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GENETIC CONTROL FOR MATURITY AND YIELD TRAITS IN MAIZE

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Abstract: An understanding of the genetic control of a trait is very important for the efficient implementation of a breeding program. This study aimed to obtain information about the genetic control of male and female flowering and crop humidity, related to the maturation and grain yield and mass attributes of a thousand seeds, through diallel analysis. Thirteen elite lines of the Coodetec breeding program were selected and seventy-eight hybrids were synthesized as a half table diallel. The hybrids and parentals were evaluated in Palotina, Mariluz and São Pedro do Iguaçu, in a 10x10 square lattice experimental design, with three replications. Male and female flowering, crop humidity, thousand seed weight and grain yield were evaluated. Analyses of individual and joint variance and of diallel analysis were performed using the Hayman methodology. Analyzes of individual variance reveal variability in all the traits studied. The genetic model was observed in at least two tests of significance of the dominant additive model. The genetic information showed that dominant alleles are found more frequently in the genitors, except for yield, which is predominantly recessive. Dominant gene effects are predominant in the control of the variables studied with an overdominance interaction between the alleles. The CD069 line shows a higher number of dominant genes for maturation and the CD038 line had a higher number of dominant genes for yield. It is possible to have greater selection gains for male and female flowering and one thousand seed weight in the Palotina environment. For crop humidity greater gains are possible in the Mariluz and Palotina environments.
Keywords: Genetic components, overdominance, diallel of Hayman.

Introduction

Corn was traditionally a typical spring-summer crop, sown between August and November (Fornasieri Filho, 2007). In Paraná, in the 70's, the cultivation of corn second season began sown between January and March and, currently, this activity represents more than 80% of corn cultivated in the state (SEAB/DERAL, 2017). The consolidation of the off-season in Paraná occurred by the great technological advance, especially by the use of simple hybrids, early cycles and adapted to the autumn-winter climatic conditions (Fornasieri Filho, 2007).

In order to meet the market demand for early, productive hybrids adapted to the growing conditions, knowledge of the genetic control of such traits is fundamental for conducting a breeding program, assisting in the selection of more efficient selection methods (Cruz et al., 2012). To this end, the use of diallel crosses is efficient for generating information on parents for population synthesis, identification of efficient selection methods and knowledge of the genetic bases that control such traits (Cruz et al., 2012; Makumbi et al., 2018).

For the study of genetic control, we highlight the methodology proposed by Hayman (1954), which is based on the knowledge of the environmental and genetic nature of means, variances and covariance, obtained from a diallel table and, in addition to genetic control, provides information on parent genetic values, selection limits, ratio of dominant to recessive genes and coefficient of genotypic determination and number of genes or gene blocks that control the variable under study (Cruz et al., 2012; Rohman et al., 2019). However, for the use of this methodology, some premises must be met, such as diploid segregation, use of homozygous parents, absence of maternal effect, absence of multiple allelism, independent distribution of genes and absence of epistasis, which may be obstacles to the use of this method (Schuelter et al., 2010; Cruz et al., 2012).

For corn cultivation, some authors used this methodology to generate information about several quantitative characters of interest, such as Lopes et al. (1995) who studied inheritance of the number of days for flowering and concluded that it is controlled by at least three genes or gene blocks and by additive and dominance effects. Saleem et al. (2002) studying the number of days for male and female flowering, number of rows of grains per cob, number of grains per row and mass of one hundred seeds, concluded that over-dominance is the gene action that controls these traits. Wattoo et al. (2009) studied days for male and female flowering, number of grain rows per bob, plant height, number of cobs per plant, number of grains per row, mass of one hundred seeds, yield and percentage of protein and oil in seeds and detected overdominance and non-additive gene action for the yield components. Sher et al. (2012) studied maturity and flowering and observed dominance action and epistatic interaction in the control of these characters.

Although traits related to maturity and yield in maize are of great importance and researchers devote their attention to it, the studies present divergent results, both in terms of gene effects, heritability and number of genes involved (Lima et al., 2008). Thus, this study aimed to obtain information on the genetic control of the attributes male flowering, female flowering and crop humidity, related to maturity and the attributes grain yield and mass of one thousand seeds, through diallel analysis.

Materials and methods

Genetic material and growing conditions

Thirteen elite lines from the Coodetec (Cooperativa Central de Pesquisa Agrícola) Southern Corn Breeding Program with late-to-late cycle selected from Friske's (2015) assessment were employed to obtain F_1 populations following a scheme of diallel crossing half table. Seeds were obtained by hand crossing block sown in summer 2014/2015 at Coodetec experimental farm in Palotina/PR.

The experiments were carried out in the second season of 2015 in the municipalities of Palotina, São Pedro do Iguaçu and Mariluz, Paraná, respecting the agroclimatic zoning of the Ministério da Agricultura, Pecuária e Abastecimento for each site being sowed on February 27th, February 17th and February 22nd of 2015, respectively.

The experiments counted on the 13 parent lines, the 78 F_1 hybrids and 9 commercial hybrids, totaling 100 treatments. The experimental design used was the 10x10 lattice with three replications.

The experimental unit was two lines with 5 meters in length and 0.76 meters of line spacing. Sowing was mechanized and between 25 and 30 days after plant emergence thinning was performed, establishing an average population of 65,000 plants ha^{-1}.

Evaluated traits

To determine the number of days for male (MF) and female (FF) flowering, visual evaluations were made of all plots of each trial with two-day periodicity between evaluations, always at the same time of day and same evaluator, considering for FM and FF the number of days between planting and when 50% + one of the plants had pollen emission and style-stigmas exposed.

To determine the mass of one thousand seeds (MTS), five ears of each plot were randomly collected, threshed and taken to the dryer until reaching 13% of humidity. The MMS value of each plot was calculated through the average weight of six samples of 100 seeds.

The percentage of humidity in the grain mass (HUM) was determined at the time of harvest through the plot harvester. The grain yield (GY) was calculated from the data of mass and humidity of each plot provided by the harvester by adding the grain weight of the 5 ears collected to determine the MTS and adjusted to 13% of humidity and expressed in kg ha^{-1}.

Harvesting was mechanized and performed in the total area of each plot. To determine the mass of one thousand seeds (MTS), five ears of each plot were randomly collected, threshed and taken to the dryer until they reached 13% humidity. The MTS value of each plot was calculated through the average weight of six samples of 100 seeds.

Genetic-statistical analysis

For all statistical analysis, the 13 progenitor lines and 78 diallel hybrids were considered. The efficiency of the lattice design was estimated for all evaluated characters, being for all of them below the 120% efficiency limit that would justify the work in this methodology, allowing to work with the randomized block statistical model (Moraes et al., 1988; Gomes and Garcia, 1991).

After defining the statistical model, individual variance analyzes were performed to detect the presence of variability in the treatments under study, experimental precision and calculation of homogeneity of residual variances. For joint analysis, the homogeneity of variances was considered by Hartley's maximum F test. The objective of this analysis was to estimate the significance of the environments, the interaction treatments x environments and the interaction of treatment outcomes (genotypes, checks and groups) with the environment. After interpretation the results were performed analyzes of individual and joint diallel variance proposed by Hayman (1954).

