

GENETICS OF SEED WEIGHT IN LENTIL (*LENS CULINARIS* MEDIK.)

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Abstract

Combining ability and genetic analysis was conducted in a four parent complete diallel for seed weight in lentil. Additive type of gene action predominantly governed by recessive genes was observed for the expression of this character. Thus, simple selection in late generations, when genes are fixed, is recommended to pick the desired transgressive segregants in the hybrids involving Mansehra-89 and Flip-86-38L as one of the parents.

Introduction

Seed size is one of the important yield components in lentil. Plumpness of lentil seed is also a desirable trait from consumer's point of view. Therefore, it is desirable to investigate the genetics of this trait in order to develop varieties with higher seed weight. The analysis of a diallel cross (a set of all possible mating among several genotypes as explained by Hayman, 1954 & Griffing, 1956) is a useful tool for plant breeders to study the inheritance of quantitative traits such as seed weight. The technique of diallel analysis has been used successfully in several legume crops such as mashbean (Singh & Singh, 1971), mungbean (Wilson *et al.*, 1985; Singh *et al.*, 1987), pea (Singh *et al.*, 1987), chickpea (Rastogi, 1979; Singh *et al.*, 1982) and lentil (Malhotra *et al.*, 1973; Singh & Singh, 1990; Singh & Singh, 1991 and Swarup *et al.*, 1991) to aid in the choice of parents for hybridization and selection of best lines from hybrid progenies. The information about the inheritance of seed weight in lentil is almost scanty. The present study was therefore, conducted to gather information on combining ability and gene action of seed weight in crosses among local and exotic lentil genotypes. The information will be useful for plant breeders aiming to improve the plumpness of lentil seed.

Materials and Methods

Two local (Masoor 85 and AARI L-337) and two exotic (Flip 86-38L and Mansehra 89) lentil genotypes were used in the present study. The genotypes were crossed among each other in a diallel fashion during winter 89. The F₁'s including reciprocals and parents were grown using randomized complete block design with three replications at the experimental fields of the National Agricultural Research Center, Islamabad during winter-1990. The hybrids and parental lines were dibbled in single row (four meter long) plots by keeping 25 and 5 cm spacing between and within rows,

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Table 1. Mean squares, components of variance and percent variance for grain weight in 4 parent diallel, Griffing's Method 1, Model 1.

Source	DF	Mean Square	Variance	Percent Variance
GCA	3	3.72000**	0.46031	89.80
SCA	6	0.04064**	0.02472	4.82
Reciprocal	6	0.05469**	0.02711	5.29
Error	30	0.00046	0.00046	0.09

respectively. The seed weight was recorded as weight (g) of 100 randomly selected seeds from 10 selected plants in each replication. Analysis of variance was performed following the methods of Steel & Torrie, (1980). Genetic analysis of the diallel cross was conducted with the help of a computer program written in "BASIC" according to the methods described by Griffing, 1956 (Method 1, Model 1) and Hayman (1954).

Results and Discussion

The analysis of variance revealed significant differences among the parents and F1's including reciprocals for the character under study. The estimates of General Combining Ability (GCA), Specific Combining Ability (SCA) and Reciprocal Effects were highly significant for seed weight. These results indicated the presence of both additive and non-additive gene-action. In 100-seed weight it seemed that both types of genetic variation are inter-linked in a complex form. Therefore, total variance due to combining ability effects were partitioned to components of variation due to combining ability effects and expressed as percentage, to get precise information (Table 1). High contribution of GCA effects (89.80%) revealed that additive gene-action was predominantly important for grain weight in lentil. The presence of high degrees of additive gene-action revealed that the population was amenable to selection in early segregating generations.

Among genotypes, Mansehra 89 proved to be the best combiner for grain weight with GCA values of 0.735 and it was followed by Flip 86-38L with GCA value of 0.426 (Table 2). Masoor 85 and AARI L-337 could not exhibit any promise for grain weight. Therefore, Mansehra 89 and Flip 86-38L should be exploited to establish pure lines of bold seeded lentil genotypes. The estimates of SCA and reciprocal effects, revealed that only two crosses (Masoor-85 x Flip86-38L and Flip86-38L x Mansehra-89) produced positive values (0.10 and 0.022) whereas all other specific crosses produced negative SCA effects (Table 2). In reciprocal effects, the cross "Mansehra 89 X Masoor 85" gave the highest value of 0.192 whereas all other crosses exhibited negative effects (Table 2).

Table 2. General combining ability (diagonal), specific combining ability (upper) and reciprocal effects (lower) for grain weight (g) in 4 parent diallel (Griffing's Method 1, Model 1).

