

DEVELOPMENT OF HIGH YIELDING TYPES OF *BRASSICA NAPUS* L. UNDER SALINITY STRESS

SHAMSA KANWAL¹, M. HAMMAD NADEEM TAHIR², HAFEEZ AHMAD SADAQAT³ AND BUSHRA SADIA⁴

^{1,3}University of Agriculture, Faisalabad, ²Muhammad Nawaz Sharif University of Agriculture, Multan, Pakistan

⁴Centre of Agriculture Biotechnology and Biochemistry, Pakistan

*Corresponding author's email: kanwalshamsa32@yahoo.com

Abstract

Six sensitive and ten salinity tolerant lines along with their resultant crosses obtained after crossing in Line × Tester mating design were evaluated at maturity stage in a pot experiment. Data were recorded on various seed yield (days to 50% flowering, days to 50% maturity, plant height, number of primary branches, number of silique per plant, seeds per silique, oil content, thousand seed weight, seed yield per plant) and salinity tolerance related traits (proline content, Na⁺/K⁺ ratio, osmotic potential). Data were recorded on yield and salinity tolerance related traits, were analyzed to assess the variability in germplasm under studies and general and specific combining ability effects. Results showed that breeding material being studied had genetic variability that can be used in development of high yielding salinity tolerant types of *Brassica napus* L. Combining ability analysis revealed that lines R-3 and 23627 and tester Faisal were best general combiners under control conditions and on exposure to higher levels of salinity also. Crosses R-3×Laclone, RBJ-8007×Laclone and ZMR-1×ZMR-3 were observed to have positive significant specific combining ability effects for most of the traits under control and salinity stress conditions that can be further evaluated for growing under saline conditions. Proline content, Na⁺/K⁺ ratio and osmotic potential might be used as salinity tolerance indicators.

Key words: Salinity, Genetic variability, Combining ability, Line × Tester, Proline, Na⁺/K⁺ ratio.

Introduction

Pakistan is deficient in edible oil production and meets its requirements through import of either edible oil. The total edible oil available in Pakistan during 2017-18 was 3.623 million tonnes, out of this only 0.431 million tonnes i.e., 12% of total availability was locally produced and 88% was imported by spending 320.893 billion rupees (Govt. of Pakistan, 2017-18). There is dire need to focus on oilseed crops for developing high yielding hybrids and varieties to meet the local requirements of oil. The most common brassica types grown for commercial purpose in subcontinent and other parts of the world include rapeseeds (*B. campestris* and *B. napus*) and mustards (*B. juncea* and *B. carinata*). Its oil is of great importance as it is the only oil which contains 2:1 optimal ratio of linoleic (20%) to linolenic acid (10%) and oleic acid (60%) (Zebarjadi *et al.*, 2006). Total area covered by Brassicas in Pakistan is 0.51 million acres and total production is 0.206 million tonnes seed and 0.067 million tonnes of oil (Govt. of Pakistan, 2017-18). Increasing area under rapeseed and developing varieties with enhanced genetic potential for seed and oil yield may contribute towards increasing edible oil production in country. As rapeseed is the 2nd leading source of edible oil in Pakistan, enhancement in its production may help in reducing the import of edible oils (Nassimi *et al.*, 2006). This might be achieved by increasing the yielding potential and increasing the area by utilization of marginal lands.

Almost 42% of the irrigated area is salt affected in Pakistan (Haq *et al.*, 2014). The main causes for increasing saline area in developing countries include less rainfall, higher rate of evapotranspiration, high level of salts in irrigation water, presence of rocks and defective methods of using and managing water (Arzani, 2008). Two lines of action may be adopted to overcome the problem of salinity: a) reclamation of saline soils through

chemical amendments and b) development of salinity tolerant cultivars. There are situations where good quality water is not available or where saline soils cannot be reclaimed due to restricted availability of natural and economic resources. In such situations development and utilization of tolerant varieties becomes useful. Major role of salt tolerant varieties is to obtain better yield of crops grown in naturally salt affected areas and provide an option of putting marginal lands under cultivation.