To test the adequacy of the data to the additive-dominant model, *i.e.*, to verify if the data of each analyzed variable meets the restrictions imposed for the use of Hayman's genetic model, three tests were used: in the first one the variances and covariance were calculated. For each row in each of the repetitions and the variation between $W_i - V_i$ values of each repetition was evaluated by a randomized block analysis of variance, using as source of variation the blocks and rows of each diallel table. If the F test was not significant for the "lines" effect, it met the assumptions of the model.

In the second test, the significance of the angular coefficient of the line (b) was tested using an $F(= t2)$ test with 1 and "$n - 2$" degrees of freedom. In the third test it was tested if the angular coefficient "b" was 1.0, using the regression analysis of W_i versus V_i to obtain the mean square value of the regression deviation and then the variance of "b", then proceeding a *t test* with "n-2"degrees of freedom. Since the angular coefficient of the line is nonzero and equal to 1.0, it met the constraints of the model.

With the adequacy of the data to the additive-dominant model, the results obtained from the diallel table were used to estimate the genetic variation components $\widetilde{H_1}$, $\widetilde{H_2}$, $\widetilde{D}$, $\widetilde{h^2}$, $\tilde{F}$, where $\widetilde{H_1}$ e $\widetilde{H_2}$ are the variation caused by the dominance effects; $\widetilde{D}$ is the measure of variation caused by additive gene effects; $\widetilde{h^2}$ the measure of variation caused by dominance effects; and $\tilde{F}$ is the mean covariance measure between additive and dominance gene effects.

The significance of each component was tested by the t-statistic, obtained by dividing the effect estimates by the respective standard deviation. When t values were above 1.98, they

were considered significant at 5% probability (Singh and Chaudhary, 1979). To calculate the standard deviation of each estimate, the variances of the components were obtained by consulting the table presented by Ferreira (1985).

The association between genetic variation components was also employed in the estimation of the following parameters:

$$(\widetilde{H}_1/\widetilde{D})^{1/2} \quad \text{(Eq. 1)}$$

Is a measure of the average degree of dominance at all loci;

$$\widetilde{H}_2/4\widetilde{H}_1 \quad \text{(Eq. 2)}$$

Is a measure of the average value of the products of the frequencies of positive and negative alleles at loci that exhibit dominance;

$$K_D/K_R = \left(\sqrt{4\widetilde{D}\widetilde{H}_1 + \widetilde{F}}\right)/\left(\sqrt{4\widetilde{D}\widetilde{H}_1 - \widetilde{F}}\right) \quad \text{(Eq. 3)}$$

Is a measure of the most often occurring allele, where a ratio close to one (1) indicates equality between the number of dominant and recessive alleles in the parent genotypes;

$$\tilde{h}^2/\widetilde{H}_2 \quad \text{(Eq. 4)}$$

Is a measure of the number of genes or gene blocks that control the character and display some degree of dominance;

$$\tilde{h}_R^2 = \left(\widetilde{D} - \tilde{F} + \widetilde{H}_1 - \widetilde{H}_2\right)/\left(\widetilde{D} - \tilde{F} + \widetilde{H}_1 - \frac{1}{2}\widetilde{H}_2 + 2\tilde{\varepsilon}\right)$$

(Eq. 5)

Is a measure of the genotypic coefficient of determination in the narrow sense;

$$\tilde{h}_A^2 = \left(\widetilde{D} - \tilde{F} + \widetilde{H}_1 - \frac{1}{2}\widetilde{H}_2\right)\Big/\left(\widetilde{D} - \tilde{F} + \widetilde{H}_1 - \frac{1}{2}\widetilde{H}_2 + 2\tilde{\varepsilon}\right)$$

(Eq. 6)

Is a measure of the genotypic coefficient of determination in the broad sense.

In addition to these parameters, the mean degree of dominance and relative genetic constitution of the parents were obtained by W_i regression in V_i. All statistical analyzes were performed using Genes computer software (Cruz, 2013).

Results and discussion

Analysis of variance

It is observed in the analysis of individual variance (Table 1) that there are significant differences between the average behavior of the lines at the 1% of probability by the F test for all environments, evidencing the existence of genetic variability, confirmed by the CV_g/CV_e ratio, greater than 1. The coefficients of variation showed good experimental accuracy for all environments, classified as low or medium as suggested by Scapim et al. (1995). The coefficients of variation for grain yield (YIELD) were considered average, which may be justified by the fact that it is a quantitative character, which makes it quite influential by the environment (Matos Filho et al., 2009).

The grain yield trait (GY) was not significant for the source of variation control, a fact linked to the low productivity of the lines (controls). It was observed that the general average of all environments was low for the productive patterns of the study region, which may be related to the presence of the parents in the trials, which presented productivities ranging from 345.11 kg ha^{-1} to 2,359.57 kg ha^{-1} (Table 2).

All variables meet the assumption of homogeneity of residual variances, allowing joint analysis of the data. However, the results of the joint analysis of variance (Table 3) show that the source of variation environment and the interaction treatment x environment and their outspread were significant for all variables, suggesting that the environments behaved differently with respect to the mean values genotype for all characters and/or that the performance of genotypes varied depending on the assessment environment, so individual analysis of each site is preferable.

Diallelic analysis

The restrictions imposed on the use of Hayman's method (1954) were evaluated by sufficiency tests of the additive-dominant model (Table 4) based on W_i - V_i heterogeneity. The results

show that, except for the humidity variable (HUM) in the medium environment, the genetic model was met in at least two tests for all variables. Similar results were presented by Schuelter et al. (2010) who, working with pepper plants, report adequacy of the studied variables to the genetic model in at least two tests.

The estimate of the average dominance degree ($\sqrt{H_1}/D$) for all variables was over 1.0, indicating over-dominance, with the GY trait presenting the highest indices, reaching 11.3467 for the Palotina environment (PTNA) (Table 5). However, they do not agree with what was obtained from the W_r graph in V_r (Figures 1, 2, 3, 4 and 5), where the regression line cuts the W_i axis above the origin, in most cases, showing possible partial dominance.

According to Cruz et al. (2012), the parameter $H_2/4H_1$ allows to evaluate the proportion of parents who are in dominant or recessive homozygosity, where values close to 0.25 indicate symmetrical distribution of alleles between parents. At this point, it is observed that only the trait GY tended to symmetry between parents, as it had values between 0.2262 to 0.2422. From the K_D/K_R ratio (Table 5), it can be concluded that the dominant alleles are more frequent in the parents of all characters, except for grain yield (GY), which has a predominance of recessives, evidenced also by the W_r in V_r graph of this variable (Figure 03), which presents influence of recessivity.

Table 1. Mean squares of individual variance analysis for male flowering (MF), female flowering (FF), grain yield (GY), crop humidity (HUM) and mass of one thousand seed (MTS) of the 13 parents and their respective 78 hybrids.

