Comunicata Scientiae
Horticultural Journal

ORIGINAL ARTICLE
published: 30 August 2025
https://doi.org/10.14295/CS.v16.4170

Genetic inheritance of quantitative characters in ornamental peppers

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Abstract

This study was carried out aimed to genetic inheritance analysis of 14 characteristics in ornamental peppers. Eight ornamental *Capsicum annuum* lines were crossed to produce a diallel set without reciprocals. The 28 F_1 hybrids and their parents were arranged in a completely randomized design, with three replicates and two plants per plot. Data were subjected to variance analysis and subsequent diallel analysis performed according to Hayman's method. The t statistic was used to test the adequacy of the additive-dominance model. Canopy diameter, plant height, first bifurcation height, stem diameter, days to fruiting, leaf length, leaf width, fruit mass, fruit dry matter content, fruit diameter and yield manifested epistasis. For days to flowering and number of fruits per plant additive effects were more important, in this way selection in segregating generations will be quite efficient. These two traits exhibited partial dominance and fruit lenght exhibited overdominance it is being recommended to explore heterosis. The expected limits for the reduction of the average number of days to flowering is 89 days, for the increase in the number of fruits it is 96 fruits and for the reduction of the fruit length it is 6 milimeters. UFSJ 1 has the highest concentration of dominant genes to reduce days to flowering and fruit length averages and UFSJ 8 has the highest concentration of recessive genes to increase the number of fruit, so these parents are indicated for selection for continued breeding program.

Keywords: Capsicum annuum, diallel analysis, genetic effects, genetic improvement, Hayman`s method

Introduction

The great value of peppers of the genus *Capsicum* is in the trade of fresh or processed fruits, as an ornamental plant and as raw material for the pharmaceutical and cosmetics industries (Ferraz et al., 2016). Among potted ornamental plants, peppers have been highlighted due to their growing acceptance by the consumer market (Rêgo et al., 2009).

The study of the genetic control of the quantitative characteristics related to the fruits and the size of the plants in the ornamental peppers is of great relevance for the efficient conduction of the genetic improvement program (Barroso et al., 2012; Fortunato et al., 2019; Marcelino & Albuquerque, 2019; Silva Neto et al., 2014; Silva et al., 2017), guiding in the choice of the best selection procedures and the most efficient methods for the conduction of the segregating populations, since genetic variability in *Capsicum* can be exploited aiming at identifying superior genotypes and obtaining hybrids (Albuquerque et al., 2021; Pessoa et al., 2021). In this context, diallel crosses are very efficient because they allow estimating useful parameters for the selection of parents for hybridization and for understanding the genetic effects involved in the determination of characters (Cruz et al., 2014; Marcelino & Albuquerque, 2019; Rêgo et al., 2015).

Among diallel analysis methods, the one proposed by Jinks & Hayman (1953) and Hayman (1954a, 1954b) is based on genetic and environmental estimates of statistics obtained from a diallel table and it generates information about genetic control and selection limits of evaluated characters and on the genetic values of the parents. This method requires the following assumptions which are jointly evaluated by sufficiency tests of the additive-dominant model: diploid segregation, homozygous parents, no reciprocal differences, no

Received: 24 February 2023
Accepted: 30 May 2023

multiple allelism, uncorrelated gene distribuitions between the parents, and no epistasis.

Thus, the objective of this work was to carry out a genetic analysis of quantitative traits in ornamental pepper plants and to estimate the genetic value of the parents in diallel crosses by Hayman`s method.

Material And Methods

Eight ornamental *Capsicum annuum* lines belonging to the germplasm bank of CSL-UFSJ (Campus Sete Lagoas, Universidade Federal de São João del Rei, Sete Lagoas, MG, Brazil) (**Table 1**) were crossed in all possible combinations to produce a diallel set without reciprocals. The 28 F_1 hybrids and their parents were arranged in a completely randomized design, with three replicates and two plants per plot.

