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Gene action for seed yield and its component traits in castor (*Ricinus communis* L.) using graphical and numerical approach of Diallel analysis

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Abstract

The experimental material consisting of 55 entries comprised of ten parents and their 45 hybrids developed through half diallel mating design were evaluated in a randomized block design with three replications. Graphical and numerical approaches of diallel analysis were used to assess the nature and magnitude of gene action governing the expression of quantitative traits. The non-significance of t^2 values assured the fulfillment of assumptions underlying diallel analysis for all the characters except seed yield per plant. Regression coefficient (b) for five characters viz; effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, 100-seed weight and oil content did not differ significantly from unity indicating the absence of epistasis. The estimate of components of variation revealed significant differences for D, H_1 and H_2 for all the characters except D for seed yield per plant and H_1 and H_2 for oil content, indicating importance of both additive and non-additive gene effects for the expression of various characters. However, predominance of dominance effect was observed in the expression of most of the traits except effective length of primary raceme and number of capsules on primary raceme. The positive sign of 'F' and more than unity ratio of K_D/K_R than unity for all the characters except shelling out turn, indicated that proportion of dominant genes were more than recessive genes. High estimates of heritability in narrow sense was observed for effective length of primary raceme and number of capsules on primary raceme.

Keywords: gene action, Diallel, numerical approach, graphical

Introduction

Castor (*Ricinus communis* L.) belongs to monospecific genus *Ricinus* of family Euphorbiaceae and it is one of the most ancient oilseeds crop of the world, having chromosome number $2n = 20$. The genus name "Ricinus" is derived from Latin term meaning "dog tick" because of its seed resembling to the common pest of dog. Castor plant is considered native to Ethiopian region of tropical East Africa and India. The Egyptians burned castor oil in their lamps more than 4,000 years ago. Castor is one of the most important non-edible oilseed crops in the world. Hayman (1954) [5] listed six assumptions as the basis for the application of additive-dominance model. These assumptions were re-emphasized by Allard (1956) [1], who further stated that if the assumptions are valid, the points on the covariance (wr)/ variance (vr) graph are expected to fall on a line of unit slope. Where the regression line is significantly different from unit slope epistasis is implicated (Manga and Sidhu, 1979; Srivastava *et al.* 1979) [10, 19]. The intercepts of regression lines determine the levels of dominant gene action. Where the intercept is below the origin, at origin or above the origin, the gene actions is overdominance, complete dominance and partial dominance, respectively (Hayman, 1954; Allard, 1956; Singh and Chaudhary, 1985) [5, 1, 14]. The positions of the points of parental array in relation to the origin separate the parents into either dominant or recessive parents (Hayman, 1954; Allard, 1956; Singh and Chahal, 1974; Sirohi and Choudhury, 1983; Jolliffe and Arthur, 1993) [5, 1, 15, 16, 7]. However, the positions of the parental array in relation to the sides of the regression line are used to determine the additive and non-additive gene actions of the parents. Where the parent points lie above the regression line, they are said to possess additive gene action whereas those below are said to possess non-additive gene action (Manga and Sidhu, 1979; Kaw and Menson, 1983; Sirohi and Choudhury, 1983) [10, 8, 16]. Sirohi and Choudhury (1983) [16] went further to add that those arrays below the regression line implicated both non-additive and epistatic gene actions. There is dearth of information in literature regarding covariance (W_r)/ variance (V_r) graphs and additive-dominance model in castor. In the light of the above, the current study is to highlight gene action using graphic method.

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Materials and Methods

The experimental material comprised of ten parents *viz.*, SKP-84, VP-1, JI-436, JI-433, JI-368, SKI-346, PCS-124, JI-35, SKI-215 and RG-43. The seeds of 45 F₁ hybrids and ten parents were produced by hand emasculating-hand pollination and selfing, respectively during *Kharif* 2016-17. These 45 F₁ hybrids along with 10 parents were evaluated in randomized block design with three replications during *Kharif* 2017-18 at Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh.

Five competitive plants per each entry in each replication were randomly selected before flowering and tagged for the purpose of recording the observations of different characters *viz.*, days to 50% flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme (cm), number of nodes up to primary raceme, length of primary raceme (cm), effective length of primary raceme (cm), number of effective branches per plant, number of capsules on primary raceme, shelling out turn (%), 100-seed weight (g), seed yield per plant (g) and oil content (%).

