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Hyman's diallel analysis to study genetic parameters of phenological traits in common bean (Phaseolus vulgaris)

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Citation

Abstract

An experiment was executed to study the genetic parameters underlying the inheritance of phenological traits of common bean: number of days to flowering and maturity. The experiment comprised of 36 genotypes (8 parents and 28 forward F1 diallel crosses) which were grown in randomized complete block design with two replicates at Mandura, North West Ethiopia. Statistical significant difference was observed between genotypes, parents and progenies for the traits considered. Significant mean squares due to 'a' and 'b' components of Hayman were observed for both the traits. Thus both additive and non-additive types of gene actions were important in governing the inheritance of these traits. However, non-additive type of gene action was more important for number of days to maturity whereas both are almost equally important for the inheritance of number of days to flowering .The b_1 and b_3 components of Hayman showed statistically significant results, implying the presence of directional dominance, and residual dominance and dominance effects specific to individual crosses, respectively in the expression of the traits. The b_2 component of Hayman, however, did not show statistically significance difference for the traits, indicating the absence of gene asymmetry in the expression of the traits. The wr/vr graph for both the traits revealed that the inheritances of both the traits were governed by over dominance with additive gene action and epistasis was not involved. The direction of dominance was confirmed that it was operating in the decreasing direction.

1. Introduction

Climate change has been becoming an issue in world agriculture in general and most sever in rain dependent agrarian countries including the Ethiopian agriculture. Drought stress is the most important limitation facing crops now and in the future. Adaptation to and mitigation of the effects of climate change strategies could be devised as an option. Cultivation of short duration crops has been becoming a recent measure taken by farmers to reduce the risk of drought. To this effect, common bean is among the crops preferred

and produced, and also is suitable for intercropping and double cropping (Legesse et al., 2006). Nevertheless, drought stress limits common bean (*Phaseolus vulgaris* L.) production worldwide and in some semi arid area of Eastern and Southern Africa, it is the major problem reducing the mean seed yield by 50 % or more (Rao, 2001; Wortmann, 1998). Thus, screening and development of adaptable early maturing common bean varieties could be a sound option to minimize the effect of drought (Polania et al., 2009). Crop yield can be characterized as a function of an organism's: adaptation to its environment; ability to effectively collect light with the photosynthetic apparatus; and ability to partition and translocate photosynthate to the economic organs as cited by (Scully and Wallace, 1990). These processes are measured in various ways by breeding programs. It could be through trait inheritance evaluation of crop Phenology (Evans, 1984). These phenological traits are important characteristics associated to earliness and have been used by researchers to measure earliness of genotypes (Bora et al., 1998; Coyne, 1978; Mohanty and Baisakh, 1999; and Wallace and Enriquez, 1980). These traits are positively and highly correlated to grain yield under intermittent drought conditions in common beans (Acosta-Diaz et al., 1999).

Effective and efficient breeding program mainly depends on the genetic information underlying the trait of interest. Nevertheless, the Ethiopian common bean improvement program has focused on screening of introduced materials and has limitations to generate genetic information pertinent to the improvement of those traits (Atnaf et al., 2013). Diallel mating design among others is mostly preferred by plant breeders in terms of generating the amount of genetic information starting from the early generation though it has limitations on coverage of populations from which the parents are selected (Acquaah, 2012). Hayman's approach to Diallel analysis is one of the preferred approach as he further

partioned the non-additive component in to three sub components in addition to the total sum of the square due to genotypes in to two components called additive and non-additive (Hayman, 1954). Moreover, the wr/vr anova and graphs are the other powerful tools in Hayman's analysis with an inbuilt test for epistasis.

Studies to generate basic genetic information of important agronomic and physiological traits of different crops including common beans (Atnaf et al., 2013; Derera et al., 2007; Gwata et al., 2005; Jaramillo et al., 2005) have been conducted in various parts of the world. However, the genetic information underlying the inheritance of phenological traits of common beans in Ethiopia is limited. The study was, therefore, designed to generate basic genetic information of two important traits of common beans: number of days to flowering and maturity.

