

Inheritance Pattern of Quantitative Characters in *Brassica napus*

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ABSTRACT

The genetic basis of variation in five varieties/lines of *Brassica napus* L. was examined. The parents were crossed in all possible combinations. The response of 20 F₁ hybrids and the five parents were studied till maturity. At maturity, data on number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot was recorded. Analysis of variance of the means of 25 families showed highly significant differences for these four characters. The two scaling tests i.e. joint regression analysis and analysis of (W_r + V_r) and (W_r-V_r) suggested that the genetic model was fully adequate for number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot. The estimated components of variation revealed that affects of the genes showing dominance properties were more pronounced than those of additive genes. Estimates of narrow sense heritability of number of seeds per pod were very low, suggesting that selection of desirable plants should be delayed till later generations. While in number of pods per plant, 1000 seed weight and seed yield per plot, the narrow sense heritability was in medium range.

Key Words: *Brassica napus*; Canola; Variation; Additive; Dominance; Diallel cross

INTRODUCTION

Although Pakistan has made impressive progress in agriculture production in some crops like cotton, wheat etc. but there was no impressive progress in oilseed crops although the country is suffering from acute deficit of edible oil. It is necessary to take important measures to improve the production potential of traditional oilseeds. Keeping in view, the magnitude of edible oil shortage, development and improvement work needs serious attention. Improvement through breeding can be made successful by knowing the genetic behaviour and creating genetic variability in *Brassica* seed especially in *Brassica napus*.

In the perspective of afore explained situation the present study was planned to evaluate the inheritance pattern of quantitative characters which influence the seed yield and oil contents in *Brassica napus*.

MATERIALS AND METHODS

The present study was carried out in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experiment comprised of five varieties of *B. napus* viz. Con-I, MLCP-048, Star, Con-II and AUB-2000, which were sown in field and crossed in a diallel fashion during 2001-02. Crosses and parents were sown in Randomized Complete Block Design with three replications during 2002-03 with row to row and plant to plant distance as 60 and 22 cm, respectively. Normal agronomic practices were followed for the crop. At maturity, 10 guarded plants were randomly selected in per replication for recording data in each cross.

Statistical procedure. Before subjecting the data to diallel analysis technique, data were subjected to analysis of variance (Steel & Torri, 1980) to see the significance of genotypic differences among F₁ hybrids and their parents.

To determine the adequacy of the additive dominance model, and to assess the validity of some of the assumptions underlying the model, preliminary analysis of the data were done following Hayman (1954a,b) and Jinks (1954). From the data set, variance of components of each array (V_r), the covariance of the parents with their offspring in each array (W_r), and the variance of parental means (V₀L₀ = V_p) were calculated. Other statistics include the computation of the means of array variance (V₁L₁), the variance of means of arrays (V₀L₁), and the mean of array covariance (W₀L₀). All these statistics were used to calculate the genetic components of variation in characters. The components under the simple additive-dominance model are: D, the component of variation due to additive effects of the genes; H₁ and H₂ the component of variation due to dominance effects of the genes; h is the direction of dominance effects whether it is toward positive or negative; F, provides an estimate of the relative frequency of dominant to recessive alleles in the parents, and variation in dominance over the loci. These estimates were obtained by removing the environmental component. E, which in the present study was halved, since reciprocal F₁ families were assumed to have identical expectations and therefore, were averaged (Mather & Jinks, 1982). Estimates of narrow sense heritability of number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot were calculated from the genetic components according to the formula given by Mather and Jinks (1982).