Brassica napus is the need of the time and salinity is crucial stress. Salinity had adverse effects on brassica species. Reduction in yield contributing traits has been observed in brassicas under salinity which ultimately affect the oil quality and quantity particularly in *B. napus* (Tantawy *et al.*, 2009; Ghuge *et al.*, 2011; Tarinejad *et al.*, 2013). Salinity affects the vegetative as well as reproductive growth in brassicas negatively due to utilization of energy resources in maintenance of plants rather than in growth and development (Gul and Ahmad, 2004). Negative influence of salinity in yield attributes results in accumulation of more sodium ions and restriction of the availability of potassium required in many metabolic processes leading to the possible way of reducing yield (Wani *et al.*, 2013). Sensitive cultivars accumulate Na⁺ ions more quickly than the tolerant one which causes cell death ultimately leading to plant death in *Brassica napus*. Plants tolerate the salinity by osmotic adjustment and through maintenance of Na⁺/K⁺ ion ratio by regulating the uptake of K⁺ and restricting Na⁺ ions from entering the cell (Ashraf & McNilley, 2004).

Understanding of genetic behavior of traits related to salinity tolerance helps in improvement through breeding. Combining ability may help in identification of potential parents, understanding the nature of gene action involved, introgressing elite traits, and maximizing yield for a successful breeding programme. Line × tester (Kempthorne, 1957) is an efficient technique for assessing

the combining ability effects of a large number of accessions. Both GCA and SCA provide accurate information for determining the genetic basis of economically important traits of plants (Singh and Chaudhury, 1977). Higher general combining ability effects show the additive component of total variance and specific combining ability effects specify non additive gene effects. The research work was planned to determine genetic variability among entries under control and salinity stress conditions. Identification of potential parents and best cross combinations under salinity stress was another great objective of this study.

Material and Methods

Ten salinity tolerant accessions (G-96, ZNR-1, ZM-M-5, 23627, R-3, ZMR-10, BLBN, RBJ-8007, ZMR-2, B-56) were used as lines (female parents) and six salinity sensitive (Legend, Laclone, Faisal, Shiralee, Long and ZMR-5) as testers (male parents) to develop crosses in a Line \times tester mating design through controlled pollinations. Crosses, parents and check varieties collected from Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad were sown in pots filled with soil. The experiment was laid out in randomized complete block design using three replications with two factorial structured treatments. Salinity level of soil was measured and three levels of salinity i.e., T1: 0mM, T2: 120mM and T3: 150mM were maintained by adding salt solution in pots filled with 12kg soil each using following protocol:

$$\text{Salts per kg of soil} = \text{TSS} \times \text{Eq. Wt of NaCl} \times \text{SP} / 1000 \times 100$$

$$\text{Total soluble salts (TSS)} = \text{Required EC} \times 10$$

$$\text{Saturation percentage (SP)} = \frac{\text{Loss in wt. oven drying}}{\text{Wt. of saturated soil paste without china dish}}$$

$$\text{Required EC} = \text{Desired EC} - \text{Original EC}$$

Calculated amount of salt i.e. 14.6 g and 18.96 g for each treatment was used to prepare one liter salt solution for each pot separately to develop the required salinity level of 120mM and 150mM respectively. The prepared salt solutions were added to the soil at the time of first irrigation. Amount of soluble salts was measured using saturated paste method (Dellavalle, 1992). Soil samples from different pots were taken from all treatments using tube sampler. Soil samples were saturated by adding double distilled water to the beaker containing sieved soil while stirring with spatula. After mixing it was allowed to stand overnight then saturated paste was transferred to Buchner funnel with filter paper in place. Vacuum was applied and saturated paste extract was collected in a flask. EC of the extract was measured using portable EC meter (HI 99300) for ensuring the required EC in each treatment. Data were noted on days to 50% flowering, days to 50% maturity, plant height, number of primary branches, and number of siliquae per plant, number of seeds per siliquae, oil contents, 1000

seed weight, and seed yield per plant after tagging of two plants of each entry in each replication.

