	Greenish white	Present	Absent	spoon	Normal	2644.97 x 1157.06	-	983.78	231.28
KT -10B	White	Present	Present	-	Normal	1860.60 x1341.61	465.45 x 212.82	578.94	243.43
KT-28A	White	Present	Absent	spoon	Normal	2073.02 x 1583.09	-	1019.11	420.09
KT -28B	White	Present	Present	-	Normal	2185.73 x 1650.48	523.78 x 341.32	872.28	117.49
KT-39A	White	Present	Absent	spoon	Normal	1453.86 x 1134.23	-	1362.43	463.78
KT -39B	White	Present	Present	-	Normal	1574.34 x 1139.87	472.20 x 279.03	1283.65	394.65
KT-47A	Greenish white	Present	Absent	spoon	Normal	1865.78 x 1232.65	-	3116.35	523.08
KT -47B	White	Present	Present	-	Normal	1975.45 x 1012.45	464.16 x 216.43	975.85	253.21
KT-62A	Greenish white	Present	Absent	spoon	Normal	1747.08 x 1345.56	-	1278.75	160.56
KT-62B	White	Present	Present	-	Normal	1954.53 x 958.23	392.49 x 282.16	1226.91	132.49
KT-80A	Greenish white	Present	Absent	spoon	Normal	1526.07 x 1210.66	-	1340.27	285.11
KT-80B	White	Present	Present	-	Normal	1756.39 x 1290.34	485.21 x 326.90	854.75	274.63
KT-95A	Greenish white	Present	Absent	spoon	Normal	50914.51 x 1676.02	-	2279.80	227.43
KT-95B	White	Present	Present	-	Normal	48791.87 x 1035.26	394.45 x 183.34	706.54	185.89

KT-98A	Greenish white	Present	Absent	spoon	Normal	1957.80 x 1106.67	-	1294.38	368.29
KT-98B	White	Present	Present	-	Normal	1398.88 x 1043.33	328.22 x 290.34	1274.42	179.38
KT-8542A	Greenish white	Present	Absent	spoon	Normal	2078.98 x 1456.56	-	1486.69	324.45
KT-8542B	White	Present	Present	-	Normal	2370.95 x 1367.45	334.69 x 194.36	1475.56	174.06

Plate 1 General view of field during crossing programme

Plate 2 General View of field trial for evaluation of hybrids

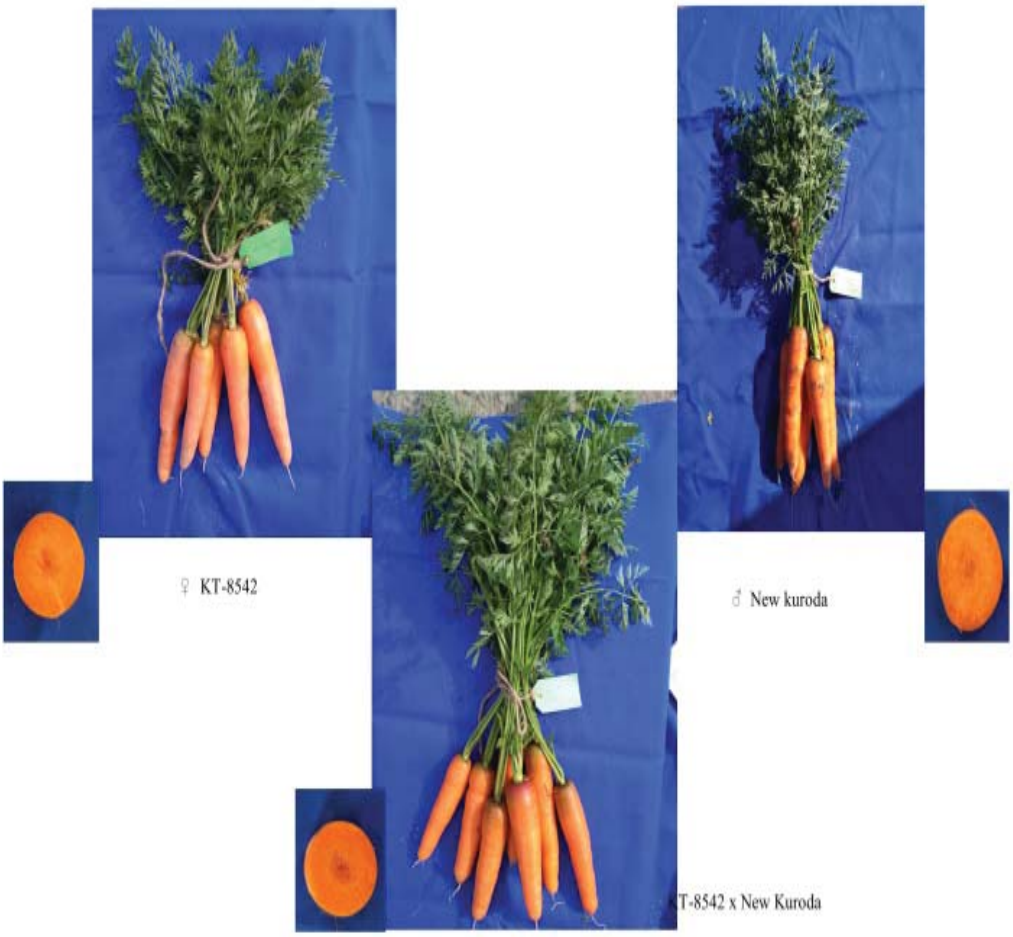


Figure 4.5.2; a). One of the best high yielding performing F1 hybrid KT-8542 x New Kuroda

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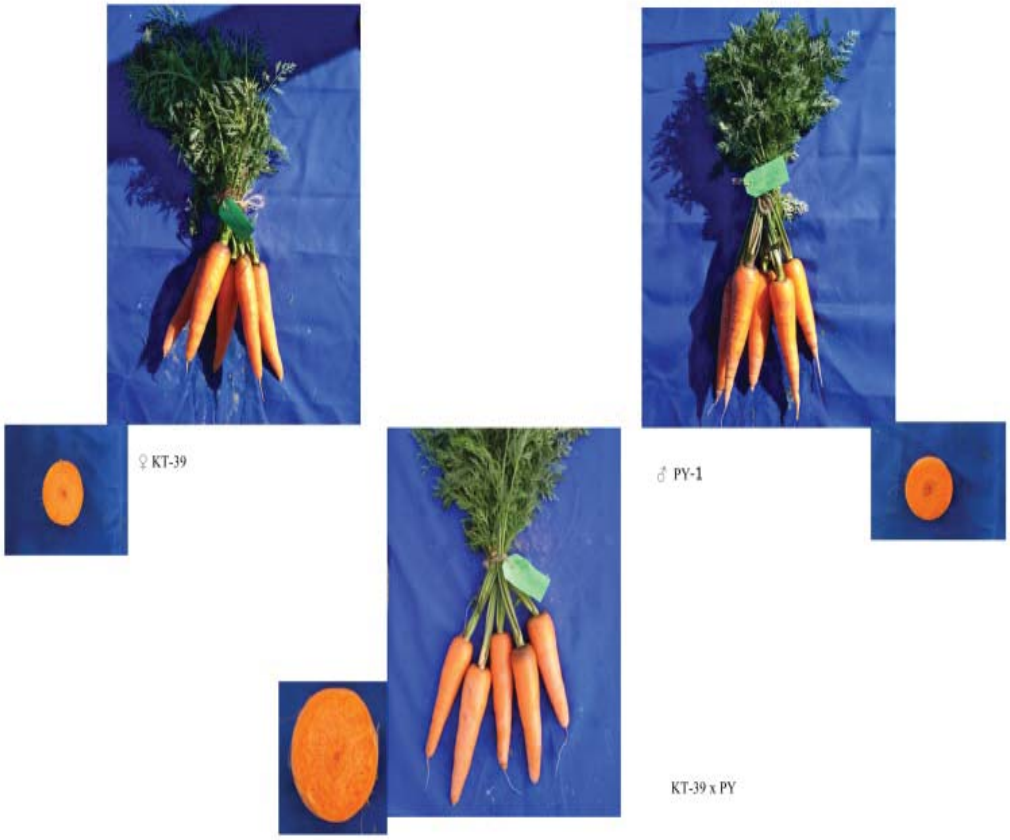


Figure 4.5.3; .b). One of the best corless F1 hybrid KT-39 x PY-1

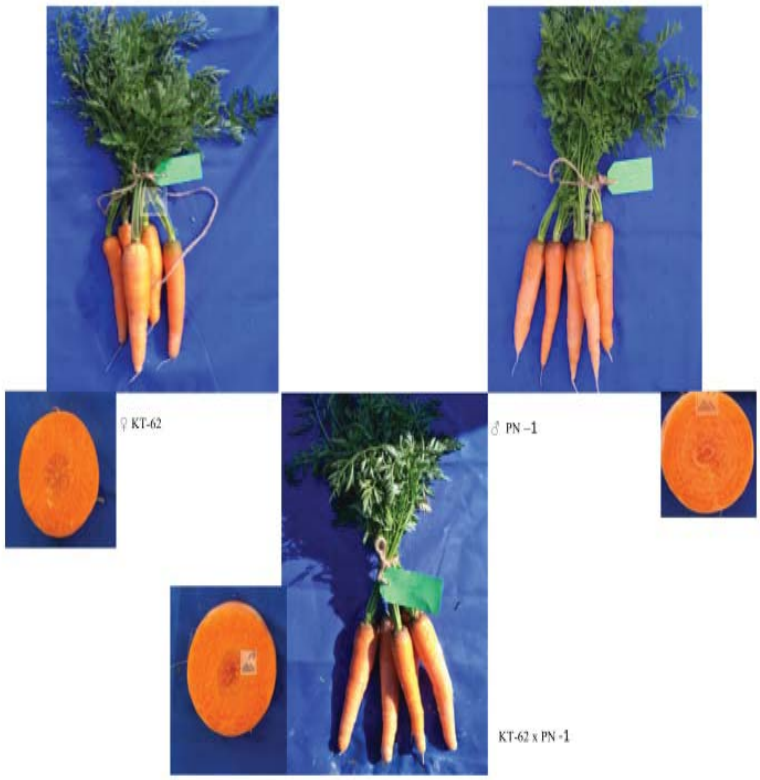
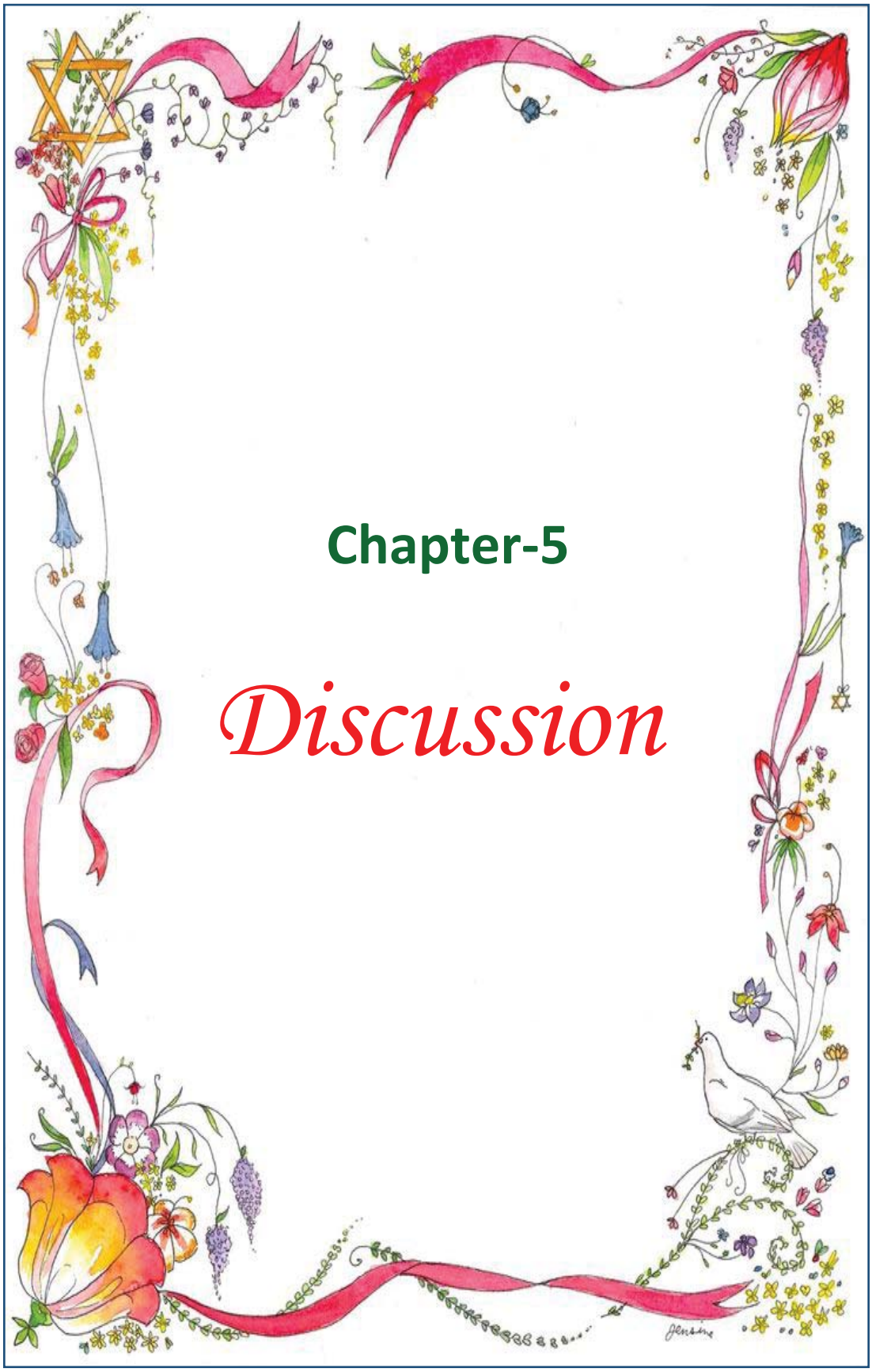


Figure 4.5.4; c). One of the best early maturity performing F1 hybrid KT-62 x PN-1

bv



Chapter-5

Discussion

Chapter 5

Discussion

5.1 Quantitative characters characterization of parents

Crop genetic diversity is the essence of plant breeding and is indispensable for the success of any crop-breeding programme. The knowledge of extent of genetic diversity of a crop species and its distribution is crucial for its effective conservation and utilization. Quantitative characters, qualitative characters and molecular markers have been exploited for assessment of genetic diversity, evaluation of breeding material and characterization of germplasm in root vegetables. Quantitative characters have been widely used for characterization and clustering of elite genotypes/lines with maximum variability and further selection of suitable lines with desirable traits for crop genetic improvement programme. The results pertaining to quantitative characters characterization of parents used in the current study were presented in the Table 4.1 and Table 4.2. The analysis of parental CMS and tester for qualitative traits revealed that all the parental genotypes were free from physiological disorders of forking, cavity spot, splitting and also free from anthocyanin coloration in its roots shoulder. All the lines and testers were having fine and smooth root texture and no secondary roots were observed at root harvesting stage in any of these genotypes. In the CMS lines, majorly all of the genotypes have orange colour roots with cylindrical shape except Kuroda, which had conical roots. In majority of the genotypes, the leaf attitude was erect for all CMS line, except in KT-7A, KT-28A, KT-47A, KT-80A and KT-95Awith semi-erect leaf division. Likewise, in all the fertile testers were had completely erect leaf attitude except KS-21. Hybrids with better quantitative and better yield parameters are desirable to fetch the market and to get higher economic benefits. In the present investigation the CMS lines KT-7A, KT-10A, KT-80A and testers KS-20, KS-73 had the highest root length of up to 25.50 cm, while the smaller roots were found in CMS lines KT-