	SV	DF	MEAN SQUARE				
			MF	FF	GY	HUM	MTS#
MARILUZ	BLOCKS	2	9.20	7.92	1106786.03	3.11	1434.89
	TREATMENTS	90	32.54**	38.80**	16405612.8**	12.71**	4327.23**
	Genotye	77	15.13**	15.86**	5292840.4**	9.82**	2517.30**
	Check	12	48.37**	64.60**	346801.8^{ns}	15.59**	3597.50**
	Genotype vs Check	1	1182.95**	1495.25**	1064794815.6**	200.98**	152448.40**
	ERROR	180	1.18	1.12	1066896.64	0.56	337.35
	TOTAL	272					
	Average		59.72	59.99	6623.09	14.84	321.72
	CV(%)		1.82	1.77	15.60	5.02	5.71
	CVg/CVe		1.99	2.09	1.15	2.36	1.47
PALOTINA	BLOCKS	2	2.77	1.31	4267.81	12.32	134.23
	TREATMENTS	90	18.37**	28.63**	10863288.7**	34.06**	6476.61**
	Genotype	77	13.56**	19.81**	3411106.4**	36.44**	4072.09**
	Check	12	14.60**	25.58**	793314.5^{ns}	21.03**	8695.30**
	Genotype vs Check	1	434.11**	744.53**	705521016.8**	7.76^{ns}	164999.99**
	ERROR	180	0.48	0.92	581338.76	2.99	251.79
	TOTAL	272					
	Average		52.63	53.39	4953.92	22.33	261.55
	CV(%)		1.31	1.80	15.39	7.75	6.07
	CVg/CVe		3.03	2.61	1.27	1.93	2.25
SÃO PEDRO DO IGUAÇU	BLOCKS	2	5.08	2.00	3203730.1	0.56	
	TREATMENTS	90	32.14**	42.20**	6679031.2**	42.98**	
	Genotype	77	16.71**	22.66**	2235917.3**	44.03**	
	Check	12	52.94**	50.61**	961514.7^{ns}	38.09**	
	Genotype vs Check	1	970.77**	1445.55**	417409003.9**	21.11^{ns}	
	ERROR	180	3.61	4.68	491127.7	2.62	
	TOTAL	272					
	Average		58.71	59.92	4445.69	25.37	
	CV(%)		3.24	3.61	15.76	6.38	
	CVg/CVe		1.10	1.13	1.09	2.29	

**: Significant at 1% of probability by F test; ^{ns}: not significant; CV (%): coefficient of variation; CVg/CVe: ratio between genetic and environmental variation. #: Performed only in Mariluz and Palotina.

Table 2. Mean values of male flowering (MF), female flowering (FF), grain yield (GY), crop humidity (HUM) and mass of one thousand seed (MTS) of the 13 parents.

	Parental	MF (days)	FF (days)	GY (kg ha^{-1})	HUM (%)	MTS# (g)
MARILUZ	CD069	59.33d	60.00e	1762.52ab	11.17cde	208.15e
	CD060	68.67a	68.67abc	1863.60ab	17.58a	287.02abc
	CD056	66.00ab	67.00abc	1122.75b	10.33e	319.36a
	CD007	65.67abc	64.67cd	1332.09ab	10.82de	239.99bcde
	CD070	59.67d	59.00e	1747.34ab	11.36cde	220.35de
	CD065	67.00a	69.00ab	1497.31ab	11.42cde	235.93bcde
	CD008	68.67a	70.33a	2023.76ab	14.07bc	262.68abcde
	CD010	62.33bcd	65.67bc	2035.96ab	12.19cde	265.06abcde
	CD067	61.67cd	60.67de	2359.57[a]	11.98cde	273.49abcd
	CD038	69.67a	71.00a	1762.01ab	16.79ab	280.05abcd
	CD063	67.33a	69.67ab	1862.89ab	13.89bcd	300.37ab
	CD072	58.33d	58.67e	2202.90ab	12.94cde	305.40a
	CD034	68.33a	70.00a	1639.10ab	11.04cde	232.08cde
PALOTINA	CD069	52.33d	53.00d	1059.88abcde	17.63f	165.77cd
	CD060	57.00ab	60.00a	662.87cde	19.75def	155.27de
	CD056	57.00ab	60.00a	345.11e	21.69bcd	195.47bcd
	CD007	57.00ab	59.00ab	1166.02abcde	22.45bcd	197.17bcd
	CD070	52.00d	52.67d	1630.46ab	22.74bcd	193.40bcd
	CD065	56.00bc	58.00b	493.94de	18.50ef	102.90e
	CD008	58.00a	60.00a	460.16de	24.40ab	182.43bcd
	CD010	56.00bc	58.00b	775.00bcde	20.87cde	217.80bc
	CD067	55.00c	55.00c	1928.55a	19.73def	195.77bcd
	CD038	58.00a	60.00a	1419.48abc	27.15a	288.63a
	CD063	57.00ab	59.00ab	487.85de	24.4ab	314.23a
	CD072	52.00d	53.00d	1357.90abcd	21.95bcd	220.83b
	CD034	57.00ab	59.00ab	1422.83abc	23.57bc	187.70bcd
SÃO PEDRO DO IGUAÇU	CD069	57.33d	62.33abcd	1037.28ab	23.06b	
	CD060	63.00abcd	64.67abcd	2332.26a	23.72b	
	CD056	66.42abc	70.42a	593.34b	23.07b	
	CD007	63.50abcd	65.50abcd	2123.57ab	35.11a	
	CD070	58.00cd	59.67d	870.44ab	21.33b	
	CD065	64.67abcd	68.00abcd	1052.84ab	21.87b	
	CD008	69.00a	70.00ab	1348.13ab	25.73b	
	CD010	64.00abcd	69.00abcd	1197.61ab	23.25b	
	CD067	63.00abcd	62.33abcd	1147.98ab	22.55b	
	CD038	60.00bcd	60.33cd	2243.77a	22.84b	
	CD063	67.33ab	69.67abc	1105.89ab	25.42b	
	CD072	57.33d	60.67bcd	1360.47ab	26.60b	
	CD034	69.67a	69.67abc	2005.57ab	26.41b	

* Means followed by the same letter in the column did not differ statistically by the Tukey test at 5% significance. #: Performed only in Mariluz and Palotina.

Table 3. Mean squares of joint analysis of variance, following the simple factorial model with additional checks for male flowering (MF), female flowering (FF), grain yield (GY), harvest humidity (HUM) in Palotina, Mariluz and São Pedro do Iguaçu and mass of one thousand seeds (MTS) in Pallottine and São Pedro do Iguaçu.