Table 1. Description of some qualitative traits of the eight ornamental pepper accessions (*Capsicum annuum*). Plant growth habit was erect for all accessions

Accessions	Traits			
	FP	IFC	MFC	PWF
UFSJ 1	Erect	Yellow	Red	Intermediate
UFSJ 2	Erect	Light yellow	Red	Persistent
UFSJ 3	Erect	Yellow	Yellow	Intermediate
UFSJ 4	Erect	Yellow	Orange	Intermediate
UFSJ 5	Erect	Greenish yellow	Orange	Intermediate
UFSJ 6	Erect	Light yellow	Orange	Persistent
UFSJ 7	Erect	Greenish yellow	Dark red	Intermediate
UFSJ 8	Pending	Light yellow	Orange and yellow	Persistent

FP = fruit position, IFC = fruit color at intermediate stage, MFC = fruit color at mature stage, PWF = persistence of pedicel with fruit.

To make the crosses, freshly opened flower buds of each male parent were collected to obtain pollen. The pollen obtained from each parent was stored in refrigerator in containers containing silica gel and properly identified. The flower buds of female parents were emasculated in the morning before anthesis using tweezers. In the same period, pollination was performed by placing pollen grains from each male parent on the stigmas of each emasculated flower. Each crossing was identified with a small aluminum plate tied with nylon thread in the pedicel of each pollinated flower.

Parents and their offspring were seeded in a 200-cell styrofoam tray. Seedlings were transplanted at the six-leaf stage into 900 mL plastic pots filled with commercial substrate (Bioplant, Brazil). Pots were kept under a mesh structure at 30% shading.

The 36 treatments were evaluated according to 14 characteristics related to fruits, plant size and yield: canopy diameter (CD), plant height (PH), first bifurcation height (FBH), stem diameter (SD), days to flowering counted from transplanting date (DTF), days to fruiting counted from transplanting date (DTFr), leaf length (LL), leaf width (LW), number of fruits per plant (NF), fruit mass (FM), fruit dry matter content (DMC), fruit length (FL), fruit diameter (FD) and yield (Y). All characteristics were evaluated based on the list of descriptors suggested by the International Plant Genetic Resources Institute (1995), and those relative to fruits were taken from 10 mature units randomly harvested on each plot.

Through the method of Jinks & Hayman (1953) and Hayman (1954a, 1954b), with the covariance between the parents and the r-th row ($\widehat{W_r}$) and the variance within the diallel row or column ($\widehat{V_r}$), three tests were applied to assess the heterogeneity of $\widehat{W_r}$ - $\widehat{V_r}$: i) variation of $\widehat{W_r}$ - $\widehat{V_r}$ was evaluated by means of analysis of variance considering as a source of variation the repetitions of the tables and the rows (or diallel table entries) within each table. In case of a significant effect of the lines, there were indications of failure in the assumptions; ii) From the linear regression analysis of $\widehat{W_r}$ as a function of $\widehat{V_r}$ the t test was applied on the linear regression coefficient to verifying the significance of the slope of the line (H_0: b=1 vs. H_a: b≠1); iii) $\widehat{W_r}$ and $\widehat{V_r}$ were weighted by 45° rotationof the axes represented by $\widehat{W_r}'$ and $\widehat{V_r}'$ and then the slope of the line after rotation was tested (H_0: b'=0 vs. H_a: b'≠0).

For the traits that met the assumptions of the additive-dominant model, the following genetic and non-genetic components were obtained: • $\widehat{\varepsilon}$ - environmental component of variation; • $\widehat{D}$ - variations due to additive effect: $\widehat{D} = \widehat{Vp} - \widehat{\varepsilon}$; • $\widehat{F}$ - covariances of additives and non-additive effects: $\widehat{F} = 2\widehat{Vp} - 4\widehat{W} - \frac{2(p-2)}{p}\widehat{\varepsilon}$; • $\widehat{H1}$ - variations due to dominance effect: $\widehat{H1} = \widehat{Vp} - 4\widehat{W} + 4\widehat{V} - \frac{(3p-2)}{p}\widehat{\varepsilon}$; • $\widehat{H2}$ - component of variation arising from the h increments of all segregating genes, or the dominance component indicating asymmetry of positive and negative effects of genes: $\widehat{H2} = 4\widehat{V} - 4\widehat{V_M} - 2\widehat{\varepsilon}$; • $\widehat{h^2}$ - is the overall mean dominance effect of heterozygous loci $\widehat{h^2} = 4\widehat{M^2} - \frac{4(p-1)}{p^2}\widehat{\varepsilon}$.

