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# GENETIC ANALYSIS FOR QUALITY ATTRIBUTES IN CHILLI (*CAPSICUM ANNUUM* L.)

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**ABSTRACT**

Genetic analysis for quality attributes in chilli (*Capsicum annuum* L.) was studied in four selected crosses ($F_1$) *viz.* LCA 710 x HC-28, LCA 712 x HC-28, LCA 712 x LCA 710 and LCA 764 x LCA 315 involving five diverse parents at HRS, Lam, Guntur, A.P. during *Kharif*, 2012-13 and their $F_2$ (Selfing of $F_1$), $B_1$ ($F_1$ x $P_1$), $B_2$ ($F_1$ x $P_2$) were developed during *kharif*, 2013-14. All the six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$) of respective four crosses were evaluated in compact family block design with three replications during *kharif*, 2014-15 for ascorbic acid, oleoresin, capsaicin, red carotenoids, yellow carotenoids, total carotenoids and total colour value. The data generated was subjected to six generation mean analysis and the results revealed that all the types of gene actions *i.e.* additive, dominance and interaction components were played an important role in the inheritance of all studied parameters in all four crosses except cross 1 for yellow carotenoids in which interaction components were absent. Maximum number of crosses were exhibited duplicate epistasis while some crosses showed complimentary epistasis which indicating that all the quality attributes can be improved either by pedigree selection, recurrent selection, delayed selection, reciprocal recurrent selection, heterosis breeding, diallel selective mating scheme or bi-parental mating system.

***Keywords*** **:** *Capsicum annuum*, Generation mean analysis, Gene effects, Epistasis and Inheritance

## Introduction

Chilli (*Capsicum annuum* L.) is an important commercial crop in India and is grown worldwide as spice cum vegetable crop. It belongs to Solanaceae family and originated in South and Central America. India is the largest producer, consumer and exporter of chilli in the world. Chilli is a rich source of health-related metabolites, such as ascorbic acid, carotenoids, flavonoids and capsaicinoids (Howard and Wildman, 2007). The 'capsaicin' is an alkaloid present in the placenta of the fruit, which can directly scavenge various free radicals (Kogure *et al*., 2002). The capsaicinoids also have antioxidant, anticancer, antiarthritic and analgesic properties (Prasad *et al*., 2006). Chilli has also acquired a great importance because of the presence of 'oleoresin', which permits better color distribution and flavor in foods. In view of the changing of food habits and health consciousness, food quality particularly perishables like fruits and vegetables is gaining importance since improved quality not only facilitates remunerative market price for the producer and also improves consumer's health.

The attempts towards improvement of quality characters along with yield in crop plants have lot of significance which can increase the income of the farmer through premium price. The basic requirement in adopting a suitable breeding method is a sound understanding of the genetic behavior and the success in development of genotypes with desired characters depends on the knowledge of genetic architecture of the traits and their inheritance pattern or gene action in different genetic backgrounds. Gene action refers to the behaviour or mode of expression of genes in a genetic population. But the efforts of crop improvement in chilli regarding quality have been constrained due to lack of adequate information on the genetic control of quality traits.

In chilli, most of the reports for gene effects refer to diallel or L × T analysis. But, the inherent drawback of diallel or L × T design is that, those designs estimates only additive and dominance components of gene action and information on epistasis cannot be estimated which is an integral component of genetic architecture of population. Therefore, the present investigation was carried out to study the nature and magnitude of gene effects involved in the expression of quality attributes in chilli using generation mean alaysis which estimates not only additive and dominance components of gene action and also estimates epistasis or non-allelic gene interactions *viz.,* additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) interactions. Similar type of research works have also been conducted by Zewdie and Bosland (2000), Dhall and Hundal (2005a), Dhall and Hundal (2005b), Kamboj *et al.* (2006), Tempeetikul *et al*. (2013) and Navhale *et al*. (2017).

