

Combining Ability Studies to Realize Maximum Heterosis for Morpho-Economic Traits in the Rapeseed, *Brassica napus* (L.)

MANOJ KUMAR*, R.K. SINGH* and MANOJ KUMAR YADAV**

*Department of Plant Breeding and Genetics,
Narain College, Shikohabad – 283135 (U.P.); and

**Department of Pharmacy, Dr.Bhimrao Ambedkar University, Agra-282002 (U.P.).

E-mail: manojkumarmnp@gmail.com

Abstract

The nature and magnitude of combining ability effects were studied for seed yield, its components and oil content in Rapeseed (*Brassica napus*). Analysis of variance for combining ability revealed that mean squares due to gca and sca were significant for all the characters. This indicates that both additive and non additive gene effects were important in the expression of these characters. The mean degree of dominance ($2sca/2gca$) was quite high for seed yield per plant, plant height, number of siliquae on main raceme and primary branch, indicating the involvement of non-additive gene effects in controlling the inheritance of these traits. The lines GSC-3A and CSM-25 were the best general combiner as judged by its consistent desirable gca effects over the F1S and F2S for six characters, namely, plant height, main raceme length, primary branches, secondary branches, number of siliquae on main raceme and seed yield per plant. The female, CAN-105, showing high gca effects for secondary branches, siliquae on main raceme, harvest index, seed yield per plant and oil content also showed high per se performance. The cross GSC-3A Sheetal and GSC-861-212 WBN-1 showed significantly high heterosis for seed yield and some of the yield contributing traits. The cross TKG-24 Neelam, BCN-25 Sheetal, CAN-101 WBN-1 and GSC-861-212 WBN-1 also exhibited high and significant heterosis for oil content per cent. As both additive and non-additive gene effects are present, breeding strategies that exploit both types of gene action such as biparental mating approach and reciprocal selections should be followed for the genetic improvement of seed yield and other traits and this will also give further opportunity for substantial release of hidden genetic variability.

Introduction

Oilseed crops and rapeseed-mustard account for 14% and 3% respectively of the gross area in India. Among the oil seed crops, rapeseed-mustard is next to groundnut, and currently it contributes nearly 22.2% and 24.2% of the oilseeds acreage and production, respectively (Kumar, 2005). *Brassica napus*, a rapeseed is grown in U.P., as well as in other

states of the country during rabi season. *Brassica napus* species is grown as a pure or a mixed crop system. But its low productivity is a major constraint in its large-scale cultivation in U.P.

Development of high yielding varieties can contribute significantly to increase productivity as well as production. Suitable breeding methodology and identification of superior parents are the pre-requisite for the development of high yielding genotypes. Sound understanding of gene effects involved in the expression of various yield attributes is of prime importance in formulating any breeding methodology. The knowledge of combining ability effects and their resulting variances are of paramount significance in deciding the selection procedure for exploiting either heterosis or obtaining new recombinants of desirable types in any crop. This possibility was explored in the present study and combining ability of desirable lines was investigated.

Materials and methods

15 lines viz., NDR-10, GSC-3A, CAN-101, RTM-365, RKN-9806, GSL-1, NUDB-38, GSC-861-212, PRM-101, HNS-003, CAN-105, BCN-25, CSM-25, TKG-24, TERI (00) R-985 and three testers namely Sheetal, Neelam and WBN-1 representing wide range of diversity were selected for the study. Experimental material consisted of 15 lines and 3 testers, which were officially received from DRMR, Sewar, Bharatpur (Rajasthan) in September, 2010 and also selected from different geographic regions considering its pedigree record. 45 possible cross combination were made during experiment I following line tester mating design of Kempthorne (1957). The parent and all F₁'s were grown in RBD with three replications during rabi season 2012-2013 and 2013-2014 as experiment II and experiment III at Agricultural Research Farm, Narain College, Shikohabad. The resulting 15 lines and 3 testers were raised in a randomized block design with a single row of 3 meters in three replications. The row to row distance was kept at 40 cm and plant to plant at 15 cm. The observations were recorded on ten characters viz; plant height, main raceme length, no. of primary branches, no. of secondary branches, harvest index,

1000-seed weight, oil content, and seed yield per plant.

