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Research Article

Hayman’s graphical analysis of yield, quality and their components traits in rice (*Oryza sativa* L.) under coastal agro ecosystem

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Abstract

Six × six full diallel mating involving six parents *viz.,* (P1) ADT 37, (P2) ADT 43, (P3) ADT 45, (P4) ASD 16, (P5) CO51 and (P6) CO47 was effected to evolve 30 hybrids in rice crop. The six parents along with their 30 F_1 hybrids were evaluated for ten agronomic traits *viz* days to 50 per cent flowering, plant height at maturity, the number of productive tillers per plant, panicle length, the number of filled seeds per panicle, seed length, seed breadth, seed L/B ratio, hundred seed weight and seed yield per plant. The traits *viz.,* seed length and seed L/B ratio were controlled by complete dominance. Incomplete dominance was found to operating in the expression of the traits *viz.,* the number of filled seeds per panicle and seed yield per plant. Partial dominance can be had as semi additivity. On the other hand, the traits *viz.,* days to 50 per cent flowering, plant height at maturity, panicle length, seed breadth and hundred seed weight were controlled by over dominance. Apart from this amphi directional dominance was well evidenced from the correlation coefficient of Yr and Wr – Vr as well as Vr – Wr graph. It is earnestly advised to inter-cross among the parents to evolve high heterotic lines and/or improved populations.

Key words

Rice, Vr-Wr graphical analysis, Coastal salinity.

INTRODUCTION

Rice (*Oryza sativa* L.) is the major food crop for Asians, Africans, Australians, Americans as well as Europeans. Rice is life for many of the Asians as well as other rice consuming peoples in the world. 100 g of rice gives about 300 calories of energy. The requirement of calories for an average Indian citizen is 1500 calories. Rice is rich in carbohydrate. 100 g of cooked rice supplies 28 g of carbohydrates, 2.7 g of proteins, as well as 0.3 g of fat (USDA, 2021). Apart from this, cooked rice also gives mineral nutrients such as sodium (1 mg), potassium (30 mg), magnesium (3%), calcium (1%) and iron (1%). Cooked rice also enriched with Threonine, Isoleucine, Leucine and Lysine amino acids.

Choice of the breeding programme depends upon the nature of gene action governing the important seed yield and its component traits. Genetic architecture of yield, quality and their component traits gains paramount importance in formulating effective breeding programme. Mating designs are extensively to obtain information on combining ability, heterosis and gene action. Out of the commonly used mating systems Dialle mating system proposed by Griffing (1956) assumes special importance, as it excavates the presence of cytoplasmic gene action apart from the role of nuclear genes and the possible inter-play of nuclear-cytoplasmic interactions in the expression of seed yield and its components traits, as well. Griffing's proposed four approaches, out of which the first approach, which includes the parents, direct hybrids as well as reciprocal hybrids gains momentum. It is customary to deduce the genetic components *viz.,* $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{H}^2$ and $\hat{E}$ by employing Hayman (1954a) additional second degree statistics. The graphic analysis proposed by Jinks and Hayman (1953) is widely used as it includes the third degree statistics *viz.,* variance and covariance.

India achieved self sufficiency in cereal grain production especially in rice and wheat. India exports rice grains to western countries and gains valuable foreign exchange. To hike the market value, improving the quality of the grains assumes special importance. Hence, the present investigation was formulated to unveil the genetic worthiness of the certain genotypes of rice, under coastal ecosystem, with relation to productivity as well as quality parameters. East coast area accounts 2378.8 km running from Tamil Nadu to West Bengal. If the productivity and production is increased in the coastal area, it will improve the livelihood of the resource poor farmers of East-Coast area.

MATERIALS AND METHODS

The experimental material consisted of six parents *viz.,* (P1) ADT 37, (P2) ADT 43, (P3) ADT 45, (P4) ASD 16, (P5) CO51 and (P6) CO47. These varieties were obtained from Tamil Nadu Rice Research Institute (TNAU), Aduthurai and sown during January – February in three spells. They were transplanted during February – March 2019 (Late Navarai). A total of three plantings were done with 15 days interval. Parents were selfed as well as mated in 6 ×6 full diallel fashion. Thus, selfed seeds of six parents and crossed seeds of 30 cross combinations were evolved. Crosses were made as per the protocol suggested by Narasimman (2005). The selfed seeds as well as the crossed seeds were harvested and thrashed separately by keeping the identify and individuality.The selfed seeds of the parents were sown separately. Similarly, the F_1s seeds of the 30 cross combinations were sown in raised beds, one meter away from the nursery bed of the parents, during July, 2019. Twenty five days old seedling were transplanted in two rows of three meter length plots, during Kuruvai 2019. The spacing adopted was 20 × 15 cm. The seedlings were planted in RBD with three replications. Recommended agronomic practices and need based plant protection measures were judiciously followed. Observations were recorded on ten agronomic traits *viz.,* X_1) Days to 50 per cent flowering, X_2) Plant height at maturity, X_3) Number of productive tillers per plant, X_4) Panicle length, X_5) Number of filled seeds per panicle, X_6) Seed length, X_7) Seed breadth, X_8) Seed L/B ratio, X_9) Hundred seed weight and X_{10}) Seed yield per plant, on five randomly selected competing plants per replication.

RESULTS AND DISCUSSION

Estimates of uniformity test, t^2, were non-significant for all the traits of interest. It indicated that the assumptions made by Hayman (1954b) for diallel analysis is valid for all the traits of interest. It may also indicate the absence of epistatic interactions (**Table 1**). The result is in conformity with the findings of Narasiman (2005) and Iftekharuddaula *et al.* (2009). However , Amardeep Kour et al (2019) reported about the presence of epistatic interaction for seed yield in rice. The deviations of regression coefficients (b) of Vr-Wr were significant for all the traits of investigation (**Table 1**). It indicated that these traits had a strong relationship between Vr (Variance of each array) and Wr (Covariance between parents and their offspring's) of the parental materials and thus Vr, Wr graph was effective for the genetical studies of the parental material with respect to these attributes. Hence, Vr-Wr can be plotted for all the traits of interest. The correlation coefficients of Yr and Wr+Vr were non significant always. It may indicate the presence of ampidirectional dominance (**Table 1**). The results are in conformity with the earlier findings of Mather and Jinks (1971).