Biometrical approaches: The recorded data were subjected to analysis of variance following Steel *et al.*, (1997). Combining abilities were computed following Line \times Tester analysis outlined by Kempthorne (1957).

Genetic variability: Table 1 presents the results for analysis of variance of yield and salinity tolerance related traits under studies. Entries differed significantly for days to 50% flowering, number of primary branches, oil contents, Na⁺/K⁺ ratio, proline contents, osmotic potential and seed yield per plant under all the treatments. Parents were found significantly different for number of primary branches, Na⁺/K⁺ ratio, proline contents, osmotic potential and oil contents under control and salt stress treatments. Significant differences among parents vs crosses were observed for plant height and days to 50% maturity, Na⁺/K⁺ ratio, proline contents and osmotic potential under control conditions as well as at higher levels of salinity. Crosses were significantly different for plant height, number of seeds per siliquae, oil contents, Na⁺/K⁺ ratio and proline contents. Lines differed significantly for thousand seed weight, oil contents, Na⁺/K⁺ ratio, proline contents and osmotic potential under all the treatments. Testers were found significantly different under all treatments for number of primary branches, Na⁺/K⁺ ratio and proline contents. Line \times tester interaction differed significantly for number of seeds per siliquae and thousand seed weight under control and salinity stress treatments.

General combining ability effects: Tables 2, 3 and 4 present the estimates of general combining ability effects for various morphological traits under T1, T2 and T3 respectively. Under T1, line R-3 and 23627 had significant and positive GCA effects for most of the traits. Among testers Faisal and Long showed significant and positive GCA effects for most of the traits. Under T2, lines R-3 and 23627 whereas, the testers Shiralee and Faisal had significant and positive GCA effects for most of the traits. Under T3, significant and positive GCA effects for most of the traits were observed for lines R-3, ZNR-1 and 23627. Testers Long and Faisal had significant and positive GCA effects for most of the traits. Under all treatments, lines R-3 and 23627 and tester Faisal had significant and positive GCA effects for most of the morphological traits. Under higher levels of salinity lines BLBN and R-3 had significant and positive GCA effects for the salinity tolerance related traits like Na⁺/K⁺ ratio, proline content and osmotic potential.

Specific combining ability effects: Specific combining ability effects of various yield attributes traits are presented in Table 5 under T1, Table 6 under T2 and Table 7 under T3. Crosses R-3 \times Laclone, RBJ-8007 \times Laclone, ZMR-1 \times ZMR-3, G-96 \times Faisal and B-56 \times Legend had significant and positive SCA effects for most of traits under T1. Under T2, significant and positive SCA effects for most of traits were observed for crosses

R-3×Laclone, RBJ-8007 × Laclone, G-96 × Long, ZMM-5×ZMR-3, ZMR-1×ZMR-3 and G-96×Faisal. Crosses R-3×Laclone, RBJ-8007 × Laclone, G-96 × Faisal, G-96 × long, 23627 × Shiralee, ZMR-1×ZMR-3 and B-56×Legend had significant and positive SCA effects for most of the traits under T3. Significant and positive SCA effects for most of traits were observed for crosses R-3×Laclone, RBJ-8007×Laclone, ZMR-1×ZMR-3 and G-

96×Faisal under all treatments. They showed significant and positive SCA effects for days to 50% flowering, days to 50% maturity, number of seeds per silique and thousand seed weight under all treatments. Crosses B-56×ZMR-3 and RBJ-8007×Legend had significant and positive SCA effects for salinity tolerance related traits like Na⁺/K⁺ ratio, proline content and osmotic potential at higher levels of salinity.

Table 1. Mean squares from analysis of variances for maturity traits under control and salinity treatments.

