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Research Article

Study of genetic architecture through haymen's graphical approach for quantitative and qualitative traits in quality protein maize (*Zea mays* L.) over environments

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Abstract
Kernel yield is a very complex trait in maize which results from the interaction of various yield contributing characters and it is highly influenced by environmental variation. Therefore, phenotypic selection cannot directly improve the characters in highly cross pollinated crops like maize unless dissected by genetic analysis. The present investigation was carried out for gene action of various quantitative and qualitative traits in a complete set of 10x10half diallel mating designed involving ten elite inbred lines. The results of Variance/Co-variance graphs revealed that preponderance of over dominance type of gene action for days to 50 % tasselling, days to 50 % silking, ear height, kernel rows per ear, 100 kernel weight, kernel yield per plant, shelling percentage and lysine content. Distribution of array points depicted that parents GWQPM 55-2 had the maximum dominant genes while GWQPM 46-2 and GWQPM 26-3 possessed maximum recessive genes for most of the character.

Key Word
Over dominance, Gene action, haymen's graphical approach, *Zea mays* L.

Introduction

Maize (*Zea mays* L.; 2n=20) being nutritionally an important crop has multiple functions in the traditional farming system, being used as food and fuel for human being and feed for livestock and poultry. In the world, maize ranked third amongst the food crops, next to rice and wheat. There is no cereal on the earth, which has diversified use as maize and therefore, it occupies the unique place as "Queen of Cereals". Being a C_4 plant, it is physiologically more efficient and resilient to climate change. It has wider genetic variability and able to grow successfully throughout the world over a wide range of environmental conditions covering tropical, subtropical and temperate agro-climatic regions. Development and adaptation of quality protein maize would increase the nutritional quality of food and feed as well. Quality protein maize (QPM) contains high quality amino acids lysine and tryptophan, which are two times higher in QPM than normal maize because QPM contains opaque-2, a single gene mutation that alter the protein composition of the endosperm protein and nearly double the essential amino acid (Akande and Lamidi, 2006).

Among various designs diallel mating design gives better control over the experimental material and thereby provides more precise information on various parameters obtained from this design. It also helps to understand the genetic architecture of various characters that enable the breeder to design effective breeding plan for the improvement of the existing breeding materials.

Material and Methods

Research was carried out at Agricultural Research Station, Anand Agricultural University, Nenpur-Snasoli, Ta: Mahemdavad, Dist. Kheda (Gujarat) during 2011 to 2014.Ten diverse inbred lines of QPM provided by Main Maize Research station, Godhra (Gujarat), *viz.*, GWQPM 6-3, GWQPM 5-1, GWQPM 55-2, GWQPM 47-4, GWQPM 46-2, GWQPM 40-3, GWQPM 26-3, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 were utilised to produce 45 F_1 hybrids using half diallel crossing system during *kharif* and *Rabi* 2011-12. The 45 hybrids along with their parents and checks (HQPM 1 and DHM 117) were evaluated in randomized block design with three replication in four different environments *viz*., E_1: *Kharif* (1st fortnight of July, 2012), E_2: Semi *rabi* (2nd fort

night of October, 2012), E_3: *Rabi* (1st fort night of December, 2012) and E_4: Summer (2nd fort night of January, 2013). Each entry was consisted of a single row of 5.0 m length with distance of 60 cm between rows and 30 cm between plants within row. The data were recorded for Days to 50 % tasselling, Days to 50 % silking, Plant height(cm), Ear height(cm), Days to 75 % maturity, Ears per plant, Ear length(cm), Ear girth(cm), Kernel rows per ear, Kernels per row, 100 kernel weight(g), Kernel yield per plant(g), Shelling percentage, Oil content(%), Protein content(%), Tryptophan content(%) and Lysine content(%). The data obtained were analyzed for graphical analysis as per method proposed by Haymen(1954).

Results and Discussion

The analysis of variance was carried out for different characters for four environments and pooled environments (Table:1).The results revealed that mean square values due to genotypes were significant for all the characters in each individual environment and pooled environments except for 100 kernel weight in E_2, indicating the presence of sufficient amount of genetic variability in the material studied under individual environments. Mean square values of environment were highly significant for all the characters which indicates environment play major role in expression of the quantitative and qualitative characters of maize.