Genetic analysis of diallel data for graphical approach (Wr-Vr graph) as well as genetic components of variation was according to method of Hayman (1954) [5] and Jinks (1954) [6]. The first three assumptions of the additive/dominance genetic model underlying an analysis of the diallel cross Hayman (1954) [5] were tested as follows: (1) diploid segregation; (2) homozygous parents each parent was maintained by inbreeding and was assumed to be homozygous; and (3) no reciprocal differences. The remaining assumptions of the simple additive dominance genetic model (Mather and Jinks, 1982) [11] are (4) independent effect of non-allelic genes (i.e. no epistasis); (5) no multiple allelism and (6) genes independently distributed between parents. Hayman's (1954) [5] method was adopted for covariance (Wr) and variance (Vr) estimates using the genotype means on MS Excel programme.

Results and Discussions

The t^2 values were calculated for all the characters (Table 1 and Table 2). The results indicated that t^2 values were non-significant for all the characters except number of nodes up to primary raceme and seed yield per plant indicating that the additive-dominance model was adequate for all the characters studied except for numbers of nodes up to primary raceme and seed yield per plant. The estimate of the components of variation revealed significant differences for variance due to additive genetic effect (D) as well as variance due to non-additive effects (H₁ and H₂) for all the characters (except D for seed yield per plant and H₁ and H₂ for oil content) (Table 1 and Table 2). The above finding indicated that both additive and dominance components were important in the inheritance of all the traits except seed yield per plant and oil content. The non-significant estimate of 'E' for all the traits except oil content indicated that environmental influence in modifying the expression of these characters was negligible.

The average degree of dominance (H₁/D)^{1/2} was found to be more than unity indicating over dominance for several characters such as, days to maturity of primary raceme, number of effective branches per plant, shelling out turn, 100-seed weight, seed yield per plant and oil content which suggested that heterosis breeding might be advantageous to get higher seed yield in castor. In that study seed yield per plant reported as overdominance in nature. These results are in general agreement with Giriraj *et al.* (1974) [4], Singh and Yadav (1981) [13], Narkhede *et al.* (1985) [12], Dobariya *et al.*

(1992) [3], Tank *et al.* (2003) [20], Sodavadiya (2010) [17] and Manga and Gila (2015) [9] in castor.

The equal distribution of positive and negative genes in the parents helps the breeders in selecting desirable traits without losing other traits of interest. In that study, asymmetrical distribution of positive and negative genes in the parental lines was revealed from the estimate of H₂/4H₁ for all the characters. Asymmetrical distribution of alleles in the parents was also noticed by Sodavadiya (2010) [17], Manga and Gila (2015) [9] in castor and Aminul *et al.* (2015) [2] in jatropha.

The positive sign of 'F' and K_D/K_R ratio was more than unity for all the characters (except shelling out turn) indicated that proportion of dominant genes were more than recessive genes, while for shelling out turn there was excess of recessive genes in the parents. The present results are in agreement with Manga and Gila (2015) [9] in castor.

Knowledge on number of gene groups which exhibit dominance and responsible for particular traits is important for the genetic progress through selection. In the present investigation, the value of h²/H₂ was low in most of the cases except days to 50% flowering of primary raceme, days to maturity of primary raceme and shelling out turn indicating that minimum one gene group with dominant effect was responsible for these traits. While for days to 50% flowering of primary raceme, days to maturity of primary raceme and shelling out turn more than one gene or group of genes generally controlled the dominance effect in inheritance of a particular character.

High estimates of heritability in narrow sense was observed for days to 50% flowering of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme and number of capsules on primary raceme suggesting that selection based on these attributes would lead to rapid genetic improvement. A high heritability for earliness, plant height and length of primary raceme was reported by Solanki and Joshi (2000) [18]. Moderate heritability was observed for number of effective branches per plant, shelling out turn and seed yield per plant, whereas for days to maturity of primary raceme, 100-seed weight and oil content displayed low heritability.

Graphical analysis of the experimental data recorded was done in order to get information about allelic constitution of the parents used in the diallel cross. In the present study, regression coefficient values (b) for eight characters *viz.* days to maturity of primary raceme, plant height up to primary raceme, length of primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, 100-seed weight and oil content did not differ significantly from unity indicating the absence of epistasis (Table 1 and Table 2). This indicated the fulfilment of the assumption that epistasis is absent for these characters. The Wr-Vr graphs for these characters have been presented in Figures 1-8. But for the rest characters regression value differs significantly. So, for these characters epistatic gene action may be present. For almost all the characters, the parental array points were scattered all along the regression line in the Wr-Vr graph. This indicates the genetic diversity among the parents for all the traits studied. Distribution of array points in Wr-Vr graph also decides relative proportions of dominant and recessive alleles present in parent.