SOV	DF	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP	Na ⁺ /K ⁺	PC	OP
T1 (0mM)													
Replications	2	254.92*	15.76	4.75	0.26**	66.93	14.97**	4.49**	19.43*	97.99	8.19**	9.20**	5.92*
Entries	75	132.35**	41.78*	34.11**	10.02	75.42**	21.63**	4.58**	3.44*	40.96*	9.71**	8.02*	2.35**
Parents (P)	15	103.96**	101.98**	39.81**	0.01	43.40	32.24	8.34**	3.42*	32.46*	17.09**	6.01**	1.91**
Crosses (C)	59	114.08**	21.95	28.90**	0.3	48.58*	64.93**	3.19**	3.40*	10.47	4.8*	9.32*	3.96**
P vs C	1	370.91**	23.38	153.52**	1.003	21.15**	24.31**	11.99**	5.10	21.64	9.00**	12.32**	4.08**
Lines (L)	9	764.50**	35.93	34.86**	2.05*	55.11**	16.18*	1.47	5.00*	62.82	22.87*	22.88*	4.50**
Testers (T)	5	930.10	49.02	24.11**	4.03	64.48*	49.75	4.71**	2.97	61.33	36.78**	2.66**	3.10
L× T	45	240.80**	33.54	28.67**	1.02	37.89*	19.51**	3.23**	3.17	29.82	1.91	0.90	0.08
Error	28	360.63	14.48	6.78	4.42	20.47	4.02	0.67	4.69	5.47	8.19**	9.20**	5.92*
T2 (120mM)													
Replications	2	67.10	31.97*	90.03**	35.86	274.83*	80.72	97.99	5.281	50.72	26.13*	23.5*	4.97**
Entries	75	90.81	15.91*	111.86	68.12	268.90*	38.52*	140.96*	51.012**	38.52*	44.74*	9.90*	2.63**
Parents (P)	15	96.21	66.23	164.79	49.41	135.15	11.66	232.46*	63.27**	11.66	31.5*	26.8*	6.31**
Crosses (C)	59	76.58*	19.88	95.69	70.30	231.69*	48.03	110.47	22.4**	18.03	10.9*	13.6*	2.24
P vs C	1	129.34*	53.55	95.67*	197.64	42.80	1.10	201.64	31.32**	1.10	26.13*	30.5*	4.93**
Lines (L)	9	59.28	83.49	155.00	76.88	424.91	89.49*	62.82	5.51**	9.49*	44.74*	19.9*	6.18*
Testers (T)	5	75.56	49.60	78.82	43.52	170.23	38.00	61.33*	9.28	38.00	13.9*	13.6*	0.75
L× T	45	60.24	21.21*	87.20	74.34	205.34*	41.74*	129.82	72.7**	41.74	0.5	2.8	0.05
Error	28	111.82	6.29	8.36	8.31	15.17	0.48	2.47	0.98	1.48	26.13*	23.5*	4.97**
T3 (150mM)													
Replications	2	16.92*	98.95*	107.10	651.07*	1001.03**	23.06	51.80*	60.12	4.83*	15.7*	9.76*	4.75
Entries	75	99.30*	52.12*	98.01	123.11*	99.06	48.02	32.10*	26.52*	8.90*	8.06*	5.80*	4.11**
Parents (P)	15	14.12	23.05	78.11	87.13	105.99	29.11	75.25*	9.66*	5.15	12.61*	19.60*	13.52**
Crosses (C)	59	95.09**	108.01**	96.08	99.08	45.79*	25.37	13.49	68.03*	21.69	1.78*	8.60*	39.81**
P vs C	1	20.09*	13.04	89.34*	29.45	39.07	119.24	66.09	0.90	8.80	15.70*	9.70*	8.90**
Lines (L)	9	99.88	145.88*	123.18	99.69	175.00	66.89*	39.01	79.39*	4.91	788.6*	4.80*	14.86**
Testers (T)	5	99.07*	100.09*	85.06	189.50*	88.22	47.32	19.03*	28.00	9.23	99.78*	7.60*	4.11**
L× T	45	108.15**	109.06**	89.04	111.01	89.10*	78.04*	23.04	22.04	5.34	0.86	1.6	0.67
Error	28	45.03	14.09	10.32	15.14	21.26	1.01	1.07	12.78	0.70	15.7*	9.76*	4.75

*= Significant at 0.05 probability level ** = Significant at 0.01 probability level

SOV= Source of variation, DF= Degrees of freedom, PH= Plant height, DTF= Days to 50% flowering, DTM= Days to 50% maturity, SP= Silique per plant, SS= Seeds per silique, TSW= Thousand seed weight, PB= Primary branches, OC= Oil content, YP= Seed yield per plant, Na⁺/K⁺ = Na⁺/K⁺ ion ratio, PC= Proline content, OP= Osmotic potential

Table 2. General combining ability effects of lines and testers for morphological traits of Brassica napus under T1 (0mM).