Additive-dominance model was satisfactory as indicated by non significant deviation of b (Wr, Vr) from unity, but significant deviation from zero (Hayman, 1954) suggesting the absence of epistatic gene effect. The material under investigation was tested for agreement with the assumptions basic to diallel analysis. Deviation of regression coefficient 'b' from zero and unity were analysed by 't' test and employed to diallel analysis for each of the characters studied (Table: 2). The regression value '' b'' was significant from zero and non significant at unity for days to 50 % tasseling (E_1), days to 50 % silking (E_1), ear height (E_2), kernel rows per ear (E_1 and E_4), 100 kernel weight (E_2,E_3 and E_4), kernel yield per plant (E_3), shelling percentage (E_2) and lysine content (E_4)which revealed the absence of digenic interactions for these characters in respective environment. Rest of the characters had non-random distribution of genes at different loci among the parents and/ or presence of interaction between the genes at different loci; hence, those have been excluded from graphical analysis approach.

The data on days to 50 % tasselling were fitted to the additive-dominance model in E_1 (Table 2). The Vr, Wr graph (Fig.1) indicated over-dominance as the regression line intercepted Wr-axis below the point of origin. The array points indicated that GWQPM 55-2 and GWQPM 40-3 were situated nearer to the point of origin and thus possessed most of the dominant alleles. Whereas, parental array of GWQPM 46-2, GWQPM 26-3, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 lay away from point of origin indicating that it possessed most of the recessive alleles. Array points of other three parents *viz.*, GWQPM 6-3, GWQPM 5-1 and GWQPM 47-4 were situated in the middle of regression line, hence they had equal frequency of dominant and recessive alleles. The additive-dominance model fitted well to the data for days to 50 % silking in E_1(Table 2). The regression line which intercepted the Wr-axis below the point of origin (Fig.2) also revealed over dominance for days to 50 % silking. In the Vr, Wr graph, parental array of GWQPM 5-1, GWQPM 55-2 and GWQPM 40-3 located nearer to the point of origin which showed presence of higher frequency of dominant alleles. Whereas, GWQPM 46-2, GWQPM 26-3, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 fell far away from the point of origin which indicated the presence of higher proportion of the recessive alleles for this trait. The array point of GWQPM 6-3 and GWQPM 47-4 were situated in the middle along the regression line, hence they had equal frequencies of dominant and recessive alleles. The results of over dominance in flowering traits were similar to the results reported by Saleem *et al.*(2002), Kumar *et al.* (2005) and Wattoo *et al.* (2009), Nagar *et al.*(2016), Lay and Razdan (2017).

The data on ear height was fitted to the additive-dominance model in E_2 (Table 2). The Vr, Wr graph (Fig.3) suggested over dominance as the regression line intercepted Wr-axis below the point of origin. Parents GWQPM 6-3, GWQPM 5-1, GWQPM 55-2, GWQPM 47-4, GWQPM 40-3, GWQPM 26-3, GWQPM 22-5 and GWQPM 17-1 whose array points were situated in the middle along the regression line, hence they had equal proportion of dominant and recessive alleles. The array point of GWQPM 46-2 was situated nearer to the point of origin and thus possessed dominant allele, while the parent GWQPM 11 was farthest from the origin indicating that they possessed the recessive alleles. Miranda *et al.* (2008), Soni and Khanorkar (2014) and Nagar *et al.*(2016) obtained the same results for ear height.