Table 1. Hayman's graphic analysis in rice crop

S. No.	Characters	t^2 values	a	B	SE	(b-0)/SE	(1-b)/SE	Correlation coefficient 'r'
1	Days to 50 per cent flowering	4.0350	-5.2127	0.5301	0.1421	3.7283*	3.3047	0.8744
2	Plant height at maturity	0.8274	-1.1349	0.9391	0.5123	1.8331*	0.1187	0.6801
3	Number of productive tillers per plant	1.7646	-0.0836	0.2747	0.1522	1.8048*	4.7654	-0.1327
4	Panicle length	4.1911	0.0524	3.2869	0.1881	17.4742*	-12.1578	-0.4538
5	Number of filled seeds per panicle	0.4514	5.3350	1.0453	0.2389	4.3740*	-0.1896	0.6785
6	Seed length	4.2913	0.0313	1.1067	2.3027	48.0607*	-4.6352	-0.9706
7	Seed breadth	0.0803	-0.0014	1.0155	0.1064	9.5441*	-0.1456	0.4380
8	Seed L/B ratio	0.1045	0.0010	1.0104	0.1166	8.6612*	-0.0895	-0.9563
9	Hundred Seed weight	0.2658	-0.0033	1.0211	0.2057	4.9638*	-0.1030	-0.9083
10	Seed yield per plant	0.5070	4.6665	0.8430	0.1444	5.8361*	1.0862	0.9169

*Significant at 1 per cent level

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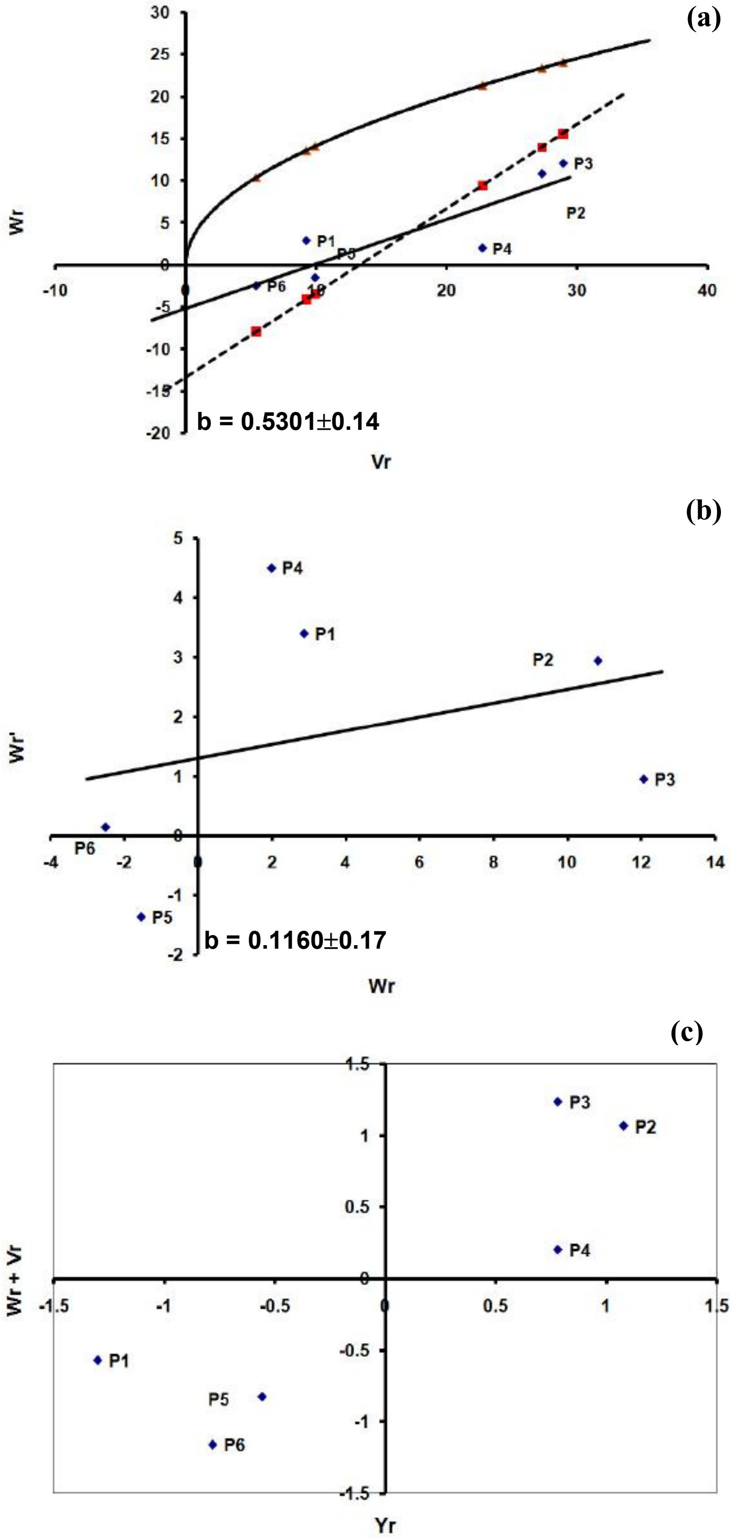
The regression line of the Vr, Wr graph intersected the Wr axis well below the origin, for days to 50 per cent flowering, plant height at maturity, the number of productive tillers per plant, panicle length, seed breadth and hundred seed weight. It may indicate the influence of over dominance in the expression of the aforementioned traits. Similar results were earlier reported by Raju *et al.* (2011), Illieva *et al.* (2013), Chaturvedi *et al.* (2015) and Akanksha and Jaiswal (2019). On the other hand the traits *viz.,* seed length and seed L/B ratio were controlled by complete dominance as the regression line of the Vr, Wr graph intersect Wr axis at the origin (**Fig. 1a to 10 a**). Similar observations have been reported earlier by Mahmood *et al.* (2004). The other traits of interest *viz.,* the number filled seeds per panicle and seed yield per plant were conditioned by partial dominance as the regression line Vr, Wr intersect Wr axis well above the origin. The results are in conformity with the earlier findings of Akram *et al.* (2007), Chaturvedi *et al.* (2015) , Patel Shashikant Kacharabhai (2015) and Priyanka and Jaiswal (2017).

The deviations of regression co-efficience from zero were significant always. It indicated that all the traits of interest had a strong relationship between Vr (Variance of each array) and Wr (Covariance between parents and off springs) of the parental material. This indicated that Vr, Wr were effective for the genetical studies of the parental material. The regression coefficience of Vr, Wr graphs were non-significantly different from unity for all the traits of interest. It may indicate that the traits of interest were controlled by additive genes.

