

Inheritance of flower traits in ornamental pepper¹

Angela Maria dos Santos Pessoa²; Elizanilda Ramalho do Rêgo³; Cristine Agrine Pereira dos Santos⁴; Michelle Gonçalves de Carvalho⁵; Júlio Carlos Polimeni de Mesquita⁶; Mailson Monteiro do Rêgo⁷

Abstract: Diallel crosses provide estimates of useful parameters in the selection of parents for hybridization. They also help in understanding the gene action behind the determination of characters of interest. The objective of this study was to determine the genetic control of flower traits in ornamental pepper based on a complete diallel with parents F₁'s and reciprocal crosses. The experiment was conducted in a greenhouse at Laboratório de Biotecnologia Vegetal, Centro de Ciências Agrárias, Universidade Federal da Paraíba (CCA-UFPB). Seven accessions of ornamental pepper belonging to the CCA-UFPB Germplasm Bank UFPB001, UFPB004, UFPB77.3, UFPB099, UFPB134, UFPB137 and UFPB390 were used. The morphological analysis was performed on following quantitative *Capsicum* descriptors: days for flowering (DFL), flower diameter (FD), petal length (PL), number of petals (NP), number of stamens (NS), anther length (AL) and fillet length (FL). The data were previously submitted to analysis of variance and then to diallel analysis. All evaluated traits were adequate to the additive-dominant model. There are possibilities of genetic gains in breeding programs, for the NP, NS, AL and FL in ornamental peppers.

Keywords: *Capsicum annuum*; genetic control; hybridization.

Herança para características de flor em pimenteira ornamental

Resumo: Os cruzamentos dialélicos propiciam estimativas de parâmetros úteis na seleção de genitores para hibridação e no entendimento da ação gênica envolvida na determinação dos caracteres de interesse. Assim objetivou-se neste trabalho determinar o controle genético das características de flor em pimenteiras ornamentais com base em dialelo completo, com pais, F₁'s e recíprocos. O experimento foi conduzido em casa de vegetação no setor de Biotecnologia Vegetal do Centro de Ciências Agrárias, Universidade Federal da Paraíba (CCA-UFPB). Foram utilizados sete acessos de pimenteira ornamental, pertencentes ao Banco de Germoplasma da CCA-UFPB: UFPB001, UFPB004, UFPB77.3, UFPB099, UFPB134, UFPB137 e UFPB390. A caracterização morfoagronômica foi realizada com base nos descritores de *Capsicum*, sendo avaliadas dias para floração (DFL), diâmetro da flor (DF), comprimento das pétalas (CP), número de pétalas (NP), número de estames (NE), comprimento da antera (CA) e comprimento do filete (CF), características quantitativas referentes à flor. Os dados foram previamente submetidos à análise de variância e, posteriormente à análise dialélica. Todas as características avaliadas se adequaram ao modelo aditivo-dominante. Há possibilidades de ganhos genéticos para NP, NE, CA e CF em pimenteiras ornamentais.

Palavras-chave: *Capsicum annuum*; controle genético; hibridação.

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²Doutora em Agronomia; Bolsista PNPd, Universidade Federal da Paraíba (UFPB), Centro de Ciências Agrária, Programa de Pós-Graduação em Agronomia, Areia-PB, CEP: 58397-000; E-mail: angelapessoapb@gmail.com

³Doutora em Genética e Melhoramento; Professora Associada, Universidade Federal da Paraíba (UFPB), Centro de Ciências Agrária, Departamento de Ciências Fundamentais e Sociais, Areia-PB, CEP: 58397-000; E-mail: elizanilda@cca.ufpb.br

⁴Mestre em Agronomia; Doutoranda, Universidade Federal da Paraíba (UFPB), Centro de Ciências Agrária, Programa de Pós-Graduação em Agronomia, Areia-PB, CEP: 58397-000; E-mail: cristineagrinerps@hotmail.com

⁵Mestre em Agronomia; Doutoranda, Universidade Federal da Paraíba (UFPB), Centro de Ciências Agrária, Programa de Pós-Graduação em Agronomia, Areia-PB, CEP: 58397-000; E-mail: carvalho.areia@hotmail.com

⁶Doutor em Agronomia; Engenheiro Agrônomo, Instituto Agronômico de Pernambuco (IPA), Recife-PE; E-mail: jcpmesquita@yahoo.com.br