Basic parameters were also estimated to obtain the following genetic information: • mean degree of dominance over all loci. With average parcial dominance this is expected to fall within the range 0-1, and with over-dominance to be greater than 1: $\sqrt{\widehat{H1} / \widehat{D}}$; • average frequency of negative versus positive alleles showing dominance in the parents. The value should have a maximum of ¼ when the positive and negative alleles were equally distributed. Unequal distribuition would result in a value less than ¼: $\widehat{H2}/4\widehat{H1}$; • the ratio of the total number of dominant to recessive alleles in all the parents: D/R = KD/DR = $\frac{\sqrt{4D\widehat{H1}+F}}{\sqrt{4D\widehat{H1}-F}}$; • number of effective factors which exhibited dominance: $\widehat{h2}/\widehat{H2}$; • broad coefficient of determination: $h_A^2 = \frac{\widehat{D}-\widehat{F}+\widehat{H1}-\left(\frac{1}{2}\right)\widehat{H2}}{\widehat{D}-\widehat{F}+\widehat{H1}-\left(\frac{1}{2}\right)\widehat{H2}+2\widehat{\varepsilon}}$, and • restricted coefficient of determination $h_R^2 = \frac{\widehat{D}-\widehat{F}+\widehat{H1}-\widehat{H2}}{\widehat{D}-\widehat{F}+\widehat{H1}-\left(\frac{1}{2}\right)\widehat{H2}+2\widehat{\varepsilon}}$

The concentrations of dominant and recessive alleles were estimated so that a fully homozygous dominant parent has variance Vr(g) and covariance Wr(g), respectively expressed by VD and WD. A fully homozygous recessive parent has variance Vi(g) and covariance Wi(g), respectively expressed by Vr and Wr. The points (VD, WD) and (VR, WR) were estimated in two ways. The first of these was through the estimators of D and H1 parameters. The other way in which the points (VD, WD) and (VR, WR) were estimated was through the graphical procedure in which they were located by the intersection between the straight line $\widehat{W}= \frac{1}{4}(\widehat{D}\text{-}\widehat{H1})+\widehat{Vr}$ and the parabola $\widehat{W_R^2} = \widehat{V_R}\,\widehat{Vp}$

Correlations between parent means (Yr) and the statistic Wr + Vr were obtained. The sign and magnitude of the correlation coefficient (r) between $\widehat{W_r}$ + $\widehat{V_r}$ and the average of the parental lines ($\overline{Y_{rr}}$) were used in the evaluation of the direction of action of the dominant genes. If r was positive and close to + 1, the dominant genes acted to reduce the character. If r was close to -1, the dominant genes acted to increase the character.

The theoretical limits of selection referring to the average value expected for the completely dominant or recessive parent in relation to the segregating genes in the diallel was estimated through the prediction equation given by: $\widehat{Y}$r = $\widehat{\alpha}_0+\widehat{\alpha}_1(\hat{W}_R+\widehat{V}_R)$.

The classification of coefficients of determination was performed according to Hallauer et al. (2010), in which: $\hat{h}^2$ <30 = low, 30< $\hat{h}^2$ <70 = intermediate, $\hat{h}^2$ >70 = high.

All analyses were performed using the Genes computer program (Cruz, 2013).

Results And Discussion

Differences among genotypes were significants for all evaluated traits (data not shown).

Days to flowering counted from transplanting date (DTF), number of fruits per plant (NF) and fruit length (FL) revealed no significance in the three tests of the dominant additive model. For the other characteristics, significance was observed in at least one of the tests and they were suppressed from subsequent analyzes due to non-adequacy to the model, on account of epistasis occurrence (**Table 2**).