Graphical analysis of Wr axis v/s Vr axis revealed that plant height up to primary raceme, length of primary raceme, effective length of primary raceme and number of capsules on primary raceme exhibited partial dominance gene action as

the regression line intercepting the W_r coordinate above the origin, confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was less than unity for these traits. The present results are in agreement with Manga and Gila (2015) [9] in castor and Aminul *et al.* (2015) [2] in jatropha.

For days to maturity of primary raceme, number of effective branches per plant and oil content regression line passed below the origin indicating that these traits were conditioned by over dominance and confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was more than unity for all these traits and for 100-seed weight regression line passed near the origin indicating that this trait was conditioned by complete dominance.

W_r - V_r graphical analysis indicated the involvement of dominant genes for most of characters except length of

primary raceme and effective length of primary raceme. This was in agreement with the assertion of Hayman (1954) [5] that the parents were either predominantly dominant or preponderantly recessive when they were close to or far away from the origin, respectively.

Since the distribution of array points reflects the parental diversity. The parents for making crosses could be selected on the basis of gca effects. However, selecting the parents on the basis of genetic diversity cannot be ignored. The crosses between the diverse parents would be the potential ones for throwing out desirable segregants. So, the crosses should preferably be between the parents located away from the origin in W_r - V_r graph analysis, subject to fulfilment of other criteria, namely good gca effect and the desirable mean values for the important traits.

Table 1: Genetic component for days to 50% flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme

Genetic component	Days to 50% flowering of primary raceme	Days to maturity of primary raceme	Plant height up to primary raceme	Number of nodes up to primary raceme	Length of primary raceme (cm)	Effective length of primary raceme (cm)
D	94.94*	93.38*	382.33*	3.79*	155.63*	241.67*
	± 11.88	± 5.42	± 23.64	± 0.52	± 7.43	± 9.12
H_1	77.34*	110.30*	200.13*	3.92*	97.97*	115.80*
	± 25.28	± 11.53	± 50.33	± 1.11	± 15.81	± 19.42
H_2	56.55*	65.75*	178.99*	2.68*	88.47*	98.68*
	± 21.49	± 9.80	± 42.78	± 0.95	± 13.44	± 16.50
h^2	67.69*	293.73*	55.77	0.16	4.99	-1.22
	± 14.38	± 6.56	± 28.63	± 0.63	± 8.99	± 11.05
F	67.44*	129.13*	171.36*	1.65	62.43*	9.13
	± 27.40	± 12.50	± 54.56	± 1.21	± 17.14	± 21.05
E	0.87	3.32*	7.10	0.12	3.97	3.48
	± 3.58	± 1.63	± 7.13	± 0.16	± 2.23	± 2.75
$(H_1/D)^{0.5}$	0.90	1.09	0.72	1.02	0.79	0.70
$H_2/4H_1$	0.18	0.15	0.22	0.17	0.23	0.21
KD/KR	2.30	4.50	1.90	1.54	1.67	1.06
h^2/H_2	1.20	4.47	0.31	0.06	0.06	-0.01
Heritability (ns) %	60.71	18.20	69.10	68.30	66.30	81.60
t^2 value	1.27	1.12	0.11	3.80	0.08	0.43
Probability for t^2	0.36	0.41	0.98	0.051	0.98	0.79
H: b = 1	2.80	1.61	0.85	4.72	0.39	1.11
Probability for b	0.02	0.15	0.42	0.002	0.71	0.30

Table 2: Genetic component for number of effective branches per plant, number of capsules on primary raceme, shelling out turn, 100-seed weight, seed yield per plant, oil content in castor

