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Department of Genetics and Plant Breeding

School of Agriculture

Study of Heterosis and Combining Ability for Yield and its Component Traits in (*Brassica juncea* L.)

Synopsis for Research Project of

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By

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Synopsis

Title:

Study of Heterosis and Combining Ability for Yield and its Component Traits in (Brassica juncea L.)

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CERTIFICATE

This is certified that this synopsis entitled "Study of Heterosis and Combining Ability for Yield and its Component Traits in (*Brassica juncea* L.)" submitted in partial fulfilment of requirements for degree – Master of Science in Genetics and Plant Breeding by Sudip Khan, Registration no. 11700334 to Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, has been formulated and finalized by the student himself on the subject.

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DECLARATION

I hereby declare that the project work entitled — "Study of Heterosis and Combining Ability for Yield and its Component Traits in (Brassica juncea L.) is an authentic record of my work carried at Lovely Professional University as requirements of Project work for the award of degree -Master of Science in Genetics and Plant Breeding, under the guidance of Dr.Nidhi Dubey, Assistant Professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab.

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1. Introduction :

Indian mustard belongs to family Brassicacae and genus Brassica. Indian mustard [Brassica juncea (Linn.) Czern & Coss] is a natural amphidiploid (2n = 36) of Brassica rapa (2n = 20) and Brassica nigra (2n = 16). The chromosome no of Brassica juncea is 2n =18. Mustard is largely self pollinated but certain amount (5 -18%) of cross pollination may take place (Labana and Banga, 1984). It originated in Asia with its major center of diversity in China . It was introduced in India from China and from where it spread to Afghanistan and other countries. India is one of the largest rapeseed mustard growing country in the world in ranking the third position in area and production after Canada and China. Mustard is most important edible oil seed crop in India . Mustard is 2nd most important oil seed crop after soybean . It accounts nearly 28% of total oilseed production in India. When compared to other edible oils it has lowest amount of harmful saturated fatty acids. As per the 2014 -2015 data mustard production was 72.82 lakh ton . Indian accounts nearly 12% of world production . It has 38 to 42% of oil and 24% protein. Since oilseeds account for nearly 14% of gross national product and 7% of the value of all agriculture products, therefore, Indian mustard assumes as an important crop. Top mustard producing state in India- 1st Rajasthan(28.96 lac tones) 43% of national production 2nd Uttar Pradesh 14% of national production. 3rd Madhya Pradesh 11% of national production

The presence of undesirable long chain fatty acids like erucic acid (50%) in the seed oil, it becomes detrimental to human health. Both linoleic and linolenic acids are essential fatty acids; however, less than 3% linolenic acid is preferred for oil stability. Beside the yield potential, oil quality from nutritional point of view is very important.

The line x tester mating analysis (Kempthorne, 1957) is one of the simple and efficient methods for preliminary evaluation of genetic studies through hybridization. It provides information about general and specific combining ability of parents and at the same time, it is helpful in estimating various types of gene effects. Analysis of GCA and SCA is also useful to know the type of gene action controlling various characters and in the development of suitable breeding strategy.

Genetics of morphological traits facilitate the breeder to improve the yield productivity in varying environments. The genetic research done for yield improvement in mustard revealed that the grain yield in this crop is mainly determined by component traits, which are highly complex and variable.

Keeping in view the aforesaid problems, the present investigation has been planned with the following objectives:

Objectives:

1. To study per se performance of parents and hybrid.

- 2. To study extent of heterosis for yield, yield attributes and oil content.
- 3. To study GCA of the parent and SCA effects of the hybrid.
- 4. To study nature and magnitude of gene action.

2. Review of Literature

The success of any plant improvement programme mainly depends on the right selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the concerned field. In mustard substantial contribution has been made to the literature regarding its genetics and breeding in the recent years. The literature pertaining to the various aspect of the present study has been reviewed under the following heads:

- 2.1 Heterosis analysis
- 2.2 Estimation of combining ability
- 2.3 Gene action

2.1 Heterosis Analysis :

The term heterosis was given by Shull 1914. It may be defined as superiority of the F_1 hybrid over its both parent in term of yield or some other characters.