2. Materials and Methods

Thirty six genotypes (eight parents and their 28 forward F1 diallel crosses) were studied in two replicates of randomized complete block design at Mandura, North west Ethiopia. Six of the parents were released varieties and being under production in different agro-ecologies of Ethiopia and two CIAT lines (BELDAKMI RR5 and SK93263) were screened at Awassa College of Agriculture for good performance. Descriptions of the eight parents used in the diallel cross study are given in Table 1. Two row plot with 1 m long and spaced 60 cm apart, and 10 cm intra-row plant-to-plant spacing were used. Twenty plants per plot were maintained at optimum plant population per plot basis. The phenological traits (days to flowering and days to maturity) considered were recorded on plot basis and the data were subjected to the analysis of variance (anova) using SAS statistical software (SAS, 2004). Existence of significant difference among genotypes justifies further analysis.

Table 1. Description of the parental lines for the 8x8 diallel crosses of common bean

Nº	Parent	Status/Origin	Seed color	Seed shape	Seed size	Growth H
1.	Roba-1	Released-1990	Cream	Elongated	Small	II
2.	Dimtu	Released-2003	Red	Round	Small	II
3.	Zebra	Released-1999	Carioca	Round	Medium	II
4.	MAM-41	Released-2003	Cream	Round	Medium	III
5.	BELDAK	CIAT	Cr. Pinto	Round	Medium	III
6.	SK 93263	CIAT	White	Round	Medium	III
7.	Tabor	Released-1999	Cream	Elongated	Medium	II
8.	Red wolayta	Released-1974	Red	Elongated	Medium	II

BELDAK, BELDAKMI RR 5; Cr. Pinto, cream pinto; Growth H, growth habit; I, determinate bush; II, indeterminate bush; III, indeterminate prostrate. Seed size based on 100 seed weight: 1 to 24 g = small seed; 25 to 39 g = medium seed; 40 g and above = large seed.

Diallel analysis was carried out according to Hayman's (1954) approach. Hayman partioned the total sum of the square due to genotypes in to two components in the case of half diallel, meaning in the absence of reciprocals; the 'a' component with p-1 degree of freedom which is equivalent to Griffing's (1956) method II GCA, and the 'b' component with

p(p-1)/2 degree of freedom which is equivalent to Griffing's method II SCA component where p is number of parents involved in the cross. The 'b' component is further partioned in to b_1 with one degree of freedom, which shows directional dominance, b_2 with p-1 degree of freedom indicating gene asymmetry where p is number of parents. If b_2 is significant, it

indicates that some parents possess more dominant genes than others. Another component, the b_3 with p(p-3)/2 degree of freedom measures residual dominance effect and also dominance effects specific to individual crosses.

The wr/vr anova and graphs are the other powerful tools in Hayman's analysis with an inbuilt test for epistasis. wr is the covariance between parents and their offspring in each array. vr is the variance of means of an array. Parents which possess smaller values of (wr +vr) have more of the dominant genes. Those with higher values of (wr + vr) possess more recessive genes.

In the absence of epistasis, the regression of wr on vr gives a linear regression line of unit slope. Therefore, the deviation of this regression line from unity is an indication of the existence of epistasis. Parents with more dominant genes lie near the point of origin of this regression line, those with more recessive genes lie furthest from the point of origin. Direct anova of (wr–vr) also tests the absence/presence of epistasis. Significance of the difference (wr-vr) is an indication of the existence of epistasis.

The intercept of the wr/vr regression line shows the degree of dominance. If the regression line intercepts the wr axis above the point of origin, this indicates incomplete dominance. If the regression line passes through the origin, then there is complete dominance. If the intercept is negative (the regression line passes below the point of origin), then over dominance contributes to the expression of the trait.

