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STUDIES ON GENE ACTION FOR GROWTH AND YIELD ATTRIBUTE TRAITS IN PARENTAL LINES AND THEIR F_1 HYBRIDS UNDER AYODHYA REGION IN PUMPKIN (*CUCURBITA MOSCHATA* DUCH. EX. POIR.)

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ABSTRACT

The present investigation was carried out to obtain the information based on gene action of parents and their combinations for genetic improvement in pumpkin. Eight promising genotypes were crossed in a diallel manner (excluding reciprocals). Half diallel set of 28 F1's in pumpkin during Zaid 2022 23 (Y1) and 2023-24 (Y2) at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) India. Based on gene action, both additive and dominance variance were found important in the inheritance of most of the traits, whereas dominance variance was more prominent than the additive variance in both seasons. Average degree of dominance revealed the presence of over dominance for all traits in both the seasons and the proportions of genes ($\hat{H}_2/4\hat{H}_1$) in the parents were less than 0.25 for all the traits indicating asymmetrical distribution of alleles at loci, In general the proportions of dominant and recessive genes in parents i.e.$(4\hat{D}_1\hat{H}_1)1/2+ 1/2 + \hat{F}/(4\hat{D}\ \hat{H}_1)\ 1/2- \hat{F}$ were more than unity with positive value for all the traits and the ratio of ($\hat{h}_2/\hat{H}_2$) which estimates the number of gene groups revealed that atleast one gene group was involved in the inheritance both seasons (Y1, Y2) and rest of traits and the positive correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) were showed for most of the characters in both the seasons.

***Keywords*: Pumpkin (*Cucurbita moschata* Duch. ex. Poir), gene action, growth and yield parameters.

Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is a significant vegetable crop in the Cucurbitaceae family. The pumpkin word derived from Greek word "pepon" meaning "large melon" or something enormous and round. Because of its great yield to farmers and its beneficial nutritional and medicinal uses, it is grown in all over the world. The origin place of pumpkin is Central Mexico.

The cultivated Cucurbita species are ranked among the top ten vegetable crops in the world based on their commercial significance. India is the world's second-largest producer of pumpkins after China other major producers include the United States, Egypt, Mexico, Ukraine, Cuba, Italy, Iran, and Turkey (Ferriol and Pico, 2008). In India, there are 0.11 million hectares of pumpkin growing, but only 2.31 million tonnes are produced, with a productivity of 20.99 t/ha (Annonymous, 2021-22).

Pumpkin showed more variability in their fruit size, colour, shape, fruit yield and also other agronomic attributes (Singh *et al.,* 2005). Similar to other gourds, pumpkins are summertime crops that can be grown all year round in the country's centre and southern regions. In contrast, it is typically grown during the summer and rainy season, which is sowed from January to July, in the northern regions of the nation, where winters are colder. Farmers in northern India seed their crops in mounds or on Introduction 4 hills near their homes in July and August, following the start of the monsoon. The developing plants are supported by thatches, hutments, and other vacant areas. The genotypes that are typically planted close to a household are land races that have historically been preserved by the locals and are known locally as Bhadhavaha Kohara, or pumpkins for the rainy season.

The ability to take advantage of heterosis requires a considerable degree of non-additive gene activation. If heterosis is strong for a particular cross combination and the findings are valid for economic characteristics such as plant production, the cross can be used. The specific combining variance is primarily the measure of dominance variance and the crop improvement can be brought about in pumpkin by assessing the genetical variability and exploitation of heterosis. Pumpkin is highly conducive to heterosis breeding due to its monoecious character, large flower size, ease of pollination, maximum fruit set of pollinated female flowers, large number of seeds per fruit, and low seed rate required per unit area. Many researchers have reported high levels of heterosis in pumpkin during the past three decades and many studies on the subject have been conducted (Mohanty, 2001; Sirohi *et al.*, 2002; Dubey and Maurya, 2003; Jha *et al.*, 2009; Pandey *et al.,* 2010; Jahan *et al.,* 2012; Nisha and Veeraragavathatham, 2014 and Tamilselvi *et al.,* 2015). For commercial cultivation, both the public and private sectors have released a number of hybrids. The yield and production of this crop have increased due to the rapid expansion of the area under F_1 hybrids.