## Materials and Methods

A total of four crosses ($F_1$) *viz.* LCA 710 x HC-28, LCA 712 x HC-28, LCA 712 x LCA 710 and LCA 764 x LCA 315 were made from five diverse parents (Table 1) at HRS, Lam, Guntur, A.P. during *Kharif*, 2012-13 and their $F_2$ (Selfing of $F_1$), $B_1$ ($F_1$ x $P_1$), $B_2$ ($F_1$ x $P_2$) were developed during *kharif,* 2013-14. All the six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$) for respective four crosses were evaluated in compact family block design with three replications during *kharif,* 2014-15. In each replication, for each cross five rows each (one row of 4 m length) of the non-segregating generations ($P_1$, $P_2$, and $F_1$), thirty rows for $F_2$ generation and twenty rows each of $B_1$ & $B_2$ generations were planted at a spacing of 75 cm x 30 cm maintaining 12 plants per row and the crop was raised as per the standard package of practices.

For each cross, the fruit samples were collected from five competitive plants of non-segregating generations ($P_1$, $P_2$ and $F_1$) at random and from all the individual plants of segregating generations ($F_2$, $B_1$ and $B_2$) to estimate qualitative traits *viz.* ascorbic acid (mg/100g), oleoresin (%), capsaicin (%), red carotenoids (mg/100g), yellow carotenoids (mg/100g), total carotenoids (mg/100g) and total color value (ASTA units). The red ripe fruits were sun dried and ground in an electronic grinder and passed through a 0.5 mm sieve and the dry chilli powder was used to measure biochemical constituents whereas mature green fruits were used for estimating the Vitamin 'C' content. Ascorbic acid content of mature green fruits was estimated by volumetric (2, 6-dichlorophenol indophenol dye) method described by Sadasivam and Balasubramanian (1987). The oleoresin content was estimated as per the procedure described by Ranganna (1986). The capsaicin content was estimated by colorimetric method described by Balasubramanian *et al.* (1982). Total red ($C^R$; capsanthin, capsorubin and capsanthin-5, 6-epoxide) and yellow ($C^Y$; zeaxanthin, violaxanthin, antheraxanthin, â-cryptoxanthin, â-carotene and cucurbitaxanthin A) carotenoid isochromic fractions were estimated following the protocol of spectrophotometric method (Hornero-Mendez and Minguez-Mosquera, 2001). Total colour value (ASTA- American Spice Trade Association units) was estimated as per the procedure given by Rosebrook *et al* (1968).

The data was subjected to generation mean analysis as suggested by Hayman (1958) and Jinks & Hayman (1958) for the estimation of genetic components of variation. The presence/absence of epistatic interactions or adequacy of additive dominance model or non-epistatic model or three parameter model for different characters in each cross has tested by employing the simple scaling tests (A, B, C and D) as described by Mather (1949) and Hayman & Mather (1955) and further confirmed by employing the joint scaling test as suggested by Cavalli (1952) and Mather & Jinks (1982). In presence of non-allelic interactions/epistatic interactions, the gene effects were estimated using six parameters model as suggested by Hayman (1958). The non-significance scaling tests indicates absence of non-allelic interactions and for such character the three parameter model as suggested by Jinks and Jones (1958) is employed.

## Results and Discussion

The inheritance patterns varied with crosses and characters. The mean values of six generations of four crosses for seven quality traits are given in table 2. Among the parents, the parent 2 ($P_2$) recorded maximum mean values for all the quality attributes in all crosses except cross 3 for ascorbic acid, cross 4 for oleoresin, crosses 1, 2 and 3 for capsaicin, cross 1 and 2 for red carotenoids, cross 1 for yellow carotenoids, total carotenoids and total colour value in which parent 1 ($P_1$) exhibited maximum mean values. The $F_1$ means of the crosses 2 and 4 for ascorbic acid, crosses 2 and 3 for oleoresin, cross 1 for capsaicin, crosses 1 and 3 for red carotenoids and cross 2 for total colour value were highest over both of their parents which revealed presence of over dominance. Whereas, the crosses 1 and 4 for oleoresin, crosses 2 and 4 for capsaicin, cross 2 for red carotenoids, crosses 2 and 3 for yellow carotenoids, crosses 1, 2 and 3 for total carotenoids and crosses 1 and 3 for total colour value were showed intermediate $F_1$ means between their corresponding parents indicating the presence of partial dominance and improvement can be made through selection. These findings are supported by earlier findings of Dhall and Hundal (2005a and 2005b) who also reported that partial dominance has more influence on the inheritance of the capsaicin and colour in chilli.