SV	DF	MEAN SQAURES				DF	MEAN SQUARE MTS#
		MF	FF	GY	HUM		
BLOCK/ENVIRONMENT	6	5.68	3.74	1438261.32	5.33	4	784.56
BLOCK	2	4.60	7.05	442322.01	9.49	2	466.64
BLOCK vs ENVIRONMENT	4	6.22	2.09	1936230.98	3.25	2	1102.48
TREATMENT	90	74.45**	99.92**	28584936.06**	52.35**	90	8711.06**
Genotypes	77	40.21**	52.46**	5814088.77**	54.35**	77	4691.74**
Check	12	93.09**	112.51**	971881.12	30.95	12	8783.97*
Groups	1	2487.54*	3603.60*	2113296836.79*	154.91	1	317324.27**
ENVIRONMENTS	2	4016.85**	3919.36**	354241706.46**	8017.28**	1	494182.53**
TREATMENT vs ENVIRONMENT	180	4.30**	4.85**	2681498.32**	18.71**	90	2092.77**
Genotype x Environments	154	2.60**	2.94*	2562887.66**	17.97**	77	1897.66**
Tester x Environments	24	11.41**	14.14**	564874.93	21.88**	12	3508.83**
Groups x Environments	2	50.14**	40.87**	37213999.75**	37.47**	1	124.12**
ERROR	540	1.75	2.24	713121.03	2.06	360	294.57
TOTAL	818					545	
Average		57.02	57.77	5340.90	20.84		291.64
CV (%)		2.32	2.59	15.81	6.88		5.89

ns: not significant; *, **: Significant at 5% and 1% probability; CV (%): coefficient of variation; #: Performed only in Mariluz and Palotina.

Table 4. Suitability test of the additive-dominant model based on the analysis of variance of W_i - V_i values and the linear regression analysis of W_i in relation to V_i for male flowering (MF), female flowering (FF), grain yield (GY), crop humidity (HUM) of Mariluz, São Pedro do Iguaçu and Palotina and mass of one thousand seeds (MTS) of Mariluz and Palotina.

Trait	Env.	ANOVA (W_i - V_i)#	Regression [$W_i = 1/4(D - H_1) + bV_i$]##	
		Mean Square	t (H_0 : b = 1)	t^2 (H_0 : b' = 0)
GY (kg ha^{-1})	MLZ	57521880807.64^{ns}	0.109^{ns}	6.696*
	SPI	427002169724.76*	0.609^{ns}	0.737^{ns}
	PTNA	87934573054.77^{ns}	0.117^{ns}	6.015*
	Average	29997786024.48^{ns}	0.138^{ns}	3.531^{ns}
HUM (%)	MLZ	2.99*	0.404^{ns}	1.845^{ns}
	SPI	100.88*	0.395^{ns}	4.056^{ns}
	PTNA	25.57*	0.549^{ns}	2.072^{ns}
	Average	4.29*	0.274^{ns}	4.937*
MTS (g)	MLZ	375944.99*	0.444^{ns}	2.672^{ns}
	PTNA	1155970.09*	0.619^{ns}	0.353^{ns}
	Average	396623.57*	0.458^{ns}	1.266^{ns}
MF (days)	MLZ	81.87*	0.733^{ns}	2.714^{ns}
	SPI	85.76*	0.673^{ns}	1.59^{ns}
	PTNA	4.76*	0.429^{ns}	2.743^{ns}
	Average	36.36*	0.720^{ns}	2.404^{ns}
FF (days)	MLZ	127.78*	0.677^{ns}	4.178^{ns}
	SPI	90.31*	0.537^{ns}	1.723^{ns}
	PTNA	21.80*	0.567^{ns}	2.449^{ns}
	Average	66.43*	0.699^{ns}	2.498^{ns}

^{ns}: not significant; *: Significant at 5% probability; ($^{\#}$: F Test ; $^{\#\#}$: t Test); t^2: t test, considering the mean values of W_i and V_i for a 45º rotation; Env: Environment.

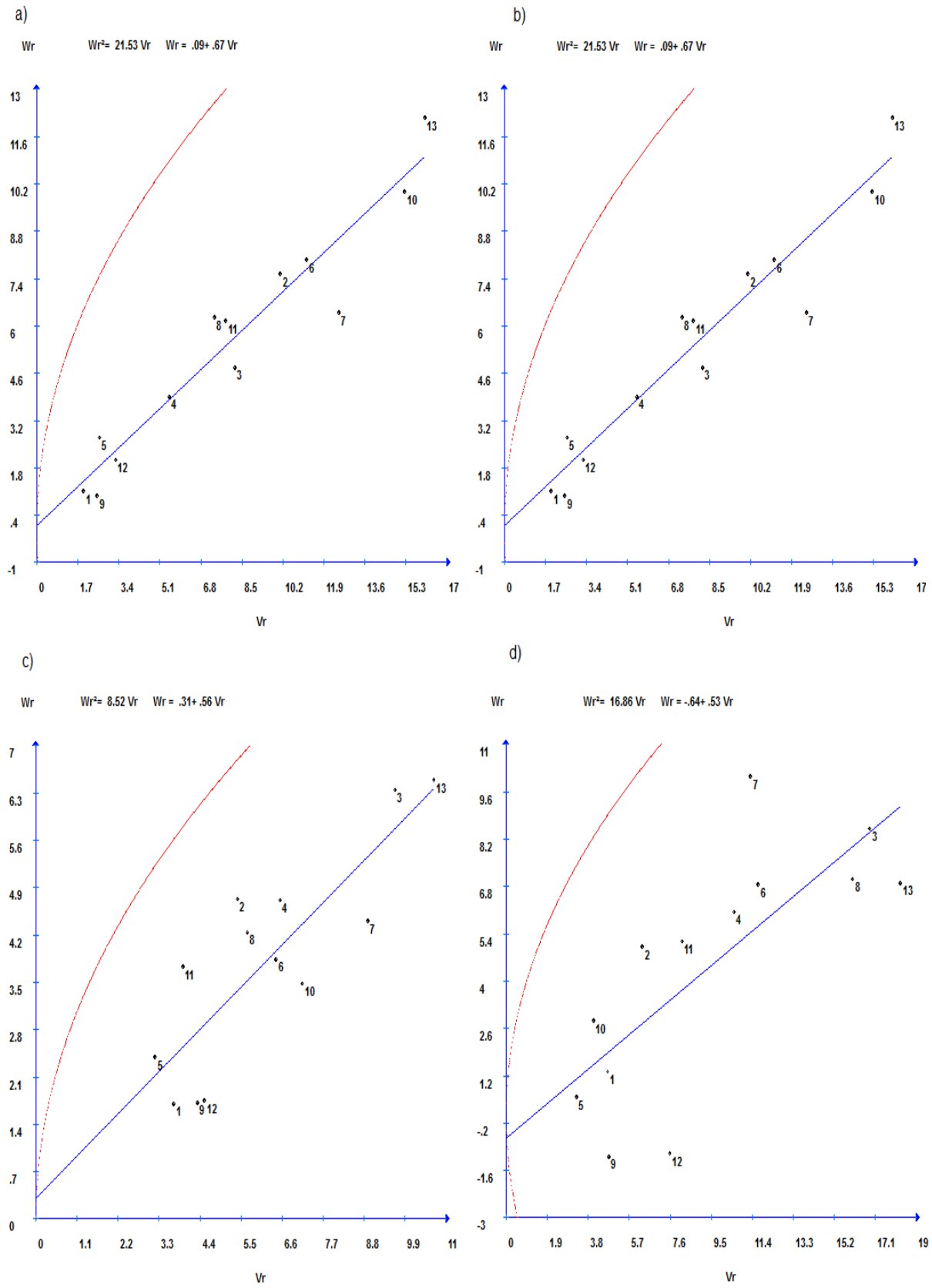

Figure 1. Regressions of W_r in V_r for female floewring (FF) for joint analysis (a), Mariluz (b), Palotina (c) and São Pedro do Iguaçu (d). 1: CD069; 2: CD060; 3: CD056; 4: CD007; 5: CD070; 6: CD065; 7: CD008; 8: CD010; 9: CD067; 10: CD038; 11: CD063; 12: CD072; and13: CD034.