The estimates of Y intercept ('a') and slope ('b') of the test fitting regression line indicated the following facts. The estimates of Y intercept ('a') were positive for panicle length, the number of filled seeds per panicle, seed length, seed L/B ratio and seed yield per plant. It indicates that the above mentioned traits involve the partial dominance in inheritance. However, the traits *viz.,* days to 50 per cent flowering, plant height at maturity, the number of productive tillers per plant, seed breadth and hundred seed weight recorded the values of Y intercept ('a') close to zero. This indicated that these traits were controlled by dominant gene action. In the Yr – (Wr+Vr) graph, the parents which falling in the I quadrant indicate the possession of parents with genes which had recessive positive effects. The parents falling in the II quadrant may have recessive genes with negative effects. The parents is falling in the III quadrant may have dominant genes with negative effects. Similarly, the parents falling in the IV quadrant may have dominant genes with positive effects (**Fig c of all the graphs**).

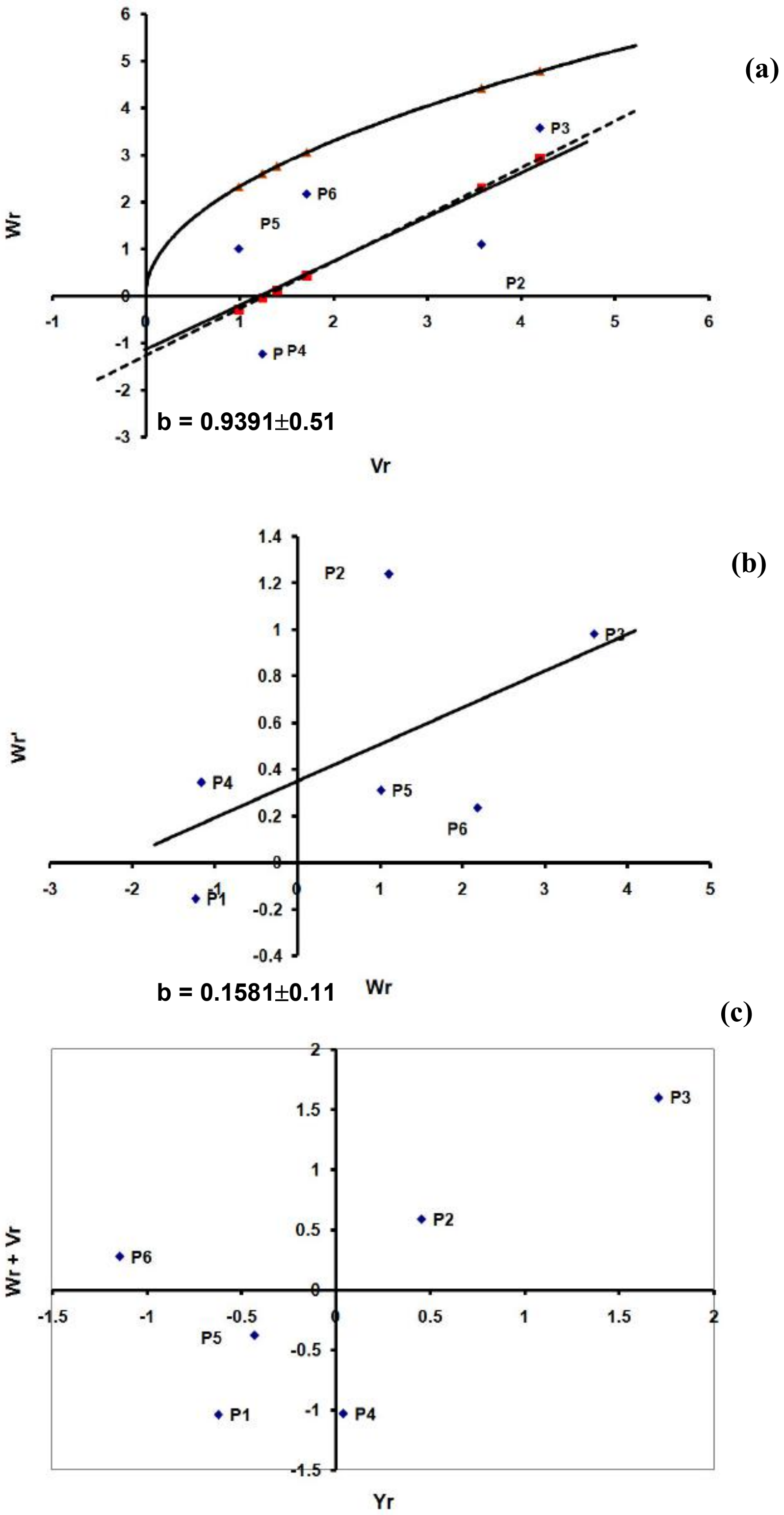
The parents P1 (ADT 37), P5 (CO51) and P6 (CO47) had most dominant genes. The parents P2 (ADT 43) and P3 (ADT 45) had most recessive genes. The parent P4 (ASD 16) was intermittent with relation to days to 50 per cent flowering. The parents P1 (ADT 37), P4 (ASD 16), P5 (CO51) and P6 (CO47) had most dominant genes and the parents P2 (ADT 43) and P3 (ADT 45) had most recessive genes for plant height at maturity. The parents P2 (ADT 43) and P4 (ASD 16) had most dominant genes and the parents P5 (CO51) and P6 (CO47) had intermittent values. The parent P1 (ADT 37) and P3 (ADT 45) had most recessive genes for the number of productive tillers per plant. The parents P1 (ADT 37), P2 (ADT 43) and P4 (ASD 16) had most dominant genes and the parents P3 (ADT 45) and P6 (CO47) had most recessive genes. The parent P5 (CO51) had intermittent value for panicle length. The parents P4 (ASD 16) and P6 (CO47) had most dominant genes and the parent P5 (CO51) had most recessive genes. The parents P2 (ADT 43) and P3 (ADT 45) had intermittent for the number of filled seeds per panicle. All the parents had most dominant genes, except P1 (ADT 37), which had most recessive genes for seed length. The parents P2 (ADT 43), P3 (ADT 45), P4 (ASD 16), P5 (CO51) and P6 (CO47) had most dominant gene and the parent P1 (ADT 37) had most recessive gene for seed breadth. Such a similar trend was also observed by seed L/B ratio. The parents P1 (ADT 37), P4 (ASD 16) and P5 (CO51) had most dominant genes and the parent P3 (ADT 45) had most recessive genes. The other parents P2 (ADT 43) and P6 (CO47) were intermittent for hundred seed weight. The parents P2 (ADT 43), P4 (ASD 16) and P6 (CO47) had most dominant genes and the parent P5 (CO51) had most recessive genes. The parent P1 (ADT 37) and P3 (ADT 45) were intermittent for seed yield per plant (**Fig. 1b to 10b**).