The $F_2$ mean values of all crosses except cross 2 for ascorbic acid, all crosses for capsaicin and cross 2 for red carotenoids were highest than their corresponding $F_1$ means and parents (Table 2) which could be due to the presence of large number of transgressive segregates. The $F_2$ mean values of cross 1 for oleoresin, cross 3 for yellow carotenoids and cross 2 for total carotenoids have registered maximum mean values only than their corresponding $F_1$ means, whereas all the remaining crosses exhibited lowest $F_2$ mean values than their corresponding $F_1$ means indicating presence of some inbreeding depression. The behaviour of back cross generations $B_1$ and $B_2$ were on expected lines in all the crosses except in cross 2 for ascorbic acid, crosses 1 & 4 for oleoresin, cross 1 for capsaicin, crosses 1 & 4 for yellow carotenoids and cross 2 for total carotenoids and total colour value indicating that in which crosses the means of back cross generations were slightly deviated from expectations.

The superiority of $F_1$ could be due to an accumulation of favorable dominant alleles while the superiority in performance of segregating generations ($F_2$, $BC_1$ and $BC_2$) might suggest a higher frequency of their transgressive segregants. Transgressions in segregating generations could occur due to a wider genetic distance between genotypes of their parents. The particular cases in which the backcross generations ($BC_1$ and $BC_2$) were superior to their matching generations ($P_1$ and $P_2$) might also indicate an accumulation of some favorable alleles in them. The reverse case, in which the $F_2$ generation was inferior to its matching progeny generations ($F_1$, $BC_1$ and $BC_2$), could be due to the maximum segregation of their desirable alleles which may result in higher frequency of inferior segregants in some crosses (Marame *et al*., 2009). The differences in performances among the generations could be caused by both the additive and dominance genes as well as their interaction effects, most of which might be manipulated through recombination and selection (Perera *et al*. 2001).

The estimates of simple scaling tests (A, B, C and D) and joint scale test of four crosses for all traits are furnished in table 3. The significance of any scaling test indicates the presence of epistasis. The significance of A or B or both A and B tests indicates the presence of all three types of epistatic interactions *viz.*, additive × additive [*i*], additive × dominance [*j*] and dominance × dominance [*l*], while the

significance of C scaling test reveals the presence of dominance × dominance [*l*] type of interaction, the significance of D scaling test indicates the presence of additive × additive [*i*] type of gene interaction and the significance of both C and D scales indicates presence of additive × additive [*i*] and dominance × dominance [*l*] types of non-allelic gene interactions (Mather, 1949). The presence of epistasis has further confirmed by joint scaling test with significant $\chi^2$ values. The joint scaling test found to be more efficient in detection of epistasis compared to individual scaling tests and Ketata *et al.* (1976) had also concluded superiority of joint scaling test over the simple scaling tests in wheat.

From the table 3, the results revealed that all the four crosses have exhibited significant one or more simple scaling tests (A, B, C and D) for all the seven quality traits except cross 1 for yellow carotenoids indicating the presence of all the three types of non-allelic gene interactions *viz.*, additive × additive [*i*], additive × dominance [*j*] and dominance × dominance [*l*] interactions and also confirmed by joint scaling test with significant $\chi^2$ values. Finally, these results revealed that the additive dominance model is inadequate for all the crosses of all the quality traits except for cross 1 of yellow carotenoids for which additive dominance model is adequate as it has showed non-significant scaling tests as well as joint scaling test. The significance of only C and D scaling tests in cross 3 of capsaicin, cross 1 of red carotenoids and cross 1 of total colour value indicating the presence of additive × additive [*i*] and dominance × dominance [*l*] types of non-allelic gene interactions, whereas the significance of only C scaling test in cross 1 of total carotenoids indicating the presence of only dominance × dominance [*l*] type of non-allelic gene interactions. These findings were relevance with the reports of Navhale *et al.* (2017) and Dhall and Hundal (2005b).