Materials and Methods

The experimental materials for the present study comprised of eight promising and diverse inbreds and varieties of pumpkin selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, A.N.D.U.A.T., Kumarganj, Ayodhya (U.P.) India. The selected parental lines *i.e.* Narendra Agrim (P_1), Narendra Amrit (P_2), Narendra Upkar (P_3), NDPK-73-1(P_4), NDPK-76-1(P_5), NDPK-12-1 (P_6), NDPK-13-1(P_7) and NDPK-17-12-1(P_8) were raised and crossed in the all possible combinations, excluding reciprocals during *Zaid*, 2022 to develop 28 F_1 hybrid seeds for gene action to fourteen quantitative traits and observations were recorded on fourteen economic traits *viz*., node number to first male flower, node number to first female flower, days to first male flower anthesis, days to first female flower anthesis, days to first fruit harvest, vine length (m), number of primary branches per plant, number of nodes per plant, internodal length (cm), polar circumference of fruit (cm), equatorial circumference of fruit (cm), average fruit weight (kg), number of fruits per plant and fruit yield per plant (kg).

Estimation of components of genetic variance

The following genetic components of variation were calculated for the analysis of numerical approach followed the method given by Jinks and Hayman (1953), Hayman (1954a) and Aksel and Johnson (1964).

$\hat{D}$ = components of variation due to additive effects of gene

$\hat{H}_1$ = components of variation due to dominance effects of gene

$\hat{H}_2$ = Dominance, indicating asymmetry of positive and negative effects of genes, = $\hat{H}_1\,[1-(\mu-v)^2]$

μ = proportion of the positive genes in the parents

v = proportion of the negative genes in the parents and

Where

$\mu + v = 1$

$\hat{F}$ = the mean of F_r over the arrays

Where,

F_r = the covariance of additive and dominance effects in single array

$\hat{h}^2$ = dominance effects (as the algebraic sum over all the loci in heterozygous phase in all the crosses)

The estimates of these components of genetic variation were determined based on the following formula suggested by Hayman (1954a).

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2V_0L_0 - 4W_0L_{01} - \frac{2(n-2)}{n}\hat{E}$$

$$\hat{H}_1 = 4V_1L_1 + V_oL_0 - 4\,W_0L_{01} - \frac{3n-2}{n}\hat{E}$$

$$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\,\hat{E}$$

$$\hat{h}^2 = 4\,(ML_1 - ML_0)^2 - \frac{4(n-1)}{n^2}\hat{E}$$

$$Fr = 2\,(V_0L_0 - W_0L_{01} + V_1L_1 - Wr - Vr) - \frac{2(n-2)}{n}\hat{E}$$

The estimates of the above formulae may be explained as follows:

N = number of parents

V_0L_0 = variance of the parents

Vr = variance of all the progenies in each parent of array

V_0L_1 = the variance of means of arrays

V_1L_1 = mean variance of the arrays (mean of all the Vr values)

Wr = the covariance between the parents and their off spring in r^{th} array

W_0L_{01} = the mean covariance between the parents and the arrays (mean of all Wr values)

ML_1 = mean of all F_1's

ML_0 = mean of parents

$\hat{E}$ = the expected environmental component of variation

In order to estimate the accuracy of the above components ($\hat{D}, \hat{H}_1, \hat{H}_2, \hat{E}, \hat{F}, \hat{h}^2$) variance, the terms of main diagonal of the matrix given by Hayman (1954a) with common multipliers S^2 was used where,

S^2 = ½ [var. (Wr-Vr)]

Consequently, the standard error of

$$S.E._D = \left[\frac{n^5 + n^4}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{H_1} = \left[\frac{n^5 + 41n^4 - 12n^3 + 4n^2}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{H_2} = \left[\frac{36n^4}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._{h^2} = \left[\frac{16n^4 + 16n^2 - 32n + 16}{n^5} S^2\right]^{\frac{1}{2}}$$

$$S.E._F = \left[\frac{4n^5 + 20n^4 - 16n^3 + 16n^2}{n^5} S^2\right]^{\frac{1}{2}}$$

and $S.E._E = \left[\frac{n^4}{n^5} S^2\right]^{\frac{1}{2}}$

Where,

n = number of inbred lines.

The significance of each component of variation was tested by means of 't' test using the respective standard errors.

The above genetic components were used in computation of following genetic ratios:

(i) $(\hat{H}_1/\hat{D})^{\frac{1}{2}}$ = mean degree of dominance over all loci

If the ratio obtained is equal to 1, this indicated presence of complete dominance; if more than 1, it indicates presence of over dominance and if less than 1, it reveals presence of partial dominance; if equal to 0, it indicates no dominance.

(ii) $\hat{H}_2/4\hat{H}_1$ = the proportion of dominant genes with positive or negative effects among the parents.

The maximum the oreticals value of this ratio is 0.25, which arises when p = q = 0.5 at all loci. A deviation from 0.25 would seem when $P \neq q$. Thus, $\hat{H}_2/4\hat{H}_1 \approx 0.25$ would means symmetrical distribution of positive and negative dominant genes in parents; and when $\hat{H}_2/4\hat{H}_1 \neq 0.25$ it means asymmetrical distribution.