Alituri et. al_{2006} . Evaluated 56 F₁ hybrids to identify mid-parent and better-parent heterosis in Brassica juncea. Out of 56 hybrids, negative mid-parent and better-parent heterosis were estimated in 15 and 10 hybrids for days to 50% emergence, in 20 and 11 hybrids for days to 50% flowering, in 34 and 49 crosses for days to physiological maturity and in 37 and 34 crosses for plant height, respectively whereas positive heterosis were estimated in 12 and 10 crosses for number of primary branches/ plant. However, significant negative mid-parent and better-parent heterosis were recorded in 5 and 4 hybrids for days to 50% emergence, in 05 and 03 for days to 50% flowering, in 10 and 8 for days to physiological maturity, in 7 and 36 for plant height while significantly positive heterosis was recorded in 27 and 4 crosses for number of primary branches/ plant respectively. Betterparent heterosis reduced to 27% for emergence, 3.85% for flowering, 4.08% for maturity and 22.63% for plant height whereas it reached to 44% for branches/plant Among parents, NUM103, NUM113, NUM123 and NUM117 proved to be superior when used as parents in most of the hybrid combinations. Hybrids NUM9xNUM113, NUM103xNUM113, NUM123xNUM117, NUM123xNUM113 and NUM123xNUM124 were best for different characters and their further utilization in breeding programs is suggested.

Aher *et. al*, (2009) Analyzed heterosis using a Line x tester of 10 lines and 4 testers in Indian mustard. In the present study, moderate heterosis was observed for seed yield per plant, number of siliqua per plant and number of secondary branch per plant whereas, in the remaining character low amount of heterosis was reported. The highest standard heterosis for seed yield was observed in RSK-87 x GM-2 (42.95%) followed by SKM-95-85 x GM-2 (40.11%) and RSK-87 x Varuna (37.67%).

Nair *et. al*, (2010) Analyzed heterosis using three way crosses in mustard. The crosses (Seeta x Rohini) x Pusa Bold and (Seeta x ACN-9) x Rohini and (Seeta x ACN-9) x PCR-7 exhibited maximum heterosis for seed yield/ plant and hence may be forwarded to later generations to identify a superior recombinant line.

Meena *et.al*, (2014) Evaluated 36 F1 hybrids to identify the heterobeltiosis and standard heterosis in Brassica juncea. Five crosses viz., DRMR 2486 × Ashirwad, DRMR 2243 × NRCHB 101, DRMR 2269 × NRCHB 101, DRMR 2341 × NRCDR 2 and DRMR 2613 × NRCDR 2 possessed high heterosis and higher per se performance over better parent and standard check. In many crosses, highly significant heterosis was observed for point to first branch, number of primary branches, main shoot length, point to first siliqua and number of seeds / siliqua. The high yielding cross combinations from this study can be utilized in future breeding programmes for development of high yielding genotypes.

2.2 Combining Ability Analysis

Verma *et. al*, (2011) Using a Line x tester of 12 lines and 3 testers in Indian mustard. The non-additive gene action was of greater importance for all the characters studied. Among parents HUJM-05-1, RGN-181, Varuna and HUJM-04-6 were appeared to be the best general combiners for seed yield/plant. The cross combinations HUJM05-1 × Kranti, RGN-173 × NDR 8501, RGN-173 × Kranti, NPJ-113 × NDRE-4 and Varuna × Kranti possessed superior specific cross combinations for seed yield and its contributing traits. The best hybrid combinations for seed yield were HUJM-05-1 × Kranti followed by RGN-H3 × NDR 8501 which showed significant heterosis over better parent to the extent of 80.97 and 77.75%, respectively.

Yadava *et. al*,(2012) Conducted an experiment in Line \times tester design involving 14 lines and 5 testers and reported that both additive and non-additive gene actions were important in controlling yield-contributing traits. Variety Pusa Mustard 25 was identified as best general combiner among the parents. Significant and positive sca effects were observed for seed yield in 17 hybrids, 1000-seed weight in nine hybrids, number of siliquae on main shoot in nine hybrids, number of primary branches in six hybrids, point to first siliqua in six hybrids, main shoot length in five hybrids and number of secondary branches in four hybrids; and significant negative sca effects for point to first branch in four crosses and plant height in two crosses. Ten hybrids exhibited >15% heterobeltiosis, highly significant sca effects and higher per se performance.

Gami and Chauhan (2013) Reported combining ability, gene action and heterosis in a set of six parental lines, four tester and their hybrids of Indian mustard following an L x T mating design. The parents PUSA BOLD and BIO-902 exhibited significant and positive GCA effects for seed yield per plant while parental genotype PCR-7 was good general combiner for 1000-seed weight. The ratio of ó2 gca / ó2 sca being less than unity for all yield attributing traits indicated predominance of non-additive gene action for all the traits. The hybrids SKM-9820 X GM-2 and PCR-7 X VARUNA revealed highest SCA effects and Heterosis over better parent and standard parent. Considering mean performance, heterosis and combining ability effects, the parents GM 2, SKM-9033, PUSA BOLD, SKM-9820 and hybrids SKM- 9820 x GM 2, PCR-7 x VARUNA and SKM-9033 x VARUNA were found to be promising for exploitation of heterosis and to undertaken crossing programme to obtain desirable segregants.