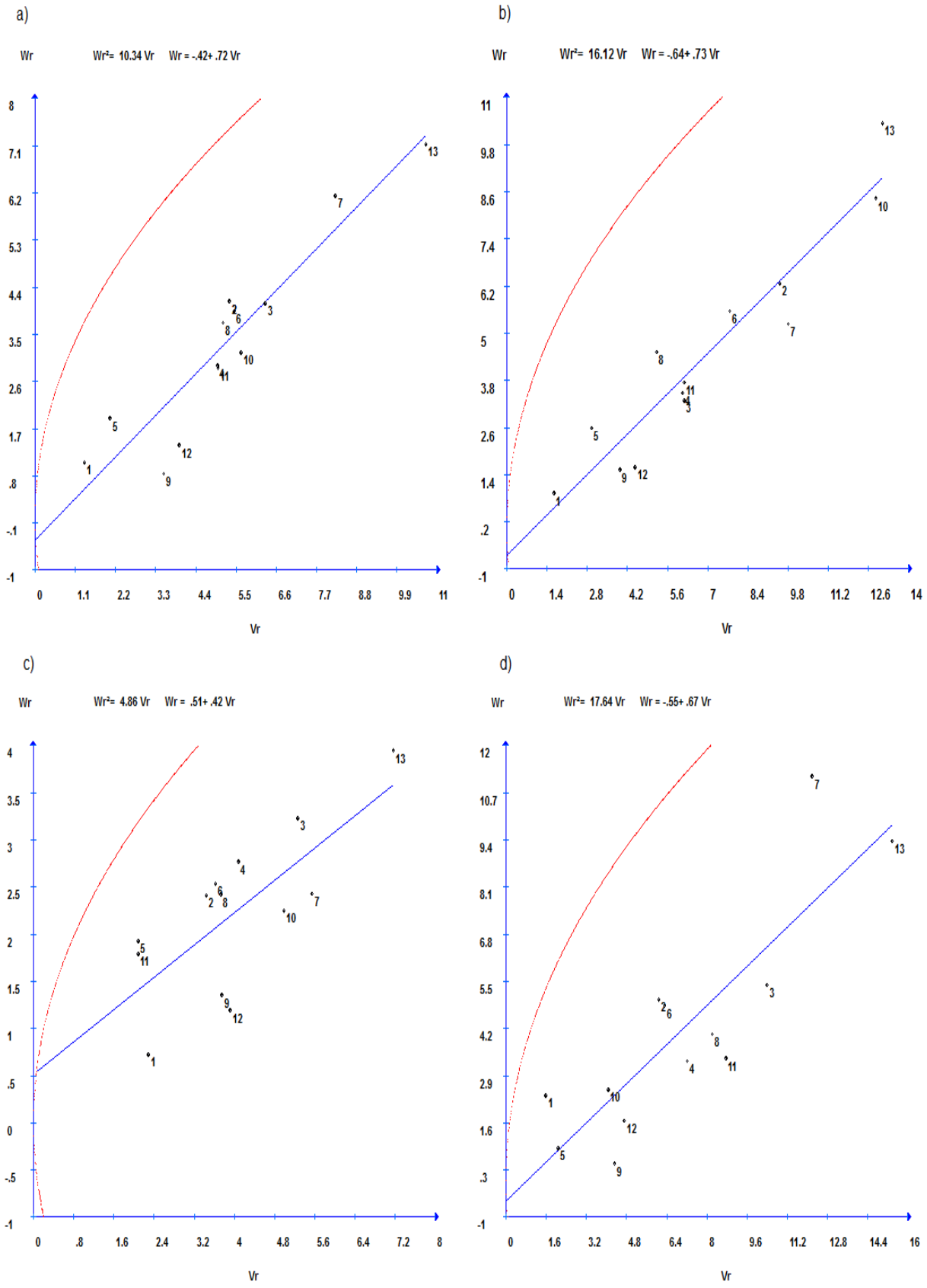

Figure 2. Regressions of W_r in V_r for male flowering (MF) for the joint analysis (a), Mariluz (b), Palotina (c) and São Pedro do Iguaçu (d). 1: CD069; 2: CD060; 3: CD056; 4: CD007; 5: CD070; 6: CD065; 7: CD008; 8: CD010; 9: CD067; 10: CD038; 11: CD063; 12: CD072; and 13: CD034.