Once dominance is confirmed as operator of inheritance of the trait being studied and the degree of dominance has been identified, then the next important step would be determining the direction of dominance whether it increases or decreases the trait. This could be judged by three options. The correlation between parental means and the value of (wr + vr), comparison of parental mean with the value of (wr + vr), and through comparison of the F1 mean with parental score. If the correlation coefficient (r) is negative, dominance tends to increase the trait and vice versa. If the highest phenotypic value of the parent is coupled with the lowest sum value of (wr + vr), dominance increases the trait. The superiority of F1 mean over the parental score indicates that dominance increases the trait considered.

3. Result and Discussions

Statistically significant differences between the 36 genotypes (8 parents and 28 forward F1 diallel crosses) were observed for the traits studied, number of days to flowering and maturity (Tables 2 and 3). Genotypes were partioned in to parents, progenies and a one degree of contrast between parents and progenies. Parents differed in number of days to flowering which shows that there is enough additive genetic variance to be exploited for the trait. Similar results were reported in an experiment to study the genetic control of number of days to flowering in common bean (Coyne, 1978; Mendes et al., 2008). Crosses were also showed statistically significant differences for the traits considered. Average heterosis which is a one degree of freedom contrast between the mean of parental performance and the progeny mean was

significant for the two traits studied suggesting the presence of directional dominance for the expression of these traits (Tables 2 and 3).

Table 2. Mean squares of genotypes, parents and crosses for number of days to flowering

Source	DF	Mean square	F-value	Probability
Replication	1	24.5	2.91	0.0968
Genotype	35	38.86	4.62	0.0001
Parents	7	39.920	4.74	0.0008
Crosses	27	34.579	4.11	0.0001
AVHET	1	147.048	17.48	0.0002
Error	35	8.414		
Total	71			

DF= Degree of freedom; AVHET= Average heterosis, which a one degree of freedom contrast between parents and crosses and when significant it indicates directional dominance

Table 3. Mean squares of genotypes, parents and crosses for number of days to maturity

Source	DF	Mean square	F-value	Probability
Replication	1	33.347	11.77	0.0016
Genotype	35	12.582	4.44	0.0001
Parents	7	4.964	1.75	0.1288
Crosses	27	7.780	2.75	0.0027
AVHET	1	195.571	69.03	0.0001
Error	35	2.833		
Total	71			

DF= Degree of freedom; AVHET= Average heterosis, which is a one degree of freedom contrast between parents and crosses and when significant it indicates directional dominance

The per se performance of the parents showed that SK 93263 was the earliest to flower and mature (Table 4). Roba-1 was one of the earliest parent taking 86 days to maturity as compared to the late maturing varieties like Red wolayta, although it was late flowering. Red wolayta was the latest maturing parent taking on average 90 days to maturity. The average numerical difference for number of days to physiological maturity between SK 93263 which is the earliest parent and Red wolyta, the latest parent, seems small, but has significance implication on grain yield under droughty condition.

Table 4. Mean performance of the genotypes (parents and progenies) for number of days to flowering and maturity

Progeny/Parent	Gen code	Days to flowering	Days to maturity
♀Roba-1 X ♂Dimtu	1	49.0	83.0
♀Roba-1 x ♂ Zebra	2	47.0	81.0
♀Roba-1 X ♂ MAM 41	3	42.5	81.0
♀Roba-1 X ♂BELDAKMI RR5	4	43.0	82.5
♀Roba-1 X ♂ sk 92263	5	38.5	80.5
♀Roba-1 X ♂ Tabor	6	49.0	85.0
♀Roba-1 X ♂ Red wolayta	7	48.5	84.5
♀Dimtu X ♂ Zebra	8	48.5	85.0
♀Dimtu X ♂ MAM 41	9	46.0	84.0
♀Dimtu X ♂ BELDAKMI RR 5	10	39.0	81.0
♀Dimtu X ♂ SK 92263	11	41.5	82.0
♀Dimtu X ♂ Tabor	12	52.0	88.0