Where,

p = proportion of dominant alleles and

q = proportion of recessive alleles

(iii) $(4\hat{D}\hat{H}_1)^{1/2}$ + F/$(4\hat{D}\hat{H}_1)^{1/2}$- $\hat{F}$ = the proportion of dominant and recessive genes among the parents when this ratio is equal to 1 it indicates nearly equal proportion of dominant and recessive alleles in parents (p = q = 0.5). If the ratio is greater than 1, it refers to preponderance of dominant alleles (p > q) and when this ratio is less than 1, it means minority of dominant alleles and excess of recessive alleles (p < q)

(iv) $\hat{h}^2/\hat{H}_2$ = the number of groups of genes which control the character and exhibit dominance.

The coefficient of correlation (r) between parental order of dominance (Wr-Vr) and parental measurements (Yr) was calculated to get an idea about the dominance of genes with positive and negative effects. Uniformity of (Wr-Vr) would indicate the validity of the hypothesis as postulated by Hayman (1954 a) with ungrouped randomization, this may be tested by using the formula mentioned below:

$$t^2 = \frac{n-2}{4} x \frac{(Var.Vr - Var.Wr)^2}{(Var.Vr\ x\ Var.Wr.) - Cov^2\ (Vr.Wr)}$$

With (n-2) degree of freedom where, n is the number of parents. Significance of t^2 indicates the failure of the hypothesis.

Result and Discussion

Choosing the right parents and using the right breeding techniques are fundamental steps in transferring traits. The parents chosen for the crossing program were assessed according to their gene action in creating superior hybrids. Below is a discussion of various field attributes result for pooled data, along with the most significant trait, fruit output per plant and the first attempt to partition the genotypic variance in to its components was made by Fisher (1918). It has subsequently been developed by Mather (1949) [12], Jinks and Hayman (1957). They were able to estimate the genetical parameters, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{F}$ (following Mather's notations) and their standard errors from second degree statistics. D-variance due to additive genetic effects, $\hat{H}_1$ the dominance variance, while $\hat{F}$ gives information on the preponderance of dominant and recessive alleles.

Days to first male flower anthesis

A perusal of Table-1 revealed that the estimates of $\hat{H}_1$, $\hat{H}_2$, and $\hat{D}$ were found significant for days to first male flower anthesis during both seasons (Y_1, Y_2). However, h^2, $\hat{E}$ and $\hat{F}$ were found non significant in both the seasons (Y1, Y2). The significance of $\hat{H}_1$, along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed complete dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect $(\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.20, 0.21 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were more than one in both the season (Y1, Y2) .which indicated that the dominant genes were more frequent than recessive ones.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.05, -and 0.14 in Y1,Y2 respectively. The 'r' values were negative and very low in Y1 and negative in Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for days to first male flower anthesis were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Days to first female flower anthesis

A perusal of Table-1 revealed that the estimates of $\hat{H}_1$ and $\hat{H}_2$ were found significant for days to first female flower anthesis during both seasons (Y_1, Y_2). However, $\hat{D}$,h^2,$\hat{E}$ and $\hat{F}$ were found non significant in both the seasons (Y1, Y2) and. The significance of $\hat{H}_1$, along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one, which showed complete dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect $(\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.24 and 0.22 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) .which indicated that the recessive genes were more frequent than dominant genes.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.15 and -0.08 in Y1,Y2. The 'r' values were negative and very low in Y1 and negative in Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for days to first female flower anthesis were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2) and over season (pooled).

Node number to first male flower appearance

A perusal of Table-1 revealed that the estimates of $\hat{H}_1$,$\hat{H}_2$, h^2, $\hat{F}$ and $\hat{D}$ were found significant for node number to first male flower appearance during both seasons (Y_1, Y_2) However $\hat{E}$ was found nonsignificant in both the seasons (Y1, Y2). The significance of $\hat{H}_1$ with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect $(\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.14 and 0.17 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) .which indicated that the recessive genes were more frequent than dominant genes.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.53 and 1.22 in Y1,Y2 respectively. The 'r' values were negative and very low in Y1, Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for node number to first male flower appearance were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Node number to first female flower appearance

A perusal of Table-1 revealed that the estimates of $\hat{H}_1$,$\hat{H}_{2,}$ h^2, and $\hat{D}$ were found significant for node number to first female flower appearance during both seasons (Y_1, Y_2). However $\hat{E}$ and $\hat{F}$ were found nonsignificant in both the seasons (Y1, Y2). The significance of $\hat{H}_1$ with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.21 and 0.21in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) .which indicated that the recessive genes were more frequent than dominant genes.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.80 and 0.95 in Y1,Y2 respectively. The 'r' values were negative and very low in Y1, Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for node number to first female flower appearance were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Days to first fruit harvest