	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
Lines									
23627	10.48	-14.34	2.14	0.05	50.57	7.53	0.24	0.04	0.07
R-3	35.37	30.65	0.80	-0.04	109.3	26.28	-0.16	-0.28	0.34
Standard error	9.89	13.93	0.61	0.03	38.60	11.49	0.19	0.51	0.27
Testers									
Long	18.96	9.86	1.58	0.02	30.77	3.81	-0.55	0.08	0.27
Faisal	-0.27	18.09	0.50	-0.07	-23.79	-6.00	0.69	0.60	0.08
Standard error	9.89	13.93	0.61	0.03	38.60	11.49	0.19	0.51	0.27

PH=Plant height, DTF= Days to 50% flowering, DTM= Days to 50% maturity, SP= Silique per plant, SS= Seeds per silique, TSW= Thousand seed weight, PB= Primary branches, OC= Oil content, YP= Seed yield per plant

Table 3. General combining ability effects of lines and testers for morphological traits of *Brassica napus* under T2 (120mM).

	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
Lines									
23627	15.54	16.56	1.30	-0.40	-29.39	18.09	-3.11	3.89	-5.15
R-3	8.49	2.14	3.77	4.66	16.78	5.04	3.83	-0.97	-2.81
Standard error	15.65	15.56	3.73	3.70	15.65	15.56	3.73	3.70	15.65
Testers									
Faisal	12.62	50.70	4.74	4.46	-8.43	0.30	1.32	4.82	-0.28
Shiralee	24.16	66.30	3.11	2.55	29.47	10.95	5.44	0.55	6.76
Standard error	13.83	13.09	2.79	3.55	13.83	13.09	2.79	3.55	5.21

PH=Plant height, DTF= Days to 50% flowering, DTM= Days to 50% maturity, SP= Silique per plant, SS= Seeds per silique, TSW= Thousand seed weight, PB= Primary branches, OC= Oil content, YP= Seed yield per plant

Table 4. General combining ability effects of lines and testers for morphological traits of *Brassica napus* under T3 (150mM).

	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
Lines									
ZNR-1	2.99	0.25	0.08	0.66	0.15	-0.10	0.07	0.07	0.26
23627	1.58	2.01	0.75	-0.44	0.13	0.22	-0.02	-0.08	-0.24
R-3	-0.01	-0.07	0.52	0.62	-0.01	0.05	-0.01	2.90	2.40
Standard error	0.91	0.88	0.44	0.30	0.15	0.03	0.06	1.41	1.12
Testers									
Long	18.96	9.86	1.58	0.02	30.77	3.81	-0.55	1.11	-0.95
Faisal	2.10	-2.16	-2.04	2.14	4.23	-1.11	-1.42	2.01	1.88
Standard error	3.23	3.27	0.57	0.75	3.16	0.36	8.54	1.37	2.54

PH=Plant height, DTF= Days to 50% flowering, DTM= Days to 50% maturity, SP= Silique per plant, SS= Seeds per silique, TSW= Thousand seed weight, PB= Primary branches, OC= Oil content, YP= Seed yield per plant

Table 5. Specific combining ability effects of crosses for morphological traits in *Brassica napus* under T1 (0mM).