For kernel rows per ear, the data were well fitted to the additive-dominance model in E_1 as well as E_4 (Table 2). The graphical presentation (Fig.4 and Fig.5) indicated that regression line intercepted Wr-axis below the point of origin suggesting over dominance. In E_1, the array points of parents GWQPM 6-3, GWQPM 40-3 and GWQPM 26-3 were situated nearer to the point of origin

suggesting that it carries more number of dominant alleles. The parents GWQPM 5-1, GWQPM 47-4, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 located in the middle of the regression line suggesting that they had equal frequencies of dominant and recessive alleles. Whereas, parents GWQPM 55-2 and GWQPM 46-2 lying farthest from the origin, indicating the higher proportion of recessive alleles. The four parents in E_4 were located nearer to the point of origin *viz.*, GWQPM 6-3, GWQPM 5-1, GWQPM 26-3 and GWQPM 22-5 which indicated that it possessed more number of dominant alleles. The parents GWQPM 46-2 and GWQPM 17-1 fell far away from the point of origin suggesting that presence of recessive alleles for this trait. Parents GWQPM 55-2, GWQPM 47-4, GWQPM 40-3 and GWQPM 11 were lying in the middle along the regression line indicating that they possessed intermediate frequency of dominant and recessive alleles .he regression co-efficient of Wr on Vr indicated adequacy of additive-dominance model in E_2, E_3 and E_4 for 100 kernel weight (Table 2). From the variance-covariance graph (Fig.6, Fig.7 and Fig.8) it was obvious that the parents had greater diversity for this trait. The regression line which intercepted the Wr-axis below the point of origin indicated over dominance in all the three environments. In E_2, maximum dominant alleles were observed in the parents GWQPM 55-2, GWQPM 47-4, GWQPM 46-2 and GWQPM 22-5. The parents, GWQPM 26-3 and GWQPM 11 exhibited farthest array points from the origin, suggesting the presence of the recessive alleles. The parents, GWQPM 6-3, GWQPM 5-1, GWQPM 40-3 and GWQPM 17-1 present in the middle along the regression line which suggested intermediate frequency of dominant and recessive alleles for this trait. In E_3,the parent, GWQPM 55-2 occupied a position nearer to the point of origin suggesting that they had higher proportion of dominant genes. Parental array of GWQPM 5-1, GWQPM 47-4, GWQPM 46-2, GWQPM 40-3, GWQPM 22-5 and GWQPM 17-1 located in the middle along the regression line, thus they had equal frequency of dominant and recessive alleles. However, the parents GWQPM 6-3, GWQPM 26-3 and GWQPM 11 situated far away from the point of origin, hence possessed higher proportion of recessive genes. The equal frequency of dominant and recessive alleles in E_4 was occupied by the parents GWQPM 5-1, GWQPM 47-4, GWQPM 46-2, GWQPM 40-3 and GWQPM 17-1. The parents GWQPM 55-2 and GWQPM 22-5 were located nearer to the point of origin suggesting that they had higher proportion of dominant genes. On the other hand, the array point of GWQPM 6-3, GWQPM 26-3 and GWQPM 11 were far away from the point of origin indicating a higher proportion of recessive alleles. The results of over dominance for both these kernel traits were same as by Saleem *et al.* (2002), Wattoo *et al.* (2009) and Lay and Razdan (2017) while Ali *et al.*(2007) reported additive genetic variance for kernel traits.

The data on kernel yield per plant was well fitted to the additive-dominance model in E_3 (Table 2).The regression line which intercepted the Wr-axis below the point of origin (Fig.9) revealed over dominance. The array point indicated that the parent GWQPM 55-2 was situated nearest to the point of origin and thus possessed most of the dominant alleles. Whereas, GWQPM 6-3 and GWQPM 26-3 lying far away from the point of origin, indicating that they possessed most of the recessive alleles. The parental points of GWQPM 5-1, GWQPM 47-4, GWQPM 46-2, GWQPM 40-3, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 located in middle along the regression line, hence it had equal frequencies of dominant and recessive alleles. The additive-dominance model was found adequate for shelling percentage in E_2(Table 2). The Vr, Wr graph (Fig.10) suggested over-dominance as the regression line intercepted Wr-axis below the point of origin. The array points indicated that GWQPM 47-4 and GWQPM 22-5 were situated nearer to the point of origin and thus possessed more number of the dominant alleles. The parents, GWQPM 46-2, GWQPM 40-3 and GWQPM 11 remain far away from the point of origin, hence possessed most of the recessive alleles. The equal frequency of dominant and recessive alleles occupied by the parents GWQPM 6-3, GWQPM 5-1, GWQPM 55-2, GWQPM 26-3 and GWQPM 17-1 for this trait. For kernel yield per plant, Muhammad *et al.* (2009), Zare *et al.* (2011) and Lay and Razdan (2017) reported similar result as discussed earlier.