⁷Doutor em Genética e Melhoramento; Professor Adjunto III, Universidade Federal da Paraíba (UFPB), Centro de Ciências Agrária, Departamento de Ciências Biológicas, Areia-PB, CEP: 58397-000; E-mail: mailson@cca.ufpb.br

1 Introduction

Peppers of the genus *Capsicum* are rich in vitamins A, C and E and present genetic diversity for several traits (Rêgo et al. 2012a). Its fruits have several compounds including carotenoids, flavonoids and essential mineral elements, as well as Capsaicin (Stommel and Bosland, 2008). Due to these characteristics, they are part of the formulation of pharmaceuticals and cosmetics, and are used as raw material for pepper spray (Neitzke et al., 2016). Pepper plants are also used as ornamental in interior and landscape design (Rêgo et al., 2011; Rêgo and Rêgo, 2016).

Flowers that stand out among foliage are of interest in ornamental peppers, as they provide beauty to the plant making them more attractive to consumers (Santos et al., 2013). This feature also facilitates the process of emasculation and manual crossing in breeding programs (Santos et al., 2013; Nascimento et al., 2013).

The inheritance of a trait is the transmission of genetic information to the offspring and that can be studied through genetic parameters obtained from controlled crosses (Baldissera et al., 2014), such as diallel crosses.

Diallel crosses provide estimates of useful parameters in the selection and understanding of the gene action involved in character (Cruz et al., 2012).

Among the various methods proposed for the analysis of diallel crosses, the Hayman method (Hayman, 1954a) provides information about important genetic parameters such as the average degree of dominance and number of genes (Vivas et al., 2013). In this context, the objective of this study was to determine the inheritance of flower characteristics in ornamental peppers based on complete diallel cross, with parents, F₁'s and reciprocal.

2 Material and Methods

The experiment was carried out in a greenhouse at the Laboratório de Biotecnologia Vegetal, Centro de Ciências Agrárias, Universidade Federal da Paraíba, (CCA-UFPB), Areia, Paraíba State, Brazil.

Seven accessions of ornamental pepper (*C. annuum* L.) belonging to the Germplasm Bank of the CCA-UFPB: UFPB001, UFPB004, UFPB77.3, UFPB099, UFPB134, UFPB137 and

UFPB390 were used.

Manual crosses were performed on flower buds, pre-anthesis, based on complete diallel, with parents, F₁'s and reciprocals.

The seeds of the 42 hybrids and seven parental were sown in polystyrene trays of 128 cells filled with commercial substrate (Plantmax®) and when they presented six definitive leaves, were transplanted into a plastic vessel containing 900 mL of the same substrate.

The morphoagronomic characterization was performed based on the *Capsicum* descriptors (IPGRI, 1995). Seven quantitative characters related to the flower were evaluated. Flower data were collected when they were fully open and during the first flowering. The flower characteristics evaluated were: Days for Flowering (DFL), Flower Diameter (FD), Petal Length (PL), Number of Petals (NP), Number of Stamens (NS), Anther Length (AL) and Fillet Length (FL). To obtain data on the dimensions, a digital caliper was used (Leetools® digital caliper) and the quantity values were taken by counting.

The experimental design was completely randomized, with 49 treatments, which consisted of 42 hybrids and seven parents, with eight replicates. Each repetition consisted of a vase with a plant. Genetic variability was detected through analysis of variance, with F test, at 5% probability.

For application of methodology proposed by Hayman (1954a), modified by Viana et al. (1999), it was necessary to test if the flower traits fulfilled the following assumptions: Mendelian inheritance and homozygous parents, absence of reciprocal effect, epistatic interactions and multiple allelism. In addition, genes must be randomly distributed between parents. These requirements were verified by the additive-dominant model adequacy test as follows: the values of W_i and V_i were used to test the data by adjusting the additive-dominant model by: a) the variation of $W_i - V_i$ was evaluated by analysis of variance, testing the occurrence of differences in the values of this expression between the lines of the crossed matrix; b) linear regression analysis of W_i in V_i , testing the significance of the angular coefficient of the straight line ($H_0: b = 1$ vs $H_a: b \neq 1$); c) weighting W_i and V_i by 45° of rotation of the axes represented by these statistics, and with

the new values of W_i and V_i , the angular coefficient of the straight line was tested after the rotation ($H_0: b = 0$ vs $H_a: b \neq 0$).