Crosses	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
G-96 × Faisal	35.30	42.03	28.20	14.46	50.16	100.61	28.30	28.46	9.42
R-3 × Laclone	45.23	25.99	14.01	34.72	95.57	166.89	15.03	33.82	35.96
ZMR-1 × ZMR-3	60.01	70.05	10.10	23.64	93.70	106.33	20.10	25.84	25.63
B-56 × Legend	32.99	70.99	19.86	34.37	107.92	84.81	17.86	35.37	6.12
B-56 × ZMR-3	40.40	80.01	20.88	10.04	5.47	-38.21	29.89	12.05	24.90
RBJ-8007 × Legend	-17.05	65.71	-14.34	4.21	-16.25	49.63	-14.44	6.91	0.12
SE	31.59	22.08	1.78	20.90	36.64	68.31	19.89	27.91	20.33

PH=Plant height, DTF=Days to 50% flowering, DTM=Days to 50% maturity, SP=Silique per plant, SS=Seeds per silique, TSW= Thousand seed weight, PB=Primary branches, OC=Oil content, YP= seed yield per plant

Table 6. Specific combining ability effects of crosses for morphological traits in *Brassica napus* under T2 (120mM).

Crosses	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
G-96 × Faisal	59.65	116.68	21.41	13.56	58.67	117.68	16.05	18.08	61.02
G-96 × Long	41.05	97.35	20.89	13.48	126.23	99.19	25.67	17.97	1.55
ZMM-5 × ZMR-3	35.62	111.25	13.81	5.85	33.18	119.22	10.36	13.61	44.54
R-3 × Laclone	39.01	150.15	17.58	17.01	111.78	95.20	31.95	39.56	42.06
ZMR-1 × ZMR-3	99.05	121.38	23.51	10.55	109.59	124.37	15.99	30.22	40.97
B-56 × ZMR-3	57.97	55.07	34.96	9.59	6.39	-44.70	33.78	14.10	29.12
RBJ-8007 × Legend	-17.02	54.09	-16.89	5.50	-19.01	58.05	-11.48	8.08	0.14
RBJ-8007 × Laclone	40.37	70.01	12.17	4.69	39.37	77.08	11.48	6.90	0.48
SE	30.19	13.08	2.18	14.39	27.15	23.67	24.05	7.21	35.33

PH=Plant height, DTF=Days to 50% flowering, DTM=Days to 50% maturity, SP=Silique per plant, SS=Seeds per silique, TSW= Thousand seed weight, PB=Primary branches, OC=Oil content, YP= seed yield per plant

Table 7. Specific combining ability effects of crosses for morphological traits in *Brassica napus* under T3 (150mM).

Crosses	PH	DTF	DTM	SP	SS	TSW	PB	OC	YP
G-96×Faisal	29.34	16.47	1.71	23.87	77.49	155.41	28.27	16.23	-14.55
G-96×Long	63.12	13.89	1.67	23.74	66.70	131.00	27.59	16.14	2.04
23627×Shiralee	36.59	22.08	0.79	22.91	96.64	208.31	12.89	15.58	-24.10
R-3×Laclone	55.89	27.33	1.41	52.25	147.62	77.79	23.22	35.53	15.55
ZMR-1×ZMR-3	54.80	-17.41	1.88	39.91	-144.73	64.25	31.05	27.14	39.58
B-56×Legend	63.12	13.89	1.67	23.74	66.70	131.00	27.59	16.14	9.45
B-56×ZMR-3	29.40	16.26	2.80	18.61	8.44	-59.03	46.17	12.66	38.46
RBJ-8007×Legend	-9.50	8.13	1.35	10.67	-25.10	76.66	-22.30	17.26	0.19
RBJ-8007×Laclone	19.68	30.79	10.17	19.12	51.99	101.79	2.87	6.20	20.64
SE	35.69	16.08	0.78	18.40	26.46	63.41	14.53	15.21	13.33

PH=Plant height, DTF=Days to 50% flowering, DTM=Days to 50% maturity, SP=Siliques per plant, SS=Seeds per silique, TSW=Thousand seed weight, PB=Primary branches, OC=Oil content, YP= seed yield per plant