The parents P2 (ADT 43), P3 (ADT 45) and P4 (ASD 16) had genes with recessive positive effects. None of the parents had genes with dominant positive effects for days to 50 per cent flowering. The parent P4 (ASD 16) had genes with dominant positive effects for plant height at maturity. The parent P5 (CO51) had genes with positive dominant effects for the number of productive tillers per plant. The parents P1 (ADT 37) and P4 (ASD 16) had genes with positive dominant effects for panicle length. None of the parents had genes with positive dominant effects for the number of filled seeds per panicle. The parents P1 (ADT 37) and P5 (CO51) had positive recessive effects for the number of filled seeds per panicle. The parents P2 (ADT 43), P3 (ADT 45), P4 (ASD 16), P5 (CO51) and P6 (CO47) had genes with positive dominant effects for seed length. For seed breadth, the parents P2 (ADT 43), P4 (ASD 16) and P6 (CO47) had genes with positive dominants. For seed L/B ratio the parents P2 (ADT 43), P3 (ADT 45) and P4 (ASD 16) had genes with positive dominant effects. The parent P5 (CO51) had genes with positive dominant effects for hundred seed weight. None of the parents had genes with positive dominant effects for seed yield per plant. The parents P1 (ADT 37) and P5 (CO51) had genes with recessive positive effects. These aforementioned parents may be crossed among themselves to evolve high heterotic line and / or improved population (**Fig. 1c to 10c**).



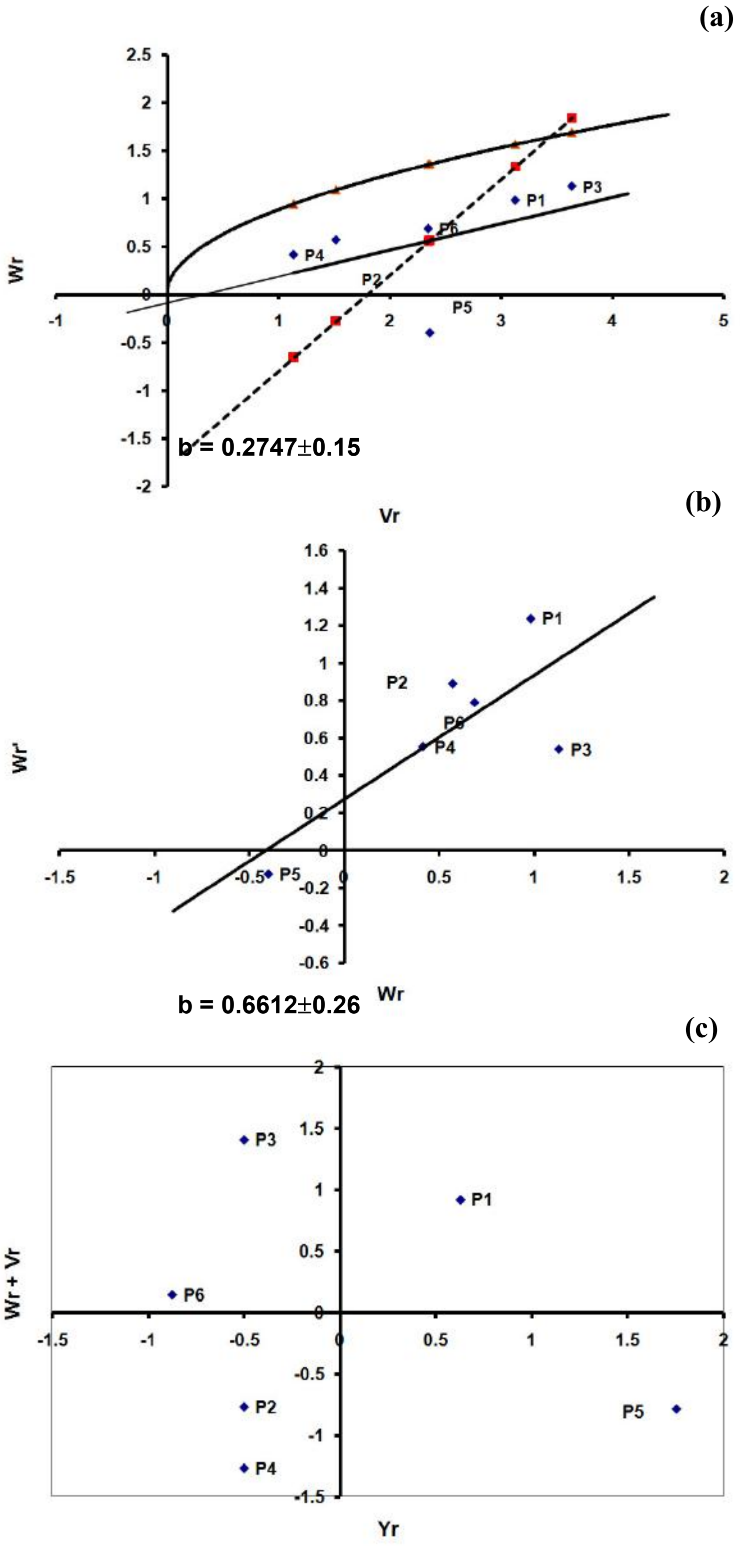
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 1. (a) Vr-Wr, (b) WrWr′and (c) Yr-Wr+Vr graphs for days to 50 per cent flowering