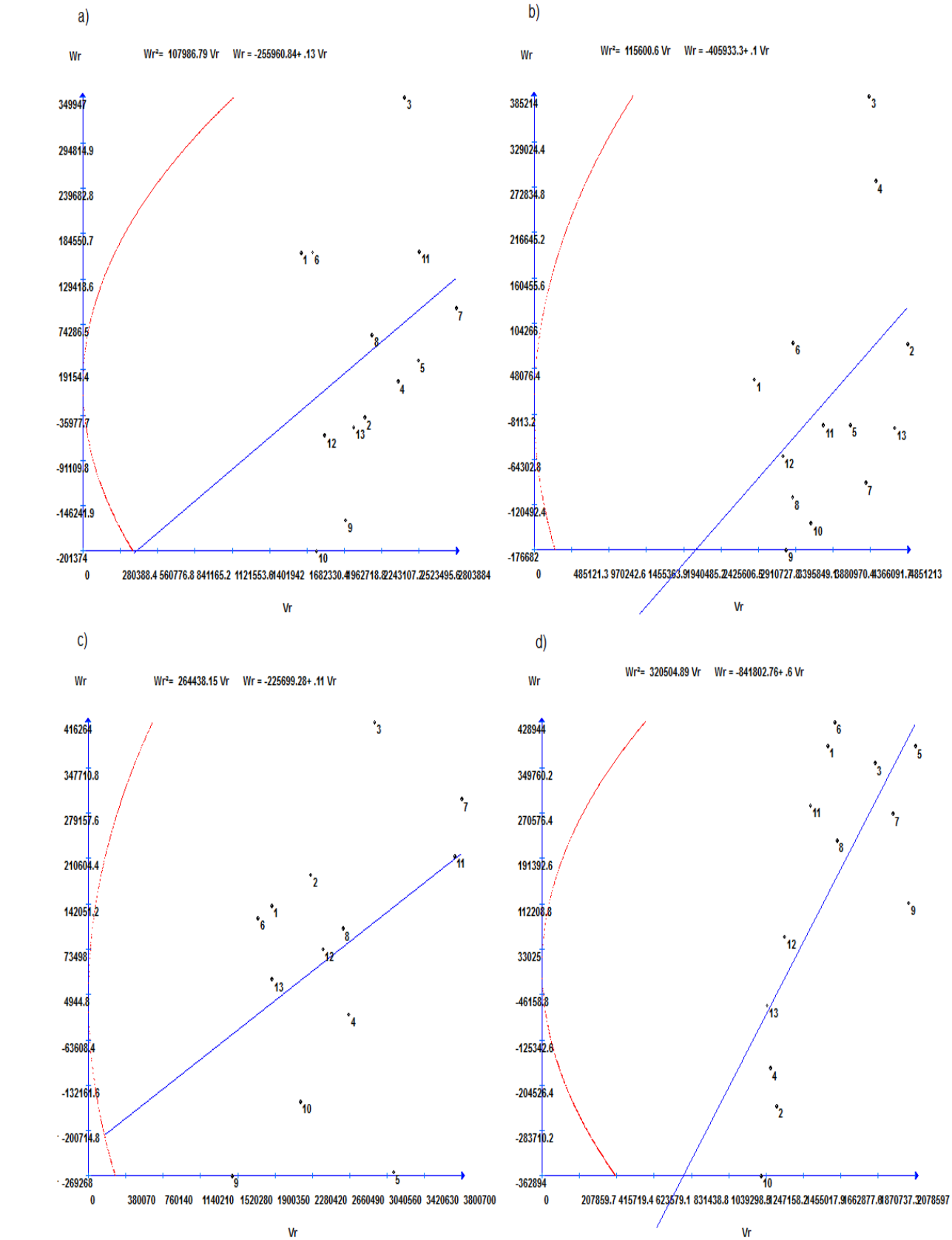

Figure 3. Regressions of W_r in V_r for grain yield (GY) for the joint analysis (a), Mariluz (b), Palotina (c) and São Pedro do Iguaçu (d). 1: CD069; 2: CD060; 3: CD056; 4: CD007; 5: CD070; 6: CD065; 7: CD008; 8: CD010; 9: CD067; 10: CD038; 11: CD063; 12: CD072; and13: CD034.

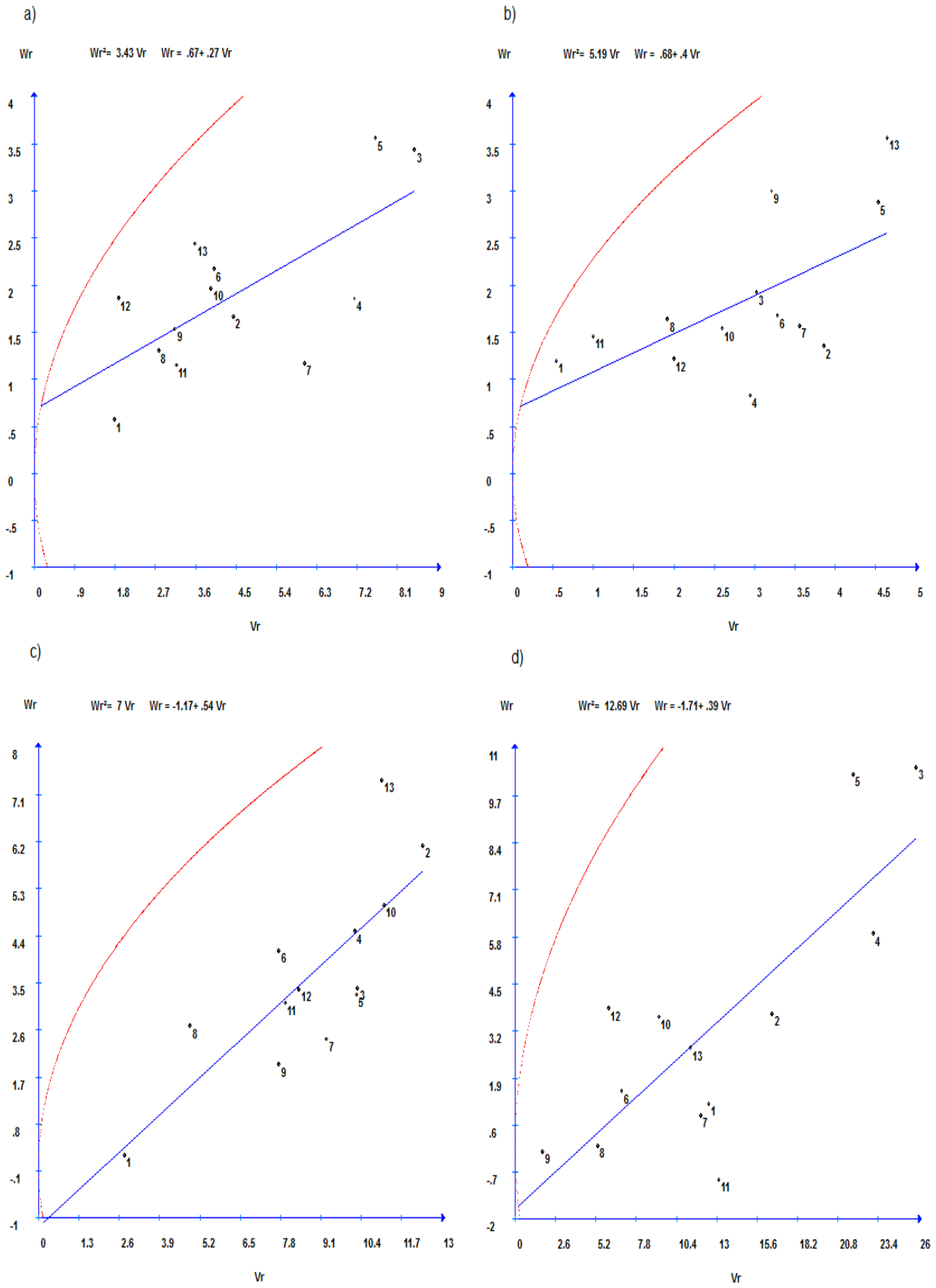

Figure 4. Regressions of W_r in V_r for crop humidity (HUM) for the joint analysis (a), Mariluz (b), Palotina (c) and São Pedro do Iguaçu (d). 1: CD069; 2: CD060; 3: CD056; 4: CD007; 5: CD070; 6: CD065; 7: CD008; 8: CD010; 9: CD067; 10: CD038; 11: CD063; 12: CD072; and 13: CD034.