After verifying the adaptation of the data to the additive-dominant model, the interpretation of the analysis of variance and the statistics obtained from the diallelic table were used to estimate the genetic and environmental components: E (Environmental variance effects); D - (Additives of genes); H_1 , H_2 and h_2 (Effects due to dominance); F - (Effect of covariance between additive and non additive effect) and D - H_1 (Component expressing the difference between the additive and dominant gene effects).

Estimates of the genetic components of the variation were divided by standard deviation and the significance was determined by t test ($p \leq 0.05$) (Singh and Chaudhary, 1979).

The following genetic parameters were also estimated: $\sqrt{H_1/D}$ (Mean degree of dominance); $H_2/4H_1$ (allele distribution among parents (symmetry), with a maximum value of 0.25); dominant and recessive relationship; number of

genes with dominance; narrow coefficient of determination; broad coefficient of determination; correlation between the average values of the parents (\hat{Y}_{ii}); sum of covariance, between parent means and r-line averages (\hat{W}_r); variance between means of the rth line (\hat{V}_r); expected values of the \hat{W}_r , \hat{V}_r and \hat{W}_D coordinates, \hat{V}_R and predicted value for the parent with maximum concentration of dominant alleles (\hat{Y}_R) and recessive (\hat{Y}_D) alleles. The meaning of the components and parameters is explained by Hayman (1954b). All analyses were performed using the Genes computational program (Cruz, 2013).

3 Results and Discussion

There were a significant differences among the treatments ($p \leq 0.05$) for all evaluated characteristics (Table 1). The significance indicates the existence of genetic variability among the evaluated genotypes and allows the inclusion of these characters in genetic breeding studies (Medeiros et al. 2014; Streck et al., 2017).

Table 1 Analysis of variance and estimates of the quadratic components for flower traits in ornamental pepper (*Capsicum annuum* L.)

| Source of variation | GL | Mean Square | | | |
|---------------------|-----|-------------|---------|---------|---------|
| | | DFL | DF | PL | NP |
| Tratamentos | 48 | 86.259** | 0.158** | 0.020** | 0.480** |
| Residual | 343 | 8.399 | 0.056 | 0.007 | 0.126 |
| Overall Mean | | 29.650 | 1.678 | 0.478 | 5.498 |
| CV (%) | | 9.775 | 12.981 | 18.924 | 6.197 |

| Source of variation | GL | Mean Square | | |
|---------------------|-----|-------------|--------|---------|
| | | NS | AL | FL |
| Tratamentos | 48 | 0.456** | 0.003* | 0.009** |
| Residual | 343 | 0.107 | 0.002 | 0.003 |
| Overall Mean | | 5.488 | 0.246 | 0.462 |
| CV (%) | | 5.960 | 20.008 | 11.862 |

DFL - Days for flowering; DF - Flower diameter; CP - Petal length; NP - Number of petals; NE - Number of stamens; CA - Length of anther and CF - Length of fillet. * and ** Significant at the level of 5 and 1% probability of error by the F test.

The coefficients of variation (CV) ranged from 5.960% (NS) to 20.008% (AL) (Table 1). In peppers, CV values vary according to the characteristic, genotype and species under study (Silva et al., 2011).

None of the studied variables presented significant effects of regression coefficients

(Table 2). The absence of significance of the regression coefficients in the sufficiency test of the additive-dominant model indicates homogeneity between the variances and covariance, which is in accordance with the constraints imposed by the model and allows the progression to the next step of the analysis.

Table 2 Test of sufficiency of the additive - dominant model for the flower characters in ornamental pepper (*Capsicum annuum* L.)

| Traits | MS Regression | MS Deviation | Regression $W_i = a + b V_i$ | | T valor and Significance ($H_0: \beta=0$) after rotation | Fit to model |
|------------|----------------------|--------------|------------------------------|--|--|--------------|
| | | | Intercept (a) Estimate (DP) | Coeff. Linear ($H_0: \beta = 1$) F Estimate (DP) | | |
| DFL | 66.226 ^{ns} | 12.807 | 2.722 (2.149) | 0.565 (0.248) ^{ns} | 0.748 ^{ns} | Adequate |
| DF | 0.001** | 0.000 | 0.007 (0.002) | 1.171 (0.147) ^{ns} | -1.633 ^{ns} | Adequate |
| CP | 0.001* | 0.000 | 0.001 (0.000) | 1.201 (0.176) ^{ns} | -1.693 ^{ns} | Adequate |
| NP | 0.003** | 0.000 | 0.008 (0.005) | 1.009 (0.114) ^{ns} | -0.368 ^{ns} | Adequate |
| NE | 0.002** | 0.000 | 0.009 (0.004) | 1.019 (0.118) ^{ns} | -0.465 ^{ns} | Adequate |
| CA | 0.000 ^{ns} | 0.000 | 0.000 (0.000) | 0.213 (0.499) ^{ns} | -0.292 ^{ns} | Adequate |
| CF | 0.000 | 0.000 | -0.000 (0.000) | 0.824 (0.197) ^{ns} | 0.319 ^{ns} | Adequate |