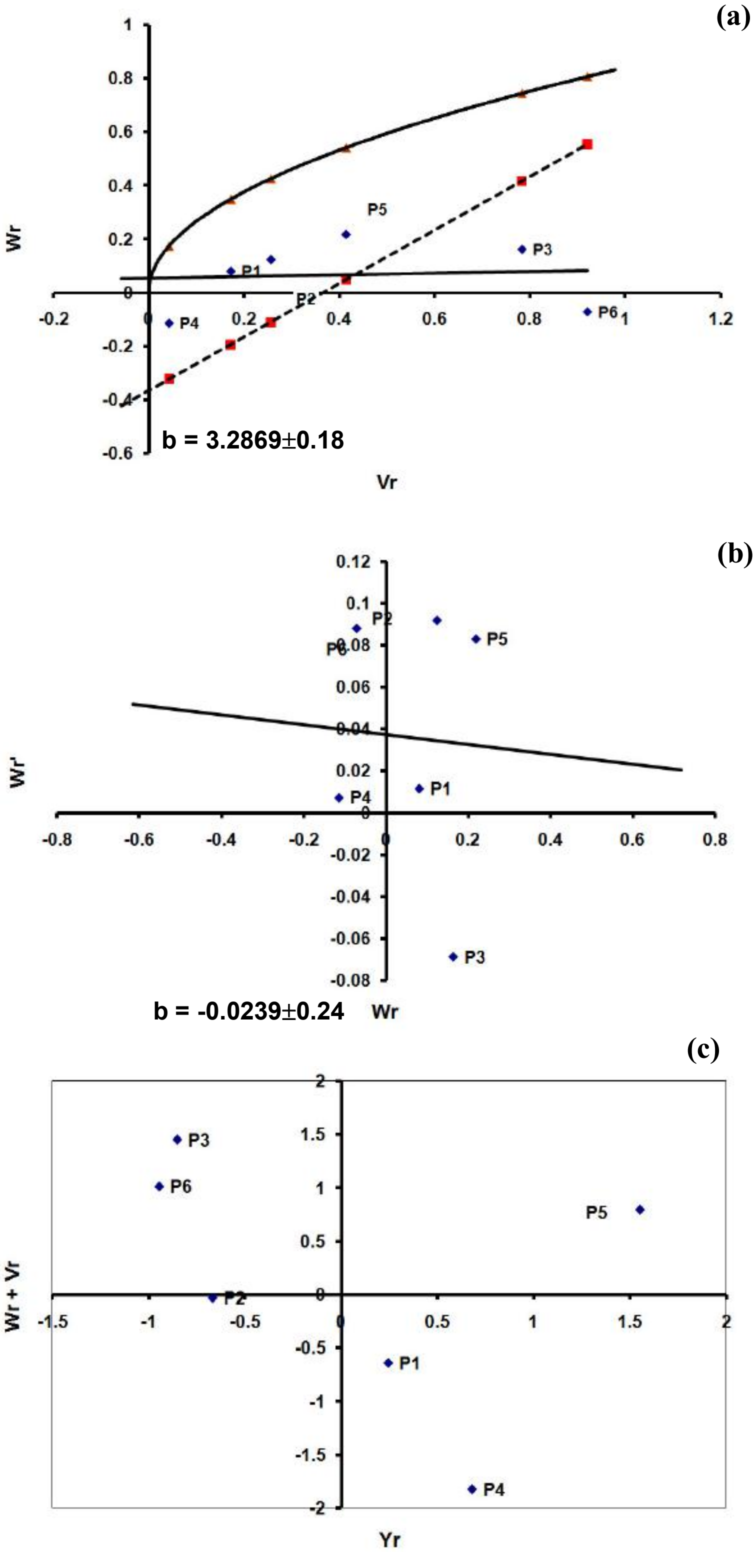
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 2. (a) Vr-Wr, (b) WrWr´ and (c) Yr-Wr+Vr graphs for plant height at maturity



P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 3. (a) Vr-Wr, (b) WrWr` and (c) Yr-Wr+Vr graphs for number of productive tillers per plant



P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 4. (a) Vr-Wr, (b) WrWr´and (c) Yr-Wr+Vr graphs for panicle length

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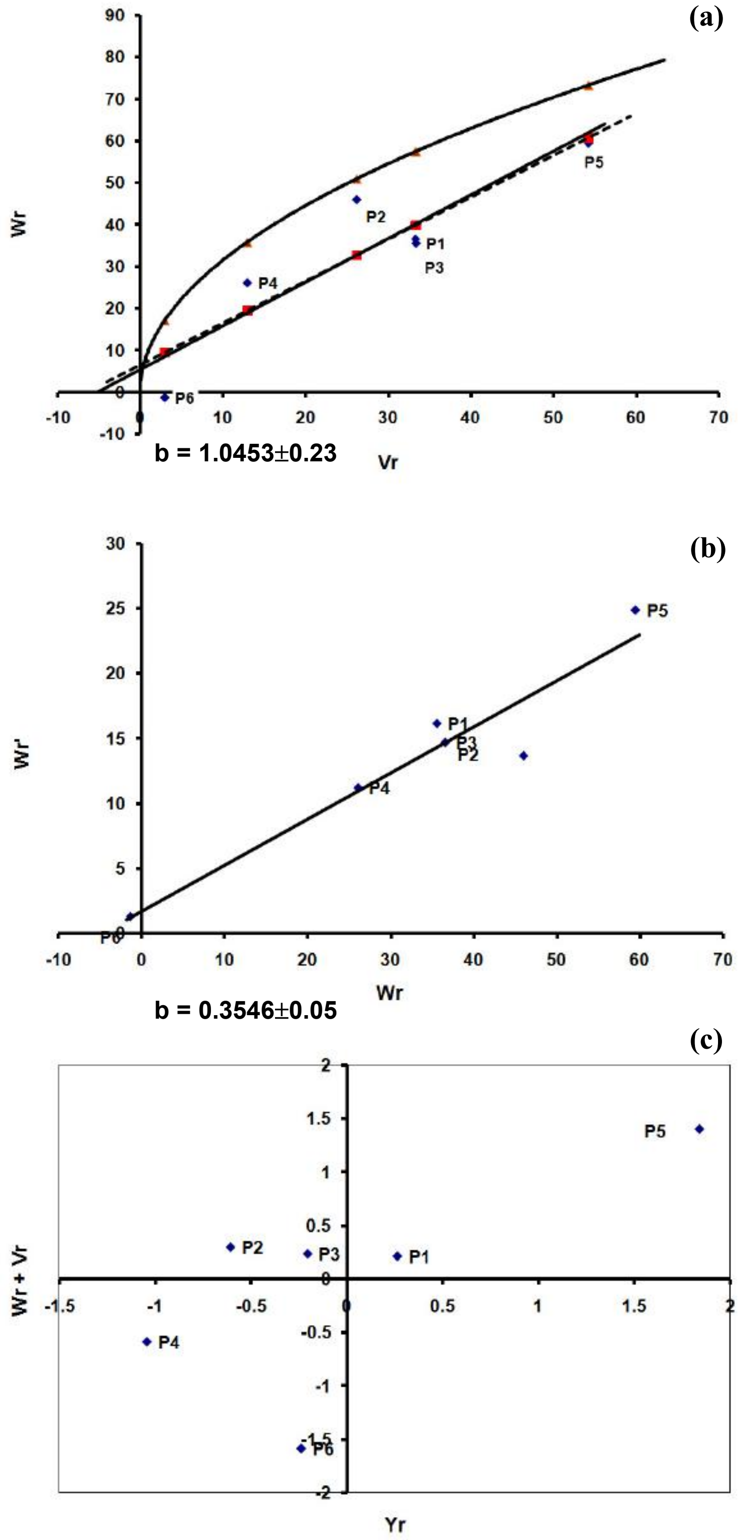
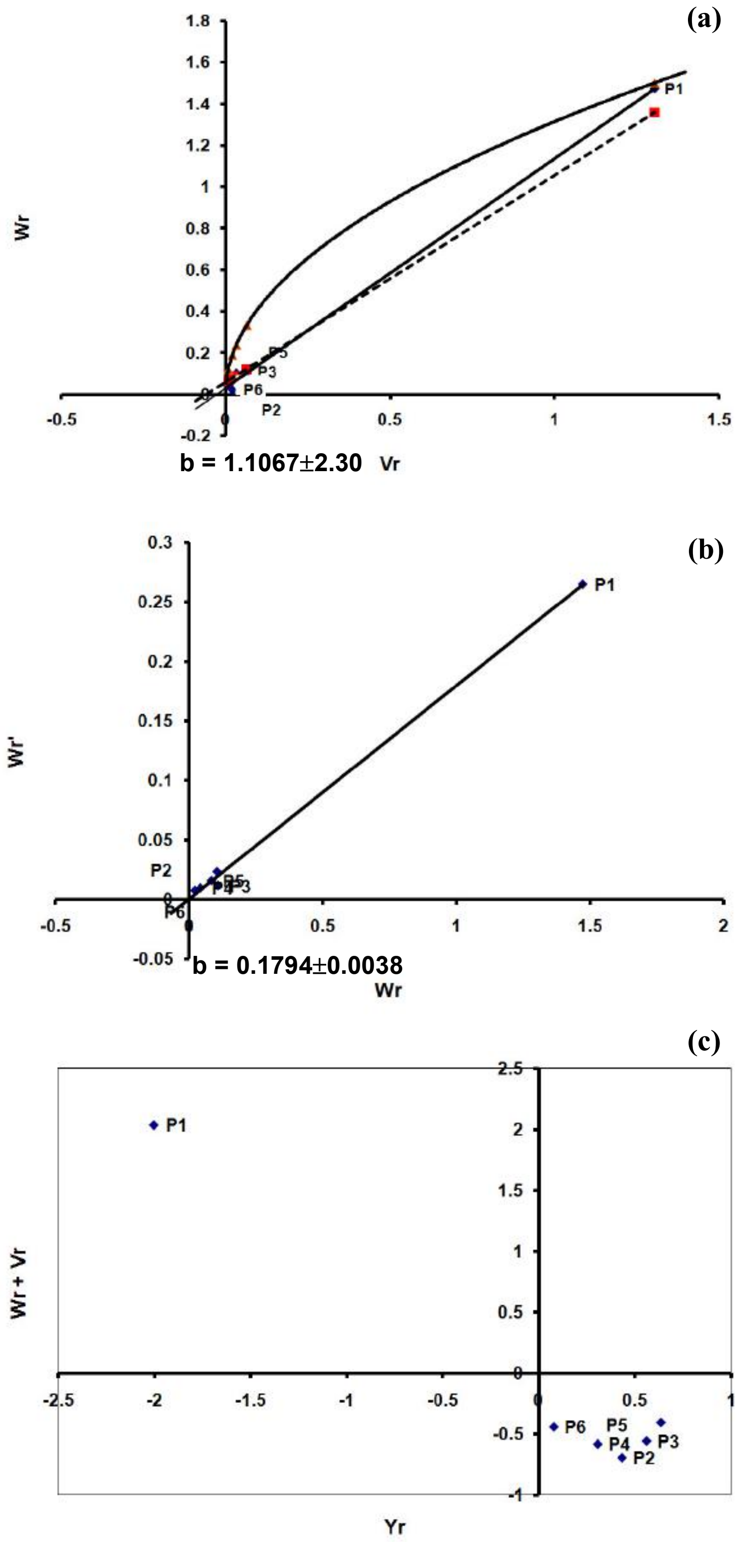