98A and KT-39A and other tester lines. The CMS lines with dwarfed plant structure would be useful for the generation of hybrid cultivars suitable for high-density planting system. Considerable variations were observed with respect to Leaf length among the lines and testers. The CMS line KT-8542A and tester NK-1 recorded highest Leaf length up to 29.50 cm. Marked differences were observed among the parental lines for root diameter, core diameter suggesting scope for selection of promising parents fordeveloping suitable hybrids with more root diameter with lesser core diameter. Results are in correspondence with Yu *et al.,* (1996, who also reported highest single root weight and other traits in study. CMS The CMS lines KT-28A, KT-47A, KT-98A and testers KS-21, KS-59 and CMS lines KT-62A, KT-47A, KT-8542A and NK-1, KS-21 performed better with respect to root diameter and core diameter. The marketable root diameter up to 17 mm and desirable minimum core diameter up to 8mm was observed. Meanwhile in case of cortex thickness, the CMS lines KT-47A, KT-28A and tester KS-21, KS-20 performed better. Consequently, these parents can be utilized for the crop improvement programme for better marketable root quality. The genotypes with small core length are desirable for having quality and similarly more root length and width for highest root size index. Considerable variability was recorded in the parental CMS lines and testers for few important quantitative characters traits as revealed by the mean performance of parents described in Table 4.2. The considerable variation indicated scope for selection of promising parents for these traits. The CMS lines KT-28A and KT-7A were having the highest root size as compared to rest of lines and best check (Pusa Nayan Jyoti). The smallest core length was observed in genotype KT-62A and KT-80A as revealed by mean performance of parents described in Table 4.2 and subsequently, these lines can be utilized for hybrid breeding of carrot with more smoothness traits. Considerable differences were observed for harvest index and total marketable yield as revealed by mean performance analysis of parental genotypes (Table 4.2), indicating scope for selection of genotypes for hybrid breeding of carrot for high

yield. The results revealed that the CMS line KT-28A, KT-7A, KT-39A, KT-98A, KT-10A and KT-39A could be used potentiality as female parent for developing high yielding F_1 hybrids in carrot in Indian conditions. The results are also in conformity with the findings of Kvasnikov and Zhidkova (1980).

5.2 Genetic components of variance for quantitative characters traits

In the present study for quantitative traits, significant negative GCA was observed for traits like leaf length, shoot weight, core diameter. The adequate knowledge of nature of gene action, genetic components of variance (additive, dominance and epistasis) accompanied with combining ability and allied genetic parameters such as heritability, degree of dominance, predictability ratio is must for plant breeders in the pursuit of rendering crop genetic improvement for different economically important traits (Sharma 1994; Dabholkar 1999). The results pertaining to variance analysis and genetic parameters with respect to quantitative characters traits in the present investigation were presented in the Tables 4.3, 4.4 and 4.5. The analysis of variance exhibited significant differences for almost all treatments for all the 13 vegetative and commercial traits, designating substantial genetic variations among parents and their testcross progenies. The results of any crop-improvement programme relies on genetic diversity of genotypes. Similar results were reported (Duan *et al*., 1996; Karkleliene *et al*., 2005) for yield and related traits. As the our study showed the studied vegetative and commercial traits were found to be under the genetic control of both additive and non-additive gene effects, as revealed by significant mean squares of lines, testers and line versus tester interactions (Table 4.3). The results are in conformity with (Kushlaf and Kalia., 2012) for plant height, marketable root weight, gross plant weight days to maturity and harvest index in carrot using CMS based inbred lines.

The analysis of GCV (Table 4.5) showed the significance of SCA in developing various cross combination as disseminate by higher value of σ^2_{sca} than σ^2_{gca} of lines and testers for majority of traits. All the quantitative characters and horticultural characters showed predominance of dominance variance (σ^2D) and greater than unity value of degree of dominance suggested over-dominance in the action of genes for quantitative characters and horticultural characters traits. Further, less than unity values of the $\sigma^2_{gca}/\sigma^2_{sca}$ and σ^2A/D indicates the non-additive genetic control of all the vegetative and commercial traits, and thus supported with high level of σ^2_{sca}. These results shows a better prospects of heterosis breeding for development of hybrids. Similar results were reported by Poleshi *et al.,* 2017 indicating negligible influence of environment on these traits. While response to natural and artificial selection depend on additive genetic variance, as the narrow sense heritability (h^2_{ns}) as it allow basis to estimate accurate selection of genotypes based on phenotypic variance attributed to additive genetic components with (Evans et al., 2018). In present experimentation, low to intermediate level of h^2ns was recorded for majority of quality and horticultural traits suggesting non-additive genetic control of these traits, which might be due to epistatic effects. Hence, the selection for quantitative characters and commercial traits would be hard due to dominance effects in the expression of phenotypic variance, and thus selection must be practiced in later generations of crop improvement programme. Further, medium to low h^2ns was observed with respect to qualitative characters and phenotypical traits, suggesting response to selection could be efficient in qualitative characters trait and indicating negligible influence of environment on these traits. Moreover, experimentation may be carried out in multiple standard environments for affirmation of these effects.

5.3 Combining ability analysis for quantitative characters traits

The combining ability analysis study have been prospectus in crop breeding for assessing parental CMS and tester performance and understanding dynamics of genes involved

in various trait expression. The general combining ability (GCA) measures shows potentiality of best parent in producing suitable breeding populations. In the current experimentation, the high GCA effects of parental lines in desirable direction with respect to various quantitative characters and horticultural traits are due to predominance of additive genetic effects of genes and additive versus additive interactions (Singh *et al*., 2018). It exhibited desirable gene flow from parents to offspring at high frequency and these parental lines showing significant GCA for the concerned traits, hence it can utilized to stack favourable alleles via recombination followed by selection (Arashida *et al*.,2017). The results obtained in the current study with respect to combining ability analysis were presented in the Table 4.5 and Table 4.6. The results exhibited that not any of parents was good general combiner for all the studied characters. The finding are in agreement with results obtained for yield and quality traits with (Kushlaf and Kalia, 2012**)** and it proposed the need of multi-location breeding programmes for the developing promising variety or hybrids while concentrating significant alleles of genes. The GCA measures signifies that the CMS lines, KT-62A and KT-8542A exhibited significant negative GCA for leaf length. Similarly, for the core diameter, the CMS lines, KT-62A, KT-10A, tester KS-20 and KS -21 were observed good combiner for negative GCA for core diameter could be utilized as parents for developing hybrids with standard coreless roots. Based on GCA, the three CMS lines viz. KT-10A, KT-98A, KT-8442A, could be better as female parent for higher yield. However, for those parental lines exhibiting GCA is in undesirable direction with respect to any traits can be employ to give rise suitable mapping population to study (Gao *et al.,*2013). The specific combining ability (SCA), which contemplate the loci having non-additive and epistatic gene effects, can make use to find out specific heterotic cross combination for respective to trait of interest. The significantly high SCA effects manifested in desirable direction by low × low testcrosses (poor GCA effects of both male and female parents) for instance KT-8542 x KS -21 for plant height and KT-8542 x

NK-1 for root and shoot ratio, may be attributed to dominance versus dominance type of interaction having especially complementary epistatic effects with (Fasahat et al., 2016). This contrary relationship of GCA and SCA for various cross combination evidence of complex interaction of genes for quantitative traits with (Su et al.,2017). The most of heterotic cross combination exhibit significantly high SCA in desirable direction. It illustrating that crosses viz., KT-8542 x KS -21 for leaf length, KT-10 x New Kuroda for cortex thickness, KT-98 x PN-1 for net root weight and may be attributed to good combiner parent depicting favourable additive effects and poor combiner parent displaying epistatic effects (Fasahat *et al*., 2016).

The heterotic cross combination demonstrate significant SCA in desirable direction for various characters with good GCA (good general combiner × good general combiner) viz.., KT-98 x NK-1 pertaning to shoot weight; KT-8542 x NK-1 for root to shoot ratio, KT-98 x NK-1 for gross root weight,KT-10 x New Kuroda for harvest index and KT-98 x PN-1 for yield indicate the role of aggregate effects of additive × additive interaction (Fasahat et al. 2016). Concurrently, some of the cross combination had poor SCA effects with respect to various characters, in spite of assuming parents with significant GCA effects, might be attributed to lack of interaction among alleles of genes hence indicated the measure of SCA in divergence to GCA in identifying particular superior crosses. Therefore , this experimentation submit conclusively that in crop improvement programme one must take care to both GCA and SCA in the selection of promising parents for the development of heterotic hybrids. Further, the recombination breeding and random mating in conjunction with recurrent selection, synthetics and composites, may be exploited to harness utility of both additive and non-additive gene effects in carrot (Gupta and Verma, 2007).

5.4 Heterosis analysis

The significant event of heterosis has long been demonstrate very useful in enhancing agricultural productivity and has continuously attract the plant breeders and geneticists to

search on this unending process. The authentic characterisation and identification of hybrid crosses of genetically varied inbred lines giving heterotic performance is the key to successful hybrid breeding programmes, presuming positive correlation of genetic divergence and average heterosis (Falconer and Mackay 1996). Heterosis results from concentration of parental genetic and epigenetic information, subsequently it display as better production of hybrid cross compare to the average of their genetically diverse parents (Bansal et al. 2012; Fujimoto *et al.,* 2018). In spite its immense economic prospects, the molecular basis behind this events are still unclear (Groszmann *et al*., 2013; Fujimoto *et al*., 2018). Until now, various hypothesis and genetic mechanisms have been propose to explain this multiplex event viz., dominance model, over-dominance model and epistasis model (Groszmann *et al.*, 2013; Fujimoto *et al.,* 2018; Li *et al.,* 2018). The results obtained in the current study pertaining to heterosis analysis for quantitative characters traits were presented in the Table 4.10, Table 4.12 and Table 4.13. For the traits related to leaf length, shoot weight and core diameter the heterosis in negative direction is desirable. In the current study, the heterosis of 0.78 % and -53.52 was obtained with respect to leaf length. Very high heterosis of up to -53.52 % was recorded for core diameter. Moderate heterosis of 10-30% was recorded for root length, while for cortex thickness the heterosis upto 150 % and 100 % for root diameter, was recorded in some of the crosses. Very high heterosis of up to 90 % and 70 % was recorded for gross root weight and root surface, respectively, in many of the heterotic crosses among 100 hybrids. Moderate level of heterosis (10-60%) was recorded for harvest index, root to shoot ratio and root weight. The heterotic crosses, KT-98 x PN-1 (55.79%), KT-8542 x New Kuroda (45.70 %) and KT-8542 x KS -50 (37.03%) exhibited very high significant heterosis for total marketable yield. The similar results were reported by (Garg and Lal, 2005).

5.5 Variance analysis and genetic parameters for antioxidant and qualitative characters traits

The results pertaining to analysis of variance and genetic components of variance with respect to antioxidant traits were presented in the Tables 4.16, 4.17 and 4.18.The variance analysis shows significant variation for all the genotypes, which is a necessary for the favourable outcome in any crop improvement programme. Similar outcome reporte in tropical carrot for quantitative traits (Poleshi *et al.,* 2017). The notable mean squares due to lines, testers and line versus tester interactions for all the studied traits (Table 4.16) at $P \leq 0.001$ indicated the prevalence of both additive and non-additive gene action for the expression of these traits. These results are in agreement with (Singh *et al*.,2009) for various qualitative characters traits. Further, the estimate of degree of dominance higher than unity indicated the role of over-dominance for accumulation of all the studied traits related to qualitative characters activity in the carrot root. Then, less than unity values of σ^2A/D and σ^2gca/σ^2sca ratios shows dominance of non-additive gene action and thus there is better opportunity of heterosis breeding for development of antioxidant rich F_1 hybrids. The favourable outcome in any crop improvement programme mainly depends on heritability, which can be defined as the ratio of variances i.e. Proportion of total variance in a population for a specific trait, which is due to variation in additive genetic or total genetic values (Visscher *et al.*, 2008). It exhibited the degree to which progenies can be expected to resemble their parents for a specific trait. Heritability can be classified into broad sense heritability ($H^2_b = V_G/V_P$; $VG = V_A + V_D + V_I$), which is the proportion of phenotypic variation due to inherent genetic base, including effects due to dominance and epistasis, secondly the narrow sense heritability ($h^2_{ns} = V_A/V_P$; $V_P = V_G + V_E$), the proportion of phenotypic variance attributed to additive genetic effects (Visscher *et al.*,2008; Evans *et al*., 2018). Narrow-sense heritability as response selection and count very

important crop improvement programme (Visscher *et al.,* 2008; Evans *et al.,* 2018). In the current experimentation the moderate to low level estimates of narrow-sense heritability for qualitative characters compounds shows the role of non-additive gene action in the inheritance of studied antioxidant traits in carrot and results are in conformity with (Karmakar *et al*., 2013). Hence the present investigation provides very useful information about the genetic variation available in carrot for the various quantitative root traits, which helps to plan a suitable strategy for the crop improvement of carrot to temperate region.

5.6 Combining ability and heterosis for antioxidant traits

The awareness on combining ability of various parental line for development of hybrids primarily significant in breeding program. Line versus tester analysis was successfully employ to find out the comparative suitability of lines and testers to identify desirable heterotic cross combinations (Kempthorne *et al.,*1957). This analysis also shows the GCA effects of parental lines and SCA effects of each cross apart from genetic component of variance and gene action to allow selection of suitable parents and identification of superior cross combinations to be utilized in heterosis breeding (Singh and Chaudhary 2014; Dey *et al.* 2014; Parkash *et al.* 2017). The estimates of general combining ability and specific combining ability were presented in the Table 4.18 and 4.19. The evaluation of breeding material and characterization of germplasm in root vegetables for qualitative characters attributes is essential for antioxidant rich breeding of root crops like carrots. In the present investigation, the pooled analysis over the environments for different antioxidant and bioactive traits revealed remarkable chemotypic variation among parental carrot types, which is prerequisite for any crop improvement program. The carotenoids are known to play a major role on human health having antioxidant potential and are accumulated in an abundant amount in commercial carrot genotypes (Jourdan *et al.,*2015). The industrial importance of carotenoids comes from their colour imparting

properties. Thus enhancement of carotenoids especially β-carotene in carrot varieties is major breeding trait for functional food and pigment industry Bogacz-Radomska and Harasym, (2018). In the present investigation the content of TCC and β-carotene among parental types varied from 0.13 to 4.34 mg/100g and 1.64 to 3.92 μg/100 g, respectively. These results are comparable to the findings of (Koley *et al.,*2014) for β-carotene in orange genotypes of carrot. The results suggested that the petaloid type CMS lines KT-62A and KT-80A can be effectively utilized in carotenoid rich breeding of carrots for enhancing their industrial potential. The results were further supported by dendrogram analysis for bioactive traits and principal component analysis (PCA) which depicted substantial genetic variation among parental chemotypes for nutrient rich breeding. Similar trends were reported by (Koley *et al*.,2014) in tropical carrot genotypes and substantial chemotypic variation among the carrot parental types could be explained by genotype, season of growing, maturity, portion of root sample and qualitative characters assay approach (Koley *et al*.,2014). Further, the analysis of variance also indicated considerable genetic variation among all the carrot genotypes comprising parental chemotypes and their testcross progenies. Thus, sufficient genetic variation is available for exploitation in crop improvement program of carrot.