For days to flowering (DTF) and number of fruits per plant (NF) the component associated with additive effects ($\widehat{D}$)had a significant result being more important than the components associated with dominance effects($\widehat{H}_1$, $\widehat{H}_2$ and $\widehat{h}_2$) (**Table 3**). Marcelino and Albuquerque (2019) also found a predominance of additive effects for both traits in this population. Similar resultas were found for these traits by Nascimento et al. (2019), Marame et al. (2009 a, b), Nascimento et al. (2012) and Santos et al. (2014). In this way selection in segregating generations will be quite efficient for these two traits (Rêgo et al., 2009), since the performance of a genotype will be inherited by its progeny. Bento et al. (2016) and Bhutia et al. (2015) also found the predominance of additive effects for NF, but different results were found for DTF by Rêgo et al. (2012) in which showed significant effects only for dominant genes. For NF the positive and significant estimate of F indicates a higher frequency of dominant than recessive genes in diallel parents (Table 3). The estimates of the mean degrees of dominance ($\sqrt{\widehat{H1}/\widehat{D}}$= 0,755 for DTF and 0,802 for NF) indicate the existence of partial dominance (values between zero and one) between the alleles that act in the control of these two traits (**Table 4**), which can also be verified by the fact that the regression line $\widehat{W_r}$ as a function of $\widehat{V_r}$ of intercepts the ordinate above the origin (**Figure 1**a, b). Due to partial dominance, it is also recommended to explore heterosis (Bhutia et al., 2015 and Pessoa, 2016) for days to flowering and for number of fruits per plant. It is known that dominant alleles can act both in increasing and decreasing the mean of a trait (Cardoso et al., 2015) and by estimating $\widehat{H}_2/4\widehat{H}_1$ (0,128 for DTF and 0,148 for NF) it is verified that the dominant alleles that act in the sense of increasing and the dominant alleles that act in the sense of decreasing the DTF and NF averages have asymmetric distribution among parents, with a predominance of dominant homozygous forms ($\widehat{K}_D/\widehat{K}_R$= 2,527 for DTF and 5,439 for NF). It was also found the presence of at least one gene or gene block acting to control these traits ($\widehat{h_2}/\widehat{H}_2$= - 0.953 for DTF and - 0.245 for NF). In fact, Bento et al. (2016) estimated 16 genes and indicated the complexity of the inheritance with the presence of a major gene involved in control of NF.

For fruit lenght (FL) the component associated with additive effects ($\widehat{D}$)and the components due to dominance deviations had significant results with the significance and negative sign of $\widehat{D}$- $\widehat{H}_1$indicative of the greater importance of the components associated with the effects due to dominance (**Table 3**). Rodrigues et al. (2012) also found additive and non-additive effects acting on the control of fruit length in *C. baccatum*. In contrast, Bento et al. (2016), Medeiros et al. (2014) and Rêgo et al. (2009) found the predominance of additive effects in genetic control of FL. The estimate of the average degree of dominance ($\sqrt{\widehat{H1}/\widehat{D}}$ was 1.426, indicating an overdominance relationship (value greater

Table 2. Adequacy test of the additive-dominant model based on the analysis of variance of $\widehat{W_r}+\widehat{V}_r$ and on the linear regression analysis of $\widehat{W_r}$ as a function of $\widehat{V}_r$, according to Hayman`s method, for quantitative traits in ornamental pepper (*Capsicum annuum*)

Character	Anova $\widehat{W_r}+\widehat{V}_r$	Regression $\widehat{W_r} = 1/4(\widehat{D}+\widehat{H}_1)+\widehat{bV_r}$		
	MS Lines	$\widehat{b}$ +Variance	t (h_0: b = 1)	F = t^2 (h_0: b´= 0) (1)
CD	1060685.1365*	1.063± 0.0906	0.208^{ns}	-1.117^{ns}
PH	113053.4640*	1.060±0.1417	0.160^{ns}	-1.294^{ns}
FBH	19624.1908^{ns}	0.469±0.0618	-2.136*	0.823^{ns}
SD	31.5946**	0.956±0.0265	-0.269^{ns}	-0.225^{ns}
DTF	958.1836^{ns}	0.433±0.0970	-1.821^{ns}	0.370^{ns}
DTFr	10348.2154*	0.820±0.0700	-0.681^{ns}	-0.174^{ns}
LL	62114.8628 **	0.670	-2.051*	1.229^{ns}
LW	5335.0367**	0.683 ±0.0234	-2.070*	1.283^{ns}
NF	92.1271^{ns}	0.3460±0.1297	-1.817^{ns}	0.142^{ns}
FM	0.2259**	1.345±0. 051	1.530^{ns}	-2.470*
DMC	0.0010**	0.980±0.054	-0.084^{ns}	-0.615^{ns}
FL	7225.5168^{ns}	0.686±0.183	-0.735^{ns}	-0.665^{ns}
FD	153.9540**	1.051±0.065	0.198^{ns}	-0.968^{ns}
Y	941.6207^{ns}	0.115±0.090	-2.949*	0.744^{ns}