Results and Discussion

The analysis of variance for combining ability revealed significant differences for all the characters studied in case of fifteen lines, which indicated the existence of genetic diversity in the parental materials. On the other hand, among testers highly significant differences were observed for plant height, main raceme length, number of primary and secondary branches. The mean sum of squares and appropriate degree of freedom are given in Table 1. The mean sum of squares due to females were found to be smaller than those due to males except for Sq/MR, Sq/L, TW and OC. Variations among line tester interaction were significant for all the characters. This indicated the manifestation of parental genetic variability in their crosses and presence of uniformity among the hybrids.

The significance of mean squares due to lines (females) and testers (male) indicated prevalence of additive variance for all the characters, except Sq/L and TW. The significance of mean squares due to line tester for all the characters provide a direct test indicating that non-additive variance was important for exploitation of the characters.

General combining ability estimates of parents are presented in Table 2. The result revealed that parents GSC-3A and CSM-25 were the best general combiner as judged by its consistent desirable *gca* effects over the F_1S and F_2S for six characters, namely, plant height, main raceme length, primary branch, secondary branches, number of siliquae on main raceme and seed yield per plant. The female CAN-105 showing high *gca* effects for secondary branches, siliquae on main raceme, harvest index seed yield per plant and oil content also showed high *per se* performance. Ghosh et al. (2002) has also reported that CAN-105 was a good general combiner for all the characters studied by them. Among the other lines, TERI(00) R-985 for plant height, main raceme length, siliqua length and oil content, GSL-1 for plant height, primary branches and secondary branches, NDR-10 for main raceme length and primary branches, RKN-9806 for primary branches and oil content, RTM-365 for main raceme length, were the best lines as revealed by their *per se* performance and *gca* effects. Among the testers, Sheetal was the best general combiner as proved by its consistent significant favourable *gca* effects over the F_1s for six characters, viz; plant height, primary branches, secondary branches, number of siliquae on main raceme, siliqua length and seed yield per plant. The tester, Neelam, exhibiting high *gca* effects for plant height, main raceme length, secondary branches and length of siliqua also expressed high *per se* performance. WBN-1 was another male parent which exhibited high *gca* effects for plant

height, 1000-seed weight and oil content along with better *per se* performance (Table 3).

The estimates of specific combining ability effects for most of the characters were lower in magnitude than *gca*. In most of the cases, the best F_1 , $1t$ hybrid combinations selected on the basis of *per se* performance recovered high *Sca* effects except plant height, harvest index and test weight. Similar results were reported by Anand & Rawat (1984), Sheikh & Singh (1998), Gosh et al. (2002) and Sridhar & Raut (2003) and Tripathi et al. (2005) In most of the 16 crosses, which exhibited desirable significant *sca* effects, one good and one poor or average general combiners were involved except GSC-3A WBN-1 (Poor Poor) for main raceme length, NDR-10 Sheetal (Poor Poor) for number of siliquae on main raceme, CSM-25 WBN-1 (Poor Poor) for length of siliqua and RKN-9806 Neelam (Poor Poor) for test weight. Similar observation of Poor Poor combinations of *gca* effects in Indian mustard have been reported by Singh et al. (1973), Krishna & Ghosh (1992) observed that poor combining parents locked the additive effects of good inbred, but were highly responsible to heterozygosis in the way of non-additive effects. Katiyar et al. (2000) reported that additive and non additive gene effects were also equally important in the inheritance of siliquae on main shoot, seed yield per plant and oil content.

Two of the three best combinations in general included one good general combiner and one poor or average general combiner in respect of the characters, main raceme length, primary and secondary branches, siliquae number and siliqua length, test weight, oil content and seed yield per plant. However, out of these best combinations viz., NDR-10 Sheetal, for main raceme length, GSL-1 Sheetal for number of primary branches and GSC-3A WBN-1 for seed yield included both the parents with high *gca* effects. It is, thus, seen that in most of the cases, the high low crosses exhibited greater *sca* effects, most likely because of the concentration of opposing alleles in the parents which showed high allelic interaction in F_1S . The high performance of the high high crosses may be described to accumulation of favorable alleles in F_1S as well as beneficial interaction effects such crosses are ideally suitable for exploitation either through pedigree selection or recurrent selection.