The variance analysis shows significant variation for majority of genotypes, which is a essential for the successfulness of any breeding program. The outcomes are in agreement with the report (Poleshi *et al.,* 2017) for root traits in tropical carrots. The pooled analysis over the years revealed significant mean squares at $P \leq 0.001$ for lines, testers and line × tester interaction for all the antioxidant and bioactive traits, which indicated the preponderance of both additive and non-additive gene action governing the expression of target traits in temperate carrots. Thus, selection and heterosis breeding would be instrumental in developing antioxidant rich carrot hybrids. These results corroborates the findings of (Semakula *et al*. 2007) for total carotenoid in cassava, (Halilu *et al*.,2016) for provitamin A in maize and (Peprah *et al*.,2020) for

provitamin A in cassava. All the studied traits were qualitative in nature; hence less influence of environment in controlling trait phenotype is evident. But, the significant mean squares of G × E interaction over the years for carotenoid concentration (TCC and β-carotene) content indicated the influence of environment for the expression of carotenoid content in carrot genotypes. Thus, the considerable variation in carotenoid concentration is both genotypic and environmental (Peprah *et al.,*2020). These results indicated the need of multi-environment testing trials of carrot genotypes for carotenoid improvement. The observed results indicated the oligogenic control of carotenoid expression (Halilu *et al*.,2016). The perusal of genetic components of variance revealed the role of specific combining ability (SCA) in the generation of heterotic hybrids as evident from higher magnitude of σ^2_{sca} as compared to σ^2_{gca} of parental types for majority of bioactive compounds (Table 4.18). The higher than unity estimates of degree of dominance shows the role of over-dominance for the concentration of characters except for carotenoids and β-carotene. Further the preponderance of non-additive (dominance and epistasis) gene action controlling the expression of CUPRAC, FRAP, anthocyanin, TPC, ascorbic acid and lycopene was observed as designate by less than unity value of σ^2A/D and σ^2gca/σ^2sca. These results emphasized the scope of hybrid breeding in development of superior varieties of carrot having industrial and nutritional potential. Then the influence of additive gene action was much pronounced in the genetic control of TCC and β-carotene as evident from σ^2A/ σ^2D ratios. There is scope of simple pure line selection for the improvement of such traits. The narrow-sense, which describes the phenotypic variance, is a promising component of crop improvement programme as response to selection relies on additive genetic effects (Karavolias *et al.,* 2020). The moderate estimates of h^2ns for majority of traits except for carotenoids indicated that selection at early generation would be impractical and must emphasize for the multi-location multi-year experiments. For such traits selection at later generation could be feasible. For the TCC and β-carotene, selection would be easy as evident

from higher estimates of h^2ns. The effects of σ^2Env × lines, σ^2Env × testers, σ^2Env × GCA and σ^2Env × SCA interaction variance were significant for TCC and β-carotene which necessitate the need of multi-year and over the environment evaluations for the selection of TCC and β-carotene during carrot breeding program. The results are in line with (Semakula *et al*.,2007) for TCC in cassava and Athanase and Rob (2019) for β-carotene in cassava. These pooled analysis results over the years indicated that the TCC and β-carotene accumulation in carrot roots is governed by few major genes. Thus, selection followed by recombination would be an appropriate approach to enhance frequency of genes controlling the target trait.

The acquaintance with the aspects of combining ability of parental types utilized for hybrid breeding and heritability analysis is crucial for crop genetic improvement program (Singh *et al.,* 2018a). The analysis of GCA effects over the years indicated that none of the parental type exhibited significant GCA in desirable direction for all the traits simultaneously. These results corroborated the findings of Athanase and Rob (2019) and suggested the need of multiple crossing in suitable breeding design for stacking favourable alleles of antioxidant capacity in carrot genotypes. The GCA effects over the years depicted that petaloid CMS lines KT-80A and KT-62A had significant GCA in desirable direction for TCC, β-carotene and ascorbic acid content. These lines can be effectively utilized as female parent for the improvement of carotenoids and ascorbic acid in temperate carrots. The GCA analysis results helped in identification of suitable combiners among parental types for the improvement of respective antioxidant and bioactive traits in carrot. The parental types with significantly high GCA in desirable direction over the years are most suitable for recombinant breeding. The SCA effects provide estimation of loci with non-additive and epistatic gene action. It also leads to identification of specific heterotic crosses for hybrid development. The considerably high SCA effects in desirable direction showed by poor × poor crosses like for the CUPRAC content in KT-98A × KS-50, for the FRAP content in KT-62A × PY-1 and for the β-carotene in KT-39A

× PY-1, could be explained by dominance × dominance type of non-allelic epistatic interaction (Singh *et al.,* 2018a; Athanase and Rob, 2019). Biparental crossing or reciprocal recurrent selection followed by hybrid breeding would be useful for improvement of target traits involving such cross combinations. The majority of the heterotic cross combinations manifesting greater SCA effect and had one of the parent with poor GCA like poor × good combiner or good × poor combiner. For instance in the cross combination KT-39A × KS-20 for FRAP content, KT-47A × KS-20 for ascorbic acid content and KT-47A × KS -59 for the lycopene content had one of the parent with poor GCA. These results could be due to additive effects of good GCA parent and epistatic effects of poor GCA parent (Singh *et al*., 2018a; Singh *et al*., 2019a). The higher estimates of SCA effects over the years in the crosses involving good × good combiners like KT-7A × KS-20 for anthocyanin content, KT-62A × KS-21 for β-carotene content and KT-62A × KS-22 for TCC could be attributed to stacking of favourable alleles of both parents for the improvement of target trait (Singh *et al*., 2018a; Singh *et al.,* 2019a; Athanase and Rob, 2019). The pooled combining ability analysis over the years in the carrot for antioxidant traits also indicated that the parents depicting high per se performance always were not having high GCA in desirable direction, which revealed the role of both GCA and SCA for the selection of parents to develop heterotic hybrids.

In majority of cases, the heterotic cross combinations menifested significant high value of MPH or heterobeltiosis in desirable direction had positive SCA effects for all the antioxidant and bioactive traits in carrot. It is evident that combining ability is positively associated with heterosis (Singh *et al.,*2019a). Concurrently, the heterotic cross combinations exhibiting highest MPH always did not revealed significant SCA effects in desirable direction such as KT-95A × KS-21 for β-carotene content, KT-98A × KS-59 for the lycopene content and KT-62A × PY-1 for the total phenolic content. Similar is true for the heterobeltiosis estimates such as KT-98A × KS-59 for TCC, KT-98A × KS-59 for lycopene content, KT-80A × KS-21 for

the FRAP assay and KT-47A × New Kuroda for the ascorbic acid content. It may be because of fact that SCA is the function of a specific cross combination while heterosis is associated with mid parent value, better parent estimates or commercial check. The interaction analysis results indicated significant positive association among the antioxidant traits under study. For instance, the significant positive association was observed for FRAP with anthocyanin content and TCC with ascorbic acid content. These results indicated that breeding for improvement of one trait will simultaneously improve the connected trait.

5.7 Cluster analysis and allelic diversity in parental lines and testers of crosses

The assessment of genetic diversity is an important component of crop genetic improvement programmes, as it provides knowledge about adaptation, extent of genetic variation contained in the studied germplasm, and history of evolution of a species, gene flow and phylogenetic relationships among different species/genera/accessions (Zhang *et al.,*2015). As quantitative characters markers are also widely used for genetic diversity analysis, but they do not provide true insights into extent of genetic variation in the studied germplasm, as they are highly influenced by environmental factors (Zhang *et al.,*2015). Nowadays, molecular markers have been proved powerful tool to assess the genetic diversity within landraces, species, and analysis of population genetic structure depicting true image of extent of genetic variation and gene flow in the existing germplasm (Zhang *et al.,* 2015; El-Esawi *et al*., 2016; Yousef *et al.,* 2018). Among the PCR-based molecular markers, the microsatellite markers (SSR: simple sequence repeats) are most favored by plant breeders and geneticists ascribed to their co-dominant inheritance, high reproducibility across the laboratories, their abundance, high polymorphism and entire genome coverage (Wu *et al.,* 2013; Zhang *et al.,* 2015; El-Esawi *et al*., 2016; Yousef *et al*., 2018). Molecular markers been proved to be useful for selection of suitable parental lines owing to their association with different alleles governing economic traits and heterosis.

The investigation of crop diversity and variance is important in selecting suitable parents for hybrid seed production. The characterisation and identification of heterotic germplasm and exploring surviving genetic diversity in CMS lines is the preparatory essentiality any breeding programme. Then examination on genetic variation at phenotypic and genotypic level has been seen as possible techniques in identification of suitable breeding lines (Baranski *et al*. 2012; Chair *et al.* 2019). By analysing principal component analysis (PCA) and UPGMA cluster analysis of 20 parental CMS lines and testers for 13 quantitative characters traits, it was obvious that majority of parental lines had adequately diverse in nature . Then first two axes PC1 and PC2 exhibited 61.41% variation, thus PCA was structured in finding out the genetic variation among all the parental lines.

The principal component analysis and NJ clustering was constructed base on molecular data which constitute proved to be decisive tool in recent plant breeding methods. The PCA analysis and NJ clustering based on 67 SSR loci confirm that majority of testers remained divided in two different sub-clusters. The CMS lines KT-10A, KT-47A, KT- 80 A and KT-8542A placed different main cluster from rest of CMS lines and remained close affinity with tester line KS- 20, KS-21and KS-22. The CMS lines KT-7A, KT-28A, KT-39A, KT-62A, KT-95A and KT-96A were remained in different main clusters and has no close affinity with any tester lines.

Then CMS line KT-62A and KT-10A found to be high GCA in positive direction few commercial traits like gross root weight, marketable net root weight, harvest index, total marketable yield thus could lead to be instrumental in advancement of high yielding hybrid carrot cross intact with all other horticultural traits. The CMS line KT-10A found to be considerable GCA effect in desirable negative direction for core diameter and KY-62A for leaf length could be used for generation of small core and less leaf hybrids. Further detailed analysis on various aspect of phenotypic and genotypic variation along with GCA analysis could play

pivotal role (Parkash *et al.,*2018) in development of CMS based hybrid in cross pollinated crops.

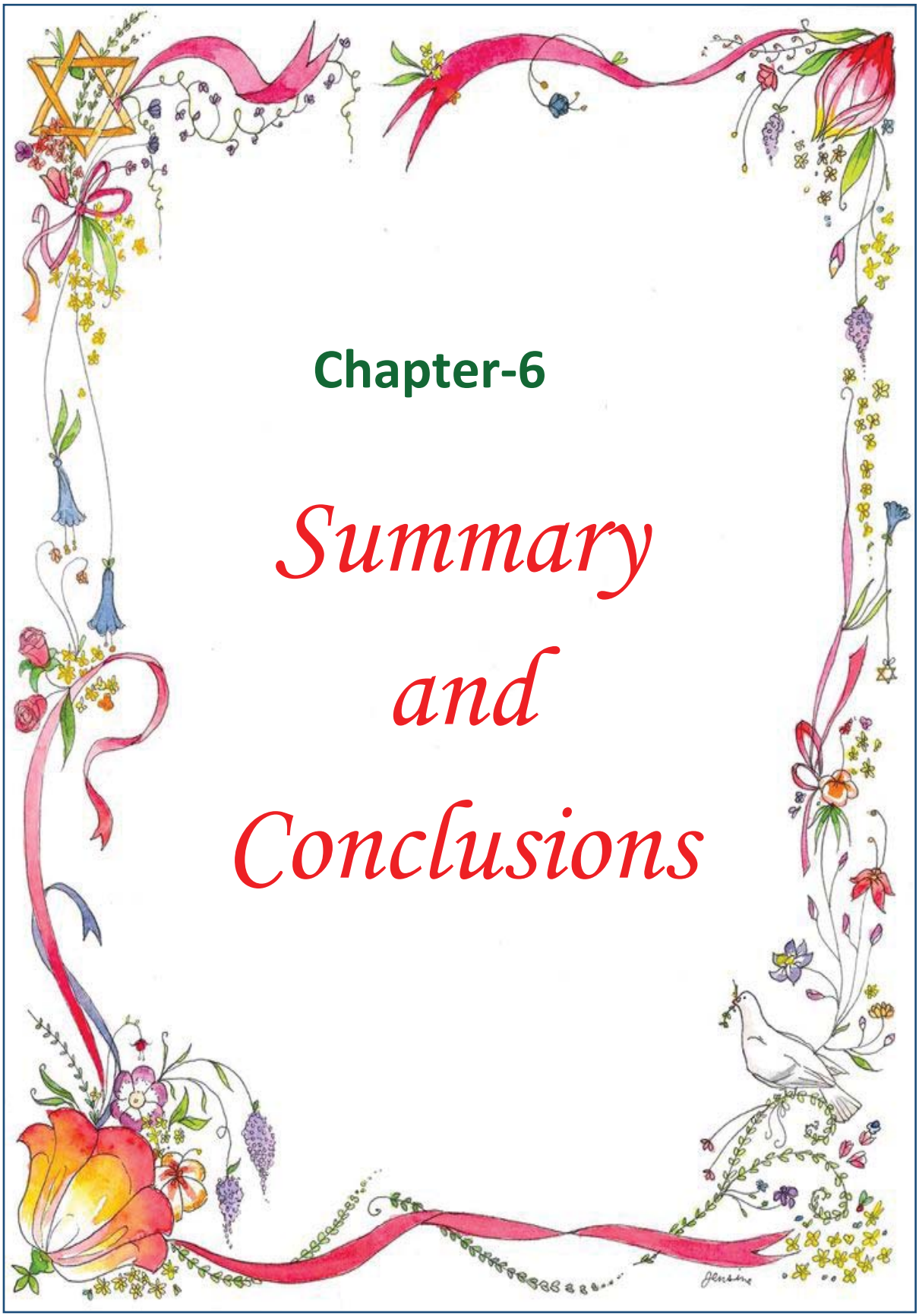
Subsequently, in our observation greater allele frequency of overall 522 alleles through 67 SSR in 20 parental CMS and tester with mean allelic frequency of 8.55 alleles per locus (Table 4.27). Hence it suggested that the allelic diversity within or adjacent to genes might be more informative functionally and have higher inherent rate to related taxa in contrast to genomic SSRs (Varshney *et al.* 2005; Taheri *et al.* 2018). Additionally, we observed greater estimates of average expected heterozygosity (H_e), which is 0.68 stipulate high genetic variation in the various used germplasm as H_e corresponds to genetic diversity. The polymorphic information content (PIC) in molecular study employ as an estimate of informativeness of a marker locus for linkage profiling (Moges *et al.,* 2016; El-Esawi *et al.,* 2016) and it group as informative markers (PIC ≥ 0.5), reasonably informative (0.5 < PIC >0.25) and slightly informative (PIC < 0.25) (Moges *et al*., 2016; El-Esawi *et al*., 2016). In the present study the PIC content of 67 polymorphic loci ranged from 0.24-0.80 (Table 4.19), which classified all the 67 loci (SSR) as slightly informative, reasonably informative (12 primers) and highly informative markers (54 primers) as per PIC content in this experimentation (Table 4.27) and conclusively proposing their ability in genetic differentiation of CMS and tester lines. (Barbara Jagosz, 2011) Genetic distances among lines were calculated using the RAPD and AFLP techniques. Significant heterosis was found for both total and marketable yield. The content of quality compounds for hybrids usually had mid-parent values. Significant correlations were found between molecular distances among lines, measured using RAPD markers, and heterosis of crosses for total yield, and among divergences of parents measured using AFLP markers and heterosis for marketable yield. This appears to contribute towards the carrot hybrid yield prediction by estimation of the genetic distances between

parents. Conclusively similar findout indicates possibility of heterosis prediction would allow for the reduction of costs and quicker identification of superior carrot hybrids.