Kang et. al, (2014) Estimated heterosis, GCA and SCA in Brassica napus in a set of 11 lines, 5 testers and 55 hybrids following L x T mating design. Data of 55 F1 hybrids and their parents were recorded for various seed yield and yield contributing traits. The results of analysis of variance differences were determined among entries for all the traits at significant level ($P \ge 0.01$ -0.05). The analysis of variance for combining ability revealed that the mean sum of squares due to lines were significant for all the traits except plant height and for testers the mean sum of squares were non- significant results. Highly significant results were found in L×T interaction for all traits except the trait days taken to 50% maturity. The estimation of SCA variance was noticed higher than GCA variance in all traits. The contributions of lines as compared to testers were greater in case of all the traits. Seven hybrid genotypes [CRS-5 × 20E, CRS-5 × KN (20-35), CRS-5 × B9527-1, S-9 × 5-F, MANROO × B9527-1, STAR × 20E, V-22 × KN(20-35)] were revealed highly significant heterosis and SCA effects for yield related traits.

2.3. Gene Action Analysis :

Gene action refers to the behavior or mode of expression of genes in a genetic population, knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also choice of appropriate breeding procedure for the genetic improvement of various quantitative characters.

Zaman *et.al*, (2010) Evaluated 18 advanced lines of mustard and were grouped into four clusters. The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity was present among the genotypes of distant group. The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence. But the highest cluster means for primary branches per plant and maximum seeds per siliquae with minimum seed yield per plant were obtained from the cluster II. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant.

Rao and Gulati (2001) Reported predominance of the non additive component for majority of the yield contributing characters. Estimates of narrow sense heritability medium to high for number of secondary branches and 1000-seed weight, high to medium for plant height and oil content, medium to low for seed yield/plant and for days to 50% flowering, days to maturity and number of seeds per siliqua.

3. Material and Method:

(Including location, place of work and facility available)

The experimental material of present study comprised of 21 hybrids developed from line x tester mating design (7 X 3). The crosses were made during *rabi* season 2017-18 by line x

tester mating design which will be evaluated during *rabi* season 2018-19 along with parents at field of Lovely Professional University, Phagwara, India.

Experimental detail

1 st season (crossing)		
Crop	:	Mustard
Mating design	:	Line x tester
Genotype	:	Difference varieties of mustard
Parent	:	10 (7 lines X 3 tester)
Experimental year	:	2017-18 (crossing)
Row to Row distance	:	45 cm
Season	:	Rabi
2 nd season (evaluation 2018 -2019)		
Number of genotype	:	31 (hybrid 21, parent 10)
Design	:	RBD (Randomize Block Design)
Replication	:	3

Statistical Analysis:

- 1. Estimation of heterosis
- 2. Analysis for varience
- 3. Combining ability analysis (kempthove 1957)
- 4. Gene action (Hill 1982, Lynch 1991)

Genotype details:

Sr.No.	Genotype name	Source
	LINES	
1.	RH-30	Directorate of Rapeseed Mustard Research, Bhartpur
2.	JD-6	Directorate of Rapeseed Mustard Research, Bhartpur
3.	TM-4	Directorate of Rapeseed Mustard Research, Bhartpur
4.	PBR-97	Directorate of Rapeseed Mustard Research, Bhartpur
5.	NRCHB-101	Directorate of Rapeseed Mustard Research, Bhartpur
6.	SRM-9	Directorate of Rapeseed Mustard Research, Bhartpur
7.	PUSA SAAG	Directorate of Rapeseed Mustard Research, Bhartpur
	TESTER	
1	JHUMKA	Directorate of Rapeseed Mustard Research, Bhartpur
2	PUSA JAIKISHAN	Directorate of Rapeseed Mustard Research, Bhartpur
3	URVASHI	Directorate of Rapeseed Mustard Research, Bhartpur

OBSERVATIONS TO BE RECORDED:

Α	Quantitative traits	B	Quality traits
1	Days to 50% flowering	1	Oil content
2	Days of maturity		
3	Plant height (cm)		
4	No of primary branches of plant		
5	Length of main raceme (cm)		
6	No of seeds per siliqua		
7	1000 seed weight(gm)		
8	Biological yield(gm)		
9	Harvest index(%)		
10	Siliqua on main raceme		
11	Siliqua length(cm)		
12	Seed yield per hector (kg)		
13	No of secondary branch of plant		
14	Siliqua size(cm)		

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