DFL - Dias para floração; DF - Diâmetro da flor; CP - Comprimento da pétala; NP - Número de pétalas; NE - Número de estames; CA - Comprimento da antera e CF - Comprimento do filete. ^{ns}não significativo, * e ** significativo, em nível de 5 e 1 % de probabilidade, respectivamente.

The correlations $r(\hat{W}_i + \hat{V}_i$ and $\hat{Y}_{ii})$ were positive for the DFL, FD, PL, NP, NS and AL characteristics and negative only for the FL variable (Table 3). This fact evidences that the recessive alleles are the ones that increase most of the characteristics, except for fillet length (FL).

For DFL, the limits of selection are 65.840 in the most recessive genotype and 28.845 in the most dominant genotype. The parents who presented the highest number of recessive alleles were UFPB77.3 and UFPB390, with values of $\hat{W}_i + \hat{V}_i$ equal to 30.507 and 19.511, respectively (Table 3). In contrast, UFPB099 (2.029), UFPB004 (6.597) and UFPB137(7.491) (Table 3 and Figure 1a) showed higher concentration of dominant alleles. It is noteworthy that for this variable the selection must lean towards dominant alleles, since the selection limit for earlier plants was 28.845, and among the parents the UFPB001 already has an average lower than the selection limit (17.257).

For the FD variable, the parents who presented the highest number of recessive alleles were UFPB004 and UFPB001, with $\hat{W}_i + \hat{V}_i$ values equal to 0.04 and 0.039, respectively (Table 3). In contrast, parents UFPB (0.016) and UFPB134 (0.022) had higher concentrations of dominant alleles (Table 3 and Figure 1a). The UFPB099 parent already has an average above the selection limit for flower diameter (1.92) (Table 3 and Figure 1b).

The selection limits for PL were 0.496 for the most recessive accession and 0.428 for the most

dominant accession. Those accessions are UFPB001, UFPB099 and UFPB004, with values of 0.505, 0.523 and 0.567, respectively (Table 3, Figure 1c).

For NP, the parents with the highest $\hat{W}_i + \hat{V}_i$ values were UFPB001 (0.138), UFPB004 (0.121) and UFPB099 (0.120) (Table 3, Figure 1d). The selection limits for this characteristic are 5.976, in the most recessive parent and 5.049 in the dominant. The parent with the highest number of petals was UFPB001, which was below the selection limit, indicating that it is possible to select superior lineages from the populations of these crosses for this variable.

As for NS, UFPB001 and UFPB099 as parents had the highest concentrations of recessive alleles (Table 3 and Figure 1e) with $\hat{W}_i + \hat{V}_i$ values of 0.132 and 0.103, respectively. It is possible to select, in the segregating generations of this diallel, plants with flowers with greater number of stamens.

The UFPB001 parents had a higher concentration of recessive alleles for AL, with a value of 0.05 (Table 3 and Figure 1f). It is possible to select plants with larger anthers in segregating generations.

Several authors have reported the importance of selection of floral components, such as corolla length, petal diameter, anther, fillet and stylet length, number of petals and stamens, in pepper intended for ornamentation both in pots and in different stratum of landscape design

(Nascimento et al., 2012, Santos et al 2014, Silva Neto et al., 2014, Ferreira et al., 2015). In addition to the previously cited authors, Santos et al. (2013), Rêgo et al. (2015) and Silva et al. (2017), emphasized the importance of the flower length

and width variables in selection of ornamental peppers in pots. Breeders should focus their research on the most important characters depending on the ideotype (Rêgo e Rêgo, 2018).