A perusal of Table-2 revealed that the estimates of $\hat{H}_1$,$\hat{H}_{2,}$ and $\hat{D}$ were found significant for days to first fruit harvest during both seasons (Y_1, Y_2). However, h^2,$\hat{E}$ and $\hat{F}$ were found non significant in both the seasons (Y1, Y2). The significance of $\hat{H}_{1,}$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one, which showed complete dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.18 and 0.20 in Y1, respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were more than one in the season Y2 except in Y1 which indicated that the dominant genes were more frequent than recessive ones.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was -0.01 and 0.34 in Y1andY2. The 'r' values were negative and very low in Y1 and negative in Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for days to first fruit harvest were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Vine length (m)

A perusal of Table-2 revealed that the estimates of $\hat{H}_1$ and $\hat{H}_2$ were found significant for vine length (m)during both seasons (Y_1, Y_2) but $\hat{D}$ was found significant only Y1and Y2. However, h^2,$\hat{E}$ and $\hat{F}$ were found non significant in both the seasons (Y1, Y2). The significance of $\hat{H}_{1,}$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one, which showed complete dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.17 and 0.23 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2} - \hat{F}]$ in the parents were more than one in the season Y2 except in Y1 which indicated that the dominant genes were more frequent than recessive ones.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 1.80 and 1.00 in Y1,Y2 respectively. The 'r' values were negative and very low in Y1 and negative in Y2 which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for Vine length (m)were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Number of primary branches per plant

A perusal of Table-2 revealed that the estimates of, $\hat{H}_1$, and $\hat{H}_2$, were found significant for Number of primary branches per plant during both seasons (Y_1, Y_2) but but $\hat{D}$ was found significant only Y2 except Y1. However, $h^2$and $\hat{E}$ were found nonsignificant in both the seasons (Y1, Y2) but $\hat{F}$ was found significant only Y2 except Y1. The significance of $\hat{H}_1$, along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.16 and 0.16 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}+ 1/2 +\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) .which indicated that the recessive genes were more frequent than dominant genes.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.04 and 0.18 in Y1, Y2 respectively. The ‘r’ values were positive and very low in Y1 and Y2 which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 for number of primary branches per plant were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Number of node per vine

A perusal of Table-2 revealed that the estimates of $\hat{H}_1$, $\hat{D}$ and $\hat{H}_2$, were found significant for Number of node per vine during both seasons (Y_1, Y_2). However, $h^2$and $\hat{E}$ were found non-significant in both the seasons (Y1, Y2) except in Y2 of h^2 but $\hat{F}$ was found non-significant during both seasons(Y_1, Y2). The significance of $\hat{H}_1$, along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.22 and 0.02 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}+ 1/2 +\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) except in Y_1 .which indicated that the recessive genes were more frequent than dominant genes. The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was -0.01 and 0.71 in Y1,Y2 respectively. The ‘r’ values were negative and very low in Y1 and Y2. Which showed excess of recessive genes during both the seasons (Y1, Y2). The values of t^2 for number of node per vine were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Internodal length (cm)

A perusal of Table-3 revealed that the estimates of $\hat{H}_1$, $\hat{D}$ and $\hat{H}_2$, were found significant for Internodal length(cm) during both seasons (Y_1, Y_2). However, $h^2$and $\hat{E}$ were found nonsignificant in both the seasons (Y1, Y2) except in Y2 of h^2 but $\hat{F}$ was found nonsignificant during both seasons (Y_1, Y2) except in Y2. The significance of $\hat{H}_1$, along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.17 and 0.22 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}+ 1/2 +\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were less than one in both the season (Y1, Y2) except in Y_1 .which indicated that the recessive genes were more frequent than dominant genes.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was -0.08 and 0.71 in Y1,Y2 respectively. The ‘r’ values were positive and very low in Y1 and Y2. Which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 internodal length(cm) were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Polar circumference of fruit (cm)

A perusal of Table-3 revealed that the estimates of $\hat{H}_{1,}$ $\hat{D}$ and $\hat{H}_{2,}$ were found significant for Polar circumference of fruit (cm)during both seasons (Y_1, Y_2). However, $h^2$and $\hat{E}$ were found nonsignificant in both the seasons (Y1, Y2) except in Y2 of h^2 and $\hat{E}$ but $\hat{F}$ was found nonsignificant during both seasons (Y2) except in Y1. The significance of $\hat{H}_{1,}$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one except inY2, which showed over dominance during both the seasons (Y1 except inY2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.68 and 1.08 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 +\hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were more than one in only Y_1 .which indicated that the dominant genes were more frequent than recessive genes. The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 2.72 and 0.35 in Y1,Y2 respectively. The 'r' values were positive and very low in Y1 except Y2. Which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 Polar circumference of fruit (cm)were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Equatorial circumference of fruit (cm)