The results obtained from the present study clearly showed that genetic improvement is possible for seed yield. In order to capitalize on both types of gene action, any method such as $1t$ mating approach that maintains some heterozygosity would be beneficial. It would be more appropriate to follow $1t$ crossing among F_1s each having both types of gene components. The capacity of a parent to transmit gene

Table 1. Pooled analysis of variance of combining ability for line x tester analysis in *Brassica napus* L.

Source of variance	d.f.	Mean squares									
		PH	MRL	PB	SB	Sq/Mr.	Sq/L	HI	SY	TW	OC
1 Replications	2	2.35	14.52	0.25	12.75	273.33	2.67	0.0007	12.32	0.47	9.14
2 Lines	14	832.51	535.46*	4.54*	56.39*	914.88*	14.16*	0.0085*	534.42*	0.42	105.53*
3 Testers	2	2847.16	664.02*	8.14*	132.65*	256.80*	8.27	0.019*	1114.65	0.82	32.52
4 Line x Testers	45	223.42*	112.94*	1.13*	20.48*	315.15*	2.97*	0.003*	82.65*	0.27*	7.86*
5 Error	126	96.76	36.76	0.43	4.65	274.20	0.84	0.0002	23.77	0.23	2.04

* Significant at 5% level.

Table 2. General combining ability effects of lines and testers pooled of two years for 10 characters in *Brassica napus*.

Lines / Testers	PH	MRL	PB	SB	Sq/MR	Sq/L	HI	SY	TW	OC
1 NDR-10	-3.42	5.25**	0.24**	0.56	-1.31	0.36	0.00	0.17	0.01	0.34
2 GSC-3A	6.63**	2.87**	0.31**	2.56**	5.27**	0.67**	0.00	4.98**	-0.11	-1.08**
3 CAN-101	-0.76	1.50	-0.10	0.52	1.56	-0.20	0.01	5.61**	0.09	0.97**
4 RTM-365	-3.01	4.42**	-0.33**	-0.61	-1.37	-0.73**	0.01	0.95	0.07	0.48
5 RKN-9806	2.03	0.10	0.34**	0.48	0.08	-0.61**	-0.01	0.95	0.14*	0.64*
6 GSL-1	14.68**	3.93	0.53**	1.16**	1.42	0.42	-0.03*	0.85	0.02	-0.54
7 NUDB-38	3.52	0.85	-0.37**	-0.08	2.04	-0.67**	0.04*	0.85	0.01	-0.56
8 GSC-861-212	2.94	0.68	0.11	1.73**	-1.65	0.48**	0.00	2.42*	-0.05	1.51**
9 PRM-101	-3.95*	-0.62	-0.44**	-2.40	-0.35	-0.68**	0.01	1.82	0.06	1.74**
10 HNS-003	3.42	-4.47**	0.11	-1.25	2.06	-0.87**	0.01	5.13**	0.17*	0.40
11 CAN-105	0.65	2.02	0.56**	1.62**	3.46**	0.21	0.04**	4.17**	0.03	0.67*
12 BCN-25	-11.67**	-2.07	-0.12	-0.42	3.65**	-0.75**	0.08**	3.37**	-0.09	1.85**
13 CSM-25	-8.64	-1.12	-0.94**	-3.82	-3.58	-0.73**	-0.03**	-5.76**	-0.13	1.06**
14 TKG-24	-1.02	3.56**	0.11	-0.15	0.75	-0.18	0.00	-0.59	-0.17	1.86**
15 TERI(00)R-985	-2.64	-4.92	0.12	0.23	-3.55	0.55	0.01	3.38**	0.07	0.18
Testers										
1 Neelam	-6.86**	0.75	-0.45**	-1.37**	1.95	-0.37**	0.02	-0.65	0.01	0.25
2 Sheetal	5.03**	-0.92	0.38**	0.56**	-3.55*	-0.45**	-0.03*	-1.67**	0.17**	1.00**
3 WBN-1	-4.96**	3.16**	-0.10	0.12	1.15	0.35**	0.01	1.35**	-0.05	0.43**

* Significant at 5% and ** Significant at 1% level.