5.10 Characterization of CMS lines for floral traits

The introgression of sterile cytoplasmic have been reported to be associated with different floral deformities in such as reduction in flower size, petaloid anthers, carpeloid stamens, poor nectarines development and curved stigma (Kalia *et al.,*2019) and also affecting the seed setting ability in the CMS lines. The results obtained with respect to characterization of CMS lines for floral and seed-related traits were presented in the Tables 4.28. The floral traits are significantly altered by cytoplasm in the CMS lines of different nuclear background (Kalia *et al.,*2019).The analysis for floral quality traits revealed that all the CMS lines had normal ovary type, floral nectarines and were devoid of viable pollen. The style shape in all the CMS lines had spoon stigma. The marked differences were observed with respect to quantitative floral traits. The considerable variation observed with respect to petal and sepal size in the studied CMS lines. Further, 'petaloid' type CMS found prominent and not a single of the CMS lines showed carpel-like structure (carpeloid).Green petal colour petaloid were predominant in CMS lines (Table 4.28). The prominent variation observed as the presence of light green, green mid-rib in petaloids, spoon type straight and curved petals encountered across the carrot CMS lines (Table 4.28). This profound diversity in petaloid shape and colour pattern may be some candidate genetic background of the transformed CMS lines, however, which needs further examination. The widest petals were observed in the CMS lines KT-95A, KT-10A and KT-8542A. The ratio of petal length to petal width was >1 in the CMS line KT-10A indicating the great reduction **i**n petal width relative to petal length with the temperate cytoplasm. (Kalia *et al*.,2019) reported similar results in the CMS lines of tropical depicting the ratio of petal length to petal width > 1 depicting a considerable change in petal size. The considerable differences were also observed in all the CMS lines with respect to style length

and the longest style was observed in the CMS line. The longest long style were observed in the CMS line KT-47A and KT-95A.The nine CMS lines were devoid of short style (KT-8542A, KT-98A, KT-10A, KT-7A, (Table 4.28). Similarly, (Kalia *et al*.,2019) reported similar results in the CMS lines of tropical CMS lines under study.



Chapter-6

Summary and Conclusions

Summary and Conclusions

Chapter 6

Carrot (*Daucus carota* subsp. *sativus*) belonging to the family *apiaceae* is an important member of root vegetable crops and is a valuable functional food imparting health benefits (Spooner 2019). The estimated production of carrot in India is around 1.64 million tonnes from an area of 0.097 million ha (NHB, 2018). It has antioxidant and anticancer properties due to the presence of secondary metabolites (Carotenoids), and nutraceuticals compounds. Attributed to its rich nutritional standards, great efforts have been made towards enhancing its yield and quality worldwide. The development of varieties/hybrids of different nutritional rich traits is prime objectives of any breeding program. Heterosis has long been proved an effective tool in plant breeding for enhancing agricultural productivity and feeding the growing population. In *carrot*, thegenetic mechanisms of cytoplasmic male sterility (CMS) have been widely used for heterosis breeding and commercial hybrid seed production. For this, the genetic combining ability analysis and study of nature of gene action have been used traditionally for the identification of suitable parental lines with desirable combining ability and to devise appropriate breeding approaches for the crop genetic improvement.

The present investigation entitled "Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus)* using Cytoplasmic male sterile (CMS) lines" was carried out during 2016-2019 at Naggar Experimental Farm of ICAR-IARI, regional station Katrain, Himachal Pradesh located along the left bank of river Beas. Study was conducted to characterize and assess the genetic diversity in parental petaloid type CMS lines and inbred testers of temperate carrots using, morphological and molecular markersThe parental genetic diversity was analysed using genomic SSRs. To assess the impact of sterile cytoplasm on CMS phenotypes, the comparative analysis of petaloid type CMS lines and their

male fertile counterparts was carried out for different floral traits. The combining ability analysis was performed for identification of superior parents and heterotic combiners for different quantitative and quality traits.

6.1 Characterization of parental types for quantitative and qualitative traits and per se hybrid performance

Crop genetic diversity is the essence of plant breeding and is indispensable for the success of any crop breeding programme. The knowledge of the extent of genetic diversity of a crop species and its distribution is crucial for its effective conservation and utilization. Quantitative, qualitative and molecular markers have been exploited for the assessment of genetic diversity, evaluation of breeding material and characterization of germplasm in carrot. Quantitative characters have been widely used for characterization and clustering of elite genotypes/lines with maximum variability and further selection of suitable lines with desirable traits for crop genetic improvement programs. The results obtained in the present investigation are first of its kind in temperate carrots in India and provide foundation for a carrot breeding program. The results obtained revealed substantial genetic variation among parental types for quantitative and quality traits for the successful utilization in carrot breeding. The analysis of parental CMS and tester lines for qualitative traits revealed that all the parental genotypes were free from physiological disorders like cavity spot, forking, splitting, etc. The results of mean performance in the present study revealed that CMS lines KT-39A (85.33 days ± 1.53), KT-47A (90.33 days ± 1.53) and KT-28A (90.67 days ± 1.53) were earliest maturity and can be better used for development of hybrids early in maturity. Similarly, among the testers, KS -73 (89.33 days ± 1.53), PY-1(Katrain local sel.8) (90.67 days ± 1.53) and PN-1 (Katrain local sel.11) (91.00 days ± 1.00) took minimum number of days for root maturity. In majority of the genotypes, the leaf attitude was erect for all CMS line, except CMS lines KT-7A, KT-28A,

KT-47A, KT-80A, and KT-95A, which had semi-erect leaf division. Likewise, in all the fertile testers were having completely erect leaf attitude except KS-21.

The carrot genotypes with small core size are desirable for having thick flesh and similarly more roots length and width are important determinant of root size and yield. The smallest core diameter was found in the genotype, KT-62A (8.00 mm ±0.02) followed by KT-47A (9.00 mm±0.15) and KT-28A (11.00 mm±0.01). Highest root diameter found in CMS lines, KT-28 (46.67 mm±0.92) followed by KT-47A (45.00mm± 0.46) and KT-95A (43.33mm±0.13). The results indicated suitability of these lines in hybrid breeding of carrot to develop coreless roots with thick cortex. There was marked differences among the parental lines suggesting scope for selection of promising parents for developing highly suitable hybrids with more roots weight and root length for higher yield. The CMS lines KT-28A (90.77g±0.87), KT-7A (82.00g±0.72), and KT-39A (79.50g±1.17), and CMS lines KT-80A (24.00cm±1.32), KT-10A (22.50cm±0.58) performed better with respect to root weight and root length respectively. The yield of the CMS lines revealed that KT-28A (36.30 tonnes/ha ±0.34), KT-7A (32.79 tonnes/ha ±0.28) and KT-10A (31.40 tonnes/ha ±0.32) could be better used as female parent for developing high yielding hybrids in carrot.

For the qualitative traits, considerable variability was found among the parental genotypes indicating scope for selection of elite lines for developing antioxidant rich cultivars in carrot. Moreover, the results revealed ample scope of improvement of carotenoids, β-carotene and other bioactive compounds in carrot for enhancing its nutraceutical and natural pigment industry potential. The results obtained in the present investigation would be useful for carrot breeders, researchers and geneticists for designing of novel carrot cultivars for functional food industry, nutraceutical and natural pigment industry. For enhancing the antioxidant value and quality breeding, the CMS parental lines viz., KT-8542A (0.56 µ moltrolox/g±0.017), KT-80A (0.54 µ moltrolox/g ±0.013), KT-39A (0.52 µ moltrolox/g ±0.022), and KT-39A (0.34 µ

moltrolox/g ±0.007), KT-95A (0.28 µ moltrolox/g ±0.012), KT-98A (0.18 µ moltrolox/g ±0.00) performed better for CUPRAC and FRAP content respectively. Hence, these could be put for further investigation for assessment of combining ability and heterosis with the objective of developing antioxidant rich hybrids. Marked differences were observed in the parental genotypes for the ascorbic acid content and the mean value for ascorbic acid content among the parental CMS lines ranged from 2.44 mg/100g (KT-95A) to 10.23 mg/100g (KT-62 A). The three lines KT-62A (10.23 mg ±0.02), KT-28 A (6.78 mg ±0.13), KT-80 A (6.43 mg ±0.14) performed better for ascorbic acid content and could be used as female parent for hybrid breeding of this trait. The mean value of total phenolic content and anthocyanins content among the CMS lines was ranged from 185.63 mg of gallic acid/100 g FW (KT-62 A) to 622.53 mg of gallic acid/100 g FW (KT-10A) and 0.05 mg/100g (KT-95 A) to 0.29 mg/100g (KT-10A), respectively. The CMS lines KT-10A (622.53 mg of gallic acid/100 g FW), KT-28 (568.98 mg of gallic acid/100 g FW), KT-39A (541.88 mg of gallic acid/100 g FW) and KT-10A (0.29mg/100g), KT-39A (0.24 mg/100g), KT-28A (0.20 mg/100g) gave higher mean performance for total phenolic content and anthocyanins content and could be better used in the breeding programmes for the genetic improvement of these traits. Similarly, top three lines for beta-carotene content and total carotenoid were KT-47A (3.92µg/100ml ±0.10), KT-8542A (3.77 µg/100ml ±0.16), KT-7A (3.36 µg/100ml ±0.15) and KT-62A (4.34mg/100g±0.09), KT-80A (2.49 mg/100g ±0.11), KT-28A (2.33 mg/100g ±0.07), respectively suggesting their potential for improvement of these traits.

6.2 Variance analysis and genetic parameters

The adequate knowledge of nature of gene action, genetic components of variance (additive, dominance and epistasis) accompanied with combining ability and allied genetic parameters such as heritability, degree of dominance, predictability ratio is must for plant breeders in the pursuit of rendering crop genetic improvement for different economically important traits. The

analysis of variance exhibited significant differences in majority of the treatments for all the 13 quantitative characters and 8 antioxidant traits, illustrating considerable genetic variation in most of parents and their testcross progenies. The traits under experimentation were found to be under the genetic control of both additive and non-additive gene effects, as exhibited by significant mean squares of lines, testers and line × tester interactions.

The results highlighted the influence of both GCA and SCA effects in selecting desirable parents for carrot improvement program. The preponderance of additive gene effects in some of the cross combinations derived from good × good GCA illustrated the scope of isolation of transgressive segregants. The studied traits were under the genetic control of both additive and non-additive gene action indicating the scope of hybrid development in carrot for horticultural and quality traits rich breeding.

The analysis of variance suggested the significance of SCA in developing various heterotic cross combination. Majority of the quantitative characters and qualitative characters showed predominance of dominance variance (σ^2D) and greater than unity value of degree of dominance suggested over-dominance in the action of genes for commercial and antioxidant traits in carrot. Further, the $\sigma^2_{gca}/\sigma^2_{sca}$ and σ^2A/D recommend the non-additive genetic control of all the traits, supported with high level of σ^2_{sca}, stipulate the possibility gene action and heterosis study in crop improvement programme of carrot with respect to these commercial and quality traits. Further, the ratio of additive to dominance variance (σ2A/D) and predictability ratio (σ2gca/σ2sca) was observed as less than unity for all the traits suggesting prevalence of non-additive gene action. The estimate of variance due to dominance variance (σ2A/D) for root length (0.80), root diameter (0.29), core diameter (0.24), and root weight (0.19) and yield (0.23). Similarly, estimate of variance due to predictability ratio (σ2gca/σ2sca) for root length (0.24), root diameter (0.22), core diameter (0.19), root weight (0.21) and yield (0.19) consecutively observed less than unity indicating the prevalence of non- additive gene

action for these important traits. The significant year × genotype interaction for the TCC and β-carotene content revealed the role of few major genes controlling expression of carotenoids in carrot root. The positive association of SCA with heterosis exhibited the possibility of non-additive gene effects in controlling the expression of various character. While lower level to mid-level of h^2_{ns} was observed for most of quantitative characters and commercial traits in study advocating non-additive genetic control traits, which might largely govern by epistatic backgrounds.

6.2.1 Combining ability and heterosis

6.2.1.1 Quantitative characters traits

The GCA estimates revealed that the CMS lines KT-8542A (1.92***), KT-28A (0.54***), KT-39A (0.017) were top three combiner for root length and CMS lines KT-98A (6.27***), KT-8542A (4.40***), KT-28A (3.31***) were best combiner for root weight and can be used in developing superior hybrids. Similarly, for the core diameter, CMS lines KT-8542A (25.33***), KT-62A (-4.17), KT-10A (-3.97) and for root diameter CMS lines, KT-10A (5.93***), KT-80A (1.73***), KT-28A (1.00***) were found top three general combiner and could be utilized as parents for developing hybrids with thick flesh roots. Based on GCA for root yield, the top three CMS lines were KT-8542A (3.54***), KT-98A (1.15**), KT-28 (0.59) and they can be used as female parent in developing hybrids for higher yield.