RESULTS

The analysis of variance of means of parents and 20 F₁ families revealed highly significant differences ($P \leq 0.01$) for number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot (Table I). These significant differences validated the use of simple additive dominance model for genetic analysis of the diallel data. To test the suitability of the present data for genetic analysis and validity of the major assumptions underlying the genetic model, two scaling tests i.e. joint regression analysis and analysis of variance of (Wr + Vr) and (Wr - Vr) were carried out. Regression coefficient (b) is expected to be significantly different from zero but not from unity if all the assumption are met (Hayman, 1954a,b; Jinks, 1954). The unite slope of regression line for number of pods per plant ($b = 0.729 \pm 0.22$, Fig. 1), number of seeds per pod ($b = 0.721 \pm 0.22$, Fig. 2), thousand seed weight ($b = 0.81 \pm 0.20$, Fig. 3), seed yield per plot ($b = 0.81 \pm 0.20$, Fig. 4) and significance of differences of (Wr+Vr) and (Wr-Vr) of the five characters (given in Fig. 1, 2, 3) revealed that additive dominance model was fully adequate for data set on number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot. The scaling test provided

Table I. Mean squares of some quantitative traits in *Brassica napus*

S.O.V	DF	Number of pods per plant	Number of seeds per pod	Thousand per seed weight	Seed yield per plot
Replication	2	38750.76**	16.20*	0.12 ^{ns}	1978.65 ^{ns}
Genotype	24	35171.11**	17.19**	0.48**	7554.34**
Error	48	6868.06	3.73	0.104	1623.87

* = Significant
 ** = Highly Significant
 NS = Non Significant

Table II. Components of variation in *Brassica napus*

Genetic Components	Number of pods per plant	Number of seeds per pod	Thousand per seed weight	Seed yield per plot
D	31746.83	5.39	0.19	3019
F	23085.28	4.99	0.01	185.82
H ₁	21624.31	15.76	0.29	5948.57
H ₂	16609.94	12.36	0.27	4110.92
H	-1983.16	8.24	-0.34	3.57
E	27.1431	1.41	0.03	620.48
$\sqrt{H_1/D}$	0.82	1.70	1.21	1.40
H ₂ /4H ₁	0.19	0.19	0.23	0.17
(4DH ₁) ^{0.5} +F/(4DH ₁) ^{0.5} -	2.57	1.74	1.06	1.04
F				
Heritability (narrow sense)	0.49	0.29	0.49	0.58

Fig. 1. Vr/Wr graph for number of pods/plant

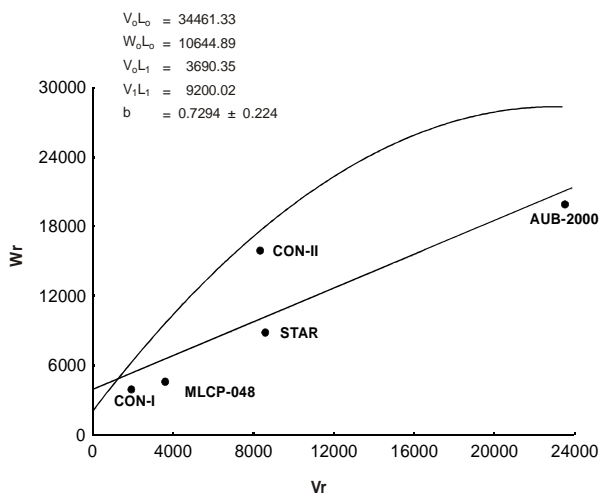
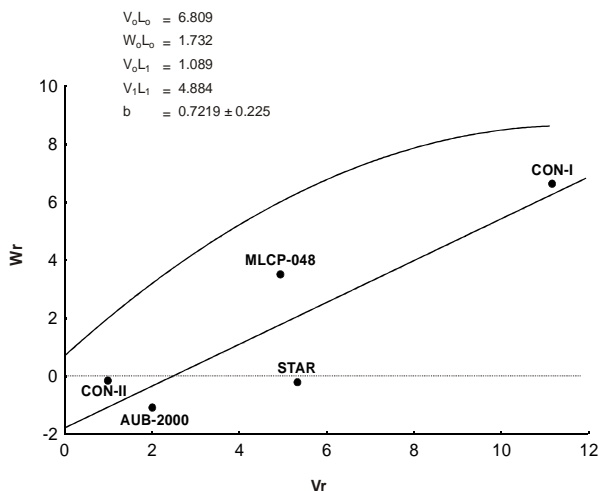


Fig. 2. Vr/Wr graph for number of seeds/pod



further evidence of the presence of non-allelic interaction in the inheritance of the character.