Progeny/Parent	Gen code	Days to flowering	Days to maturity
♀Dimtu X ♂ Red wolayta	13	52.5	87.5
♀Zebra X ♂ MAM 41	14	43.5	84.5
♀Zebra X ♂ BELDAKMI RR 5	15	38.5	83.5
♀Zebra X ♂ SK 92263	16	40.5	83.5
♀Zebra X ♂ Tabor	17	45.5	84.5
♀Zebra X ♂ Red wolayta	18	43.0	85.0
♀MAM 41 X ♂ BELDAKMI RR 5	19	41.0	84.5
♀MAM 41 X ♂ SK 92263	20	46.0	84.0
♀MAM 41 X ♂ Tabor	21	46.5	81.5
♀MAM 41 X ♂ Red wolayta	22	41.5	84.5
♀BELDAKMI RR5 X ♂ SK 92263	23	42.0	81.0
♀BELDAKMI RR5 X ♂ Tabor	24	40.5	83.5
♀BELDAKMIRR5X♂Red wolayta	25	40.5	83.5
♀SK 92263 X ♂ Tabor	26	39.5	81.5
♀SK 92263 X ♂ Red wolayta	27	40.5	80.5
♀Tabor X ♂ Red wolayta	28	49.5	85.0
Roba-1	29	51.0	86.0
Dimtu	30	52.5	87.5
Zebra	31	46.5	89.0
MAM-41	32	48.0	88.0
BELDAKMI RR 5	33	41.5	88.0
SK 92263	34	40.5	85.0
Tabor	35	49.5	86.0
Red wolayta	36	51.0	89.5
Progeny mean		44.13	83.41
Parental mean		47.56	87.38
Genotype Mean		44.90	84.29
LSD (5%)		5.89	3.42
CV (%)		6.46	1.20

Gen code=Genotype code

Significant mean squares due to 'a' and 'b' components

Table 5. Hayman's diallel analysis for number of days to flowering

Source	DF	Sum of squares	Mean square	F-value	Probability
Genotype	35	1360.1110	38.8600	4.6200	0.00010
a	7	831.3000	118.7570	14.1142	0.00000
b	28	528.8100	18.8860	2.2446	0.01211
b1	1	147.0500	147.0500	17.4768	0.00018
b2	7	19.6000	2.7990	0.3328	0.93360
b3	20	363.1700	18.1080	2.1521	0.02293
Error	35	294.5000	8.4140		

a = additive genetic variance, b = non-additive genetic variance, b_1 = tests overall difference between parental and F_1 means(direction of dominance), b_2 = measures consistency of mean dominance deviation over arrays (gene asymmetry), and b_3 = measures non-additive deviations unique to each F_{1s}

Table 6. Hayman's diallel analysis for number of days to maturity

Source	DF	Sum of squares	Mean square	F-value	Probability
Genotype	35	440.3750	12.5820	4.4412	0.00001
a	7	110.1750	15.7390	5.5556	0.00023
b	28	330.2000	11.7930	4.1627	0.00005
b1	1	195.5710	195.5710	69.0332	0.00000
b2	7	25.2000	3.6000	1.2707	0.29296
b3	20	109.4290	5.4710	1.9312	0.04301
Error	35	99.1530	2.8330		

a = additive genetic variance, b = non-additive genetic variance, b_1 = tests overall difference between parental and F_1 means(direction of dominance), b_2 = measures consistency of mean dominance deviation over arrays (gene asymmetry), and b_3 = measures non-additive deviations unique to each F_{1s}.

observed for number of days to flowering and maturity (Tables 5 and 6). Thus both additive and non-additive types of gene actions were important in governing the inheritance of these traits. However, non-additive type of gene action was more important for number of days to maturity as the variance component due to 'b' was greater than 'a' component (the ratio of 'a': 'b' variance component was less than unity) whereas the magnitude of 'a' and 'b' variance component for number of days to flowering was almost equal (ratio =1.054). This result is in good agreement with Melaku (1993) who reported the importance of both additive and non-additive types of gene actions in the inheritance of these traits and Navale and Patil (1982) who reported that non-additive gene action was more important in the inheritance of number of days to maturity. Contrary to the present study, however, Barelli et al (2000) reported the preponderance of additive type of gene action in the inheritance of number of days to flowering.