The results of lysine content were fitted to the additive-dominance model in E_4 (Table 2). The Vr, Wr graph (Fig.11) suggested over dominance as the regression line intercepted Wr-axis below the point of origin. Parents GWQPM 6-3, GWQPM 5-1, GWQPM 55-2, GWQPM 47-4, GWQPM 40-3, GWQPM 22-5 and GWQPM 17-1 whose array points were situated nearer to the point of origin, hence possessed most of the dominant alleles. The array points of GWQPM 26-3 and GWQPM 11 were situated in the middle along the regression line, hence they had equal proportion of dominant and recessive alleles, while the parent GWQPM 46-2 was found farthest from the origin indicating that they possessed recessive alleles. For lysine content, no such related study was reviewed having over dominance genetic variance.

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Table 1.Pooled analysis of variance for different traits in maize.

Source of variation	Df	Mean sum of square						
		Days to 50 % tasselling	Days to 50% silking	Plant height	Ear height	Days to 75 % maturity	Ears per plant	Ear length
Environments	3	19906.00**	20650.18**	243182.75**	29781.44**	19777.30**	0.14**	255.27**
Replications	2	-	-	-	-	-	-	-
Genotypes	56	24.23**	24.54**	1724.68**	232.89**	14.02**	0.06**	14.10**
Error	448	1.40	1.63	60.22	21.47	3.60	0.004	0.54

*, ** Significant at 0.05 and 0.01 levels of probability,

Table 1. Cont.....

Source of variation	df	Mean sum of square									
		Ear girth	Kernel rows per ear	Kernels per row	100 kernel weight	Kernel yield per plant	Shelling %	Oil	Protein	Tryptophan	Lysine
Environments	3	314.02**	37.34**	3540.81**	150.75**	63092.74**	192.09**	0.56**	48.11**	0.06**	0.66**
Replications	2	-	-	-	-	-	-	-	-	-	-
Genotypes	56	2.30**	2.81**	15.96**	25.79**	2617.23**	31.32**	0.94**	1.50**	0.02**	0.25**
Error	448	0.32	0.28	1.48	0.77	64.69	3.32	0.003	0.06	0.0002	0.002

*, ** Significant at 0.05 and 0.01 levels of probability,

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Table 2. Regression coefficient of Wr on Vr with their standard errors and deviation from zero and unity for various characters in maize

Characters	E_1				E_2			
	b	SE (b) ±	(b - 0)/SE	(b-1)/SE	b	SE (b) ±	(b - 0)/SE	(b-1)/SE
Days to 50 % tasselling	0.56	0.21	2.64*	-2.08	0.33	0.34	0.98	-1.98
Days to 50 % silking	0.70	0.22	3.23*	-1.39	0.29	0.29	1.00	-2.50
Plant height	0.42	0.29	1.43	-1.97	0.20	0.32	0.63	-2.48
Ear height	-0.03	0.34	-0.09	-3.07	0.66	0.26	2.50*	-1.28
Days to 75 % maturity	-0.24	0.38	-0.64	-3.28	0.68	0.36	1.91	-0.90
Ears per plant	0.07	0.15	0.44	-6.22	0.06	0.10	0.57	-9.43
Ear length	0.24	0.14	1.75	-5.58	0.35	0.23	1.57	-2.88
Ear girth	-0.15	0.13	-1.14	-8.95	0.27	0.24	1.13	-3.09
Kernel rows per ear	0.70	0.26	2.71*	-1.16	0.02	0.28	0.07	-3.44
Kernels per row	0.56	0.39	1.41	-1.13	0.47	0.28	1.69	-1.87
100 kernel weight	0.26	0.14	1.80	-5.25	0.44	0.11	4.16**	-5.34
Kernel yield per plant	0.28	0.15	1.90	-4.98	0.28	0.27	1.04	-2.64
Shelling percentage	0.11	0.27	0.43	-3.30	0.75	0.22	3.34*	-1.12
Oil content	0.04	0.21	0.17	-4.53	-0.16	0.32	-0.50	-3.64
Protein content	0.16	0.17	0.92	-4.91	-0.18	0.21	-0.85	-5.73
Tryptophan content	0.57	0.26	2.19	-1.63	-0.19	0.26	-0.73	-4.55
Lysine content	-0.25	0.22	-1.15	-5.78	0.44	0.33	1.36	-1.71