The specific combining ability (SCA), which contemplate the loci having non-additive and epistatic gene effects, can employed to find out specific heterotic crosses with respect to many trait of interest. Significant differences were observed in SCA effects of 100 crosses and the heterotic crosses with significant SCA effect in desirable direction were observed for all the traits indicating the role of non-additive gene action in the genetic control of these traits. Among the 100 hybrids, 19, 27 and 41 cross combination and has performed significant SCA

effects for few horticultural traits viz., root traits namely, root length, root to shoot ratio and root diameter. Similarly for other the commercial traits viz. gross root weight (GRW), root size (RS), net root weight (NRW), out of 100 crosses, 27,22 and 33 (Table 4.7). For the quantitative characters, in 100 crosses, 18 and 23 crosses showed significantly SCA effects for leaf length (LL), leaf weight (LW) respectively. For the harvest index (HI%) and total marketable yield (TMY), among 100 hybrids, 22 and 20 hybrids displayed significantly high positive SCA effects, respectively (Table 4.7). Whereas, significantly high positive SCA estimate of core size was observed in KT-8542 x New Kuroda (196.73 ***) (significant GCA x significant GCA), followed by KT-28 x PY-1(5.20) (poor combiner × poor GCA), KT-39 x KS -50 (4.66) (poor combiner × poor GCA). Similarly, for root diameter, the highest positive significant SCA estimate was observed in the hybrid KT-10 × New Kuroda (26.42***) (significant GCA × good general combiner) followed by KT-47 × KS -22 (11.62***) (poor combiner × significant GCA) and KT-98 × PN-1 (8.19***) (significantly poor combiner × significantly poor combiner). As far as the root length is concern, the greater SCA effect recorded in the hybrid cross of KT-47 × KS -21 (2.30***) (non-significant GCA × significant good GCA) followed by KT-8542 × PN-1 (2.36***) (significant GCA × good general combiner) and KT-62 × KS -50 (2.16***) (poor combiner × non-significant GCA). For the marketable net root weight, hybrid KT-98 x PN-1 (49.88***) (significant general good combiner × non-significant poor combiner) KT-98 x New Kuroda (23.52***) (significant general good combiner × significant good combiner), KT-95 x KS -73 (21.40***) (non-significant poor combiner × poor combiner) showed highest positive significant SCA effects. Importantly, for the yield, the cross KT-98 × PN-1 (12.44***) (significant GCA × good combiner) exhibited highest significant positive SCA effect followed by the cross combination KT-10 × NK-1 (8.29***) (good combiner × poor combiner) and KT-8542 × New Kuroda (significant good combiner × significant good GCA).

At variance with of GCA and SCA of various cross combination, indicates of complexity of interaction of genes for traits. The most of testcross progenies shows high SCA in positive direction but one of the parents exhibiting poor GCA effects (poor × good general combiner or good × poor general combiner). It may be due to good combiner parent exhibiting suitable additive effects and poor combiner parent displaying epistatic effects. Simultaneously, few crosses has poor SCA effects, despite involvement of parents with significant GCA, might be attribute to deficiency of any interaction among the positive alleles of genes. Further, our findings demonstrate that much attention need to give for both GCA and SCA in the selection suitable parents for the development of heterotic hybrids.

Average and better parent heterosis

Similarly, among the 100 crosses, 46 hybrids exhibited the significant heterosis for root length in desirable direction over mid parent heterosis. The highest heterosis in desirable direction for roots length was observed in the cross KT-8542 x KS -21 (33.76 %) followed by KT-10 x NK-1 (22.51%) and KT-47 x KS -21 (21.03%). The highest significant heterosis in desirable direction for root diameter was recorded in the hybrid Kt-10 x New Kuroda (100.68%), followed by KT-47 x KS-22 (59.3%) and Kt-62 x NK-1 (39.24%). Similarly, the highest heterosis over mid parent in desirable negative direction for core diameter was observed in the cross KT-28 x KS -21 (-53.52%) followed KT-39 x PY-1 (-50.78%) and KT-39 New Kuroda (-47.25%). The highest heterosis over mid parent in desirable direction for root weight was observed in the cross KT-98 x PN-1 (61.14%) followed by KT-8542 x KS-50 (45.76%) and Kt-8542 x New Kuroda (44.82%). Significantly high heterosis in desirable positive direction for total marketable yield over mid parent was recorded in the cross KT-98 x PN-1 (55.79%) followed by KT-8542 x New Kuroda (45.70%) and KT-8542x KS -50 (37.03%).

The highest significant heterosis over better parent in desirable direction for root length was found in the cross combination Kt-8542 x KS-21 (24.42%) followed by Kt-8542 x PN-1 (21.41%) and Kt-47 x KS-21 (14.03%). Likewise for the root weight the highest significant heterosis over the better parent was observed in the cross Kt-98 x PN-1 (87.79%) followed by Kt-8542 x New Kuroda (41.45%) and Kt-8542 x KS-50 (40.22%). The significantly high heterosis in positive direction for root yield was found in Kt-98 x PN-1 (45.94%) followed by Kt-8542 x New Kuroda (39.02%).

Economic Heterosis

The estimates of heterosis for various quantitative characters traits of top 3 hybrids over commercial check were documented. The heterosis for root length, core diameter and root diameter ranged from 8.55% (KT-10 x NK-1) to 17.95% (KT-8542 x KS -21), 6.00% (KT-8542 x KS -22) to 92.67% (KT-10 x New Kuroda), -0.46% (KT-8542 x KS -50) to -59.02% (KT-28 x KS -21), respectively. For the root length, the highest heterosis over commercial check in desirable direction was observed in the cross, KT-8542 × KS -21 (17.95%) followed by KT-8542 × PN-1 (15.11 %) then KT-10 × NK-1 (8.55%). For the core diameter, the highest heterosis over commercial check in desirable negative direction was observed in the cross, KT-28 x KS -21 (-59.02%) followed by KT-62 x KS -73 (-53.17 %), KT-39 x Py-1 (--53.17%). Similarly, significantly high heterosis over commercial check in desirable direction for root diameter was recorded in the cross, KT-10 × New Kuroda (92.67%) followed by KT-47 × KS-22 (44.50%), KT-95 x KS -50 (32.45 %). Highest standard hetrosis heterosis in desirable direction for the root weight, observed in the hybrid KT-98 x PN-1 (52.69%) followed by KT-98 x New Kuroda (35.22%) and KT-8542 x New Kuroda (27.21%). The range of heterosis over commercial check for marketable yield ranged from 19.36 % to 51.07. For the root yield, the hybrid KT-98 x PN-1 (51.07 %) followed by KT-8542 x New Kuroda (34.11%) and KT-

8542 x KS-22 (25.93%) exhibited significantly high heterosis over commercial check in the favourable direction.

6.2.1.2 Antioxidant traits

The significant GCA effects of parents exhibited in positive direction, credit to activity of genes, which are experience additive effects, and additive versus additive interactions and can be used through hybrid breeding followed by selection programmes. The estimates of GCA effects revealed that the CMS line CMS lines KT-28A (2.75***), KT-80A (1.91***), KT-95 and KT-28A (2.84***), KT-80A (1.44***), KT-95 (0.85***) was good general combiner for β-carotene and total carotenoid content respectively, KT-98A (0.45***) for CUPRAC, KT-80A (0.08***) for FRAP, and KT-8542A (87.81***) for phenols could be used as parents in hybrid breeding programs. The line KT-47 exhibited significant GCA effects for FRAP (0.03**), ascorbic acid (1.13**), phenols (32.62**) except all other traits. The line KT-62A found significantly poor general combiner for all the antioxidant compounds except CUPRAC, total phenol. Out of 100 hybrids, for the CUPRAC content, the 45 crosses exhibited positive significant SCA effects in desirable direction. Among the 100 test cross progenies (Table 4.15), the high SCA effects in desirable direction were found in 31 crosses for FRAP content; 32 crosses for ascorbic acid content; 32 crosses for total phenolic content; 34 crosses for anthocyanin concentration; 40 crosses for lycopene content; 41 crosses for β-carotene concentration and 40 crosses for total carotenoid content. As far to CUPRAC content is concern, the significant SCA effect in positive direction was observed in the cross combination KT-98 x KS-50 (5.06***) (good general combiner × good general combiner) followed by KT-47 x PN-1 (0.33***) (good general combiner × poor general combiner) and KT-28 x KS-73 (0.30***) (poor general combiner × poor general combiner). Similarly, for the FRAP content, the hybrids KT-39 x KS-20 (0.31***) (good general combiner × poor combiner GCA) and

hybrid KT-80 x KS-50 0.25*** (good general combiner × good general combiner) had significantly the highest value of SCA effects in desirable direction.). These two hybrids depicting highest SCA for FRAP content were followed by the crosses, KT-98 x PY-1 (0.16***) (good general combiner × good general combiner). Out of 100 hybrids, 27 and 17 hybrids exhibited significant heterosis in desirable direction for the ascorbic acid content over mid parent and better parent, respectively. The cross KT-47 x KS-20 (155.58**) (good GCA combiner x poor GCA combiner) followed by KT-95 x New Kuroda, (129.44**) (good GCA combiner x poor GCA combiner) showed significantly highest heterosis for ascorbic acid content over mid parent and better parent, respectively. The significantly highest heterosis for phenolic content in desirable direction was observed in the 15.38 % (KT-98 x KS-59) to 1546.38 % (KT-62 x KS-21) mid parent. The hybrid 6.15% (KT-10 x KS-50) to 320.60% (KT-62 x KS-21) and 8.03 % (KT-39 x PN-1) to 225.10 % (KT-39 x PY-1), respectively exhibited significantly highest heterosis over both mid parent and better parent in desirable direction for beta–carotene content. Among 100 crosses, 79 and 73 crosses, respectively, exhibited significant heterosis over mid parent and better parent for total carotenoid content. The significantly high total carotenoid content, the mid parent and better parent heterosis was observed, ranged from 6.76 % (KT-62 x KS-20) to 390.38% (KT-28 x KS-59) and 19.18% (KT-80 x PY-1) to 312.88 % (KT-98 x PY-1), respectively. For the antioxidant capacity related traits, CUPRAC and FRAP the estimates of standard hetrosis varied from -9.51% (KT-47 x PN) to 737.63% (KT-98 x KS -50) and -12.82% (KT-62 x PY-1) to -94.23% (KT-7*KS -20) respectively. Similarly, for the FRAP content the measure of significant standard heterosis was depicted in the heterotic cross KT-47A × KS-59 (-22.44%) followed by KT-47A × KS-21(19.23%). The measures of standard heterosis for the ascorbic acid content varied from 8.45% (KT-28 x KS -21) to (74.23%) KT-47 × KS -20. The cross combinations, KT-47A × KS-20 (74.23%), KT-95A × New Kuroda (12.45%) depicted significantly high positive

heterosis for the ascorbic acid content in desirable direction. The significantly highest estimates of standard hetrosis for the total phenolic content in desirable direction was recorded in the crosses KT-98A × PN-1(173.69%) followed by KT-98A × KS-50 (157.35%) and KT-8542A × KS-59(108.56%). The hybrid combination KT-62A × KS-21 (278.67%) followed by KT-7A × KS-20 (114.67%) and KT-8542A × KS-50 (98.00%) exhibited significantly high estimates of heterosis for the anthocyanin content. Similarly, the cross combination KT-98A × KS-59 (4.60%) followed by KT-47A × PN-1(-46.34%) and KT-98A × NK-1(-2.36%) exhibited significantly high estimates of heterobeltiosis for lycopene content. The hybrid combination KT-62A × KS-21(186.87%) followed by KT-80A × New Kuroda (117.09%) and KT-62A × KS-59 (114.68%) exhibited significantly high standard heterosis in desirable direction for the β-carotene content. The significantly high estimates of heterosis in desirable direction for the total carotenoid content was observed in the cross combinations KT-28A × KS-59 (260.94%) KT-98A × PY-1 (133.91%) and KT-98A × KS-22 (124.61%).

6.3 Molecular diversity in parental lines

As quantitative characters markers are also widely used for genetic diversity analysis, but they do not provide true insights into extent of genetic variation in the studied germplasm, as they are highly influenced by environmental factors. Nowadays, molecular markers have been proved powerful tool to assess the genetic diversity within landraces, species, and analysis of population genetic structure depicting true image of extent of genetic variation and gene flow in the existing germplasm. Very high allele frequency of overall 511 alleles through 67 SSR markers in 20 parental CMS and tester lines with average allelic frequency of 5.87 alleles per locus was recorded suggesting the true sense of genetic variability in the studied parental lines.

High estimates of mean expected heterozygosity (H_e), i.e. 0.68 was found which designate high genetic variation is. The polymorphic information content (PIC) as a measure

of informativeness of a marker locus is useful in linkage study. The PIC analysis classified all the 67 polymorphic loci (g-SSRs) firstly slightly informative, then reasonably and finally highly informative markers as per PIC content, indicating ability in genetic differentiation of CMS and tester lines of carrot under study.

6.4 Characterization based on floral traits

Different floral deformities have been observed in male sterile lines viz., reduction in floral size and petaloid anthers. In this regard the CMS lines were also characterized for different floral traits. The examination on floral characters in CMS and its maintainer lines presented in Table 4.20. It has been seen that Green petal colour and light green petaloid were predominant in CMS lines. Variation in presence of light green/light green mid-rib in petaloid was also encountered in the CMS lines. The lines KT-7A had white petaloid while a range of white and greenish white petaloid colours were also seen in KT-28A, KT-39A and KT-10A, KT- 47A, KT-62A, KT-80A, KT-98A and KT-8542A respectively. However only 'petaloid' type CMS was observed and none of the CMS lines showed carpel-like structure (carpeloid). The Petaloid shape was identical as it was spoon type in all CMS lines; in spoon type, straight and curved petals were also seen. The prominent variation observed as the presence of light green, green mid-rib in petaloids, spoon type straight and curved petals encountered across the carrot CMS lines (Table 4.20). This profound diversity in petaloid shape and colour pattern may be some candidate genetic background of the transformed CMS lines, however, which needs further examination. The widest petals were observed in the CMS lines KT-95A (50914.51 x 1676.02 µm) , KT-10A (2644.97 x 1157.06 µm) and KT-8542A (2078.98 x 1456.56 µm). The ratio of petal length to petal width was >1 in the CMS line KT-10A indicating the great reduction in petal width relative to petal length with the temperate cytoplasm. Kalia et al. (2019) reported similar results in the CMS lines of tropical depicting the ratio of petal length to petal width > 1 depicting a considerable change in petal size. The considerable differences were also

observed in all the CMS lines with respect to style length and the longest style was observed in the CMS line. The longest long style were observed in the CMS line KT-47A (3116.35 µm), KT-95A (2279.80 µm) and KT-39A (1362.43 µm). Nectary size as well as ovary development was proper in all the observed CMS lines, indicating better potential for seed setting.