Table 3 Parameters estimated in the diallel, by the Hayman method (1954) for flower characteristics in ornamental pepper (*Capsicum annuum* L.)

| Accessions | DFL | | FD (cm) | | PL (cm) | | NP | |
|---------------------------------------|---|-------------------------|---|-------------------------|---|-------------------------|--|-------------------------|
| | Mean | $\hat{W}_i + \hat{V}_i$ | Mean | $\hat{W}_i + \hat{V}_i$ | Mean | $\hat{W}_i + \hat{V}_i$ | Mean | $\hat{W}_i + \hat{V}_i$ |
| UFPB001 | 17.257 | 17.257 | 1.843 | 0.039 | 0.505 | 0.004 | 5.8333 | 0.138 |
| UFPB004 | 31.000 | 6.597 | 1.853 | 0.040 | 0.567 | 0.004 | 5.666 | 0.121 |
| UFPB77.3 | 39.875 | 30.507 | 1.287 | 0.034 | 0.355 | 0.003 | 5.125 | 0.050 |
| UFPB099 | 28.875 | 2.029 | 1.920 | 0.033 | 0.523 | 0.002 | 5.875 | 0.120 |
| UFPB134 | 31.875 | 9.302 | 1.598 | 0.022 | 0.464 | 0.005 | 5.333 | 0.079 |
| UFPB137 | 30.375 | 7.491 | 1.602 | 0.016 | 0.430 | 0.004 | 5.333 | 0.018 |
| UFPB390 | 38.500 | 19.511 | 1.520 | 0.036 | 0.371 | 0.003 | 5.166 | 0.043 |
| $r(\hat{Y}_i, \hat{W}_i + \hat{V}_i)$ | 0.717 | | 0.283 | | 0.141 | | 0.876 | |
| (\hat{W}_R, \hat{V}_R) | (39.896. 65.779) | | (0.033. 0.022) | | (0.004. 0.003) | | (0.087. 0.078) | |
| (\hat{W}_D, \hat{V}_D) | (2.921. 0.352) | | (0.009. 0.001) | | (0.001. 0.001) | | (0.007. 0.008) | |
| Prediction equation | $\hat{Y}_i = 27.662 + 0.361(\hat{W}_i + \hat{V}_i)$ | | $\hat{Y}_i = 1.430 + 7.196(\hat{W}_i + \hat{V}_i)$ | | $\hat{Y}_i = 0.417 + 10.746(\hat{W}_i + \hat{V}_i)$ | | $\hat{Y}_i = 4.991 + 5.930(\hat{W}_i + \hat{V}_i)$ | |
| \hat{Y}_R Limit | 65.840 | | 1.836 | | 0.496 | | 5.976 | |
| \hat{Y}_D Limit | 28.845 | | 1.510 | | 0.428 | | 5.049 | |
| Accessions | NS | | AL (cm) | | FL (cm) | | | |
| | Mean | $\hat{W}_i + \hat{V}_i$ | Mean | $\hat{W}_i + \hat{V}_i$ | Mean | $\hat{W}_i + \hat{V}_i$ | | |
| UFPB001 | 5.833 | 0.132 | 0.252 | 0.005 | 0.414 | 0.001 | | |
| UFPB004 | 5.625 | 0.099 | 0.245 | 0.003 | 0.422 | 0.008 | | |
| UFPB77.3 | 5.125 | 0.053 | 0.211 | 0.004 | 0.396 | 0.002 | | |
| UFPB099 | 5.833 | 0.103 | 0.248 | 0.004 | 0.431 | 0.001 | | |
| UFPB134 | 5.291 | 0.084 | 0.268 | 0.004 | 0.462 | 0.008 | | |
| UFPB137 | 5.333 | 0.020 | 0.234 | 0.001 | 0.525 | 0.001 | | |
| UFPB390 | 5.125 | 0.0474 | 0.218 | 0.001 | 0.437 | 0.001 | | |
| $r(\hat{Y}_i, \hat{W}_i + \hat{V}_i)$ | 0.805 | | 0.387 | | -0.057 | | | |
| (\hat{W}_R, \hat{V}_R) | (0.083. 0.072) | | (0.001. 0.007) | | (0.002. 0.002) | | | |
| (\hat{W}_D, \hat{V}_D) | (0.010. 0.001) | | (0.001. 0.001) | | (-0.003. 0.001) | | | |
| Prediction equation | $\hat{Y}_i = 4.953 + 6.460(\hat{W}_i + \hat{V}_i)$ | | $\hat{Y}_i = 0.223 + 50.896(\hat{W}_i + \hat{V}_i)$ | | $\hat{Y}_i = 0.447 - 3.724(\hat{W}_i + \hat{V}_i)$ | | | |
| \hat{Y}_R Limit | 5.961 | | 0.718 | | 0.428 | | | |
| \hat{Y}_D Limit | 5.028 | | 0.228 | | 0.446 | | | |

DFL - Days for flowering; FD - Flower diameter; PL - Petal length; NP - Number of petals; NS - Number of stamens; AL - Anther Length and FL - Fillet length.