F test weighing the average values of $\widehat{W_r}$ and $\widehat{V}_r$ by means of their 45º rotation. CD = canopy diameter (mm), PH = plant height (mm), FBH = first bifurcation height (mm), SD = stem diameter (mm), DTF = days to flowering counted from transplanting date, DTFr = days to fruiting counted from transplanting date, LL = leaf length (mm), LW = leaf width (mm), number of fruits per plant (NF), FM = fruit mass (g), DMC = fruit dry matter content (g), FL = fruit length (mm), FD = fruit diameter (mm) and Y = yield (g). ^{ns} no significant, */** significant at 1% and at 5% probability by F-test and t-test.

Table 3. Estimates of genetic and non-genetic components for days to flowering counted from transplanting date (DTF), number of fruits per plant (NF) and fruit length (FL), according to Hayman`s method, in ornamental pepper (*Capsicum annuum*)

Character	Component(1) Standard Deviation (2)						
	$\hat{\mathcal{E}}$	$\widehat{D}$	$\widehat{H}_1$	$\widehat{H}_2$	$\widehat{h_2}$	$\widehat{F}$	$\widehat{D}-\widehat{H}_1$
DTF	37.27±7.65*	37.27±19.72*	37.53±53.26	19.19±45.43	-18.28±25.98	43.01±45.97	28.24±24.37
NF	7.47±3.43*	38.69±8.84*	24.89±23.88	14.71±20.37	-3.60±11.65	42.78±20.62*	13.80±10.93
FL	4.68±15.26	119.91±39.34*	243.75±106.27*	224.15±90.65*	21.84±51.83	-62.44±91.73	-123.84±48.62*

$\hat{\mathcal{E}}$ - environmental component of variation; $\widehat{D}$ - variations due to additive effect; $\widehat{H}_1$ - variations due to dominance effect; $\widehat{H}_2$- dominance component indicating asymmetry of positive and negative effects of genes; $\hat{h}_2$- is the overall mean dominance effect of heterozygous loci; $\widehat{F}$ - covariances of additives and non-additive effects; $\widehat{D}-\widehat{H}_1$ – component that expresses the difference between additive anddominant genetic effects. (2) t values obtained by dividing the effect estimate by its respective standard deviation (Singh & Chaudhary, 1979). ns no significant. * significant at 5% probability (values greater than 1.96).

Table 4. Estimates of genetic and non-genetic parameters for days to flowering counted from transplanting date (DTF), number of fruits per plant (NF) and fruit length (FL), according to Hayman`s method in ornamental pepper (*Capsicum annuum*)

Character	Parameter Estimates (1)					
	$\sqrt{\widehat{H1}/\widehat{D}}$	$\widehat{H2}/4\widehat{H1}$	$\widehat{K}_D/\widehat{K}_R$	$\widehat{h2}/\widehat{H}2$	h^2_R	h^2_A
DTF	0.755	0.128	2.527	-0.953	0.328	0.405
NF	0.802	0.148	5.439	-0.245	0.214	0.473
FL	1.426	0.230	0.691	0.097	0.624	0.971

$\sqrt{\hat{H}_1}/\widehat{D}$ mean degree of dominance over all loci; $\hat{H}_2/4\hat{H}_1$ average frequency of negative versus positive alleles showing dominance in the parents; $\widehat{K}_D/\widehat{K}_R$ ratio of the total number of dominant to recessive alleles in all the parents; $\hat{h}_2/\hat{H}_2$: number of effective factors which exhibited dominance; h^2_R: Strict coefficient of determination; h^2_A: Broad coefficient of determination.