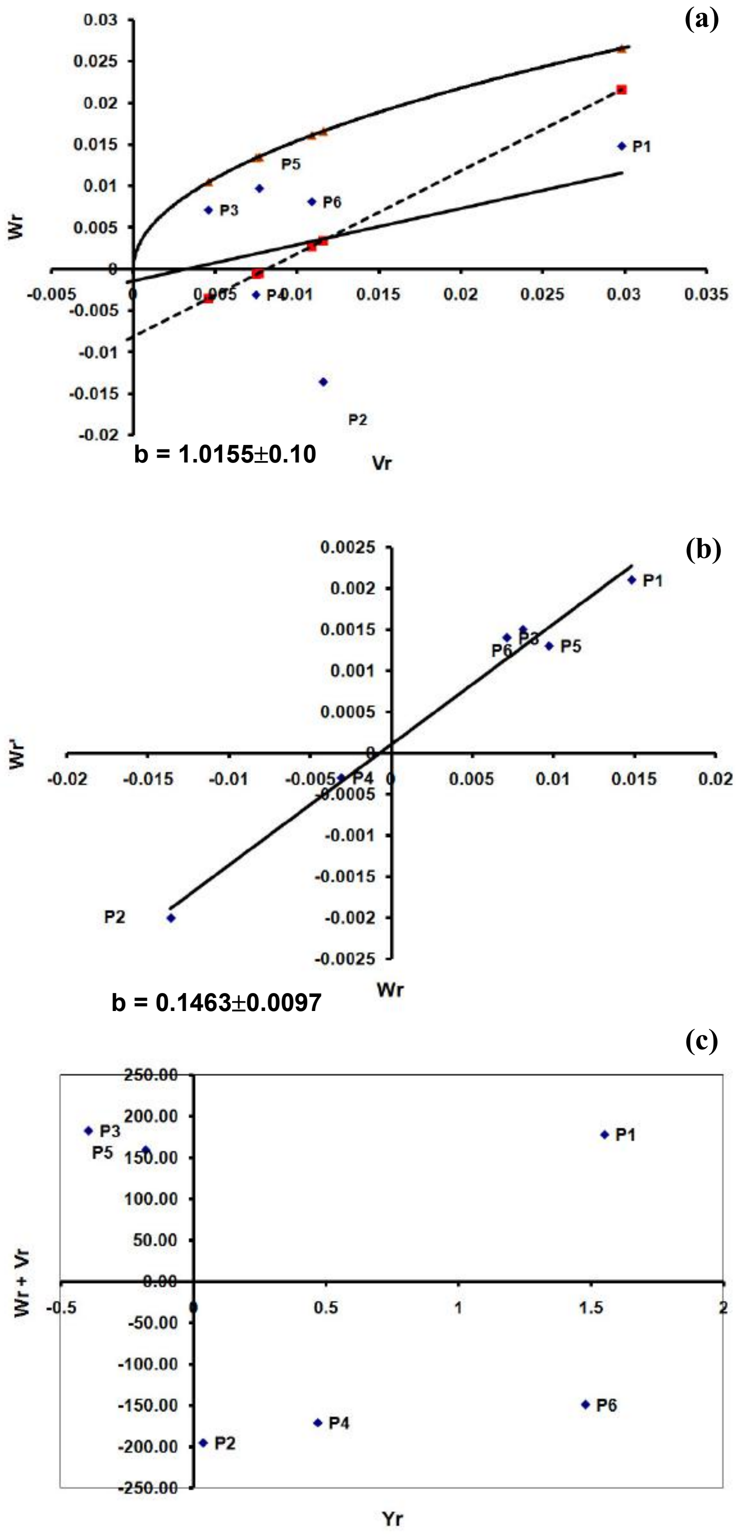
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 5. (a) Vr-Wr, (b) WrWr´ and (c) Yr-Wr+Vr graphs for number of filled seeds per panicle