$\hat{W}_i + \hat{V}_i$: Allele concentration, r: correlation coefficient between $\hat{W}_i + \hat{V}_i$ and \hat{Y}_i . Maximum values of dominant (\hat{W}_D, \hat{V}_D) and recessive homozygosity (\hat{W}_R, \hat{V}_R), \hat{Y}_R and \hat{Y}_D : limit of selection order of classification of the parents with concentration of recessive and dominant genes. cm (centimeter).

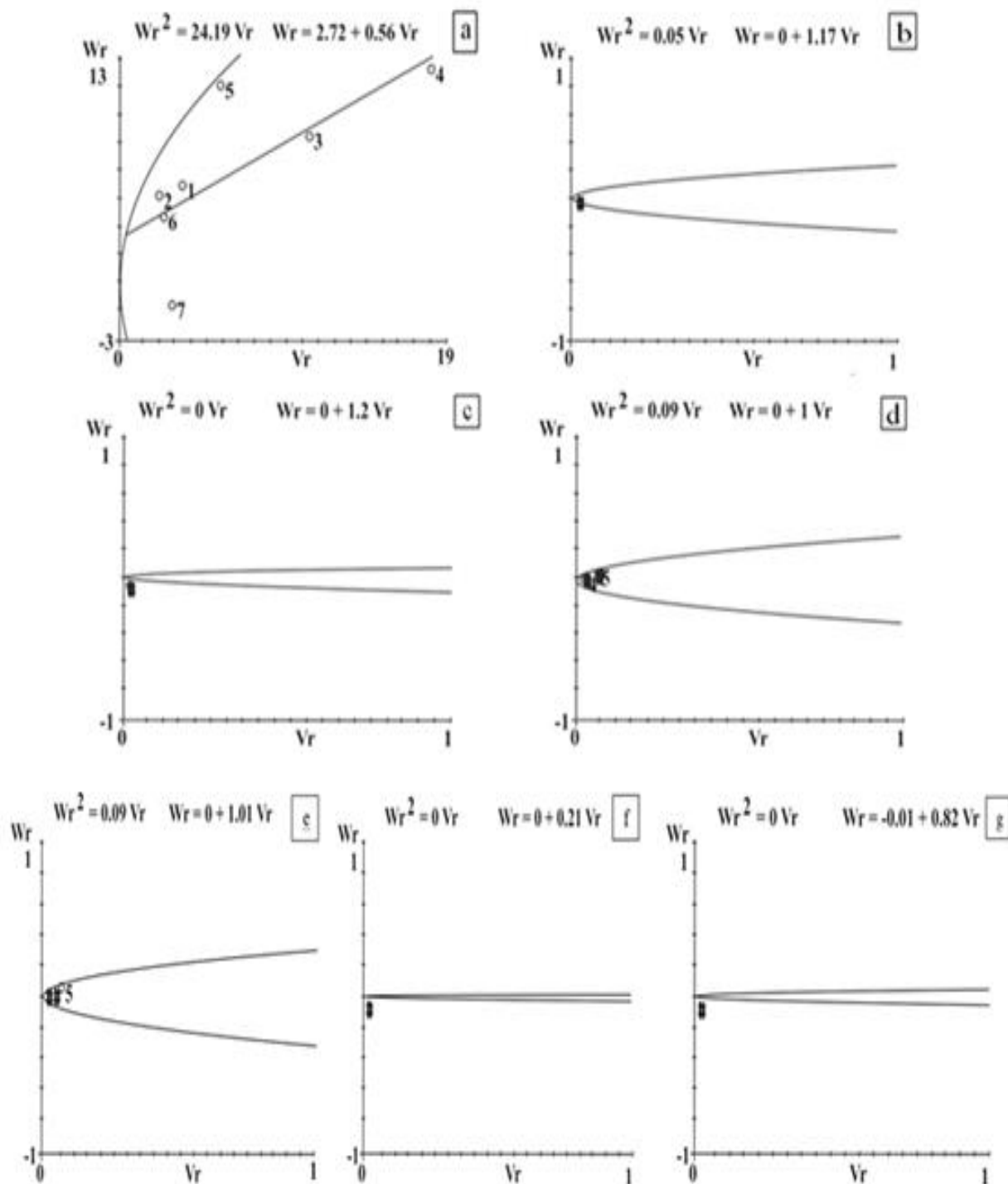


Figure 1 Straight line and parabola established by the relationships between covariance W_i , between means of parent and means within the i -th row, and the variance V_i , between means within the row for the traits of ornamental pepper flowers (*Capsicum annuum* L.): (a) days for flowering, (b) flower size, (c) length of da pétala, (d) number of petals, (e) number of stamens, (f) anther length and (g) fillet length. Parents: **1** = UFPB134, **2** = UFPB137, **3** = UFPB390, **4** = UFPB77.3, **5** = UFPB001, **6** = UFPB004 and **7** = UFPB099. Straight line established by $\hat{W}_i = \hat{a} + \hat{b}\hat{V}_i$, and parabola established by $\hat{W}_i^2 = \hat{V}_p\hat{V}_i$.

Table 4. Estimates of genetic parameters of variation due to the additive effects of genes (D), due to dominance (H₁, H₂ and h₂), the effect of covariance between additive and non-additive (F) and environmental (E) effects of diallel related to seven flower traits in ornamental pepper (*Capsicum annuum* L.)

| Estimation parameters ± deviation | Traits | | | |
|---|------------------------------|------------------------------|------------------------------|------------------------------|
| | DFL | FD (cm) | PL (cm) | NP |
| E | 1.049 ± 1.109 ^{ns} | 0.006 ± 0.000** | 0.001 ± 0.001** | 0,014 ± 0,001** |
| D | 23.147 ± 3.136** | 0.045 ± 0.000** | 0.005 ± 0.001** | 0,083 ± 0,004** |
| H ₁ | 22.151 ± 7.549* | -0.002 ± 0.003 ^{ns} | -0.004 ± 0.00 ^{ns} | 0,024 ± 0,010* |