The b_1 and b_3 components of Hayman showed statistically significant results, implying the presence of directional dominance and dominance effects specific to individual crosses, respectively in the expression of number of days to flowering and maturity. The b_2 component of Hayman, however, did not show statistically significance difference for the traits, indicating the absence of gene asymmetry in the expression of the traits.

The wr/vr graph for number of days to flowering (Fig. 1) revealed that the regression line intercepted the wr-axis well below the point of origin (intercept = -4.13), indicating that the inheritance of number of days to flowering was governed by over-dominance with additive type of gene action. The estimated regression line did not significantly deviate from
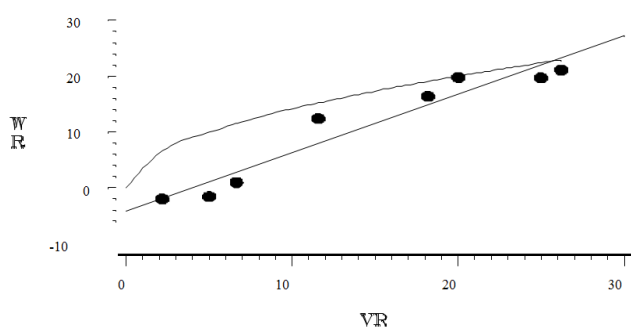
unit slope. Thus epistasis was not involved in the inheritance of number of days to flowering, justifying the adequacy of additive model. BELDAKMI RR 5 was closest to the point of origin, indicating that more dominant genes were present in it, whereas Red wolayta possessed the maximum recessive genes being farthest from the point of origin. However, gene asymmetry was not present as the b2 component of Hayman was not significant. The scattered distribution of array points on the regression line depicted that genetic variation among parents existed for number of days to flowering.

Table 7. *Variance and covariance, and different related statistics for days to flowering*

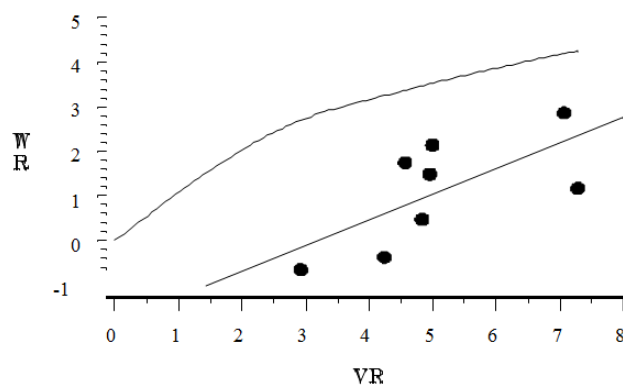| Parents	P score	vr	wr	(wr+vr)[*]	(wr-vr)[ns]
Roba-1	51.00	21.3482	16.6429	37.9911	-4.7054
Dimtu	52.50	28.9643	21.3214	50.2857	-7.6429
Zebra	46.50	16.2500	10.9821	27.2321	-5.2679
MAM-41	48.00	15.5357	3.2857	18.8214	-12.25
BELDAKMI RR 5	41.50	7.7679	-1.2589	6.5089	-9.0268
SK 93263	40.50	8.6786	-1.0357	7.6429	-9.7143
Tabor	49.50	21.1429	19.5000	40.6429	-1.6429
Red wolayta	51.00	30.3929	21.4821	51.8750	-8.9107
$b_{Wr,Vr} = 1.044^{ns}$	Intercept = -4.13^{ns}				

P score= Parental score; vr= Variance of all the progenies in each parental array (an array is a group of crosses involving a particular parents), wr= Covariance between parents and their offspring's in each array and $b_{Wr, Vr}$= Regression of wr on vr and test for $b_{Wr,Vr}$=1, and Intercept= The point where the regression line intercepted the wr-axis, test for Intercept=0. Significance of (wr+vr) and (wr-vr) is from the direct anova of the parameters.