Genetic component	Number of effective branches per plant	Number of capsules on primary raceme	Shelling out turn (%)	100-seed weight(g)	Seed yield per plant (g)	Oil content (%)
D	12.71*	3659.30*	9.07*	12.60*	9865.75	0.09*
	± 2.96	± 205.19	± 4.25	± 3.90	± 5916.80	± 0.04
H_1	27.47*	2398.48*	31.16*	45.01*	43522.75*	0.11
	± 6.32	± 436.77	± 9.04	± 8.29	± 12594.46	± 0.08
H_2	21.85*	1180.99*	28.59*	35.04*	33410.83*	0.05
	± 5.36	± 371.21	± 7.68	± 7.04	± 10703.89	± 0.07
h^2	9.71	1010.00*	31.91*	2.19	5909.80	-0.03
	± 3.59	± 248.47	± 5.14	± 4.71	± 7164.77	± 0.05
F	13.57*	3948.07*	-2.43	19.38*	7419.80	0.09
	± 6.84	± 473.44	± 9.80	± 8.99	± 13651.83	± 0.09
E	1.25*	18.53	2.33	2.23	2800.06	0.12*
	± 0.89	± 61.87	± 1.29	± 1.17	± 1783.98	± 0.01
$(H_1/D)^{0.5}$	1.47	0.81	1.85	1.89	2.10	1.08
$H_2/4H_1$	0.20	0.12	0.23	0.19	0.19	0.12
KD/KR	2.14	4.99	0.86	2.37	1.44	2.84
h^2/H_2	0.44	0.85	1.12	0.06	0.17	-0.55
Heritability (ns) %	26.20	59.70	42.60	12.60	36.00	15.70
t^2 value	0.95	0.80	2.00	0.64	14.47*	0.08
Probability for t^2	0.48	0.55	0.18	0.65	0.001	0.99
H: b = 1	2.21	1.66	4.30*	1.82	6.61*	1.44
Probability for b	0.05	0.13	.003	0.11	0.00	0.19