The estimates of gene effects of four crosses for respected quality traits are presented in table 4. The results revealed that additive x dominance (*j*) type of gene interactions were showed non-significance for all the crosses as well as for all the studied traits indicating the lesser importance in governing the respected traits. For all the traits and for all the crosses, the magnitude of dominance gene actions (*h*) was higher than that of additive gene actions (*d*) except cross 3 for ascorbic acid, crosses 2 and 4 for yellow carotenoids and cross 4 for total colour value revealed that the dominance gene effects (*h*) plays an important role in the inheritance of quality traits.

For ascorbic acid, the gene effects *viz.,* additive (*d*) for crosses 1, 2 and 3; dominance (*h*) for crosses 1 and 2; additive x additive (*i*) for crosses 1, 2 and 4 and dominance x dominance (*l*) type of interactions for cross 2 and 3 were significant. The dominance (*h*) and dominance x dominance (*l*) types of gene effects have opposite signs in cross 1 and 2 indicated that presence of duplicate epistasis whereas cross 3 and 4 have showed complementary epistasis with same signs of dominance (*h*) and dominance x dominance (*l*) types of gene effects. These results are in agreement with findings of earlier works of Kamboj *et al.* (2006).

With respect to oleoresin, the crosses 1, 2 and 4 have exhibited significant additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) gene effects, while the cross 3 showed only significant additive (*d*) gene effects and also recorded the duplicate (cross 3) and complementary (cross 1, 2 and 4) epistasis with higher magnitude of dominance x dominance (*l*) gene interactions. For Capsaicin content, the significant additive effects in crosses 2 and 3; significant dominance (*h*) and additive x additive (*i*) effects in crosses 1 and 3; and dominance x dominance (*l*) type of gene effects in crosses 1, 3 and 4 were observed. The crosses 1, 3 and 4 have recorded duplicate epistasis whereas the cross 2 has showed complementary epistasis. Similar findings are reported by Zewdie and Bosland (2000), Dhall and Hundal (2005a), Tempeetikul *et al.* (2013) and Navhale *et al.* (2014).

In respect of red carotenoids, the gene effects *viz.,* additive (*d*) for crosses 1, 2 and 4; dominance (*h*) and additive x additive (*i*) gene interactions for cross 1 and 3; and dominance x dominance (*l*) gene interactions for cross 2 and 4 were found significant. The duplicate epistasis was observed in crosses 1, 2 and 4 whereas complimentary epistasis was observed in cross 3 with higher magnitude of dominance (*h*) gene effects (cross 1 and 3) and dominance x dominance (*l*) gene interactions (cross 2 and 4). For yellow carotenoids, the additive (*d*) gene effects were significant in crosses 2, 3 and 4 whereas dominance (*h*) gene effects were significant in cross 3 and dominance x dominance (*l*) type of gene effects were significant in cross 4. The crosses 2, 3 and 4 have exhibited the duplicate epistasis with higher magnitude of dominance (*h*) gene effects (cross 3) and dominance x dominance (*l*) gene interactions (cross 2 and 4).

Regarding total carotenoids, the significant additive (*d)* effects in cross 2 and significant dominance x dominance (*l*) gene interactions in cross 4 were observed. The duplicate epistasis was observed in crosses 1 and 2 whereas the complementary epistasis was recorded in crosses 3 and 4 with higher magnitude of dominance (*h*) gene effects in crosses 1, 3 and dominance x dominance (*l*) gene interactions in crosses 2 and 4. With respect to total colour value, the additive (*d*) gene effects in cross 2 and 4; dominance (*h*) and additive x additive (*i*) type of gene interactions in cross 1 and dominance x dominance (*l*) gene interactions in cross 4 were found significant. The crosses 1, 2 and 4 have recorded duplicate epistasis whereas the cross 3 has showed complementary epistasis. These results are in line with earlier findings of Dhall and Hundal (2005b).

From the results of simple scaling tests (A, B, C and D), joint scaling test and gene effects, it can be concluded that all the studied characters in all crosses were inherited by all the types of gene actions *i.e.* additive, dominance and interaction components and indicating that these four crosses can be improved by either pedigree selection, recurrent selection, reciprocal recurrent selection, diallel selective mating scheme or bi-parental mating system (Comstock *et al.*, 1949, Navahale *et al.*, 2014).