The estimates of genetics of variation in number of pods per plant, number of seeds per pod, 1000 seed weight and seed yield per plot are given in Table II. Although D, H₁ and H₂ items were positive and significant for number of seeds per pod, 1000 seed weight and seed yield per plot, the greater magnitude of H₁ and H₂ than that of D revealed that genes with non additive effects were important. As the magnitude of H₁ is greater than H₂ therefore distribution of negative and positive alleles were unequally distributed in the parents and further proof of this unequal distribution of alleles over loci is provided by the ratio H₂/4H₁, which is lesser than its maximum value 0.25 (Table II). Positive value of F of these three characters suggested that dominant alleles were more abundant than the recessive alleles in the parents, and this claim was supported by the ratio of (4DH₁)^{0.5}+F/(4DH₁)^{0.5}-F which is more than one in

number of seeds per pod, 1000 seed weight and seed yield per plot. Positive value of h in number of seeds per pod and seed yield per plot indicated the trend of dominance towards the parent with higher number of seeds per pod and seed yield per plot (Table II). The ratio of $\sqrt{H_1/D}$ is greater than 1, and therefore presence of over dominance in the genes was revealed. Narrow sense heritability of number of seeds per pod (0.29) is very low while in 1000 seed weight and seed yield per plot is medium enough. The study of W_r/V_r graph in Fig. 1 shows that Con-II had maximum number of dominant genes and Con-I being away from origin carried maximum number of recessive genes for number of seeds per pod. In Fig. 2 and 3 shows that MLCP-048 had maximum number of dominant genes and Star being away from origin carried maximum number of recessive genes for 1000 seed weight and seed yield per plot.

The genetic components of variation for number of

Fig. 3. V_r/W_r graph for 1000 seed weight

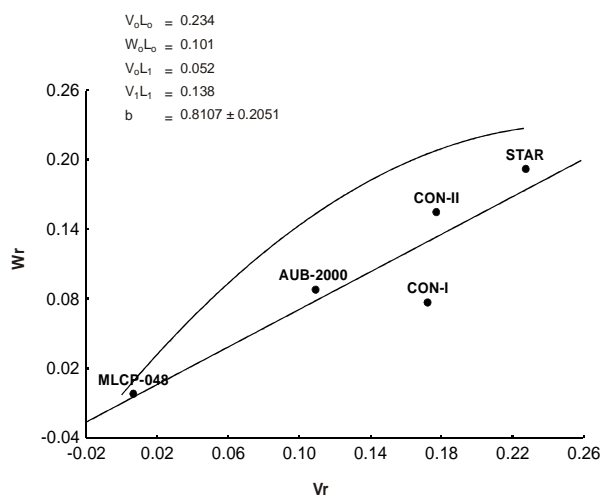
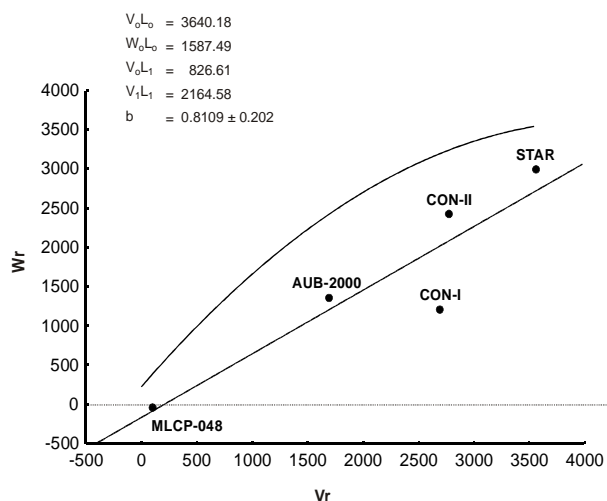