Conclusion

- The significant mean squares of parents and their crosses, revealed the presence of sufficient genetic variation, which can be utilized for crop improvement programme through heterosis breeding. CMS lines KT-39A (85.33 days ± 1.53), KT-47A (90.33 days ± 1.53) and KT-28A (90.67 days ± 1.53) were earliest maturity and can be better used for development of hybrids with early in maturity. The carrot genotypes with small core length are desirable for having thick flesh. The smallest core diameter found in genotype, KT-62A (8.00 mm±0.02) followed by KT-47A (9.00 mm±0.15) and KT-28A (11.00 mm±0.01) as revealed by mean performance of parents. The widest root diameter found in CMS lines, KT-28 (46.67 mm±0.92), KT-47A (45.00mm± 0.46), KT-95A (43.33mm±0.13). Subsequently, these lines can be utilized for hybrid breeding of coreless roots with high cortex thickness. The CMS lines KT-28A (90.77g ±0.87), KT-7A (82.00g±0.72), KT-39A (79.50g±1.17) and KT-7A (25.50 cm±0.11), KT-80A (24.00cm±1.32), KT-10A (22.50cm±0.58) performed better with respect to root weight and root length respectively. The results also revealed that the CMS lines, KT-28A (36.30 tonnes/ha.±0.34), KT-7A (32.79 tonnes/ha ±0.28) and KT-10A (31.40 tonnes/ha±0.32) could be better used as female parent for developing high yielding hybrids in carrot.
- The estimates of heterosis for various quantitative characters traits of top 3 hybrids over commercial check are as follows. The heterosis for root length, core diameter and root

diameter ranged from 8.55% (KT-10 x NK-1) to 17.95% (KT-8542 x KS -21), 6.00% (KT-8542 x KS -22) to 92.67% (KT-10 x New Kuroda), -0.46% (KT-8542 x KS -50) to -59.02% (KT-28 x KS -21), respectively. For the root length, the highest heterosis over commercial check in desirable direction was observed in the cross, KT-8542 × KS -21 (17.95%) followed by KT-8542 × PN-1 (15.11 %) then KT-10 × NK-1 (8.55%). For the core diameter, the highest heterosis over commercial check in desirable negative direction was observed in the cross, KT-28 x KS -21 (-59.02%) followed by KT-62 x KS -73 (-53.17 %), KT-39 x Py-1 (--53.17%). Similarly, significantly high heterosis over commercial check in desirable direction for root diameter was recorded in the cross, KT-10 × New Kuroda (92.67%) followed by KT-47 × KS-22 (44.50%), KT-95 x KS -50 (32.45 %). Highest standard hetrosis heterosis in desirable direction for the root weight, observed in the hybrid KT-98 x PN-1 (52.69%) followed by KT-98 x New Kuroda (35.22%) and KT-8542 x New Kuroda (27.21%). The range of heterosis over commercial check for marketable yield ranged from 19.36 % to 51.07. For the root yield, the hybrid KT-98 x PN-1 (51.07 %) followed by KT-8542 x New Kuroda (34.11%) and KT-8542 x KS-22 (25.93%) exhibited significantly high heterosis over commercial check in the favourable direction.

- For enhancing the antioxidant value and quality breeding, the CMS parental lines viz., KT-8542A (0.56 µmoltrolox/g±0.017), KT-80A (0.54 µmoltrolox/g ±0.013), KT-39A (0.52 µ moltrolox/g ±0.022), and KT-39A (0.34 µmoltrolox/g ±0.007), KT-95A (0.28 µmoltrolox/g ±0.012), KT-98A (0.18 µmoltrolox/g ±0.00) performed better for CUPRAC and FRAP content respectively. Marked differences were observed in the parental genotypes for the ascorbic acid content and the mean value for ascorbic acid content among the parental CMS lines ranged from 2.44 mg/100g (KT-95A) to 10.23 mg/100g (KT-62 A). The three lines KT-62 A (10.23±0.02), KT-28 A (6.78±0.13), KT-

80 A (6.43±0.14) performed better for ascorbic acid content. The mean value of total phenolic content and anthocyanins content among the CMS lines was ranged from 185.63 mg of gallic acid/100 g FW (KT-62 A) to 622.53 mg of gallic acid/100 g FW (KT-10A) and 0.05 mg/100g (KT-95 A) to 0.29 mg/100g (KT-10A), respectively. The lines KT-10A (622.53 mg of gallic acid/100 g FW), KT-28 (568.98 mg of gallic acid/100 g FW), KT-39A (541.88 mg of gallic acid/100 g FW) and KT-10A (0.29mg/100g), KT-39A (0.24 mg/100g), KT-28A (0.20 mg/100g) gave higher mean performance for total phenolic content and anthocyanins content. For beta-carotene content and total carotenoid, top 3 lines were KT-47A (3.92µg/100ml ±0.10), KT-8542A (3.77µg/100ml±0.16), KT-7A (3.36µg/100ml±0.15) and KT-62A (4.34mg/100g±0.09), KT-80A (2.49 mg/100g ±0.11), KT-28A (2.33 mg/100g ±0.07), respectively.

- For the antioxidant capacity related traits, CUPRAC and FRAP the estimates of standard heterosis varied from -9.51% (KT-47 x PN) to 737.63% (KT-98 x KS -50) and -12.82% (KT-62 x PY-1) to -94.23% (KT-7 x KS -20), respectively. Similarly, for the FRAP content the measure of significant standard heterosis was depicted in the heterotic cross KT-47A × KS-59 (-22.44%) followed by KT-47A × KS-21(19.23%). The measures of standard heterosis for the ascorbic acid content varied from 8.45% (KT-28 x KS -21) to 74.23% (KT-47 × KS -20). The cross combinations, KT-47A × KS-20 (74.23%) and KT-95A × New Kuroda (12.45%) depicted significantly high positive heterosis for the ascorbic acid content in desirable direction. The significantly high estimates of standard hetrosis for the total phenolic content in desirable direction was revealed in the crosses KT-98A × PN-1(173.69%) followed by KT-98A × KS-50 (157.35%) and KT-8542A × KS-59(108.56%) . The hybrid combination KT-62A × KS-21 (278.67%) followed by KT-7A × KS-20 (114.67%) and KT-8542A × KS-50

(98.00%) exhibited significantly high estimates of heterosis for the anthocyanin content. Similarly, the cross combination KT-98A × KS-59 (4.60%) followed by KT-47A × PN-1(-46.34%) and KT-98A × NK-1(-2.36%) exhibited significantly high estimates of standard heterosis for lycopene content. The hybrid combination KT-62A × KS-21(186.87%) followed by KT-80A × New Kuroda (117.09%) and KT-62A × KS-59 (114.68%) exhibited significantly highest standard heterosis in desirable direction for the β-carotene content. The significantly high estimates of heterosis in desirable direction for the total carotenoid content was observed in the cross combinations KT-28A × KS-59 (260.94%) KT-98A × PY-1 (133.91%) and KT-98A × KS-22 (124.61%).

6.2 Variance analysis and genetic parameters

- The adequate knowledge of nature of gene action, genetic components of variance (additive, dominance and epistasis) accompanied with combining ability and allied genetic parameters such as heritability, degree of dominance, predictability ratio is must for plant breeders in the pursuit of rendering crop genetic improvement for different economically important traits. The analysis of variance exhibited significant differences in majority indicated the scope for development of hybrids with higher concentration of these compounds. The estimate of variance due to dominance variance (σ2A/D) for root length (0.80), root diameter (0.29), core diameter (0.24), and root weight (0.19) and yield (0.23). Similarly, estimate of variance due to predictability ratio (σ2gca/σ2sca) for root length (0.24), root diameter (0.22), core diameter (0.19), root weight (0.21) and yield (0.19), consecutively observed less than unity indicating the prevalence of non- additive gene action for these important traits. Concurrently, the high significant SCA effects of top heterotic crosses revealed the value of SCA and

non-additive gene action for heterosis breeding in temperate carrot for antioxidant pigments.

- GCA estimates of CMS lines KT-28A (2.75***) and KT-28A (2.84***) was found good general combiner for β-carotene and total carotenoid content respectively, KT-98A (0.45***) for CUPRAC, KT-80A (0.08***) for FRAP, and KT-8542A (87.81***) for phenols could be used as parents in hybrid breeding programs. Hence decisively can be used as breeding material for enhancing antioxidant activity in temperate carrot. The current investigation highlighted the importance of both GCA and SCA in the selection of suitable parents for the improvement of yield and commercial traits and predicting appropriate breeding strategies for the crop genetic improvement in temperate carrot. The GCA measures confirm that the CMS lines, KT-10A, KT-28A and KT-80A and tester KS-21, KS-22, KS-50 and New Kuroda had significant GCA effects in useful direction with respect to root diameter at root harvesting stage. The CMS lines, KT-8542 and KT-28 and tester KS-20, KS-21 and KS- 22, exhibited significantly high GCA effects for root length. For marketable net root weight, CMS lines KT -100A, KT-28A, KT-98A and KT- 8542A showed considerable high GCA. Similarly, CMS lines, KT-100A, KT-98A and KT-8542A had significantly high GCA for marketable yield.
- Highly significant correlation of SCA with heterosis suggested the role of non-additive gene effects in heterosis. Majority of traits were found to be under the genetic control of both additive and non-additive gene effects, as revealed by significant mean squares of lines, testers and line versus tester interactions. Whereas, significant highest positive SCA estimate of **core size** was observed in KT-8542 x New Kuroda (196.73 ***), followed by KT-28 x PY-1(5.20) and KT-39 x KS -50 (4.66). Similarly, for root diameter, the highest positive significant SCA estimate was observed in the hybrid KT-10 × New Kuroda (26.42***) followed by KT-47 × KS -22 (11.62) and KT-98 × PN-

1 (8.19***). As far as the root length is concern, the greater SCA effect recorded in the hybrid cross of KT-47 × KS -21 (2.30***) followed by KT-8542 × PN-1 (2.36***) and KT-62 × KS -50 (2.16***). For the marketable net root weight, hybrid KT-98 x PN-1 (49.88***) KT-98 x New Kuroda (23.52***), KT-95 x KS -73 (21.40***) showed highest positive significant SCA effects. Importantly, for the yield, the cross KT-98 × PN-1 (12.44***) exhibited highest significant positive SCA effect. After that, the cross combination KT-10 × NK-1 (8.29***) followed by KT-8542 × New Kuroda exhibited significant positive SCA effects for yield character.

- The result suggested that in the short term the top three hybrids for root yield, KT-98 x PN-1 (54.20t/ha), KT-98 x New Kuroda (47.40t/ha) and KT-8542 x KS -22 (43.80 t/ha) should be proposed under multilocation trial under AICRP (Vegetable Crops) for their identification and release as commercial hybrids.
- In long term there is need to study the further the inheritance of different economically important traits including root yield to confirm the different components of additive and non-additive gene effects. The in depth and extensive study will facilitate the improvement programme of temperate carrot in developing high yielding varieties and hybrids with better nutritional traits.
- Significant differences found for most of the traits among parental CMS and tester lines using quantitative characters and molecular markers. The 67 pairs of SSR markers depicting high PIC of > 0.5 can be better used for predicting the genetic diversity in temperate carrot genotypes.
- The findings of our study further suggested that genetic distances of genomic-SSR based molecular data can be used as reliable predictor of heterosis for commercial traits in CMS and tester based heterotic crosses of temperate carrot. Although, the contrasting results obtained in different studies by different researchers previously across the crops

regarding efficacy of genetic distances in prediction of heterosis, invites further investigation with a different sets of large number of molecular markers covering entire genome, and different set of parental germplasm, in multiple standard environments.

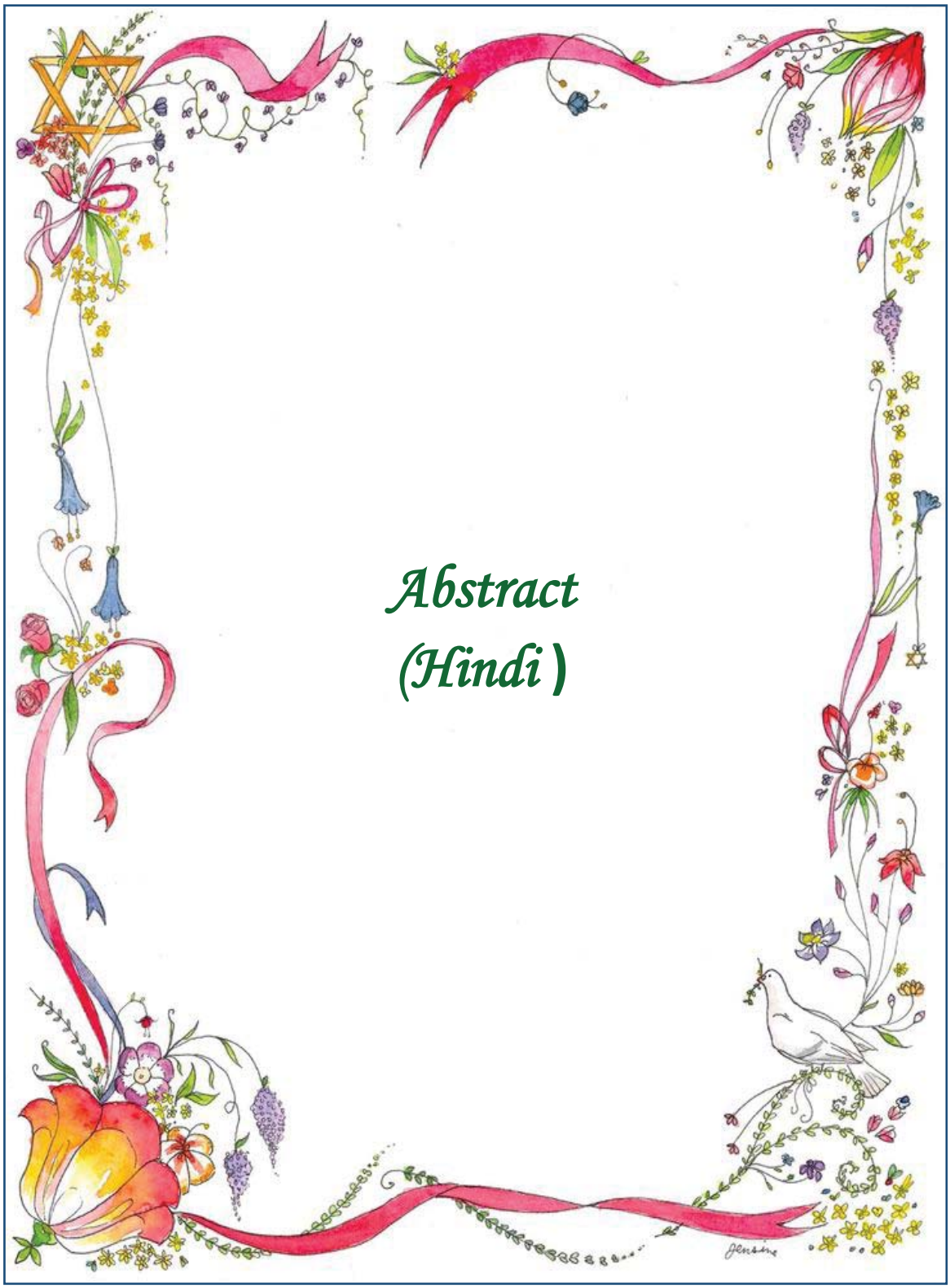
- The mitochondrial markers can be effectively utilized for identification of cytoplasm types, assessment of cytoplasmic diversity and variability in mitochondrial genome of male sterility systems. The information obtained would be helpful in determining the origin of cytoplasmic sources in different CMS lines and further understanding of molecular mechanism of male sterility in temperate carrot.