than one) between the alleles that act in the control ofthis trait (Table 4), which can also be verified by the fact that the regression line, established by the relationships between the covariance Wi and the variance Vi, intercepts the ordinate near the origin (**Figure 1**c). Rêgo et al. (2022) also found overdominant allelic interaction and occurrence of transgressive individuals for maximum and minimum values for FL. These authors recommended, in according to Silva et al. (2015), the selection of individuals with minimum values for FL aiming ornamental purposes. Due to the predominance of dominance effects and the interaction of overdominance between the alleles that govern fruit length, the best genetic improvement strategy for this trait is to obtain hybrids (Gonçalves, 2011) through the capitalization of heterosis in specific crosses. Additionally, these hybrids can be registered and protected more quickly compared to the time required to obtain a new cultivar by means of selection in segregating populations (Rêgo et al., 2022). Due to the estimate of $\widehat{H2}/4\widehat{H1}$(0.230) being around 0,25 it is verified that dominant alleles acting to increase and to decrease the mean of this characteristic have a symmetrical distribuition among the parents with a balance of homozygous forms dominant and recessive for fruit lenght($\widehat{K}_D/\widehat{K}_R$= 0.691). There is at least one gene or gene block acting to control this trait ($\widehat{h2}/\widehat{H2}$= 0.097). Concerning this, Bento et al. (2016) estimated 5 genes and indicated presence of major gene involved in control of FL.