Fig. 4. V_r/W_r graph for seed yield/plot



pods per plant (Table II) revealed that genes with additive properties influenced the inheritance of the character, as the value of D (31746.83) is greater than H_1 (21624.31). The higher value of H_1 (21624.31) than H_2 (16609.94) indicated the unequal distribution of genes, and this claim is strengthened by the ratio of $[H_2/4H_1 = 0.19]$, which is lesser than 0.25. The lesser ratio of $[\sqrt{H_1/D} = 0.82]$ indicated partial dominance occurring in the inheritance. The negative value of h (-1983.16) suggested, the direction of dominance towards the lesser number of pods per plant. The positive value of F (23085.28) revealed the presence of more dominant genes, and is evidenced by the ratio of $[(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F = 2.57]$. The estimate of narrow-sense heritability is 0.49, which is medium in magnitude pointing out better inheritance of the character for future selection. The regression line intercepted the W_r -axis above the origin, which indicated the presence of partial dominance (Fig. 4). The relative distribution of array points along the regression line indicated that Con-I had the maximum number of dominant genes, whilst AUB-2000 being away from the origin had recessive genes for number of pods per plant.

DISCUSSION

In order to bring improvement, through selection, the availability of genetically based variation is essential in any breeding population. In the present studies, the statistical analysis of the data showed that the genotypes differed significantly from each other for these five quantitative characters (Table I).

For rapid genetic improvement, thorough understanding about the pattern of inheritance of variation in different plant characteristics is an essential pre-requisite for plant breeder. The information on different genetic components of variation, i.e. additive, non-additive, epistasis and linkage may be useful to develop an appropriate selection protocol while handling the segregating generations.

Diallel cross technique is commonly used by the breeders to collect such genetic information for the plant material at hand. The analysis of the data reported in this research provided valuable information about the mechanisms of genetically controlled variation in some quantitative characters of Brassica plants.

According to Mather and Jinks (1982) significant genotypic differences for the character may be manifested by additive genetic effects. However to derive some useful and authentic information from the data, additive-dominance model of Hayman (1954a,b) and Jinks (1954) is a useful technique. Joint regression analysis of the data was carried out to test the validity of the data as suggested by Hayman (1954a,b).

The results of genetic analysis showed that three characters i.e. number of seeds per pod, 1000 seed weight

and seed yield per plot were revealed to be predominantly influenced by the over dominant gene action (non-allelic interaction). Similar results have been reported by Ghosh and Gulati (2001), Kamala (1999) and Varsha *et al.* (1999). While number of pods per plant revealed to be predominantly influenced by the additive gene action (with partial dominance effect), which may be beneficial to a research worker looking for promising genotypes from the segregating progenies, since it is the additive genetic component of the total genetic make up which is transmitted from parents to the offspring. Similar nature of gene action for these characters had been reported by Satija *et al.* (2001), Larik and Rajput (2000) and Singh *et al.* (2000).

Straight forward selection from the segregating population of the characters does not seem to be possible, the genetic variation existed in these characters could be improved successfully following reciprocal recurrent selection. Furthermore these characteristics in which over dominance was involved may advantageously to be utilized by the breeders to develop hybrid, as suggested by Rao and Gulati (2001). However, before deriving some conclusive inferences, this information must be substantiated. The scatter of array points along the regression line for different characteristics suggested the existence of genetic diversity in the parental material meaning thereby that sufficient variation is present in the plant material which could be explored by following an appropriate breeding programme. In view of the above discussion, it may be concluded that the plant traits involving additive type of gene action in their inheritance pattern, simple selection procedure would be useful for their improvement, whereas the traits involving over dominance type of gene action might be considered

when heterosis is to be exploited in appropriate improvement programme.

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