Abstract (English)

Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus)* using Cytoplasmic male sterile (CMS) lines

Abstract

Carrot belonging to plant family Apiaceae is one of the most widely consumed root crops rich in bioactive compounds and phytochemicals. The variation in mitochondrial genome cytoplasm based 10 male sterile lines was analyzed using mitochondrial (genome specific and mt-SSR) markers. The parental CMS lines and fertile testers were crossed to develop 100 F_1 hybrids in line × tester mating design. The resulting 100 test cross progenies along with 1 standard checks were evaluated in with three replications at Naggar Experimental Farm of ICAR-IARI, Regional Station, Katrain, Himachal Pradesh. As there has been increasing interest in pigmented carrots rich in carotenoids and flavonoids as source of natural food dye. On account of antioxidant and anticancer properties, the consumption of carrot and its by-products is increasing steadily. Hence, to meet the increasing demand with superior horticultural and quality traits, the identification of ideal parental chemotypes or inbreds of carrot with desirable combining ability is of utmost importance for the generation of quality cultivars. The petaloid type cytoplasmic male sterility (pt-CMS) has been instrumental in developing heterotic hybrids in carrot. In this context, the 10 pt-CMS lines of temperate carrot developed after more than nine generation of backcrossing were crossed with 10 inbreds used as testers in line × tester mating design to generate 100 testcross progenies. The resulting 100 hybrids along with 20 parental types and commercial checks were evaluated for thirteen horticultural traits and eight different bioactive compounds consecutively for two years. The pooled estimates of variance analysis over the years revealed significant mean squares of lines, testers and line × testers, which indicated the influence of both additive and non-additive gene effects in the expression. The pooled analysis estimates of *per se* performance, principal component analysis and dendrogram analysis over the years indicated remarkable genetic variation among the parental types for their exploitation in heterosis breeding. The higher magnitude of σ^2_{sca} as compared to σ^2_{gca} highlighted the relevance of specific combining ability in the generation of heterotic crosses for both horticultural and bioactive compounds. The CMS lines KT-8542A (3.54**) , KT-98A (1.15**) and KT-28A (0.59) were good combiner for root yield . CMS lines viz. KT-8542A (1.92**) could be better as female parent for higher root length. CMS lines KT-10A (5.93**), for cortex thickness and core diameter KT-8542A(25.33**) and could be utilized as parents for developing hybrids with thick flesh and coreless roots. The crosses KT-98 x PN-1, KT-98 x New kuroda can be recommended for further evaluation trial for developing hybrids with higher marketable roots and its contributing traits. The significant year × genotype interaction for the TCC and β-carotene content revealed the role of few major genes controlling expression of carotenoids in carrot root. The positive association of SCA with heterosis indicated the influence of non-additive gene effects in controlling the expression of traits. The significant genotype × environment interaction variance for total carotenoid and β-carotene indicated the role of both genotype and environment controlling expression of these traits, which necessitated the need of multi-year and multi-environment evaluation for the selection of genotypes for carotenoid content. The pooled analysis results also determined that the carotenoid content in carrot root is under the genetic control of few major genes (oligogenic). The high estimates of h^2_{ns} over the years for carotenoid and β-carotene indicated that selection would be effective for these traits. GCA effects over the years CMS lines KT-28A (2.75***) and KT-28A (2.84***) shown good general combiner for β-carotene and total carotenoid content respectively, KT-98A (0.45***) for CUPRAC, KT-80A (0.08***) for FRAP, and KT-8542A (87.81***) for phenols could be used as parents in hybrid breeding programs. The significantly highest heterosis for phenolic content in desirable direction was observed in the 15.38 % (KT-98 x KS-59) to 1546.38 % (KT-62 x KS-21) mid parent. The hybrid 6.15% (KT-10 x KS-50) to 320.60% (KT-62 x KS-21) and 8.03 % (KT-39 x PN-1) to 225.10 % (KT-39 x PY-1), respectively exhibited significantly highest heterosis over both mid parent and better parent in desirable direction for beta–carotene content. Significantly high total carotenoid content over the mid parent and better parent heterosis was observed, 6.76 % (KT-62 x KS-20) to 390.38% (KT-28 x KS-59) and 19.18% (KT-80 x PY-1) to 312.88 % (KT-98 x PY-1), respectively The molecular analysis revealed that Out of 100 microsatellite primers, 67 primers showed high polymorphism among the parental lines. The PIC content ranged from 0.35 to 0.86 and genetic distance varied from of 0.46 to 0.89, found significant association of genetic distance based on polymorphic genomic-SSR with heterosis for commercial traits indicated the utility of genetic distances in prediction of heterosis in carrot. Moreover green petal colour and light green petaloid were predominant in CMS lines, encountered variation in their mid-ribs. Variation in petaloid shape and colour pattern could may be due to influence of genetic background of the transformed CMS lines, however, it need further investigations. The overall results obtained would be instrumental for carrot breeders, geneticists and food scientists for enhancing potential of carrot for agro-food, pharmaceutical and natural pigment industry.

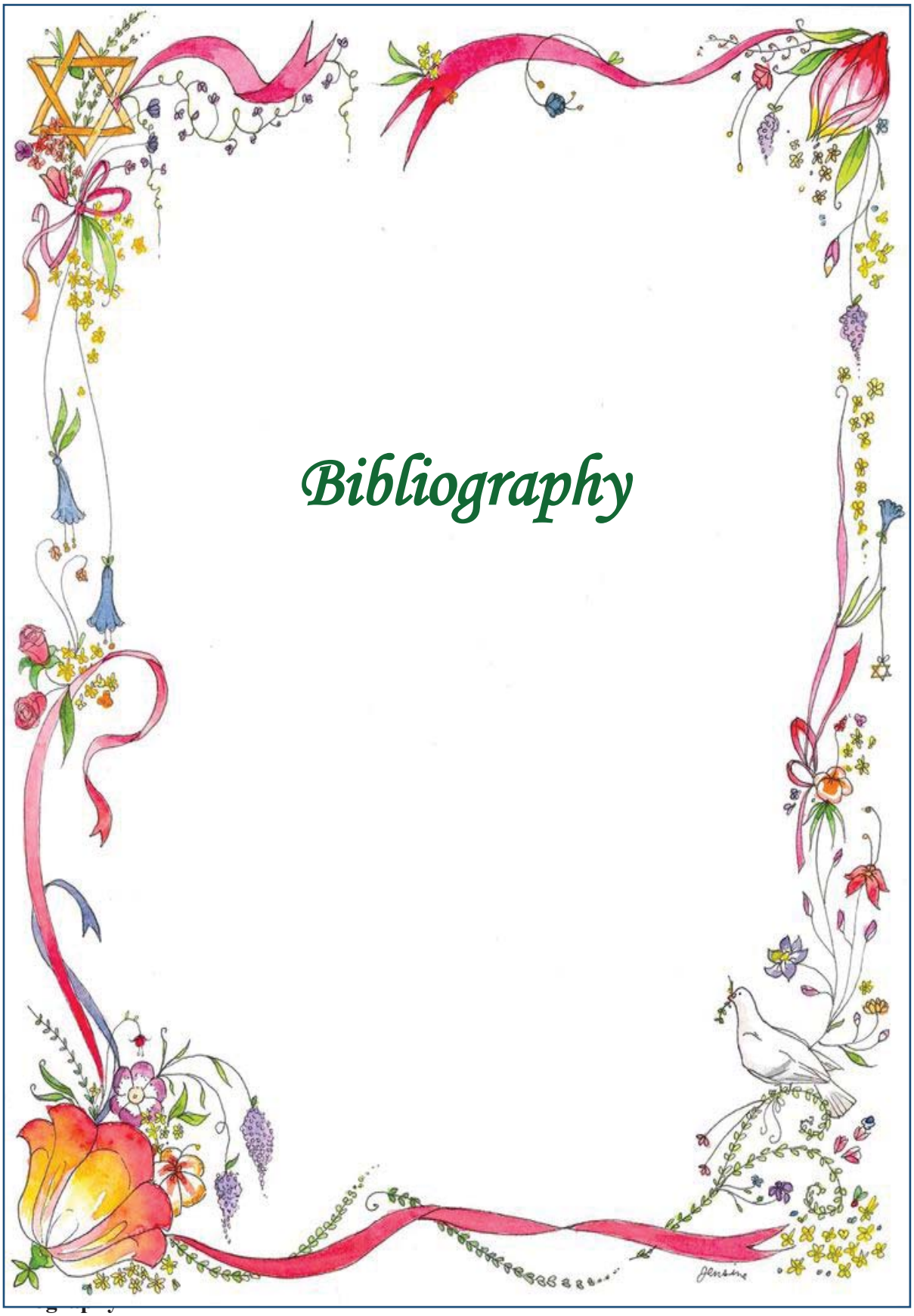


Abstract (Hindi)

सिएमएस वंशक्रमों का उपयोग कर शीतोष्ण गाजर (डॉकस कैरोटा ली.) में अनुवंशिक अध्ययन

सार

पादप परिवार अपियासी से संबंधित गाजर जैव सक्रिय यौगिकों और फाइटोकेमिकल्स से भरपूर जड़ वाली फसलों में से एक है। माइटोकॉन्ड्रियल जीनोम साइटोप्लाज्म आधारित 10 पुरुष बाँझ लाइनों में भिन्नता का विश्लेषण माइटोकॉन्ड्रियल (जीनोम विशिष्ट और एमटी-एसएसआर) मार्करों का उपयोग करके किया गया था। पैतृक सीएमएस लाइनों और उपजाऊ परीक्षकों को लाइन × परीक्षक संभोग डिजाइन में 100 एफ 1 संकर विकसित करने के लिए पार किया गया था। परिणामी 100 परीक्षण क्रॉस संततियों के साथ 1 मानक जांच का मूल्यांकन आईसीएआर-आईएआरआई, क्षेत्रीय स्टेशन, कटरीन, हिमाचल प्रदेश के नग्गर प्रायोगिक फार्म में तीन प्रतिकृति के साथ किया गया था। चूंकि प्राकृतिक खाद्य डाई के स्रोत के रूप में कैरोटेनॉयड्स और फ्लेवोनोइड्स से भरपूर रंजित गाजर में रुचि बढ़ रही है। एंटीऑक्सीडेंट और कैंसर रोधी गुणों के कारण गाजर और इसके उपोत्पादों का सेवन लगातार बढ़ रहा है। इसलिए, बेहतर बागवानी और गुणवत्ता के लक्षणों के साथ बढ़ती मांग को पूरा करने के लिए, वांछित संयोजन क्षमता वाले आदर्श पैतृक रसायन या गाजर की नस्ल की पहचान गुणवत्ता वाले किस्मों की पीढ़ी के लिए अत्यंत महत्वपूर्ण है। गाजर में हेटेरोटिक संकर विकसित करने में पेटलॉइड प्रकार के साइटोप्लाज्मिक पुरुष बाँझपन (पीटी-सीएमएस) का महत्वपूर्ण योगदान रहा है। इस संदर्भ में, बैकक्रॉसिंग की नौ से अधिक पीढ़ी के बाद विकसित समशीतोष्ण गाजर की १० पीटी-सीएमएस लाइनों को १०० टेस्टक्रॉस संतानों को उत्पन्न करने के लिए लाइन × टेस्टर संभोग डिजाइन में टेस्टर्स के रूप में उपयोग किए जाने वाले १० इनब्रेड के साथ पार किया गया था। परिणामी 100 संकरों के साथ-साथ 20 पैतृक प्रकार और वाणिज्यिक जांचों का मूल्यांकन तेरह बागवानी लक्षणों और आठ अलग-अलग जैव सक्रिय यौगिकों के लिए लगातार दो वर्षों तक किया गया था। वर्षों में विचरण विश्लेषण के अनुमानित अनुमानों ने लाइनों, परीक्षकों और लाइन × परीक्षकों के महत्वपूर्ण माध्य वर्गों का खुलासा किया, जिसने अभिव्यक्ति में योगात्मक और गैर-योज्य दोनों जीन प्रभावों के प्रभाव का संकेत दिया। वर्षों से प्रति प्रदर्शन, प्रमुख घटक विश्लेषण और डेंड्रोग्राम विश्लेषण के जमा विश्लेषण अनुमानों ने हेटेरोसिस प्रजनन में उनके शोषण के लिए माता-पिता के प्रकारों के बीच उल्लेखनीय आनुवंशिक भिन्नता का संकेत दिया। σ^2gca की तुलना में σ^2sca के उच्च परिमाण ने बागवानी और जैव सक्रिय यौगिकों दोनों के लिए विषम क्रॉस की पीढ़ी में विशिष्ट संयोजन क्षमता की प्रासंगिकता पर प्रकाश डाला। CMS लाइन KT-8542A (3.54**), KT-98A (1.15**) और KT-28A (0.59) रूट यील्ड के लिए अच्छे कॉम्बिनर थे। सीएमएस लाइनें अर्थात। KT-8542A (1.92**) अधिक जड़ लंबाई के लिए महिला माता-पिता के रूप में बेहतर हो सकता है। CMS लाइन KT-10A (5.93**), कोर्टेक्स मोटाई और कोर व्यास KT-8542A (25.33**) के लिए और मोटे मांस और कोरलेस जड़ों के साथ संकर विकसित करने के लिए माता-पिता के रूप में उपयोग किया जा सकता है। क्रॉस केटी-98 x पीएन-1, केटी-98 x न्यू कुरोडा को उच्च विपणन योग्य जड़ों और इसके योगदान लक्षणों के साथ संकर विकसित करने के लिए आगे के मूल्यांकन परीक्षण के लिए अनुशंसित किया जा सकता है। टीसीसी और β-कैरोटीन सामग्री के लिए महत्वपूर्ण वर्ष × जीनोटाइप इंटरैक्शन ने गाजर की जड़ में कैरोटीनॉयड की अभिव्यक्ति को नियंत्रित करने वाले कुछ प्रमुख जीनों की भूमिका का खुलासा किया। हेटरोसिस के साथ एससीए के सकारात्मक जुड़ाव ने लक्षणों की अभिव्यक्ति को नियंत्रित करने में गैर-योज्य जीन प्रभावों के प्रभाव का संकेत दिया। कुल कैरोटीनॉयड और β-कैरोटीन के लिए महत्वपूर्ण जीनोटाइप × पर्यावरण अंतःक्रियात्मक भिन्नता ने इन लक्षणों की अभिव्यक्ति को नियंत्रित करने वाले जीनोटाइप और पर्यावरण दोनों की भूमिका का संकेत दिया, जिससे कैरोटीनॉयड सामग्री के लिए जीनोटाइप के चयन के लिए बहु-वर्षीय और बहु-पर्यावरण मूल्यांकन की आवश्यकता हुई। एकत्रित विश्लेषण परिणामों ने यह भी निर्धारित किया कि गाजर की जड़ में कैरोटीनॉयड सामग्री कुछ प्रमुख जीन (ऑलिगोजेनिक) के आनुवंशिक नियंत्रण में है। कैरोटीनॉयड और β-कैरोटीन के लिए वर्षों से h^2ns के उच्च अनुमानों ने संकेत दिया कि इन लक्षणों के लिए चयन प्रभावी होगा। वर्षों में जीसीए प्रभाव सीएमएस लाइनों केटी-28ए (2.75***) और केटी-28ए (2.84***) ने क्रमशः β-कैरोटीन और कुल कैरोटीनॉयड सामग्री के लिए अच्छा सामान्य संयोजन दिखाया, केटी-98ए (0.45 ***) के लिए FRAP के लिए CUPRAC, KT-80A (0.08***), और फिनोल के लिए KT-8542A (87.81***) को संकर प्रजनन कार्यक्रमों में माता-पिता के रूप में इस्तेमाल किया जा सकता है। वांछनीय दिशा में फेनोलिक सामग्री के लिए उल्लेखनीय रूप से उच्चतम हेटेरोसिस 15.38% (केटी-98 x केएस-59) से 1546.38% (केटी-62 x केएस-21) मध्य माता-पिता में देखा गया था। संकर 6.15% (KT-10 x KS-50) से 320.60% (KT-62 x KS-21) और 8.03% (KT-39 x PN-1) से 225.10% (KT-39 x PY-1), क्रमशः बीटा-कैरोटीन सामग्री के लिए वांछनीय दिशा में मध्य माता-पिता और बेहतर माता-पिता दोनों पर उच्चतम विषमता का प्रदर्शन किया। मध्य माता-पिता की तुलना में उल्लेखनीय रूप से उच्च कुल कैरोटीनॉयड सामग्री और बेहतर माता-पिता हेटेरोसिस देखा गया, 6.76% (KT-62 x KS-20) से 390.38% (KT-28 x KS-59) और 19.18% (KT-80 x PY-1)) से 312.88% (KT-98 x PY-1), क्रमशः आणविक विश्लेषण से पता चला कि 100 माइक्रोसेटेलाइट प्राइमरों में से 67 प्राइमरों ने पैतृक लाइनों के बीच उच्च बहुरूपता दिखाया। पीआईसी सामग्री 0.35 से 0.86 तक थी और आनुवंशिक दूरी 0.46 से 0.89 तक भिन्न थी, व्यावसायिक लक्षणों के लिए हेटेरोसिस के साथ पॉलीमॉर्फिक जीनोमिक-एसएसआर पर आधारित आनुवंशिक दूरी का महत्वपूर्ण जुड़ाव गाजर में हेटेरोसिस की भविष्यवाणी में आनुवंशिक दूरी की उपयोगिता को दर्शाता है। इसके अलावा सीएमएस लाइनों में हरी पंखुड़ी का रंग और हल्का हरा पंखुड़ी प्रमुख था, उनकी मध्य-पसलियों में भिन्नता का सामना करना पड़ा। पेटलॉइड आकार और रंग पैटर्न में बदलाव, परिवर्तित सीएमएस लाइनों की आनुवंशिक पृष्ठभूमि के प्रभाव के कारण हो सकता है, हालांकि, इसके लिए और जांच की आवश्यकता है। समग्र परिणाम गाजर प्रजनकों, आनुवंशिकीविदों और खाद्य वैज्ञानिकों के लिए कृषि-खाद्य, फार्मास्युटिकल और प्राकृतिक वर्णक उद्योग के लिए गाजर की क्षमता बढ़ाने के लिए सहायक होंगे।