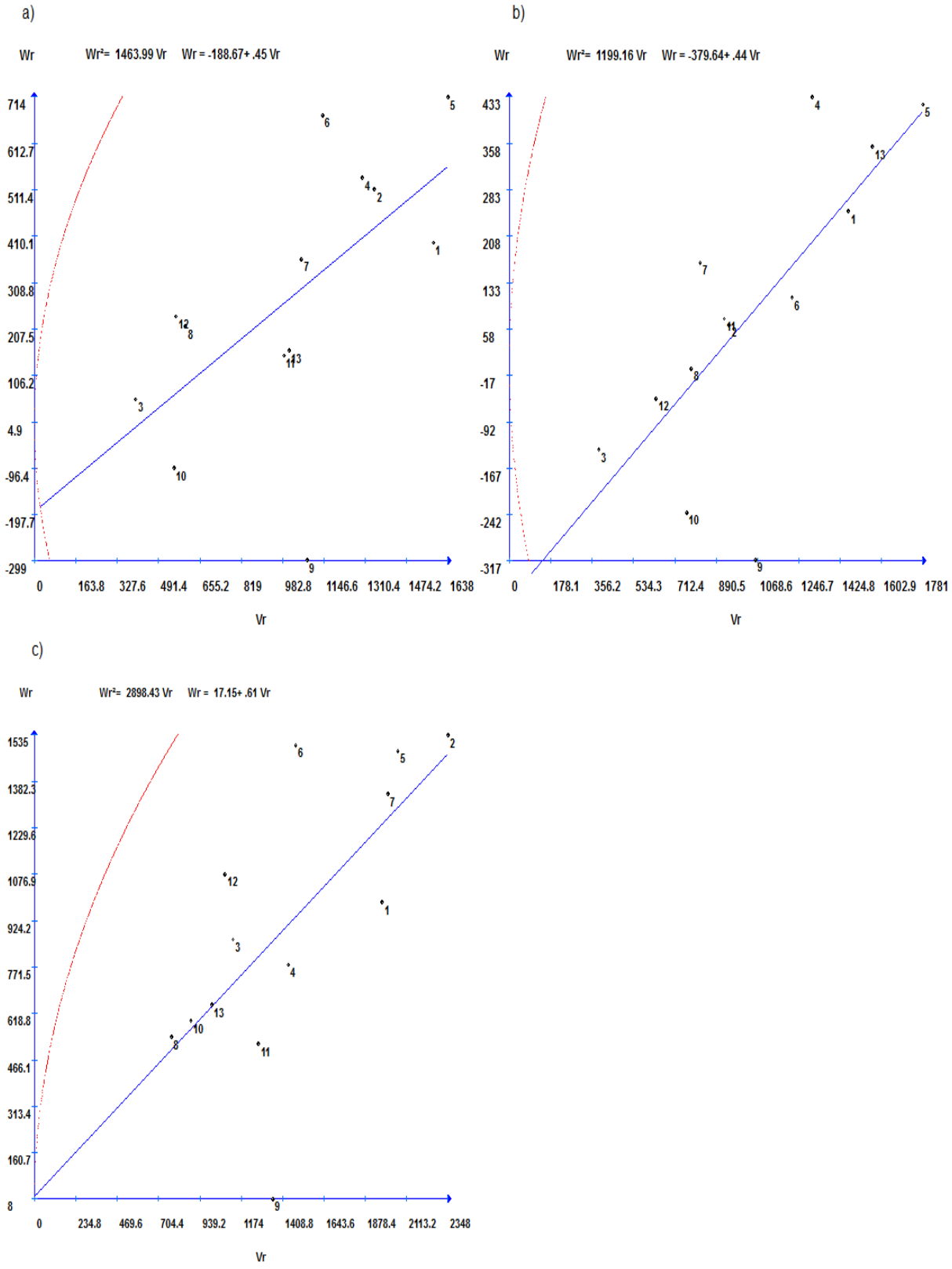

Figure 5. Regressions of W_r in V_r for mass of one thousand seeds (MTS) for the joint analysis (a), Mariluz (b) and Palotina. 1: CD069; 2: CD060; 3: CD056; 4: CD007; 5: CD070; 6: CD065; 7: CD008; 8: CD010; 9: CD067; 10: CD038; 11: CD063; 12: CD072; and13: CD034.

Table 5. Estimates of genetic and non-genetic parameters for male flowering (MF), female flowering (FF), grain yield (GY), crop humidity (HUM) of Mariluz, São Pedro do Iguaçu and Palotina and mass of a thousand seeds (MTS) of Mariluz and Palotina.

Trait	Env.	Parâmetros					
		$\sqrt{H_1/D}$	$H_2/4H_1$	K_D / K_R	h^2/H_2	h^2_R	h^2_A
MF (days)	MLZ	1.2402	0.1858	2.1055	6.7012	0.4518	0.9560
	SPI	1.1915	0.1642	2.4577	6.4330	0.4407	0.8663
	PTNA	1.5415	0.1798	1.0783	5.4936	0.6272	0.9728
	Average	1.2678	0.1827	1.7249	7.2194	0.5322	0.9447
FF (days)	MLZ	1.1856	0.1807	2.3618	7.0870	0.4414	0.9636
	SPI	1.3925	0.1840	1.9020	6.7250	0.4135	0.8697
	PTNA	1.4157	0.1907	1.1171	6.0332	0.6110	0.9653
	Average	1.3531	0.1970	1.5623	6.8011	0.5230	0.9979
GY (kg ha^{-1})	MLZ	-	0.2306	-	8.5071	0.1515	0.9148
	SPI	5.8714	0.2422	0.8520	8.1180	0.1384	0.9042
	PTNA	11.3467	0.2262	0.9215	8.7314	0.1820	0.9296
	Average	8.8841	0.2369	1.0634	8.8933	0.1094	0.9999
HUM (%)	MLZ	1.2951	0.1758	1.5351	3.5432	0.6013	0.9546
	SPI	1.9768	0.1973	1.5895	0.0517	0.3535	0.9434
	PTNA	1.9480	0.1787	0.8221	0.2983	0.5933	0.9201
	Average	1.9928	0.1881	0.8946	0.5147	0.5942	0.9969
MTS (g)	MLZ	2.0529	0.1638	2.4328	4.6968	0.3490	0.9997
	PTNA	1.3180	0.1891	1.7801	4.4164	0.5096	0.9998
	Average	1.7393	0.1980	2.1094	5.1306	0.3689	0.9997

$\sqrt{H_1/D}$: mean degree of dominance; $H_2/4H_1$: distance of alleles (symmetry); K_D / K_R: dominant/recessive ratio; h^2/H_2: number of genes with dominance; h^2_R: coeficiente of determination in then arrow sense; h^2_A: coeficiente of determination in the broad sense. -: unable to estimate the parameter; Env: Environment.

The results of h^2/H_2 indicate a high number of genes in dominance within the lines used for all variables except humidity (HUM), where the values do not indicate dominance for this trait. Amaral Junior et al. (1999) reported low reliability and low robustness of the results of the h^2/H_2 statistics, where they found atypicalities in the results. Similarly, it is observed that for the humidity variable (HUM) the $\sqrt{H_1/D}$ estimator indicates overdominance and the h^2/H_2 estimator indicates that there are no dominant genes for this trait.