A perusal of Table-3 revealed that the estimates of $\hat{H}_{1,}$ $\hat{D}$ and $\hat{H}_{2,}$ were found significant except $\hat{H}_1$ and D for Equatorial circumference of fruit (cm)during both seasons (Y_1, Y_2). However, $h^2$and $\hat{E}$ were found nonsignificant in both the seasons (Y1, Y2) except in Y1 of h^2 but $\hat{F}$ was found nonsignificant during both seasons (Y2) except in Y1. The significance of $\hat{H}_{1,}$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were less than one except which showed over recessive during both the seasons (Y1 and Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.24 and 0.22 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 +\hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were less than one in only Y_1 .which indicated that the recessive genes were more frequent than dominant genes. The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 1.66 and 0.11 in Y1,Y2 respectively. The 'r' values were positive and very low in Y1 and Y2. Which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 Equatorial circumference of fruit (cm)were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Average fruit weight (kg)

A perusal of Table-3 revealed that the estimates of $\hat{H}_{1,}$ $h^2$and $\hat{H}_{2,}$ were found significant for Average fruit weight (kg)during both seasons (Y_1, Y_2). However, $\hat{D}$ and $\hat{E}$ were found nonsignificant in both the seasons (Y1, Y2) but $\hat{F}$ was found nonsignificant during both seasons (Y2 and Y2) . The significance of $\hat{H}_{1,}$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\ \hat{D}_1)^{1/2}$ were more than one which showed over dominant during both the seasons (Y1 and Y2). The value of proportion of genes with +/- effect ($\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.20 and 0.22 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 +\hat{F}/(4\hat{D}\ \ \hat{H}_1)^{1/2}- \hat{F}]$ in the parents were less than one in both seasons(Y1and Y2) .which indicated that the recessive genes were more frequent than dominant genes. The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 1.17 and 0.70 in Y1,Y2 respectively. The 'r' values were positive and very low in Y1 except Y2. Which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 average fruit weight (kg)were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Number of fruits per plant

A perusal of Table-4 revealed that the estimates of $\hat{H}_{1,}$ h^2 and$\hat{H}_{2,}$ were found significant for number of fruit per plant during both seasons (Y_1, Y_2) However $\hat{E}$,$\hat{D}$ and$\hat{F}$ were found nonsignificant in both the seasons (Y1, Y2). The significance of $\hat{H}_1$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect $(\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.21and 0.20 in Y1, Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}+1/2+\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}-\hat{F}]$ in the parents were more than one in both the season (Y1, Y2) which indicated that the dominant genes were more frequent than recessive ones.

The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 1.87 and 1.00 in Y1,Y2 respectively. The 'r' values were positive and very low in Y1 except Y2 which showed excess of dominant genes during both the seasons (Y1, Y2). The values of t^2 for number of fruits per plant were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2) and over season(pooled).

Fruit yield per plant (Kg)

A perusal of Table-4 revealed that the estimates of $\hat{H}_1$, $\hat{H}_2$, and h^2were found significant for Fruit yield per plant (Kg)during both seasons (Y_1, Y_2) and over seasons (pooled) However $\hat{D}$,$\hat{E}$ and $\hat{F}$ were found nonsignificant in both the seasons (Y1, Y2). The significance of $\hat{H}_1$ along with higher value in both the seasons (Y1, Y2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D}_1)^{1/2}$ were more than one, which showed over dominance during both the seasons (Y1, Y2). The value of proportion of genes with +/- effect $(\hat{H}_2/4\hat{H}_1)^{1/2}$ in parents were found 0.21and 0.22 in Y1and Y2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $[(4\hat{D}_1\hat{H}_1)^{1/2}+1/2+\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}-\hat{F}]$ in the parents were less than one in both the season (Y1and Y2) which indicated that the recessive genes were more frequent than dominant genes.The number of groups of genes $(\hat{h}^2/\hat{H}_2)$ that control the character and exhibit dominance was 0.56and 0.50 in Y1,Y2 respectively. The 'r' values were positive and very low in Y2 and negative in Y1 which showed excess of dominant genes during both the seasons (Y1, Y2) and over season (pooled). The values of t^2 for Fruit yield per plant (Kg) were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (Y1, Y2).