The duplicate epistasis for many traits in four crosses was found and it will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistatic effects (Dhall and Hundal, 2006). However, Jindal *et al.* (1993) and Amawate and Behl, (1995) suggested that duplicate epistasis might restrict the expression and selection of a trait in early segregating generations. The selection in early generations would not be effective for fixable components of variation. Such gene effects can however be exploited by intermating the selected segregants and delaying the selection to the advanced generations (Jindal *et al.*, 1993). Delayed selection (Sharma and Sharma, 1995) or selection

after biparental intermating (Misra *et al.,* 1994) would be more effective to get a good response in such cases. The complementary epistasis was found for some crosses which is fixable and thus can be exploited effectively for the improvement of the traits through pedigree method of selection and heterosis breeding (Ram, 1994). Considering all these observations together, the pedigree or recurrent selection or modified bulk method is recommended for varietal improvement of chilli (Navahale *et al*., 2014).

**Table 1:** Salient features of five parents involved in four crosses used in generation mean analysis of chilli

| S. No | Crosses | |
|---|---|---|
| 1 | LCA-710 x HC-28 | |
| 2 | LCA-712 x HC-28 | |
| 3 | LCA-712 x LCA-710 | |
| 4 | LCA-764 x LCA-315 | |
| **S. No.** | **Parents** | **Features** |
| 1 | LCA-710 | Erect but dwarf plant, cluster and pendent bearing habit |
| 2 | HC-28 | Erect plant with two or three primary branches, cluster and erect bearing habit |
| 3 | LCA-712 | High yielding line, more no. of fruits, solitary and pendent fruit bearing |
| 4 | LCA-764 | Dense branching habit, solitary and pendent fruit bearing |
| 5 | LCA-315 | Virus resistant, fruits are long and dark green |