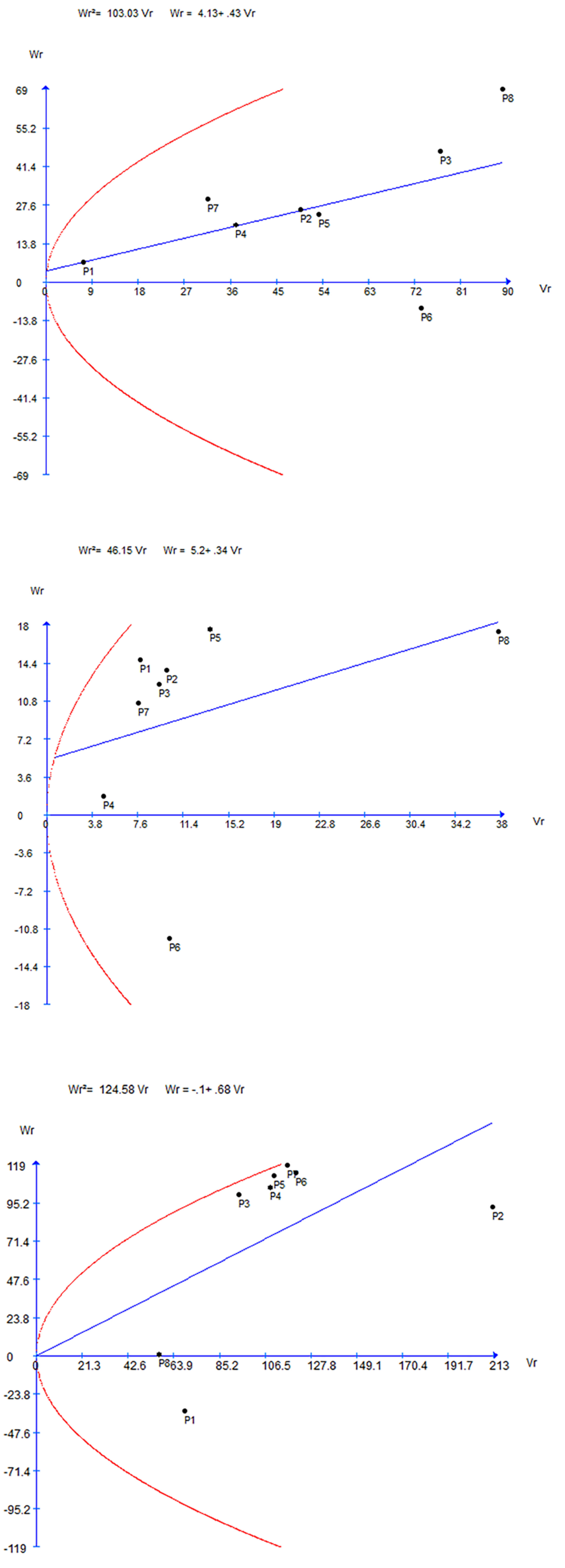

Figure 1. Straight line and parabola established by the relationship between covariance between the means of parents and the means of the r-th row ($\hat{w}_r$variance between the means of the r-th row ($\hat{V}_r$) for quantitative traits in ornamental pepper (*Capsicum annuum* L.): (a) days to flowering counted from transplanting date (DTF), (b) number of fruits per plant (NF) and (c) fruit length (FL). Parents: P1 = UFSJ 1, P2 = UFSJ 2, P3 = UFSJ 3, P4 = UFSJ 4, P5 = UFSJ 5, P6 = UFSJ 6, P7 = UFSJ 7 and P8 = UFSJ 8. Straight line established by $\hat{W}_R = 1/4(\widehat{D}+\widehat{H}_1)+\hat{V}_R$ and parabola established by $\hat{w}_R^2 = \hat{V}_R + \hat{V}_p$

For days to flowering, the correlation between the average of the parents and the mean of the concentration of dominant and recessive genes (r = 0.5561) indicates that the dominant genes act to reduce the mean of the character, as also verified by Rêgo et al. (2012) and Pessoa (2016). The expected limit for the average reduction of this characteristic is 89 days ($\widehat{Y_D}$) (**Table 5**) . UFSJ 1 has the highest concentration of dominant alleles while UFSJ 8 has the highest concentration of recessive alleles for DTF (**Table 6** and Figure 1a). The parent with maximum dominant homozygosity for days to flowering should have $\widehat{W_l}+\widehat{V_l}$= 4,3821 (= $\widehat{W_D}+\widehat{V_D}$). It is verified that, among the parents, UFSJ 1, despite retaining the highest concentration of dominant alleles, has $\widehat{W_1}+\widehat{V_1}$ = 14.4464, which shows the possibility of obtaining lines with even earlier flowering from selection in segregating populations derived from the diallel (**Tables 5** and **6**).

In ornamental pepper breeding programs, increasing the number of fruits is desirable (Nascimento et al., 2014), since it makes the plants more attractive due to the greater contrast between the color of fruits and leaves (Neitzke et al., 2016). For the number of fruits per plant, the correlation between the average of the parents and the mean of the concentration of dominant and recessive genes (r = 0.4203) indicates that recessive genes act to increase the average of the character, as also verified by Pessoa (2016). The expected limit for the increase in the mean of this characteristic is 96 fruits ($\hat{Y}_R$). (Table 5). UFSJ 6 has the highest concentration of dominant alleles while UFSJ 8 has the highest concentration of recessive alleles (Table 6 and Figure 1b). The parent with maximum recessive homozygosity for NF must present $\widehat{W_l}+\widehat{V_l}$ = 483,6173 ($\widehat{W_R}+\widehat{V_R}$). UFSJ 8 despite retaining the highest concentration of recessive alleles has $\widehat{W_8}+\widehat{V_8}$ = 55.2361 which shows the possibility of obtaining lines with an even greater number of fruits in the segregating generations (Tables 5 and 6).

Silva et al. (2015) report that smaller fruits are more proportional to the dwarf size of ornamental pepper plants. In this work it was verified that the correlation between the average of the length of the fruits in the parents and the average of the concentration of dominant and recessive genes (r = 0.7882) indicates that the dominant genes act in the sense of reducing the average of the character being the expected limit for this reduction of 6 millimeters ($\hat{Y}_D$). (Table 5). UFSJ 1 has the highest concentration of dominant alleles while UFSJ 2 has the highest concentration of recessive alleles (Table 6 and Figure 1c). The parent with maximum dominant homozygosity for FL should present $\widehat{W_l}+\widehat{V_l}$ = -

Table 5. Estimates of the correlations between the mean values of the parents ($\bar{Y}_{rr}$) and the sum of the covariance between the means of parents and the means of the r-th row ($\hat{W}_r$) with the variance between the means of the r-th row ($\widehat{V}_R$), expected values of coordinates $\hat{W}_R$, $\widehat{V}_R$ and $\hat{W}_D$, $\widehat{V}_D$ and the predicted value for the parents with the maximum concentration of dominant alleles ($\widehat{Y}_D$) and recessives ($\widehat{Y}_R$) for transplanting date (DTF), number of fruits per plant (NF) and fruit length (FL), according to Hayman`s method