Conclusion

Gene activity revealed that dominant variance was more significant than additive variance in both seasons, although both were found to be significant in the inheritance of the majority of the traits. Average degree of dominance revealed the presence of over dominance for all traits in both the seasons and the proportions of genes (H2ˆ/4 H1ˆ) in the parents were less than 0.25 for all the traits indicating asymmetrical distribution of alleles at loci, In general the proportions of dominant and recessive genes in parents i.e.$(4\hat{D}1\hat{H}_1)1/2+1/2+\hat{F}/(4\hat{D}\ \hat{H}_1)\ 1/2-\ \hat{F}$ were more than unity with positive value for all the traits and The ratio of $(\hat{h}_2/\hat{H}_2)$ after selection, the hybrids could be used as a new variety and subjected to multi-locational trials before being released for commercial cultivation. This is because the estimation of the number of gene groups showed that at least one gene group was involved in the inheritance both seasons (Y1, Y2), and the remaining traits and the positive correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) were demonstrated for the majority of the characters in both seasons.

Table 1 : Estimates of components of variation and their related statistics in 8×8 dialled crosses of pumpkin over two seasonsY_1 (2022-23) and Y_2(2023-24)

Hybrids	Days to first male flower anthesis			Days to first female flower anthesis			Node number to first male flower appearance			Node number to first female flower appearance		
	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled
$\hat{D}$ (Additive effect)	7.274**	3.192**	5.273**	1.897	2.260	2.249	1.063**	0.608**	0.777**	2.046**	2.438**	2.221**
SE±	1.240	0.729	0.975	1.270	1.258	1.338	0.166	0.214	0.178	0.933	0.969	0.966
$\hat{F}$ (Mean for over arrays)	5.913*	0.531	2.993	-0.048	-1.582	-0.229	-0.423	-1.068**	-0.84**	-1.325	-1.948	-1.642

SE±	2.930	1.723	2.305	3.000	2.972	3.163	0.391	0.506	0.420	2.205	2.290	2.283
$\widehat{H1}$ (Dominance effect)	8.880**	3.783**	5.658**	7.222**	8.150**	7.693**	1.498**	2.687**	1.924**	5.915**	5.920**	5.834**
SE±	2.850	1.676	2.242	2.919	2.891	3.077	0.381	0.493	0.409	2.145	2.228	2.221
$\widehat{H2}$ Dominance indicating asymmetry)	7.218**	3.260**	4.942**	7.191**	7.404**	7.027**	0.869**	1.889**	1.258**	5.115**	5.109**	5.026**
SE±	2.480	1.458	1.951	2.540	2.516	2.677	0.331	0.429	0.356	1.866	1.939	1.932
h^2	0.367	-0.480	-0.232	1.125	-0.606	0.381	0.467**	2.307**	1.221**	4.125**	4.873**	4.512**
SE±	1.663	0.978	1.308	1.703	1.687	1.795	0.222	0.287	0.239	1.252	1.300	1.296
$\hat{E}$ (Environmental component)	1.116	1.396	0.711	1.796	1.778	0.971	0.052	0.040	0.028	0.169	0.120	0.085
SE±	0.413	0.243	0.325	0.423	0.419	0.446	0.055	0.071	0.059	0.311	0.323	0.322
$(\hat{H}_1/\hat{D}_1)^{1/2}$ (Mean degree of dominance)	1.105	1.089	1.036	1.951	1.899	1.849	1.187	2.102	1.574	1.700	1.558	1.621
$(\hat{H}_2/4\hat{H}_1)^{1/2}$ (Proportion of genes)	0.203	0.215	0.218	0.249	0.227	0.228	0.145	0.176	0.163	0.216	0.216	0.215
$[(4\hat{D}_1\hat{H}_1)^{1/2}+1/2+\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}-\hat{F}]$ (Proportion of dominant and recessive genes)	2.164	1.165	1.755	0.987	0.689	0.946	0.713	0.411	0.488	0.680	0.592	0.629
$(\hat{h}^2/\hat{H}_2)$ (Number of gene groups)	0.051	-0.147	-0.047	0.156	-0.082	0.054	0.538	1.221	0.971	0.806	0.954	0.898
Heritability (narrow)	0.341	0.419	0.435	0.216	0.387	0.366	0.797	0.707	0.769	0.590	0.650	0.635
R(Correlation coefficient)	-0.835	-0.779	-0.929	-0.055	-0.312	-0.229	-0.615	-0.767	-0.732	-0.828	-0.829	-0.841
t^2	0.435	0.071	0.017	1.27	2.24	2.22	3.21	3.49	3.27	7.92	7.57	8.11

Table 2 : Estimates of components of variation and their related statistics in 8×8 dialled crosses of pumpkin over two seasonsY_1 (2022-23) and Y_2(2023-24)