Estimates of the number of genes or gene blocks with dominance, indicated by h^2/H_2 values, indicate the existence of at least five to seven genes or gene blocks in dominance for male flowering (MF), six or seven for female flowering (FF), eight or nine for grain yield (GY), one to four for crop moisture (HUM) and four or five for mass of one thousand seed (MTS). However, according to Cruz et al. (2012) this estimator underestimates the number of genes that exhibit little or no dominance.

Genotypic coefficients of determination in the broad sense were high (above 0.86) in all variables, while in the narrow sense they were moderate to low. When analyzing the values of the coefficient of determination in the narrow sense (h^2_R), it shows that it is possible to have different selection gains for each trait in different locations. For male and female flowering (MF and FF) and mass of one thousand seeds (MTS) the Palotina environment (PTNA) was more promising, with h^2_R value of 0.6272. For harvest humidity (HUM) the best selection environments were Mariluz (MLZ) and Palotina (PTNA) with values of 0.60 and 0.59 respectively.

These results show the possibility of genetic gain and obtaining superior segregants for these traits, considering that, according to Cardoso et al. (2015), these magnitudes propose that the desirable alleles will be transmitted to the next generations with greater reliability. For grain yield (GY), a low coefficient of determination in the narrow sense is observed, showing that direct selection gains for this trait are more difficult.

In the estimates of the genetic components, it is noticed a greater importance of the components related to the dominance effects (H_1, H_2 and h^2) than the components associated with the additive effects (D) for all studied variables (Table 6). Fact also evidenced by the negative value of D-H_1, showing predominance of dominance gene effects in the gene control of these variables and denoting potential gain through obtaining superior segregants.

Table 6. Estimation of the genetic components of the characters male and female flowering (FM and FF), grain yield (GY), crop humidity (HUM) and mass of one Thousand seeds (MMS), according to Hayman's methodology (1954).

Trait	Env.	Component						
		E	D	H_1	H_2	h^2	F	D-H_1
MF (days)	MLZ	0.391^{ns}	15.730*	24.196*	17.980*	120.489*	13.889*	-8.465*
	SPI	1.204*	16.442*	23.342*	15.328*	98.608*	16.518*	-6.900*
	PTNA	0.158^{ns}	4.708*	11.189*	8.047*	44.212*	0.547^{ns}	-6.480*
	Average	0.391^{ns}	9.952*	15.996*	11.693*	84.421*	6.713*	-6.044*
FF (days)	MLZ	0.374^{ns}	21.159*	29.745*	21.495*	152.337*	20.325*	-8.585*
	SPI	1.560*	15.309*	29.686*	21.845*	146.907*	13.252*	-14.377*
	PTNA	0.307^{ns}	8.217*	16.471*	12.566*	75.816*	1.287*	-8.253*
	Average	0.019^{ns}	12.491*	22.851*	18.006*	122.465*	7.412*	-10.370*
GY (kg ha^{-1})	MLZ	355632.21*	-240031.60*	13821029.3*	12748762.3*	108454735.4*	-433158.36*	-14061060.98*
	SPI	163709.23*	156795.66*	5405319.57*	5236238.1*	42507785.2*	-147160.75*	-5248523.90*
	PTNA	193779.59*	70658.57*	9097133.01*	8231652.2*	71873685.8*	-65529.14*	-9026474.44*
	Average	2.15*	107984.64*	8522996.57*	8075959.5*	71821952.2*	58974.19*	-8415011.93*
HUM (%)	MLZ	0.185^{ns}	5.010*	8.403*	5.767*	20.434*	2.739*	-3.393*
	SPI	0.874^{ns}	11.823*	46.201*	36.458*	1.885*	10.640*	-34.377*
	PTNA	0.997^{ns}	6.011*	22.811*	16.306*	0.486^{ns}	-2.286*	-16.800*
	Average	0.199^{ns}	3.419*	13.578*	10.217*	5.258*	-0.757^{ns}	-10.159*
MTS (g)	MLZ	0.333^{ns}	1198.833*	5052.298*	3309.278*	15543.112*	2054.432*	-3853.464*
	PTNA	0.333^{ns}	2898.101*	5034.710*	3809.173*	16822.837*	2143.732*	-2136.609*
	Average	0.333^{ns}	1463.662*	4428.016*	3152.980*	16176.647*	1816.610*	-1964.354*

E: environmental variance component; D: variance component associated with additive effects; $H_1$and H_2: variance components associated with dominance deviations; h^2: quadratic component determined by the mean difference between hybrids and parents; F: component associated with covariance between additive and non-additive effects; D-H_1: component that expresses the difference between additive and dominant gene effects. *and ^{ns}: significant at 5% and not significant by t-test.

The highest concentration of dominant alleles for male flowering (MF) and female flowering (FF) are detected in the CD069, CD070, CD067, and CD072 lines (Figures 1 and 2), suggesting that the presence of dominant alleles provides greater precocity in male and female flowering (Table 8) and that it is possible to synthesize new populations with a higher degree of dominance thus reducing the time for flowering (Figures 1 and 2). The lineage with the highest concentration of recessive alleles is CD034, followed by the lineage CD008, which, due to its recessiveness, provides later flowering.

For grain yield (GY), we note a lineage positioning that indicates the presence of mainly recessive alleles for all lines for this trait (Figure 3), thus evidencing the low selection gain for grain yield in this group of lineages. The lines closest to the dominance regions of the graphs are the CD067 and CD038, and the line with the greatest presence of recessive alleles is the CD056. Analyzing the distribution of the strains in the graphs, it can be stated that hybrids and populations from the crossing of these lines will have low productive potential, since it is attributed by dominant alleles.

The line CD069 stands out with a higher number of dominant alleles for the harvest moisture variable (HUM) (Figure 4), which provide a higher rate of moisture loss and, consequently, greater precocity. For mass of one thousand seeds (MTS), we highlight the strains

CD0056, CD038 and CD072 as those with the largest number of dominant alleles, evidencing the possibility of obtaining more dominant segregants or hybrids and possibly with the largest mass of one thousand seeds (MTS) (Figure 5).

Conclusions

Dominant alleles were found more frequently in parents, except for grain yield where there is a predominance of recessives. There is a predominance of dominance gene effects in the control of the studied variables with overdominance interaction between alleles.

At least five to seven gene blocks control male flowering, six or seven female flowering, eight or nine yield, one to three crop humidity, and four or five thousand seed masses in this parent group.

It is possible to have greater selection gains for male and female flowering and mass of one thousand seeds in Palotina environment. For crop humidity, higher gains are possible in Mariluz and Palotina environments.

The CD069 strain is recommended for use for breeding work because it has a larger number of genes in dominance for maturation providing earlier.

The CD038 strain is recommended for breeding work because it has a higher number of genes in dominance for grain yield and mass of one thousand seeds.

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