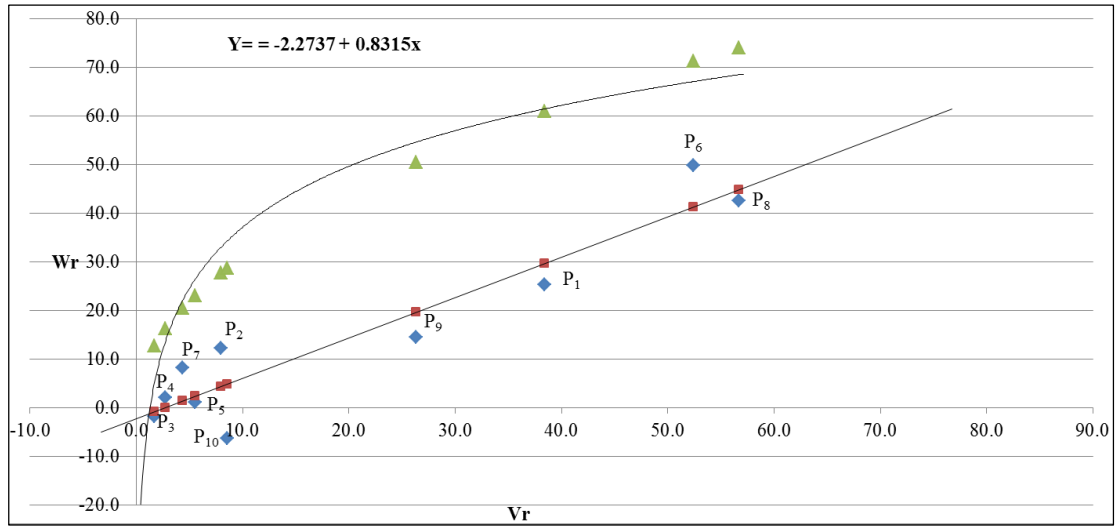


Fig 1: Wr-Vr graph for days to maturity of primary raceme

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

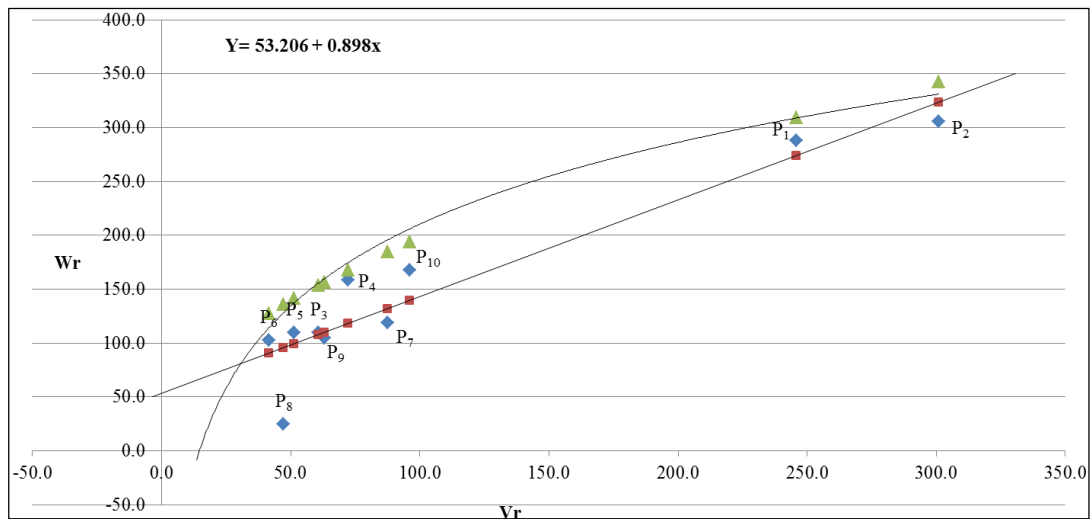


Fig 2: Wr-Vr graph for plant height up to primary raceme

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

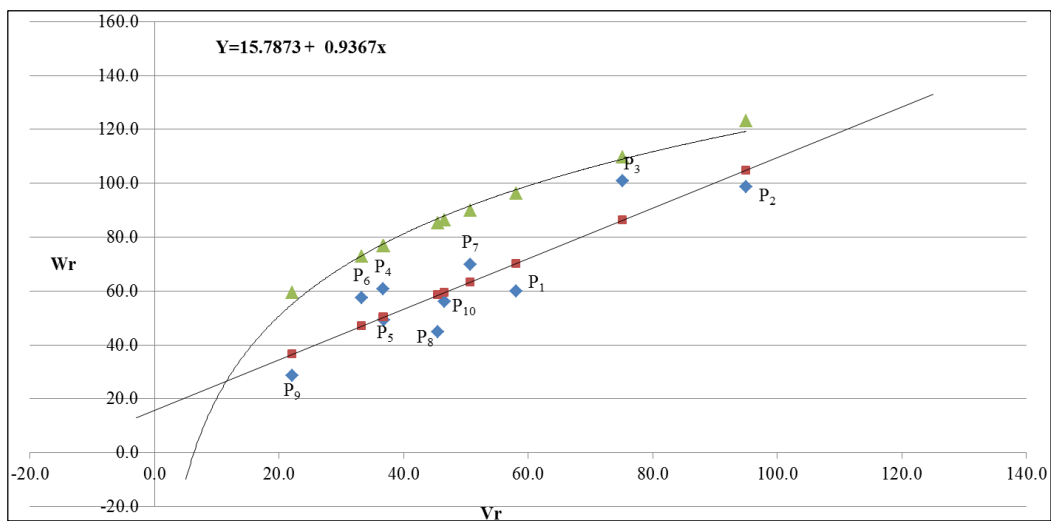


Fig 3: Wr-Vr graph for length of primary raceme

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

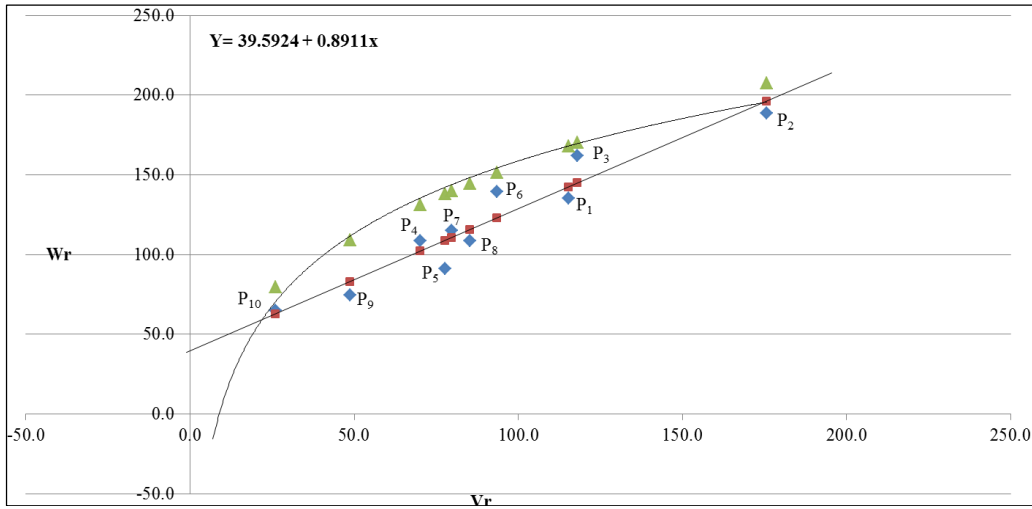