	Masoor 85	AARI-L 337	Flip 86-38L	Mansehra 89
Masoor 85	-0.598	-0.090	0.100	-0.016
AARI-L 337	-0.060	-0.562	-0.131	-0.130
Flip 86-38L	-0.095	-0.147	0.426	0.022
Mansehra 89	0.192	-0.160	-0.260	0.735
SE (gi)	0.00004	SE(s _{ii} -s _{ij})	0.00058	
SE (r _{ij} -r _{kl})	0.00046	SE(s _{ij})	0.00013	
SE (r _{ij})	0.00021	SE (g _i -g _j)	0.00011	
SE (s _{ij} -s _{ik})	0.00032	SE (S _{ij} -s _{kl})	0.00021	

The relationship between the variance (Vr) of 4 parents and the covariance (Wr) of parents with their offspring is shown in Fig.1. The linear regression (Vr,Wr) and the limiting parabola (Wr²=VpVr) is also shown in the same figure. The regression line differs significantly from a slope b=0 but not from b=1. Since the regression of (Vr,Wr) agrees well with a slope of unity, the gene system controlling the seed weight can be deduced to be additive without the complication of interallelic gene interaction. According to Hayman (1954), regression line of (Vr,Wr) with slope b=1 would pass through the origin if dominance of the genes is complete. In case of overdominance the regression line would cut the Wr axis below the origin, and in the absence of

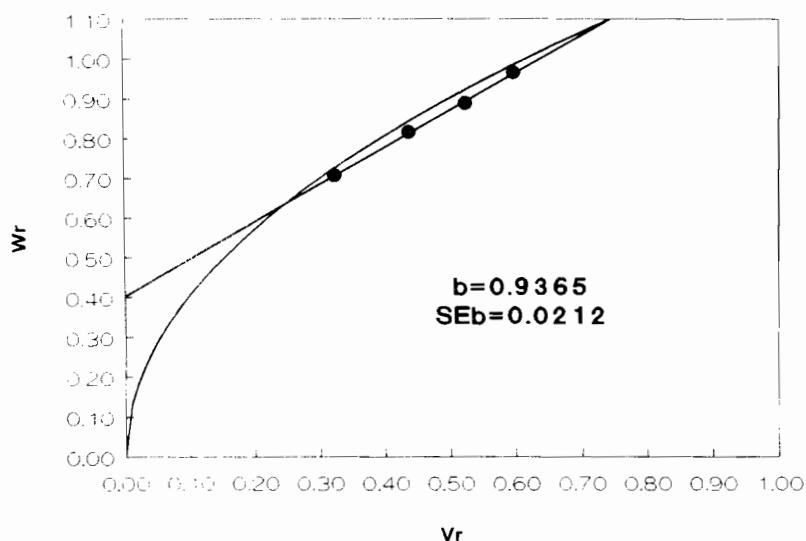


Fig.1. Vr-Wr graph for seed weight in lentil.

Table 3. Average seed weight (g) of F₁'s (Upper), Parents (Diagonal) and Reciprocals (Lower) in lentil.

	Masoor 85	AARI-L 337	Flip 86-38L	Mansehra 89
Masoor 85	1.72	1.60	2.74	3.22
AARI-L 337	1.72	2.13	2.49	2.79
Flip 86-38L	2.93	2.79	3.50	3.83
Mansehra 89	2.84	3.11	4.35	4.50

dominance the points would cluster about the position where the slope of the parabola is + 1. In the present study the regression line being near to that of a tangent to the parabola, indicates little dominance (Fig. 1). The order of the array points on the regression line indicates the distribution of dominant and recessive genes among the parents. Thus, AARI-L-337 appears to possess most dominant while Mansehra-89 possesses most recessive genes for seed weight in lentil.

The information extracted from Fig. 1, can be very useful when designing a breeding programme for increased seed weight. The array means for F₁'s of four parents (Masoor-85, AARI-L-337, Flip-86-38L, Mansehra-89) are presented in Table 3. Mansehra-89 array is the one which in the F₁ shows the most promise, and as the gene system controlling seed weight is additive, this array will hold its superiority in later generations. The Flip-86-38L is the next highest and its cross with Mansehra-89 is the highest cross (Table 3). Thus, the crosses with Mansehra-89 and especially the Flip-86-38L x Mansehra-89 cross is the most promising for improvement of seed weight in lentil. Moreover, the point representing the Mansehra-89 array (Fig. 1) on the regression line is farthest from the origin. Therefore, it appears that recessive genes are more important for the expression of this character.

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