**Table 2:** *Per se* performance of six generations of four crosses for seven quality traits in chilli

| S.No. | Characters | Crosses | $P_1$ | $P_2$ | $F_1$ | $F_2$ | $B_1$ | $B_2$ |
|---|---|---|---|---|---|---|---|---|
| 1. | Ascorbic acid (mg/100g) | LCA-710 x HC-28 | 28.10 | 29.24 | 22.33 | 48.19 | 30.03 | 37.92 |
| | | LCA-712 x HC-28 | 29.10 | 29.64 | 51.20 | 41.95 | 58.93 | 46.64 |
| | | LCA-712 x LCA-710 | 29.30 | 27.90 | 23.54 | 51.50 | 56.57 | 44.30 |
| | | LCA-764 x LCA-315 | 27.49 | 31.29 | 36.58 | 53.50 | 42.35 | 49.85 |
| 2. | Oleoresin (%) | LCA-710 x HC-28 | 10.48 | 11.55 | 10.93 | 11.19 | 15.39 | 13.57 |
| | | LCA-712 x HC-28 | 9.46 | 11.55 | 12.27 | 11.33 | 7.72 | 9.70 |
| | | LCA-712 x LCA-710 | 9.80 | 10.88 | 12.36 | 10.53 | 9.85 | 10.92 |
| | | LCA-764 x LCA-315 | 11.85 | 8.46 | 11.62 | 9.48 | 10.69 | 12.09 |
| 3. | Capsaicin (%) | LCA-710 x HC-28 | 0.40 | 0.23 | 0.48 | 0.69 | 0.47 | 0.49 |
| | | LCA-712 x HC-28 | 0.44 | 0.23 | 0.39 | 0.59 | 0.60 | 0.46 |
| | | LCA-712 x LCA-710 | 0.46 | 0.40 | 0.29 | 0.59 | 0.41 | 0.30 |
| | | LCA-764 x LCA-315 | 0.27 | 0.38 | 0.27 | 0.58 | 0.61 | 0.66 |
| 4. | Red carotenoids (mg/100g) | LCA-710 x HC-28 | 166.10 | 112.19 | 179.52 | 120.99 | 171.90 | 133.72 |
| | | LCA-712 x HC-28 | 134.49 | 112.19 | 130.86 | 145.25 | 174.36 | 138.31 |
| | | LCA-712 x LCA-710 | 140.49 | 166.10 | 189.03 | 143.26 | 153.05 | 154.95 |
| | | LCA-764 x LCA-315 | 134.45 | 162.39 | 124.93 | 105.21 | 88.69 | 112.23 |
| 5. | Yellow carotenoids (mg/100g) | LCA-710 x HC-28 | 146.06 | 133.88 | 129.51 | 128.79 | 125.43 | 129.68 |
| | | LCA-712 x HC-28 | 100.51 | 145.88 | 120.59 | 107.89 | 100.05 | 115.19 |
| | | LCA-712 x LCA-710 | 100.51 | 153.46 | 104.11 | 122.55 | 110.54 | 121.40 |
| | | LCA-764 x LCA-315 | 98.53 | 109.29 | 94.64 | 65.73 | 74.05 | 60.59 |
| 6. | Total carotenoids (mg/100g) | LCA-710 x HC-28 | 312.15 | 246.06 | 309.03 | 250.41 | 285.44 | 260.65 |
| | | LCA-712 x HC-28 | 235.01 | 266.06 | 251.46 | 253.15 | 280.70 | 248.50 |
| | | LCA-712 x LCA-710 | 235.01 | 312.15 | 296.14 | 260.48 | 267.63 | 274.91 |
| | | LCA-764 x LCA-315 | 234.98 | 253.68 | 223.57 | 167.39 | 171.92 | 183.57 |
| 7. | Total colour value (ASTA units) | LCA-710 x HC-28 | 122.43 | 96.20 | 121.48 | 97.49 | 114.18 | 102.44 |
| | | LCA-712 x HC-28 | 90.77 | 96.20 | 97.09 | 98.22 | 106.84 | 96.15 |
| | | LCA-712 x LCA-710 | 90.77 | 122.03 | 111.95 | 101.95 | 103.55 | 107.24 |
| | | LCA-764 x LCA-315 | 90.76 | 103.51 | 81.12 | 65.44 | 60.98 | 73.56 |

Where, $P_1$, $P_2$ = Parents, $F_1$=$P_1$ x $P_2$, $F_2$ = Selfing of $F_1$, $B_1$= $F_1$ x $P_1$ and $B_2$ = $F_1$ x $P_2$