Fig 4: Wr-Vr graph for effective length of primary raceme

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

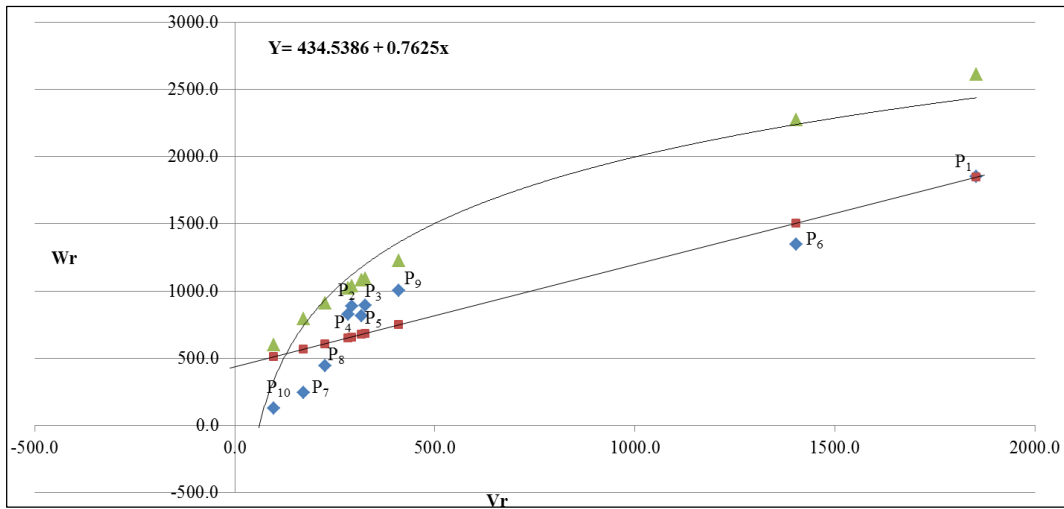


Fig 5: Wr-Vr graph for number of capsule in primary raceme

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

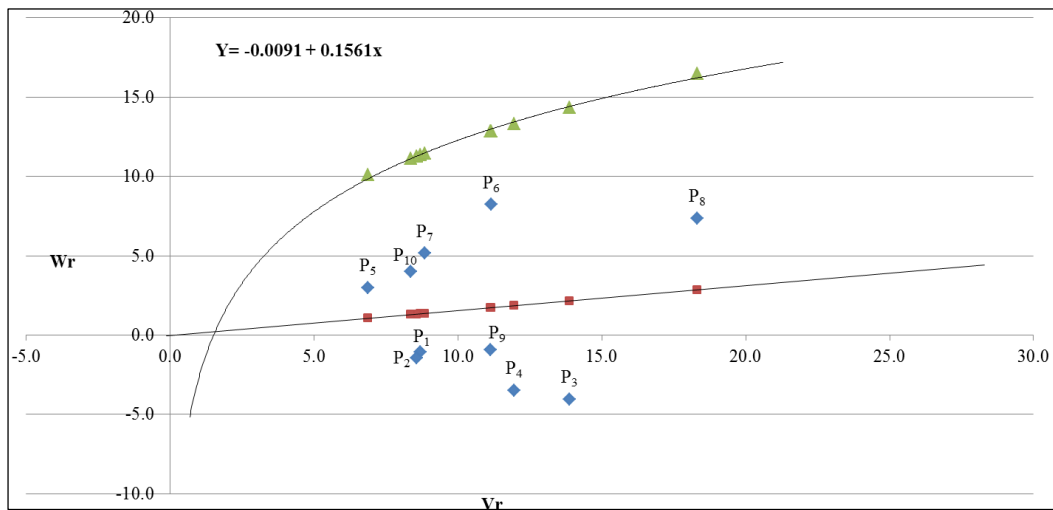


Fig 6: Wr-Vr graph for 100-seed weight

P1: SKP-84, P2: VP-1, P3: JI-436, P4: JI-433, P5: JI-368, P6: SKI-346, P7: PCS-124, P8: JI-35, P9: SKI-215, P10: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