| H ₂ | 16.848 ± 6.652* | -0.002 ± 0.002 ^{ns} | -0.002 ± 0.000 ^{ns} | 0,027 ± 0,009* |
| h ² | 30.754 ± 4.468** | -0.003 ± 0.002 ^{ns} | -0.001 ± 0.000 ^{ns} | -0,005 ± 0,006 ^{ns} |
| F | 20.811 ± 7.523* | 0.010 ± 0.003** | 0.001 ± 0.000** | -0,006 ± 0,010 ^{ns} |
| D - H ₁ | 0.996 ± 6.553 ^{ns} | 0.047 ± 0.002** | 0.006 ± 0.000** | 0,058 ± 0,009** |
| Genetic information | | | | |
| Mean degree of dominance (root of H ₁ /D) | 0.978 | 0.655 | 0.570 | 0,542 |
| Symmetry (H ₂ / 4H ₁) | 0.190 | 0.167 | 0.142 | 0,280 |
| Dominant/recessive ratio | 2.700 | 0.750 | 0.341 | 0,865 |
| Number of dominant genes | 1.825 | 1.609 | 0.716 | -0,189 |
| Narrow coefficient of determination | 0.421 | 0.755 | 0.674 | 0,669 |
| Broad coefficient of determination | 0.884 | 0.737 | 0.651 | 0,775 |
| Correlation($\hat{Y}_{ii} \cdot \hat{w}_i + \hat{v}_i$) | 0.717 | 0.284 | 0.142 | 0,877 |
| Estimation parameters ± deviation | Traits | | | |
| | NS | AL (cm) | FL (cm) | |
| E | 0.0134 ± 0.001** | 0.003 ± 0.000** | 0.000 ± 0.000** | |
| D | 0.082 ± 0.004** | 0.000 ± 0.000 ^{ns} | 0.001 ± 0.000** | |
| H ₁ | 0.019 ± 0.009* | -0.000 ± 0.000 ^{ns} | 0.001 ± 0.000** | |
| H ₂ | 0.020 ± 0.008* | -0.000 ± 0.000 ^{ns} | 0.001 ± 0.000** | |
| h ² | -0.001 ± 0.005 ^{ns} | 0.000 ± 0.000 ^{ns} | 0.002 ± 0.000** | |
| F | -0.002 ± 0.009 ^{ns} | -0.000 ± 0.000 ^{ns} | 0.000 ± 0.000 ^{ns} | |
| D - H ₁ | 0.063 ± 0.008** | 0.000 ± 0.000 ^{ns} | -0.000 ± 0.000 ^{ns} | |
| Informações genéticas | | | | |
| Mean degree of dominance (root of H ₁ /D) | 0.488 | 0.901 | 1.029 | |
| Symmetry (H ₂ / 4H ₁) | 0.261 | 0.022 | 0.182 | |
| Dominant/recessive ratio | 0.949 | 0.122 | 1.305 | |
| Number of dominant genes | -0.059 | -0.807 | 1.521 | |
| Narrow coefficient of determination | 0.693 | 0.177 | 0.523 | |
| Broad coefficient of determination | 0.778 | 0.172 | 0.722 | |
| Correlation($\hat{Y}_{ii} \cdot \hat{w}_i + \hat{v}_i$) | 0.805 | 0.388 | -0.058 | |