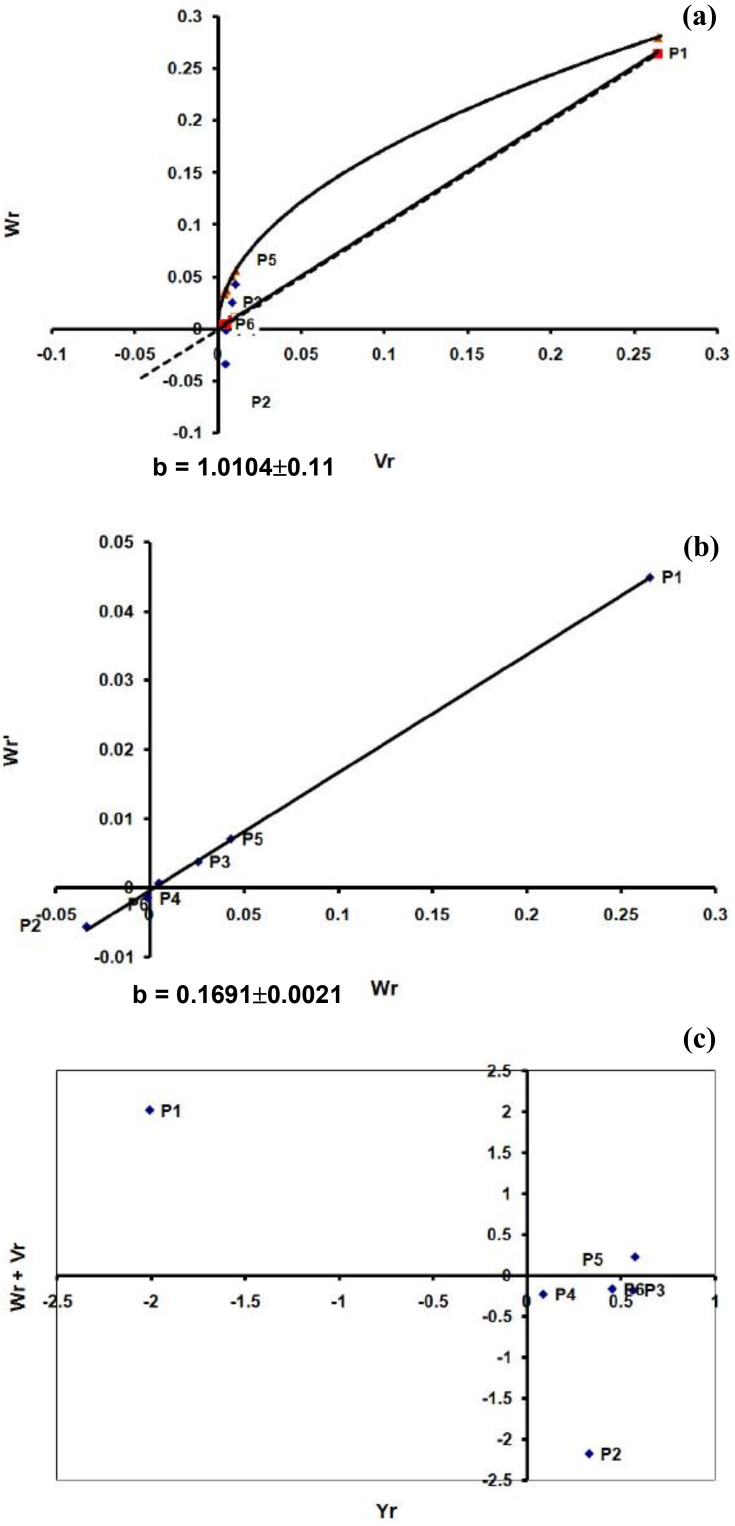
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 6. (a) Vr-Wr, (b) WrWr´ and (c) Yr-Wr+Vr graphs for seed length



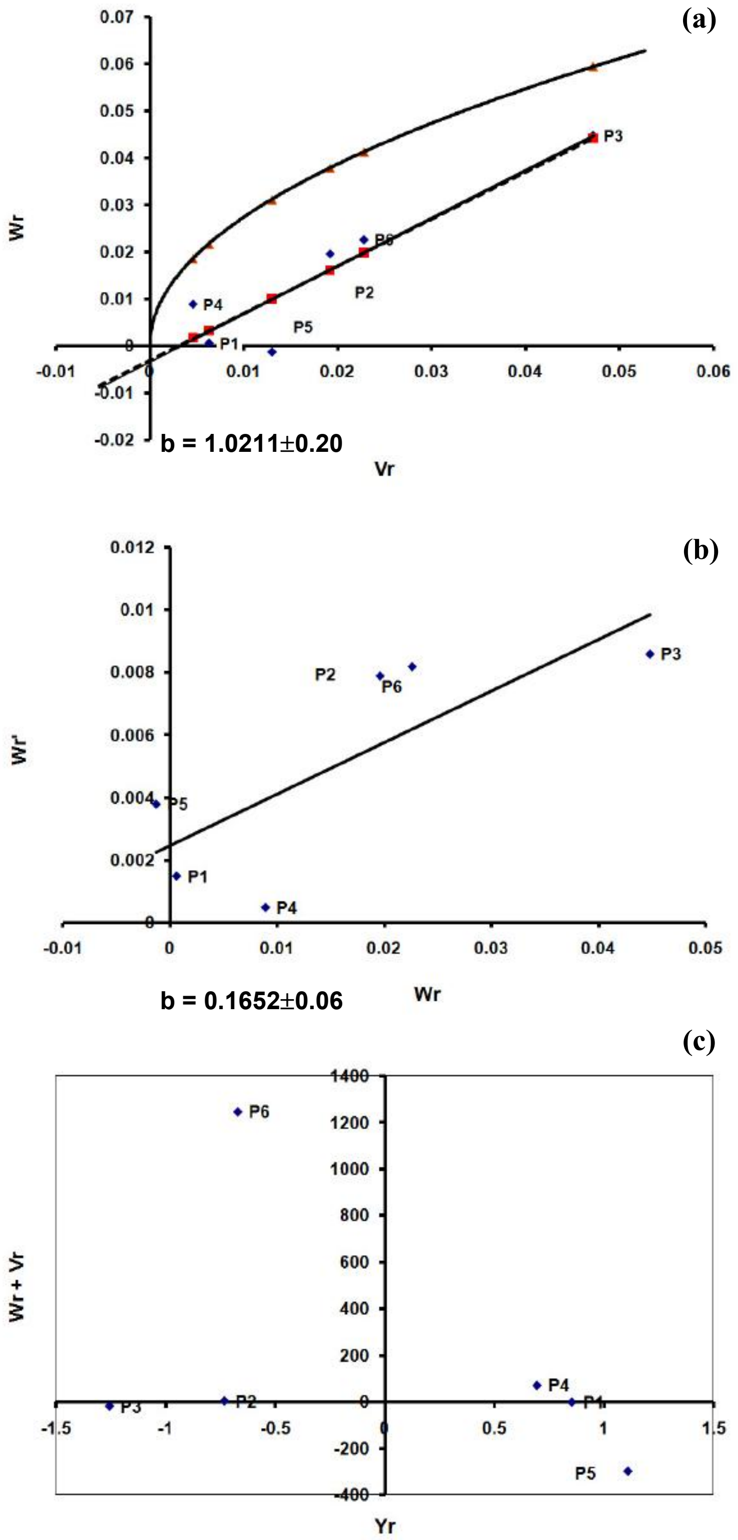
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 7. (a) Vr-Wr, (b) WrWr´and (c) Yr-Wr+Vr graphs for seed breadth