Table 2. Cont....

Characters	E_3				E_4			
	b	SE (b) ±	(b - 0)/SE	(b-1)/SE	b	SE (b) ±	(b - 0)/SE	(b-1)/SE
Days to 50 % tasselling	0.32	0.31	1.04	-2.21	0.38	0.30	1.26	-2.10
Days to 50 % silking	0.33	0.26	1.25	-2.57	0.30	0.25	1.20	-2.75
Plant height	0.29	0.16	1.78	-4.44	0.28	0.15	1.87	-4.86
Ear height	0.08	0.25	0.32	-3.73	0.06	0.09	0.69	-10.65
Days to 75 % maturity	0.40	0.75	0.53	-0.80	-0.23	0.29	-0.77	-4.16
Ears per plant	0.18	0.27	0.66	-3.05	0.08	0.13	0.64	-6.90
Ear length	0.003	0.10	0.03	-10.26	0.19	0.14	1.35	-5.58
Ear girth	0.65	0.33	1.94	-1.06	0.26	0.14	1.78	-5.15
Kernel rows per ear	-0.04	0.08	-0.48	-12.99	0.48	0.16	2.93*	-3.14
Kernels per row	-0.01	0.17	-0.05	-5.96	0.30	0.16	1.89	-4.33
100 kernel weight	0.20	0.05	3.99**	-16.01	0.31	0.12	2.62*	-5.85
Kernel yield per plant	0.11	0.04	2.81*	-22.31	0.29	0.17	1.70	-4.12
Shelling percentage	-0.11	0.12	-0.91	-9.11	0.16	0.34	0.46	-2.51
Oil content	-0.22	0.22	-1.01	-5.62	-0.36	0.24	-1.49	-5.58
Protein content	0.25	0.17	1.48	-4.54	-0.17	0.12	-1.43	-9.97
Tryptophan content	0.01	0.31	0.05	-3.19	0.68	0.63	1.08	-0.51
Lysine content	0.25	0.28	0.92	-2.70	0.78	0.21	3.80**	-1.04

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Fig 1. Vr, Wr graph for days to 50 % tasselling in E1