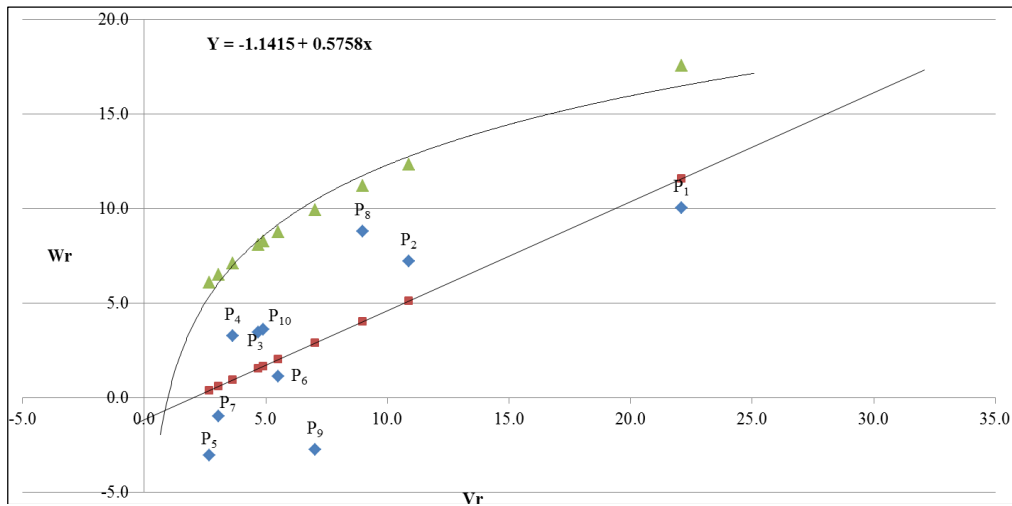


Fig 7: W_r - V_r graph for number of effective branches per plant

P₁: SKP-84, P₂: VP-1, P₃: JI-436, P₄: JI-433, P₅: JI-368, P₆: SKI-346, P₇: PCS-124, P₈: JI-35, P₉: SKI-215, P₁₀: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

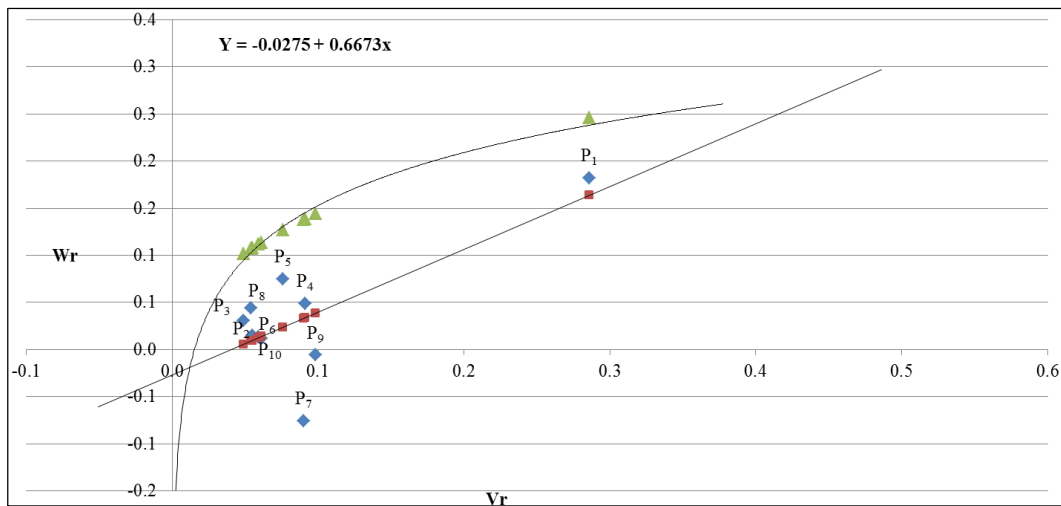


Fig 8: W_r - V_r graph for oil content

P₁: SKP-84, P₂: VP-1, P₃: JI-436, P₄: JI-433, P₅: JI-368, P₆: SKI-346, P₇: PCS-124, P₈: JI-35, P₉: SKI-215, P₁₀: RG-43

◆ Parental array points ■ Regression ▲ Parabola — Linear (Regression) — Log. (Parabola)

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