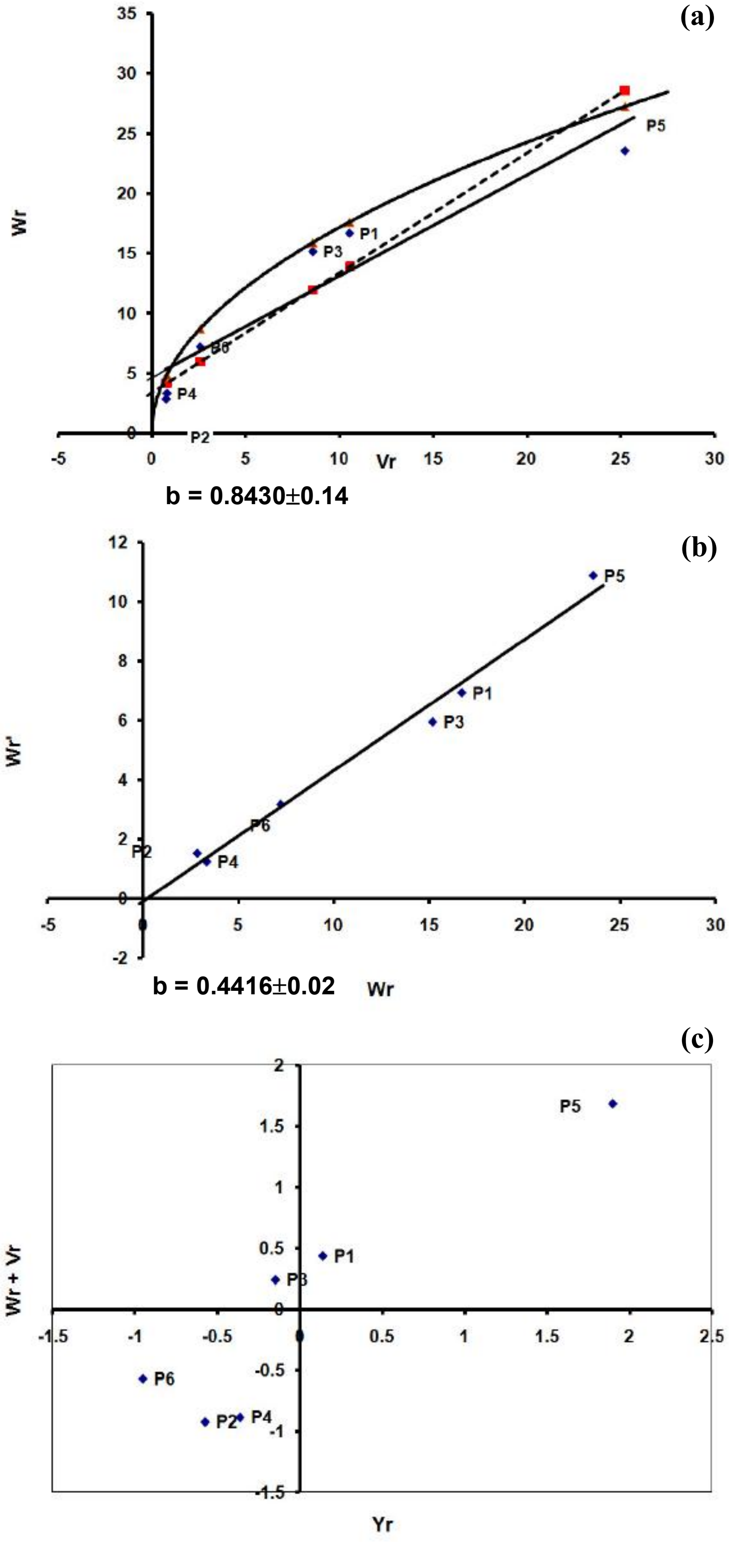
P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 8. (a) Vr-Wr, (b) WrWr´and (c) Yr-Wr+Vr graphs for seed L/B ratio



P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 9. (a) Vr-Wr, (b) WrWr´ and (c) Yr-Wr+Vr graphs for hundred seed weight



P1-ADT 37, P2-ADT 43, P3-ADT 45, P4-ASD 16, P5-CO51, P6-CO47

Fig. 10. (a) Vr-Wr, (b) WrWr´and (c) Yr-Wr+Vr graphs for seed yield per plant

The parents *viz.,* (P5) (CO51) and (P3) (ADT 45) have been identified as potential parents based on *per se* performance, *gca* effects coupled with a high standard heterosis (Satheeshkumar *et al.,* 2021). None-of these parents had dominant genes with positive effects for seed yield per plant. However, the parent *viz.,* (P5) (CO51) possessed dominant genes for the traits *viz.,* the number of productive tillers per plant, seed length and hundred seed weight and the parent (P3) (ADT 45) had dominant genes with positive effect for seed L/B ratio. They may be intercrossed to evolve superior lines with acceptable seed quality.

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