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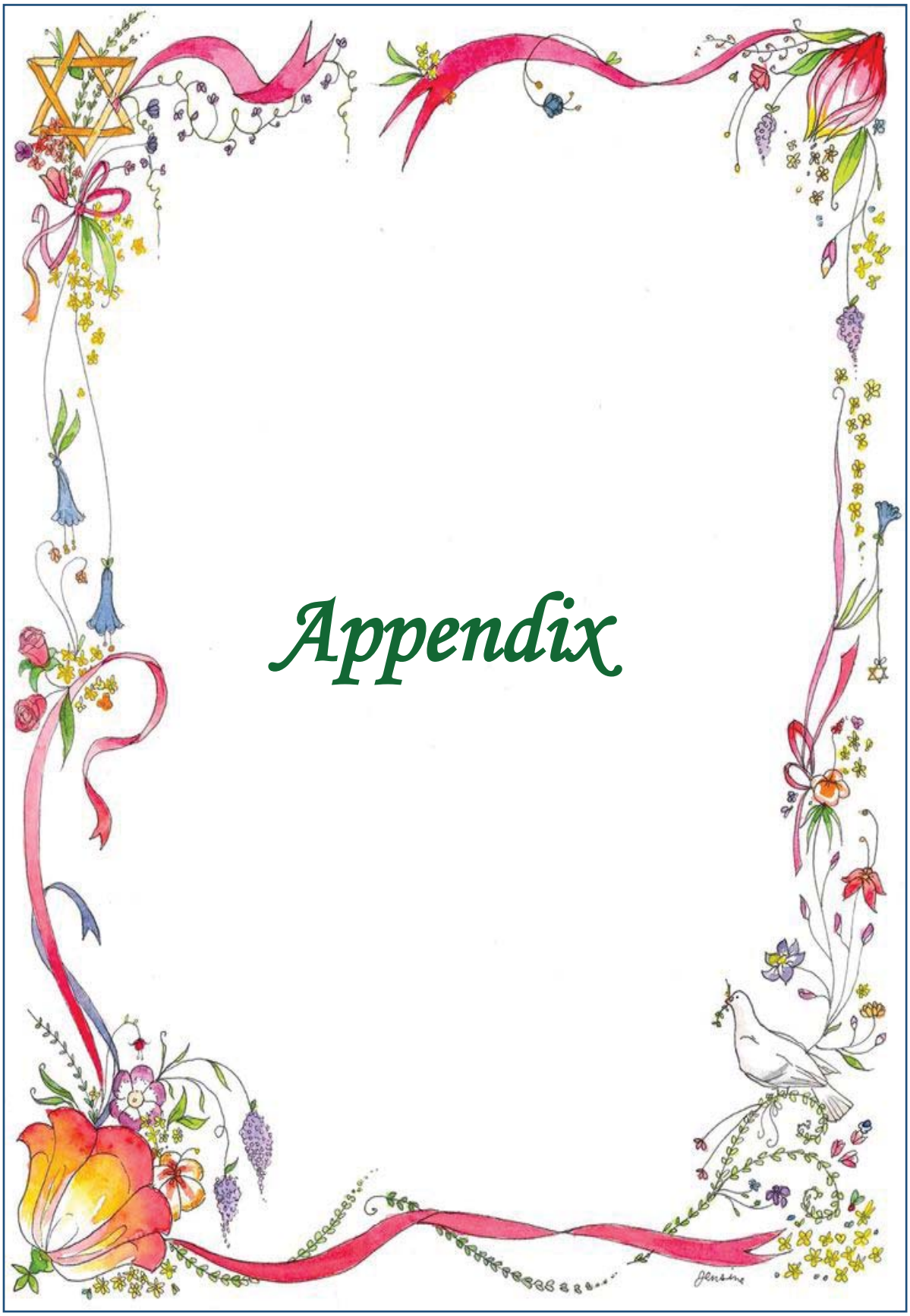

Appendix

Appendix I

List of microsatellite markers used in the study

SSR	Forward primer (5'-3')	Reverse primer (5'-3')	annealing temp. (ºC)	Amplicon size (bp)
GSSR-1	AGCCAACGTCTCCAAATGATAG	AAGTGGAAGTGGGGTTTCTTCT	55	293
GSSR-5	ATAATAAACCCAACCAGACCCC	ATCAGGCAAATCCCATACTGAC	54	120
GSSR-15	CCACCTTTTACACATACTTTCACAC	GTCTCCACGGTCTCCAAAA	54	330
GSSR-20	CATAGCGTTAGAGAGAGAGAAAG	AACTCCCCAACTCAAACTGC	54	234
GSSR-25	CCAGAAACTGATTTTTAATTTAGGC	CGTTTTTCAATAAAACCTCAATC	55	209
GSSR-30	AAGGATTAACACGATGGGAG	TGGCTCCCACTACTGCTAAT	56	223
GSSR-35	AATTCACAATCACCGACTCTCC	ACGTCAAAGCTCCTGTTCATTT	55	173
GSSR-40	TAGAAGCTCCAACAAATCACCC	CAAGGAACCCTAGATCACAAATG	55	171
GSSR-45	GTCCAACTATCCACTTCTTGGC	GCTATGTAAAATCTCCCACTACCTCT	56	379
GSSR-51	ACAGAGAGATAGGGATAGAG	GTTTGGACTCCACTTGCTC	54	234
GSSR-55	CATCCATCAATCAAAAGGAGC	CCAAGAAATGTGGAATGCTG	54, 56	201
GSSR-60	CACGAGTCATTTGATTGATTGAT	TGAATACATTGTTTTGCCGC	54	366
GSSR-65	ACTGCAAAACAGAAACCCAGA	TAGGTCATGGCGATTGATGTAG	57	384
GSSR-70	CAATGTGGTGTTGTGAACTGC	CCAGTCGTTTTGAGTAGCACAG	57	363
GSSR-75	CATGCCGATAGACTTTTCATCA	ACGTTACATTGGTCTTCACTAAG	54	283
GSSR-80	ATGGGGTCAAAGGTAGGCTAT	TTTCGTCCGGTGCTTCTTT	54	181
GSSR-84	GATTTGGGAAAGAAAGGAACG	AAGTTGCATCACCTCACCATC	58	324
GSSR-91	ATTCACCTTCAGTGCCTCCTAA	GAATTGTGTGTGGTGCCTTCTA	55	244
GSSR-96	AGCGTCGTTTTCGCGAGT	CGCGGTTAAAGCAAAGCTAAT	55	334
GSSR-101	TGGGGTGGTTTTGTCGTATT	GGTTCTCCTCTCTATCTC	54	328
GSSR-105	CTCCTAAAGTTCGAGTGAGGGA	GTTCAGGTATGGGGAAGGAAAT	54	292
GSSR-109	GGTGAAACCTTGATGGGTAAAA	AATAGCTTGCTCCAGAATCGAC	55	246
GSSR-115	TGGAGAAGATGGAGGTGGA	GGAGATTTTCACCAATTTCCG	55	346
GSSR-125	GCGTCTCCGTAGTTGTATGTGT	AATCGCTTCGGGAAAAGTC	55	188
GSSR-130	CATTTAGGTCGTCCAGGGTTAG	TGACATCTTCTGAGTGTTGCTTG	54	535
GSSR-135	CAGATACGACAACAAACTCGTCA	TTGATATTCTCTCAATTCCATATTCC	55	309

GSSR-140	GGATACGAAGGAAAGACTCCAC	AGGAGAGTAAAAGATTGAGGACTTG	56	158
GSSR-145	ACTCGATTGTAAACCCGATTGT	GGCCTCCACTTCATCTACTGA	56	282
GSSR-151	TGCATGGTCTTCTTAGCCAAT	CTAGCAACTTACACCACCACCA	56	392
GSSR-155	ACGTACGTACGTATGTATGTATG	TGCAATTAGCAAGTCCACAAC	55	183
BSSR-1	TTCTTGGTCTGTTGATGTCAGTGTAG	TGGATATAGAAGCCATCAGACTTGAG	56	180
BSSR-5	ACGACCGTAAAATTCCAAGTATGT	TACACCCCTTGACTTTATTGAGGT	54	174
BSSR-10	CCAATCTAAGAGCTTGTAAAATGAA	CAAGAGTAGTAAGCATAAGGAGTGG	51	271
BSSR-15	TGTAATCGACTTATTATCGTCTTTTG	AAGGATGATGTAGAGGTGAATGAT	50	259
BSSR-21	TATGGATCTTGAAAACCGTAATTAGA	TGCCTCAATCAAGACACAATTTAT	51	259
BSSR-25	GTTGTTCCTATTCAGAGGACTTGT	GGTAGTCTTGGAGGAGTTGAAGT	54	250
BSSR-26	TTCAACATGTTGTTTCTACCTCTGA	AAAATCTCTGATCAATTTCAGGTAAG	53	191
BSSR-30	ATGCTGGACTAGCTGAAGCATGCA	AGCAGCGAGCAATTTATGAATAAGAG	57	203
BSSR-33	TATGATCCCAAGTCACTGTATCTTT	GCCATCTATCTACTTCATCTCAAAA	53	271
BSSR-39	ACACAACGTTACAGAATTGATGTTCA	CCGGTTCACTTGGTGAATGTATTTAT	54	211
BSSR-43	CTTCTGATGCAAGTAACAACCCTAGT	AGTAATAGCTGGGCAAATGCTACAA	56	225
BSSR-49	TTCCTTTTCTTGTCTTGATTCCTTCT	CTGGACTATCCTCTGCAGTCAG	54	221
BSSR-53	GCTTTAGAACTTCTTCTAGTCGTCCA	CTCATGAGCTCACTTCATCTAACTCC	55	190
BSSR-61	GGGATGATTCTTTGAGGTATGTGAAG	GCAAACACATAAATTCCAAACAAAAGG	54	227
BSSR-65	GGAAAAATTGCACCAGTAGTTGAAGCT	CGGTCTGTTTAAGGTGACAAAACTTG	57	256
BSSR-70	AAATAGGGGTGTGTTAGGTCCAGATA	CCCTGTCGAATTTATTCTACGAACTT	56	208
BSSR-75	ATGAAAGCAGGGATAAAAGTATCCAG	AGAAGAAGGATTCAAGAAATGGCACA	54	258
BSSR-80	TCTTTATATCGTCCTAGGCCTTCA	TTGGAGGCTTATTATCACAAATTC	54	178
BSSR-87	TAAATGTGAATTCTCAAATGTCTCG	GAGTTAGTGTAAATTGGGGCTTTTT	51	190
BSSR-90	AACATGACATTATTTGTGCCCTTTA	TTGATCTCGCTTTAACTCAATTCAT	52	199
BSSR-97	TTGTGCTATTAAGCTCCTTGTTGTT	TATCTCCAACCATTTCTGTCATCAT	54	183
BSSR-101	AGCTCGATTTCTTAGTCAACAGTCA	GCCTTATATATTTAACGTCAGGAATGGA	55	180
BSSR-105	AGTAGGGGTGAGCATTCGGTTC	CAGGAGCTTCAAATCAGGTTTTAATTTT	57	248
BSSR-110	TCCTACAACCTACTATGCACATTTCA	TAATTTGAAACTCAACTCACCATCTG	55	184
BSSR-116	TCCTGTCGAATTTATTCTACGAACTT	AATTGTTAGGTCCTGAAACGATTGTA	53	199
BSSR-120	TGTTAATGGATTTTTGTGTGGTATTG	CACAACGTAATGACAGCAATAGACTT	52	216
BSSR-125	GTTACTCCAGCCTCCAGAAAACTATC	AGTGAAGAAAGAAGAATCACATTGCT	56	183

BSSR-130	GAAACTGCAAGAATCTCCTCTCTTG	ATCGCATTGGTGATAAGTTCT CTAGT	55	179
BSSR-137	CACCTCCCTAAATTCTATCTCACAAT	CCGTCCAACTTTGAGAGGTCT AT	54	190
BSSR-141	GTCTTCCCCTGTTCAACAAACAGT	AGCTACTTGTAGTTTTGCGTA CATCA	57	185
BSSR-146	GAGGTCCTTGCATAATTCATTGTT	GTACTTGTCTTCAGTGTGCGT TAAAA	53	183