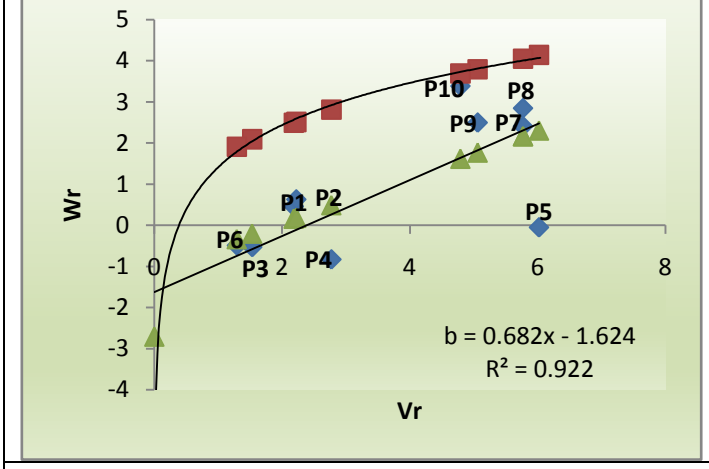


Fig 2. Vr, Wr graph for days to 50 % silking in E1

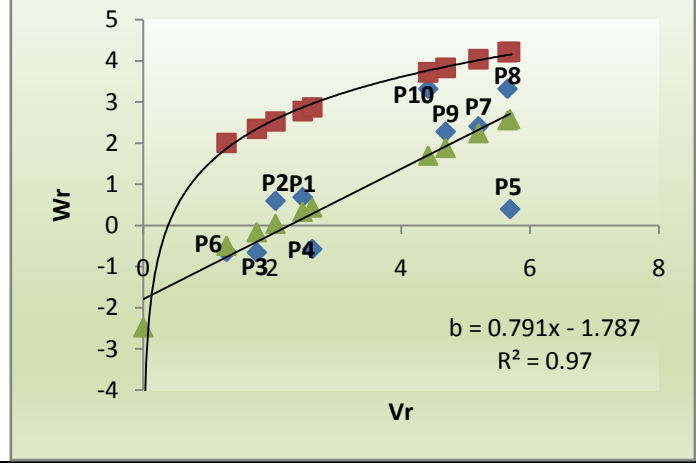


Fig 3. Vr, Wr graph for Ear height in E2

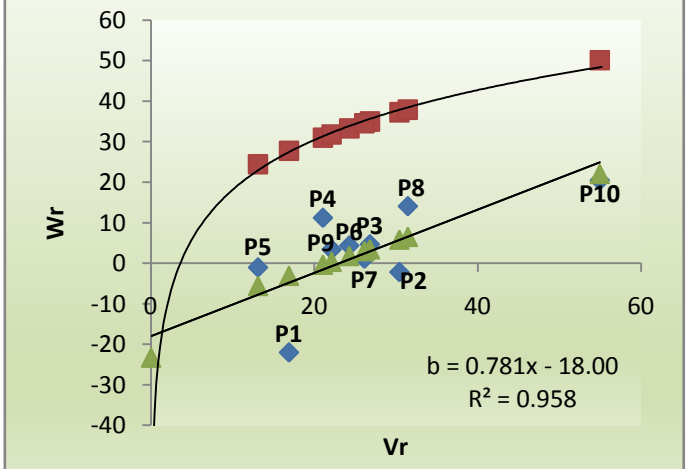


Fig 4. Vr, Wr graph for kernel rows per ear in E1

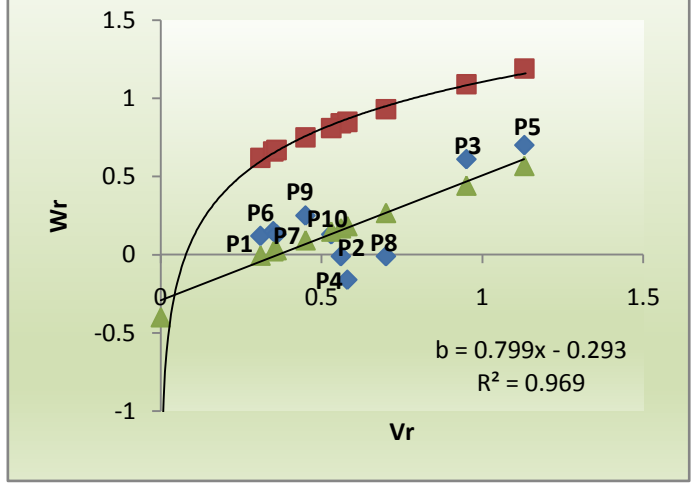


Fig 5. Vr, Wr graph for kernel rows per ear in E4