**Table 3:** Estimates of scaling tests and joint scaling test of four crosses for seven quality traits in chilli .

| S. No. | Characters | Crosses | Simple scaling tests | | | | Joint scaling test | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | A | B | C | D | *m* | *d* | *h* | $\chi^2$ |
| 1. | Ascorbic acid (mg/100g) | LCA-710 x HC-28 | 9.63* | 24.28** | 90.75** | 28.43** | 31.43** | -1.16 | -1.88 | 129.82** |
| | | LCA-712 x HC-28 | 37.57** | 12.45** | 6.66 | -21.68** | 30.33** | 0.33 | 21.64** | 53.36** |
| | | LCA-712 x LCA-710 | 60.31** | 37.15** | 101.73** | 2.14 | 30.56** | 0.57 | -3.90** | 119.63** |
| | | LCA-764 x LCA-315 | 20.64** | 31.83** | 82.06** | 14.80** | 31.40** | -1.97* | 8.02** | 81.35** |
| 2. | Oleoresin (%) | LCA-710 x HC-28 | 9.38** | 4.68** | 0.87 | -6.60** | 11.45** | -0.19 | 2.05** | 49.65** |
| | | LCA-712 x HC-28 | -6.29** | -4.41** | -0.24 | 5.24** | 9.59** | -1.15** | 1.68** | 88.57** |
| | | LCA-712 x LCA-710 | -2.47* | -1.40 | -3.31 | 0.29 | 9.91** | -0.71** | 1.54** | 8.28* |
| | | LCA-764 x LCA-315 | -2.08* | 4.11** | -5.63** | -3.83** | 10.23** | 0.33 | 1.28** | 115.63** |
| 3. | Capsaicin (%) | LCA-710 x HC-28 | 0.07 | 0.27** | 1.16** | 0.41** | 0.33** | 0.09** | 0.35** | 62.65** |
| | | LCA-712 x HC-28 | 0.38** | 0.30** | 0.90** | 0.12 | 0.40** | 0.17** | 0.14** | 32.88** |
| | | LCA-712 x LCA-710 | 0.06 | -0.10 | 0.89** | 0.47** | 0.47** | 0.06** | -0.15** | 48.49** |
| | | LCA-764 x LCA-315 | 0.69** | 0.67** | 1.14** | -0.12 | 0.50** | -0.03 | 0.01 | 121.28** |
| 4. | Red carotenoids (mg/100g) | LCA-710 x HC-28 | -1.83 | -24.27 | -153.38** | -63.65** | 134.06** | 30.16** | 36.70** | 10.94* |
| | | LCA-712 x HC-28 | 83.37** | 33.57* | 72.61* | -22.17 | 135.01** | 17.81** | 14.98 | 24.44** |
| | | LCA-712 x LCA-710 | -23.43* | -45.23** | -111.60** | -21.48* | 141.85** | -7.61* | 32.69** | 37.72** |
| | | LCA-764 x LCA-315 | -82.02** | -62.86** | -125.86** | 9.51 | 119.39** | -18.41** | -14.56 | 52.47** |
| 5. | Yellow carotenoids (mg/100g) | LCA-710 x HC-28 | -24.72 | -4.02 | -23.82 | 2.46 | 137.79** | 4.54 | -12.29 | 3.93 |
| | | LCA-712 x HC-28 | -21.01 | -36.09** | -56.00** | 0.55 | 117.35** | -21.16** | -1.15 | 23.80 ** |
| | | LCA-712 x LCA-710 | 16.46* | -14.76 | 28.00 | 13.16 | 128.85** | -22.69** | -23.43** | 8.81* |
| | | LCA-764 x LCA-315 | -45.08** | -82.75** | -134.19** | -3.19 | 80.16** | 4.82 | -12.38 | 84.82** |
| 6. | Total carotenoids (mg/100g) | LCA-710 x HC-28 | -50.31 | -33.81 | -174.64** | -45.27 | 268.55** | 34.75** | 13.59 | 12.76** |
| | | LCA-712 x HC-28 | 74.95** | -20.52 | 8.62 | -22.91 | 254.68** | -0.81 | -0.99 | 10.75* |
| | | LCA-712 x LCA-710 | 4.12 | -58.48** | -97.54** | -21.59 | 260.15** | -26.59** | 32.05** | 17.47** |
| | | LCA-764 x LCA-315 | -114.72** | -110.12** | -266.25** | -20.71 | 197.46** | -16.07* | -3.71 | 87.53** |
| 7. | Total colour value (ASTA units) | LCA-710 x HC-28 | -15.56 | -12.80 | -71.65* | -21.66* | 105.26** | 13.98** | 6.28 | 13.58** |
| | | LCA-712 x HC-28 | 25.84* | -1.00 | 11.75 | -6.55 | 95.81** | 1.45 | 3.40 | 7.27 |
| | | LCA-712 x LCA-710 | 4.39 | -19.49* | -28.91 | -6.90 | 104.19** | -10.14** | 3.36 | 10.48* |
| | | LCA-764 x LCA-315 | -49.92** | -37.52** | -94.77** | -3.67 | 81.56** | -9.25** | -18.97** | 60.70** |