Figure 1. *wr/vr graph for number of days to flowering*

The Wr/Vr graph for number of days to maturity (Fig. 2) showed that the estimated regression line intercepted the wr-axis below the point of origin, indicating that the trait is governed by over-dominance with additive type of gene action. The regression line did not significantly deviate from unit slope. Thus a non-allelic interaction was not involved, justifying the adequacy of additive model. SK 93263 was closest to the point of origin, indicating the presence of more number of dominant genes in it. Red wolayta being farthest from the point of origin had the maximum recessive genes.

Figure 2. *wr/vr graph for number of days to maturity*

Table 8. *Variance and covariance, and different related statistics for days to maturity*

Parents	P score	vr	wr	(wr+vr)[ns]	(wr-vr)[ns]
Roba-1	86.00	4.81250	-0.41964	4.3929	-5.2321
Dimtu	87.50	9.48214	1.07143	10.5536	-8.4107
Zebra	89.00	7.12500	2.75000	9.8750	-4.3750
MAM-41	88.00	6.12500	1.25000	7.3750	-4.8750
BELDAKMI RR 5	88.00	6.13393	1.40179	7.5357	-4.7321
SK 93263	85.00	4.19643	-0.57143	3.6250	-4.7679
Tabor	86.00	5.91071	0.98214	6.8929	-4.9286
Red wolayta	89.50	8.12500	3.39286	11.5179	-4.7321
$b_{Wr,Vr} = 0.575^{ns}$	Intercept = -1.83^{ns}				

P score= Parental score; vr= Variance of all the progenies in each parental array (an array is a group of crosses involving a particular parents), wr= Covariance between parents and their offspring's in each array and $b_{Wr, Vr}$= Regression of wr on vr and test for $b_{Wr,Vr}$=1, and Intercept= The point where the regression line intercepted the wr-axis, test for Intercept=0. Significance of (wr+vr) and (wr-vr) is from the direct anova of the parameters.

The correlation between parental means and the value of (wr + vr) for both traits were positive indicating that dominance dictates the trait in the decreasing direction (Tables 7 and 8). Similarly, the comparison of progeny mean (F1) with parental score for both traits revealed that dominance operates the trait in the decreasing direction (Table 4). However, similar confirmation was not found with the other option through comparison of parental mean score with the corresponding value of wr + vr (Tables 7 and 8).

4. Conclusion

Effective and efficient breeding program mainly depends on the genetic information underlying the trait of interest. An experiment to study the genetic information underlying the inheritance of phenological traits in common bean was undertaken at Mandura, North West Ethiopia. The importance of both additive and non-additive types of gene actions operating the inheritance of the traits were confirmed from the significant mean squares of the 'a' and 'b' components of Hayman. However, non-additive type of gene action was more important for number of days to maturity whereas both are almost equally important for the inheritance of number of days to flowering. The preponderance of non-additive gene action for the inheritance of number of days to maturity would imply that simple selection methods would not be effective to improve the trait. The b_1 and b_3 components of Hayman showed statistically significant results, implying the presence of directional dominance, and residual dominance, respectively in the expression of the traits. The wr/vr graph for both the traits revealed that the inheritance of both are governed by over dominance with additive gene action and epistasis was not involved. The direction of dominance was confirmed that it operates in the decreasing direction. A breeding program that aims to improve earliness under droughty conditions would consider this genetic information about the inheritance of days to flowering and maturity.

Acknowledgement

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