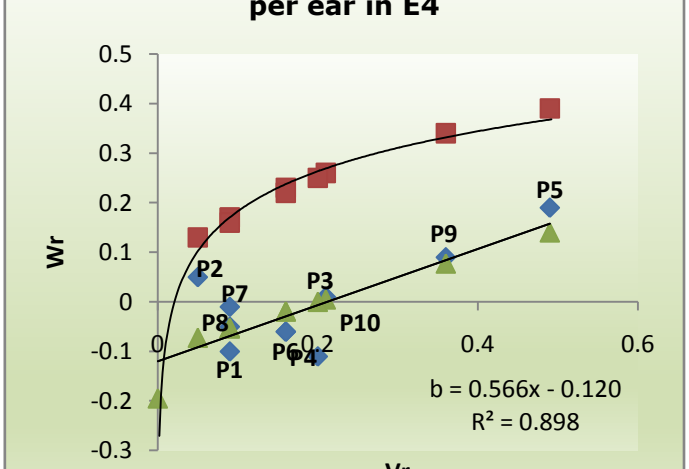


Fig 6. Vr, Wr graph for 100 kernel weight in E2

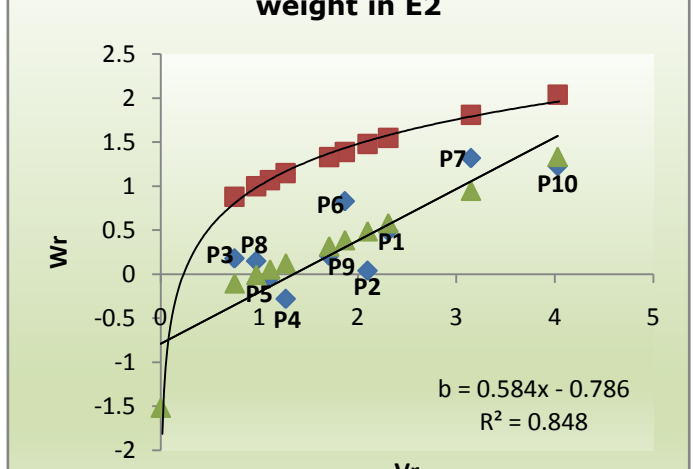


Fig 7. Vr, Wr graph for 100 kernel weight in E3

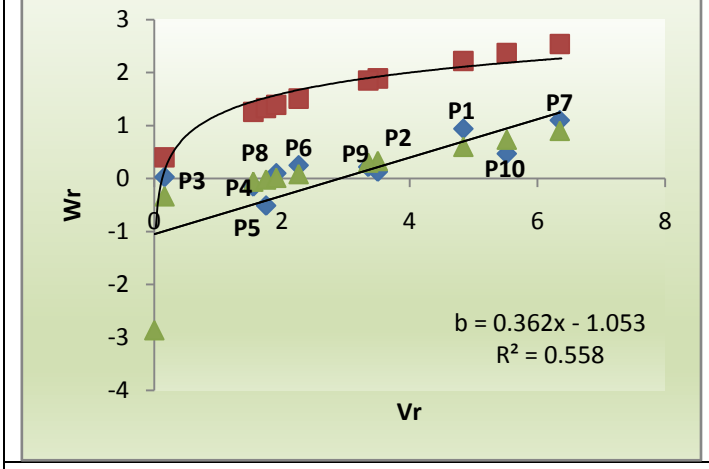


Fig 8. Vr, Wr graph for 100 kernel weight in E4

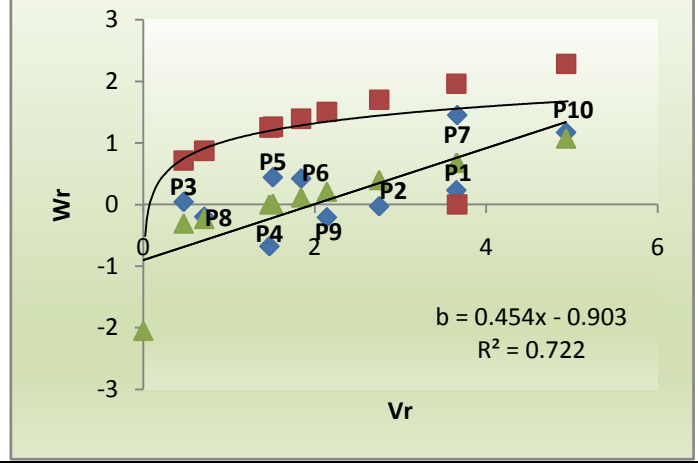


Fig 9. Vr, Wr graph for kernel yield per plant in E3

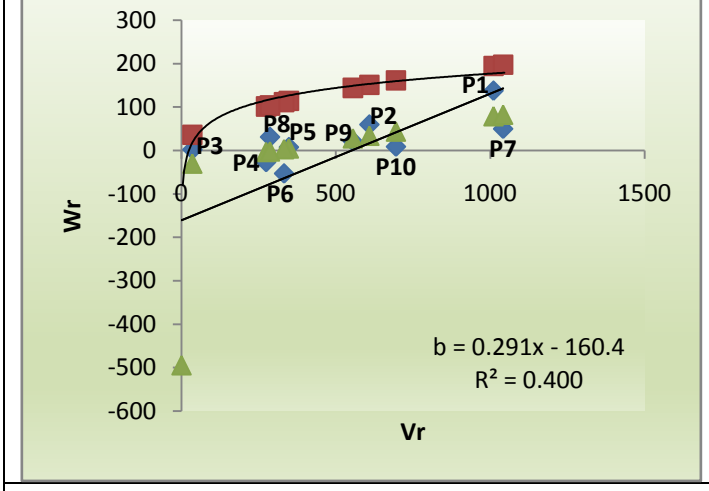