* Significant at 5% level; ** Significant at 1% level

**Table 4:** Estimates of gene effects of four crosses for seven quality characters in chilli

| S.No. | Characters | Crosses | *m* | *D* | *h* | *i* | *j* | *l* | Type of epistasis |
|---|---|---|---|---|---|---|---|---|---|
| 1. | Ascorbic acid (mg/100g) | $C_1$ | 48.19** | -7.90** | -63.19** | -56.85** | -7.33 | 22.94 | Duplicate |
| | | $C_2$ | 41.95** | 12.30** | 65.19** | 43.36** | 12.57 | -93.37** | Duplicate |
| | | $C_3$ | 51.51** | 12.28* | -9.33 | -4.27 | 11.58 | -93.19** | Complementary |
| | | $C_4$ | 53.50** | -7.50 | -22.41 | -29.60* | -5.60 | -22.87 | Complementary |
| 2. | Oleoresin (%) | $C_1$ | 11.19** | 1.82* | 13.10** | 13.19** | 2.36 | -27.23** | Duplicate |
| | | $C_2$ | 11.34** | -1.99** | -8.70** | -10.47** | -0.94 | 21.16** | Duplicate |
| | | $C_3$ | 10.53** | -1.08* | 1.46 | -0.57 | -0.54 | 4.43 | Complementary |
| | | $C_4$ | 9.49** | -1.40** | 9.11** | 7.65** | -3.10 | -9.67** | Duplicate |
| 3. | Capsaicin (%) | $C_1$ | 0.69** | -0.02 | -0.66** | -0.82** | -0.10 | 0.49* | Duplicate |
| | | $C_2$ | 0.59** | 0.15* | -0.17 | -0.23 | 0.05 | -0.44 | Complementary |
| | | $C_3$ | 0.59** | 0.11* | -1.07** | -0.93** | 0.08 | 0.97** | Duplicate |
| | | $C_4$ | 0.59** | -0.05 | 0.17 | 0.23 | 0.02 | -1.58** | Duplicate |
| 4. | Red carotenoids (mg/100g) | $C_1$ | 120.99** | 38.18* | 167.68** | 127.30* | 11.23 | -101.21 | Duplicate |
| | | $C_2$ | 145.26** | 36.06** | 51.85 | 44.33 | 24.91 | -161.26** | Duplicate |
| | | $C_3$ | 143.27** | -1.91 | 78.68** | 42.95* | 10.90 | 25.71 | Complementary |
| | | $C_4$ | 105.22** | -23.55** | -42.50 | -19.01 | -9.58 | 163.88** | Duplicate |
| 5. | Yellow carotenoids (mg/100g) | $C_1$ | 128.79** | -4.26 | -15.38 | -4.92 | -10.35 | 33.65 | - |
| | | $C_2$ | 107.90** | -15.15* | -3.70 | -1.10 | 7.54 | 58.19 | Duplicate |
| | | $C_3$ | 122.55** | -10.87* | -49.18* | -26.31 | 15.61 | 24.62 | Duplicate |
| | | $C_4$ | 65.73** | 13.46** | -2.90 | 6.38 | 18.84 | 121.45** | Duplicate |
| 6. | Total carotenoids (mg/100g) | $C_1$ | 250.42** | 24.80 | 120.46 | 90.54 | -8.26 | -6.43 | Duplicate |
| | | $C_2$ | 253.15** | 32.21* | 46.74 | 45.82 | 47.74 | -100.24 | Duplicate |
| | | $C_3$ | 260.48** | -7.28 | 65.74 | 43.18 | 31.30 | 11.18 | Complementary |
| | | $C_4$ | 167.39** | -11.65 | 20.67 | 41.42 | -2.30 | 183.42** | Complementary |
| 7. | Total colour value (ASTA units) | $C_1$ | 97.49** | 11.74 | 55.47* | 43.31* | -1.38 | -14.96 | Duplicate |
| | | $C_2$ | 98.23** | 10.70* | 16.70 | 13.10 | 13.42 | -37.94 | Duplicate |
| | | $C_3$ | 101.95** | -3.70 | 19.35 | 13.80 | 11.94 | 1.31 | Complementary |
| | | $C_4$ | 65.44** | -12.58** | -8.69 | 7.34 | -6.21 | 80.10** | Duplicate |

Where $C_1$=LCA-710 x HC-28, $C_2$=LCA-712 x HC-28, $C_3$=LCA-712 x LCA-710 and $C_4$=LCA-764 x LCA-315; *m* = mean, *d* = additive effect, *h* = dominance effect, *i* = additive x additive type gene interaction, *j* = additive x dominance type gene interaction and *l* = dominance x dominance type gene interaction. * Significant at 5% level; ** Significant at 1% level

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