Discussions

The yield enhancement and breeding for new varieties with salinity tolerance requires information about the combining ability effects of accessions and nature of gene action governing various traits. This information may be utilized in identification of potential parents, superior cross combinations and studying the inheritance pattern of traits (Dudley & Moll, 1969; Lippman & Zamir, 2007; Bi *et al.*, 2015). Additive portion of total variance are given in terms of GCA effects which shows that trait is more influenced by the inherent genetic makeup of the accessions (Cruz and Regazzi, 1994). Lines R-3 and 23627 and tester Faisal had positive significant GCA effects for most of the morphological traits under all the treatments. Lines BLBN and R-3 had positive significant GCA effects for traits like Na^+/K^+ ratio, osmotic potential and proline contents which are related to salinity tolerance. These lines and testers may be used as parents for hybridization program aiming at yield improvement and enhancement of salinity tolerance in *Brassica napus*. (Skoric, 1992; Rameeh, 2012). Specific combining ability effects indicate the non-additive genetic effects of total variance owing to the dominance and/or epistasis. Crosses R-3×Laclone, RBJ-8007×Laclone, G-96×Faisal and ZMR-1×ZMR-3 had significant and positive SCA effects for most of the morphological traits under all treatments. Crosses B-56×ZMR-3 and RBJ-8007×Legend had significant and positive SCA effects for salinity tolerance related traits like Na^+/K^+ ratio, proline content and osmotic potential at higher levels of salinity. Combination of high × low, low × high and low × low general combiners such as R-3×Laclone (high × low), G-96×Faisal (low × high), ZMR-1×ZMR-3 and RBJ-8007×Laclone (low × low) for various traits under normal and salt stress conditions and B-56×ZMR-3 and RBJ-8007×Legend (low × low) for salinity tolerance related traits under high salt stress resulted in crosses with significant positive SCA effects. Crosses having at least one parent with good general combining ability effects like R-3×Laclone and G-96×Faisal would enhance the crop productivity by increasing the frequency of favorable genes. This may be

attributed to interaction of dominant and recessive genes of good and poor combiners. The high SCA effects of crosses involving low × low general combiners may be due to over dominance or dominance × dominance type of gene action. Such crosses may be exploited for heterosis breeding. Significant and positive GCA and SCA effects for various yield and salinity tolerance related traits in *Brassica napus* breeding material studied in present research indicate the contribution of both additive and non-additive type of gene action in inheritance of these traits (Sabaghnia *et al.*, 2010). In present studies hybrids with high positive SCA effects were produced by the combination parents with high and low GCA effects indicated that there is no direct association between GCA effects of parents and SCA effects of hybrid combinations. It may be explained on the basis of gene action as GCA effects are mostly due to additive type of gene action and SCA effects are due to dominance and epistasis (Rosamma & Vijaykumar, 2005). Improvement of the varieties superior in desired traits is possible through reshuffling of the genes through hybridization of selected parents (Rameeh, 2012).

The results suggest that breeding material used in present research can be used for the improving seed yield and tolerance to salinity in *Brassica napus*. Lines ZMR-2, R-3, 23627 and testers Faisal and Shiralee may be used as parents in hybridization. Crosses R-3×Laclone, RBJ-8007×Laclone and ZMR-1×ZMR-3 may be further evaluated under saline environments for checking their potential under different agro-climatic environments. Selection is suggested in segregating generations for improving all yield related traits.

References

- Arzani, A. 2008. Improving salinity tolerance in crop plants: a biotechnological view. *Vitro Cell. Dev. Biol. Plant*, 44: 373-383.
- Ashraf, M. and T. McNeilly. 2004. Salinity tolerance in Brassica oilseeds. *Crit. Rev. Plant Sci.*, 23(2): 157-174.
- Bi, Y., W. Li, J. Xiao, H. Lin, M. Liu, X. Luan, B. Zhang, X. Xie, D. Goo and Y. Lai. 2015. Heterosis and combining ability estimates in isoflavone content using different parental soybean accessions: wild soybean, a valuable germplasm for soybean breeding. *Plos One*, 10(1): 1-13.