The importance of selection for precocity in ornamental peppers was reported by Rego et al (2012b, c). The segregating generations obtained

in this work constitute single material where the selection for some of these components can be practiced with greater probability of genetic

gains.

The genetic components of variation, due to the additive effects of the genes (D), were significant at the 1% probability level by the t test for DFL, FD, PL, NP, NS and FL. The effects of dominance (H_1 and H_2) were significant at 5% probability for DFL, NP, NS and significant at 1% for FL (Table 4). The estimates indicating the presence of dominance effects by means of D - H_1 were significant at 1% and 5% probability, by the t test, for FD, PL, NP and NS. For the AL characteristic, only the environmental effect (E) was significant (Table 4).

The mean degree of dominance for DFL, FD, PL, AL, NP and NS indicates the existence of partial dominance while FL presented over dominance interaction (Table 4). Both types of allelic interaction allow to differentiate the hybrid from the homozygotes, when compared to the presence of complete dominance. This fact facilitates if one wishes to introduce genes for the FD, PL, NP and NS variables through backcrosses, since it is possible to identify heterozygous and homozygotes without the need of self-fertilization, making possible negative selection of the dominant and, saving time and labor in the breeding program.

The characteristics FD, PL, NP, NS and FL presented high heritability values in the broad and restricted sense, above 0.651 and above 0.523, respectively (Table 4). The heritability values in the restricted sense found in this work, for these variables, indicate that the effects due to the additivity are more influential in their determination. Several authors have reported high values of heritability in the broad sense in ornamental pepper (Nascimento et al., 2012, Silva Neto et al. 2013; Costa et al. 2016; Silva et al. 2016; Naegele et al., 2016; Devi et al. 2017). In recent years, several papers have also reported that heritability in the narrow sense is involved in the determination of quantitative characters of ornamental peppers (Santos et al., 2012, Santos et al., 2004, Silva Neto et al. et al. 2015; Fortunato et al. 2015; Rêgo et al. 2015 and Silva et al. 2017). Ferreira et al. (2015) and Fortunato et al. (2015) determined that only the additive gene effects determine the number of stamens and corolla length traits. On the other hand, Ferreira et al. (2015) determined that the number of petals is determined, for the most part, by dominant effects. Rêgo et al. (2012b) detected dominant effects determining fillet length.

In cases where the predominant effects are additive, selection may be practiced in early generations with a greater chance of genetic gain. Breeding methods based on selection or the backcrossing method will be more effective in these cases (Rêgo et al., 2009, Rêgo et al., 2015, Rêgo et al., 2016).

For those characters with a predominance of gene effects due to dominance, it is indicated the selection in advanced generations or the exploration of hybrids (Rêgo et al., 2009, Rêgo et al., 2015, Fortunato et al. and Rêgo 2016), or selection in advanced generation with the use of more complex methods such as Pedigree or Recurrent Selection (Rêgo et al., 2009, Rêgo et al., 2015, Rêgo and Rêgo 2016).

4 Conclusion

It is possible to select, in early segregating generations of the crosses carried out in this work, genotypes with higher number of petals and stamens and with a longer fillet length.

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