Hybrids	**Days to first fruit harvest**			**vine length**			**Number of primary branches per plant**			**Number of node per vine**		
	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled
$\hat{D}$ (Additive effect)	4.694**	11.579**	6.696**	0.143**	0.120**	0.064	0.258	0.425**	0.341**	5.586**	9.101**	5.270**
SE±	2.506	3.200	2.960	0.069	0.030	0.039	0.158	0.128	0.142	2.590	3.806	2.510
$\hat{F}$ (Mean for over arrays)	5.996	-4.427	-1.012	0.209*	0.059	0.053	-0.287	-0.338**	-0.295	0.070	-1.616	-4.120
SE±	5.920	7.562	6.995	0.163	0.070	0.092	0.374	0.302	0.335	6.120	8.992	5.930
$\widehat{H1}$ (Dominance effect)	31.817**	9.852	14.895**	0.414**	0.457**	0.351**	1.218**	1.126**	1.201**	31.500**	44.460**	33.621**
SE±	5.760	7.357	6.806	0.159	0.068	0.089	0.364	0.294	0.326	5.954	8.749	5.769

$\widehat{H2}$ Dominance indicating asymmetry)	23.421**	7.930	11.600**	0.296**	0.428**	0.305**	0.806**	0.738**	0.788**	28.448**	36.343**	29.781**
SE±	5.011	6.401	5.921	0.138	0.060	0.078	0.316	0.256	0.284	5.180	7.611	5.019
h^2	-0.225	2.700	0.033	0.534**	0.428**	0.479**	0.037	0.133	0.090	-0.436	25.792**	7.729**
SE±	3.361	4.293	3.971	0.093	0.040	0.052	0.212	0.172	0.190	3.474	5.104	3.366
$\hat{E}$ (Environmental component)	1.745	3.326	0.899	0.017	0.008	0.007	0.043	0.056	0.021	1.625	1.707	0.723
SE±	0.835	1.067	0.987	0.023	0.010	0.013	0.053	0.043	0.047	0.863	1.269	0.837
$(\hat{H}_1/\hat{D}_1)^{1/2}$ (Mean degree of dominance)	2.604	0.922	1.491	1.704	1.956	2.347	2.172	1.628	1.876	2.375	2.210	2.526
$(\hat{H}_2/4\hat{H}_1)^{1/2}$ (Proportion of genes)	0.184	0.201	0.195	0.179	0.234	0.217	0.165	0.164	0.164	0.226	0.204	0.221
$[(4\hat{D}_1\hat{H}_1)^{1/2}+1/2+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}]$ Proportion of dominant and recessive genes)	1.650	0.657	0.904	2.513	1.289	1.432	0.593	0.607	0.626	1.005	0.923	0.732
$(\hat{h}^2/\hat{H}_2)$ (Number of gene groups)	-0.010	0.340	0.003	1.802	1.001	1.573	0.046	0.181	0.114	-0.015	0.710	0.260
Heritability (narrow)	0.318	0.628	0.592	0.220	0.282	0.256	0.662	0.705	0.707	0.329	0.466	0.448
R Correlation coefficient)	0.001	-0.123	-0.951	-0.603	-0.871	0.352	0.249	0.394	-0.691	-0.534	-0.663	0.053
t^2	2.68	7.90	7.81	6.95	1.58	3.80	16.66	17.44	20.21	1.88	5.07	2.92

Table 3 : Estimates of components of variation and their related statistics in 8×8 dialled crosses of pumpkin over two seasonsY_1 (2022-23) and Y_2(2023-24)

Hybrids	**Internodal length(cm)**			**Polar circumference of fruit (cm)**			**Equatorial circumference of fruit(cm)**			**Average fruit weight(kg)**		
	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled	Y1	Y2	Pooled
$\hat{D}$ (Additive effect)	0.143**	0.250**	0.168**	6.031**	27.333**	13.749**	6.453**	24.118**	14.598**	0.078	0.091	0.075
SE±	0.063	0.050	0.040	0.978	0.559	0.303	1.663	4.859	3.062	0.045	0.061	0.052
$\hat{F}$ (Mean for over arrays)	-0.098	-0.186**	-0.173**	-2.892**	0.848	-4.558**	-4.078**	5.685	0.461	-0.057	-0.045	-0.064
SE±	0.148	0.118	0.093	2.312	1.322	0.716	3.930	11.481	7.235	0.105	0.144	0.124
$\widehat{H1}$ (Dominance effect)	0.640**	0.401**	0.492**	9.658**	4.128**	1.432*	5.624	11.069	9.060	0.320**	0.314**	0.305**
SE±	0.144	0.115	0.091	2.249	1.286	0.697	3.823	11.169	7.039	0.103	0.140	0.120