- Cruz, C.D. and A. Regazzi. 1994. *J. Biometric models applied to genetic improvement*. Vicoso, MG: University Press, 390.
- Dellavalle, N.B. (ed.). 1992. Determination of soil-paste pH and conductivity of saturation extract. In *Handbook on reference methods for soil analysis. Soil and Plant Analysis Council, Inc. Athens, GA*. 40-43.
- Dudley, J.W. and R.H. Moll. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. *Crop Sci.*, 9: 257-262.
- Ghuge, S.A., A.N. Rai, B.G. Khandagale and S. Penna. 2011. Salt-induced stress responses of Brassica (*Brassica juncea* L.) genotypes. *Arch. Agron. Soil Sci.*, 57: 127-136.
- Government of Pakistan. 2017-18. Pakistan Economic Survey, Ministry of Finance, Economic Advisor's Wing, Islamabad.
- Gul, H. and R. Ahmad. 2004. Effect of different irrigation intervals on growth of canola (*Brassica napus* L.) under different salinity levels. *Pak. J. Bot.*, 36: 359-372.
- Haq, M.A., S. Akram, J. Akhtar, M. Saqib, Z.A. Saqib, G.H. Abbasi and M. Jan. 2014. Morpho-physiological characterization of sunflower genotypes (*Helianthus annuus* L.) under saline condition. *Pak. J. Agri. Sci.*, 50: 49-54.
- Kemphorne, O. 1957. *Introduction to Genetic Statistics*. Jhon Wiley and Sons, Inc. New York, USA.
- Lippman, Z.B. and D. Zamir. 2007. Heterosis: revisiting the magic. *Trends in Genetics*, 23: 60-66.
- Nassimi, A. W., Raziuddin, S. Ali, G. Hassan and N. Ali. 2006. Combining ability analysis for maturity and other traits in rapeseed (*Brassica napus* L.). *J. Agron.*, 5: 523-526.
- Rameeh, V. 2012. Combining ability analysis of plant height and yield components in spring type of rapeseed varieties (*Brassica napus* L.) using line \times tester analysis. *Int. J. Agri. Forest.*, 2(1): 58-62.
- Rosamma, C.A. and N.K. Vijayakumar. 2005. Heterosis and combining ability in rice (*Oryza sativa* L.) hybrids developed for Kerala state. *Ind. J. Genet.*, 65(2): 119-120.
- Sabaghnia, N., H. Dehghani, B. Alizadeh and M. Mohghaddan. 2010. Heterosis and combining ability analysis for oil yield and its components in rapeseed. *Aust. J. Crop Sci.*, 4: 390-397.
- Singh R.K. and B.D. Chaudhary. 1977. *Biometrical methods in quantitative genetic analysis*, Kalyani Publishers, New Delhi 57-58.
- Skoric, D. 1992. Achievements and future directions of sunflower breeding. *Field Crops Res.*, 30: 231-270.
- Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. *Principles and Procedures of Statistics; A biometrical approach* (2nd ed). McGraw Hill Book Co. Inc. Singapore.
- Tantawy, A.S., A.M.R. Abdel-Mawgoud, M.A. El-Nemr and Y.G. Chamoun. 2009. Alleviation of salinity effects on tomato plants by application of amino acids and growth regulators. *Eur. J. Sci. Res.*, 30: 484-494.
- Tarinejad, A., H. Ghayoumi and B. Alizadeh. 2013. Effect of different natural salinity levels on yield and yield components of canola cultivars. *Tech. J. Engin. App. Sci.*, 3(9): 768-775.
- Wani, S.H., N.B. Singh, A. Haribhushan and J.I. Mir. 2013 - Compatible solute engineering in plants for abiotic stress tolerance - role of glycine betaine. *Current Genomics*, 14: 157165.
- Zebarzadi, A.R., M.J. Javaran, A.H. Salmanian, G. Karimzadeh., A. Moeini and A. Mousavi. 2006. Transformation of rapeseed (*Brassica napus* L.) plants with sense and antisense constructs of the fatty acid elongase gene. *Iranian J. Biotech.*, 4: 79-87.

(Received for publication 3 January 2018)