Character	Parameters Estimates					
	$r(\bar{Y}_{rr}, \hat{W}_r+\widehat{V}_r$	$\hat{W}_R$, $\widehat{V}_R$	$\hat{W}_D$, $\widehat{V}_D$	Prediction Equation	$\widehat{Y}_R$ limit	$\widehat{Y}_D$ limit
DTF	0.5561	233.8637, 530.7882	4.2101, 0.1720	$\bar{Y}_{rr}$= 88.7383 + 0.1286 ($\hat{W}_r+\widehat{V}_r$)	187.0923	89.3019
NF	0.4203	128.1020, 355.5153	5.4214, 0.63676	$\bar{Y}_{rr}$= 14.2372 + 0.1691 ($\hat{W}_r+\widehat{V}_r$)	96.0182	15.2617
FL	0.7882	181.8042, 265.3019	-.0915, 0.000067	$\bar{Y}_{rr}$= 6.0344 + 0.0946 ($\hat{W}_r+\widehat{V}_r$)	48.3232	6.0257

Table 6. Values of the sum of the covariance between means of parentes and means of the r-th row ($\hat{W}_r$) with the variance between means of the r-th row ($\widehat{V}_r$) and means traits days to flowering (DTF), number of fruits per plant (NF) and fruit length (FL), according to Hayman`s method

Lines	DTF		NF		FL	
	$\hat{W}_r+\widehat{V}_r$	Mean (days)	$\hat{W}_r+\widehat{V}_r$	Mean(number)	$\hat{W}_r+\widehat{V}_r$	Mean(mm)
UFSJ 1	14.4464	85.6667	55.2361	19.0000	34.6441	12.3800
UFSJ 2	75.7619	97.6667	23.7758	19.6667	305.0808	48.3933
UFSJ 3	124.0476	100.6667	21.8075	15.0000	194.3770	20.2167
UFSJ 4	57.5813	93.6667	6.5060	12.0000	213.6860	20.2333
UFSJ 5	77.6349	99.0000	31.2679	22.6667	223.0277	24.2400
UFSJ 6	63.9702	97.3333	-1.4206	10.3333	223.0277	24.3100
UFSJ 7	61.3909	96.0000	18.2996	14.0000	235.5494	26.6100
UFSJ 8	158.2222	121.3333	55.2361	31.3333	57.7263	13.6533

0,091433 (= $\widehat{W_D}+\widehat{V_D}$). UFSJ 1 despite retaining the highest concentration of dominant alleles has $\widehat{W_l}+\widehat{V_l}$ = 34.6441 which shows the possibility of obtaining lines with even shorter fruit lengths from selection in future generations obtained through this diallel (Tables 5 and 6). It is noteworthy that due to the predominance of dominance effects and the interaction of overdominance, reciprocal recurrent selection will be quite effective in improving this trait (Paulan & Pupin, 2019).

According to Hallauer et al. (2010) the genotypic determination coefficients in the narrow sense for NF (h^2_R = 21.4%) is considered low and for DTF (h^2_R = 32.8%) and FL (h^2_R = 62.4%) intermediate (Table 4). Yunandra et al. (2018) found close coefficients for NF (h^2_R = 19,0%), DTF (h^2_R = 44,0%) and FL (h^2_R = 57,0%). Pessoa (2016) and Rêgo et al. (2009) suggest that for traits with low heritability value in the narrow sense, recurrent selection and breeding methods based on selection in advanced generations are recommended. In the case of days to flowering and number of fruits although the additive component was more important than the dominance effects the effects of environmental variance were also significant indicating that in the subsequent stages of the breeding program actions that increase environmental control should be implemented.

Conclusions

For the traits in which the additive effects were more important the selection of lines in segregating generations will be quite efficient.

Hybrid production is recommended for traits in that partial dominance and overdominance interactions are observed.

UFSJ 1 and UFSJ 8 are indicated for crosses aiming reduce days to flowering and fruit length and to increase the number of fruits per plant to continue breeding program.

Acknowledgments

This work was supported by Universidade Federal de São João del Rei – UFSJ and Fundação de Amparo à Pesquisa do Estado de Minas Gerais – FAPEMIG. The authors declare no conflict of interest.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.