$\widehat{H2}$ Dominance indicating asymmetry)	0.438**	0.362**	0.380**	4.982**	-2.755**	0.749	5.477	9.992	8.261	0.263**	0.283**	0.266**
SE±	0.125	0.100	0.079	1.957	1.119	0.606	3.326	9.717	6.124	0.089	0.122	0.105
h^2	-0.038	0.260**	0.065	13.587**	-1.006	3.283**	9.142**	1.170	4.985	0.309**	0.200**	0.249**
SE±	0.084	0.067	0.053	1.312	0.750	0.407	2.231	6.517	4.107	0.060	0.082	0.070
$\hat{E}$ (Environmental component)	0.089	0.053	0.033	2.369**	2.321	1.265**	1.879	3.151	1.530	0.001	0.001	0.001
SE±	0.021	0.017	0.013	0.326	0.187	0.101	0.554	1.620	1.021	0.015	0.020	0.018
$(\hat{H}_1/\hat{D}_1)^{1/2}$ (Mean degree of dominance)	2.118	1.265	1.713	1.265	0.389	0.323	0.934	0.677	0.788	2.020	1.857	2.019
$(\hat{H}_2/4\hat{H}_1)^{1/2}$ (Proportion of genes)	0.171	0.226	0.193	0.129	-0.167	0.131	0.243	0.226	0.228	0.206	0.225	0.218
$[(4\hat{D}_1\hat{H}_1)^{1/2}{}_+ 1/2 + \hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2} - \hat{F}]$ Proportion of dominant and recessive genes)	0.721	0.545	0.537	0.681	1.083	0.321	0.494	1.421	1.041	0.696	0.764	0.651
$(\hat{h}^2/\hat{H}_2)$ (Number of gene groups)	-0.086	0.718	0.172	2.727	0.365	4.384	1.669	0.117	0.603	1.176	0.707	0.936
Heritability (narrow)	0.528	0.624	0.640	0.653	0.885	0.867	0.622	0.633	0.675	0.590	0.539	0.570
R Correlation coefficient)	0.047	0.217	-0.509	0.533	-0.481	-0.904	-0.772	-0.850	0.446	-0.044	0.189	0.098
t^2	2.93	0.66	1.84	0.69	2.48	0.99	2.05	2.06	2.15	17.23	10.91	13.63

Table 4 : Estimates of components of variation and their related statistics in 8×8 dialled crosses of pumpkin over two seasonsY_1 (2022-23) and Y_2(2023-24)

Hybrids	Number of fruit per plant			Fruit yield per plant(kg)		
	Y1	Y1	Y1	Y1	Y2	Pooled
$\hat{D}$ (Additive effect)	0.001	1.067	1.067	1.067	1.676	1.258
SE±	0.099	2.208	2.208	2.208	2.391	2.282
$\hat{F}$ (Mean for over arrays)	0.046	-1.403	-1.403	-1.403	-1.337	-1.430
SE±	0.234	5.216	5.216	5.216	5.649	5.392
$\widehat{H1}$ (Dominance effect)	1.024**	11.548**	11.548**	11.548**	13.098**	12.007**
SE±	0.228	5.075	5.075	5.075	5.496	5.245
$\widehat{H2}$ Dominance indicating asymmetry)	0.898**	9.838**	9.838**	9.838**	11.966**	10.602**
SE±	0.198	4.415	4.415	4.415	4.781	4.563
h^2	1.687**	5.551**	5.551**	5.551**	6.008**	5.782

SE±	0.133	2.961	2.961	2.961	3.206	3.060
$\hat{E}$ **(Environmental component)**	0.018	0.062	0.062	0.062	0.057	0.029
SE±	0.033	0.736	0.736	0.736	0.797	0.761
$(\hat{H}_1/\hat{D}_1)^{1/2}$ **(Mean degree of dominance)**	29.218	3.290	3.290	3.290	2.796	3.089
$(\hat{H}_2/4\hat{H}_1)^{1/2}$ **(Proportion of genes)**	0.219	0.213	0.213	0.213	0.228	0.221
$[(4\hat{D}_1\hat{H}_1)^{1/2}{}_{+}1/2+\hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2}-\hat{F}]$ **Proportion of dominant and recessive genes)**	4.814	0.667	0.667	0.667	0.750	0.689
$(\hat{h}^2/\hat{H}_2)$ **(Number of gene groups)**	1.879	0.564	0.564	0.564	0.502	0.545
Heritability (narrow)	0.141	0.453	0.453	0.453	0.405	0.433
R (Correlation coefficient)	0.089	-0.053	-0.053	-0.053	0.170	0.584
t^2	11.71	35.94	35.94	35.94	7.59	16.19

Future scope

The results validate the subsequent recommendations for further investigation: These studies should be repeated in the next two to three years to confirm the results. These cultivars can be evaluated at different sowing dates depending on the agroclimatic conditions in the area. Other types can be utilized in subsequent experiments.

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