Fig 10. Vr, Wr graph for Shelling percentage in E2

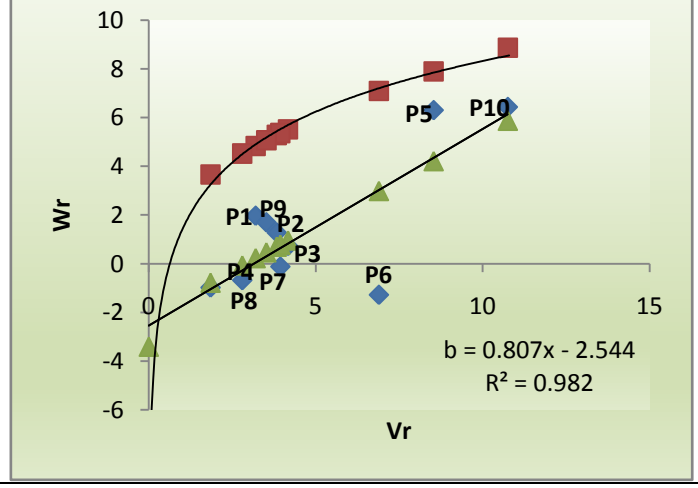
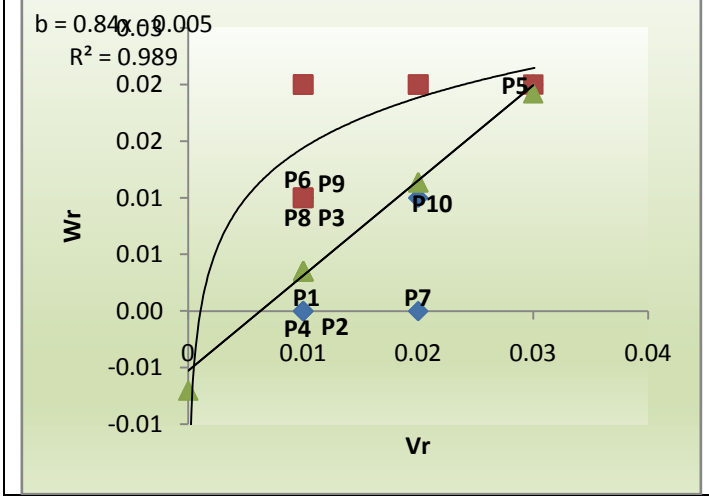


Fig 11. Vr, Wr graph for lysine content in E4



P1: GWQPM 6-3
P2: GWQPM 5-1
P3: GWQPM 55-2
P4: GWQPM 47-4
P5: GWQPM 46-2
P6: GWQPM 40-3
P7: GWQPM 26-3
P8: GWQPM 22-5
P9: GWQPM 17-1
P10: GWQPM 11
BLUE = Wr
RED = Regression &Vr
GREEN = Parabola &Vr