Table 3. Superior general combiners for 10 characters in *Brassica napus*.

Characters	Lines	Testers
1 Plant height (PH) (Dwarfness)	BCN-25, CSM-25, PRM-101, NDR-10, RTM-365	Neelam, WBN-1
2 Main raceme length (MRL)	NDR-10, RTM-365, GSL-1, TKG-24, GSC-3A	WBN-1
3 Number of primary branches (PB)	CAN-105, GSL-1, RKN-9806, GSC-3A, NDR-10	Sheetal
4 Number of secondary branches (SB)	GSC-3A, GSC-861-212, CAN-105, GSL-1, BCN-25	WBN-1
5 Number of siliquae on main raceme (Sq/MR)	GSC-3A, BCN-25, CAN-105	Neelam
6 Length of siliqua (Sq/L)	GSC-3A	WBN-1
7 Harvest index (HI)	BCN-25, NUDB-28, CAN-105	Neelam
8 1000-seed weight (Test weight, TW)	HNS-003, CSM-25	Sheetal
9 Seed yield per plant (SY)	CAN-101, HNS-003, GSC-3A, BCN-25, CAN-105, TERI(00) R-985, GSC-861-212	WBN-1
10 Oil content (%) (OC)	TKG-24, BCN-25, PRM-101, TERI(00) R-985, GSC-861-212, CAN-101	Sheetal, WBN-1

complex for traits to its progeny is known from the status of its gca effects. A variety may be good, poor or an average combiner for a given trait and when all the traits are considered, a variety will be combination of different levels of combining ability effects.

References

- Anand, I.J. & Rawat, D.S. 1984. Genetic diversity, combining ability and heterosis in Indian mustard. *Indian J. Genet.*, 44 : 226-234.
- Ghosh, S.K. & Gulati, S.C. 2002. Parental diversity to realize maximum heterosis in Indian mustard (*Brassica juncea* (L.) Czern & Coss). *Indian J. Genet.*, 62(1) : 25-28.
- Katiyar, R.K., Chamola, R. & Chopra, V.L. 2000. Heterosis and combining ability in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Indian J. Genet.*, 60 : 477-481.
- Kempthorne, O. 1957. *An Introduction to Genetic Statistics*. John Wiley and Sons, Inc. New York.
- Krishna Pal & Ghosh, S.K. 1992. Heterosis in relation to genetic divergence in rapeseed and mustard. *J. Oilseeds Res.*, 9 : 169-174.
- Kumar, Arvind 2005. Rapeseed-Mustard in India : Current and future prospects. In: *Advances in Rapeseed-Mustard Research Technology for Sustainable Production of Oilseeds*. National Research Centre on Rapeseed-Mustard (ICAR) 2005. Sewar, Bharatpur : 278-287.
- Sheikh, I.A. & Singh, J.N. 1998. Combining ability of seed yield and oil content in *Brassica juncea* (L.) Czern & Coss. *Indian J. Genet.*, 58 : 507-511.
- Singh, S.P. 1973. Heterosis and combining ability estimates in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Crop Sci.*, 13 : 497-499.
- Sridhar, K. & Raut, R.N. 2003. Estimation of gene effects for yield components and oil content in Indian x Exotic crosses of Indian mustard (*Brassica juncea* (L.) Czern & Coss). *Indian J. Genet.*, 63(1): 81-82.
- Tripathi, A.K., Ram Bhajan & Kamlesh Kumar 2005. Combining ability analysis for seed yield and its components over environments in Indian colza (*Brassica rapa* L. var. yellow sarson). *Indian J. Genet.*, 65(2): 137-138.

Gujarat Donkeys

Blood samples have been drawn from 70 donkeys each from Kutch and Jamnagar region. The donkeys are being genetically profiled and may soon stake claim as a separate breed! Gujarat's Banni buffalo, Kathiawari horse and Kharai camel have already been granted independent-breed status by the National Bureau of Animal Genetic

Resources (NBAGR), authority for registration of new breeds.

Gujarat primarily has two breeds of donkeys — Kutchi and Halari. Kutchi donkeys have smaller frame and darker complexion. They are very sturdy and are used for long journeys and for climbing mountains.