Frontiers in Crop Improvement, Vol. 6 (1) : 52-55 (2018)
Print ISSN : 2393-8234, Online ISSN : 2454-6011

ASTHA FOUNDATION
Meerut (U.P.) INDIA

GENETIC DIVERGENCE IN YELLOW SARSON USING NON HEIRARCHICAL EUCLIDEAN CLUSTER ANALYSIS

Kumari Shanti[1], Kamlesh Kumar[2] and Krishna Kumari[3]
[1]*Division of Genetics, IARI, New Delhi,* [2]*Deptt. of Genetics and Plant Breeding, NDUA & T., Faizabad*
[3]*Deptt. of Botany, C.C.S. University, Meerut*

ABSTRACT

Genetic divergence among 44 germplasm lines of yellow sarson (*Brassica rapa* var. yellow sarson) was investigated to select the parents for hybridization using Mahalanobis D^2 statistics. Cluster analysis was used for grouping 49 yellow sarson genotypes. The genotypes fall into 8 distinct non-overlapping clusters. Cluster first comprises of 16 genotypes, evolving as the largest cluster, followed by cluster seventh with 10 genotypes, cluster second and seventh with 6 genotypes each, cluster third comprises of 5 genotypes, cluster fifth comprises of 3 genotypes, cluster fourth comprises of 2 genotypes, whereas cluster six emerged as mono-genotypic. The maximum intra-cluster distance (D^2) was found in cluster fourth (D^2=39.433), followed by cluster fifth (27.206), seventh (18.085), second (13.641), eighth (12.780), first (11.22), third (9.369) and the remaining one cluster i.e. sixth had minimum intra-cluster value (0.000). The maximum inter-cluster distance was found between cluster fourth and sixth (69.204), followed by cluster second and fourth (54.957), third and sixth (52.819), first and sixth (52.627) and cluster fifth and sixth (49.277). The minimum inter-cluster distance was observed between cluster first and third (17.089), first and second (18.492), which indicated the genotypes in these clusters were less divergent.

Key words : *Genetic divergence, cluster hybridization, brassica rapa var. yellow sarson.*

Among Oilseed crops, especially *Brassica* species play a pivotal role in the agricultural economy of India. The important oilseed crops grown in the country in order of importance are groundnut, rapeseed-mustard, sesame, in seed, safflower, castor, sunflower and *niger*. Among these, *Brassica rapa var.*yellow *sarson*is *rabi* crop of eastern India comprising Uttar Pradesh, Bihar, West Bengal and Assam. India is one of the leading oilseed producing country in the world and it is a rich center of diversity for rapeseed-mustard. *Brassica* (Rapeseed-mustard) is the second most important edible oilseed crop in the India after groundnut and accounts for nearly 30% of the total oil seeds produced in the country. When compared to other edible oils, the rapeseed-mustard oil has the lowest amount of harmful saturated fatty acids. It also contains adequate amount of two essential fatty acids, linoleic and linolenic, which are not present in many of the other edible oils. Indian cultivars have high erucic acid 40-50 % in oil and high glucosinolate (18-120 μ moles (g) in seed meal). So there is an urgent need to make concerted efforts for breeding varieties with improved quality of oil (<2 % erucic acid) and meal(<22 μ moles /g fat free meal glucosinolate) at par with inter-national quality norms

Rapeseed and mustard occupy an important position among oilseeds. In world the total area under rapeseed-mustard during 2012-2013, was 34.19 m ha with the production of 63 m t and productivity was 1850 kg/ha. In India the total area under rapeseed-mustard during 2012-13 was 6.3 m ha with the production of 7.4 mt and productivity of 1176 kg/ha. During 2011-12 in Uttar Pradesh, the total area of rapeseed was 0.64 m ha with the production of 0.79 mt and productivity of 1236 kg/ha.

Botanically, the genus *Brassica* has six species *B.campestris*, *B. oleracea*, *B. nigra, B. juncea, B. napu* and *B. carinata*). Among them first three species are elementary and diploid with 2n=20,18 and 16 chromosomes and other three are tetraploids with chromosome number 2n=36, 38 and 34. Yellow *sarson* (*B.rapa* L. *var. yellow sarson*), which is cultivated under the genus *Brassica*, all over India and throughout the world, belongs to family Cruciferae (Brassicaceae). Yellow *sarson* is the major *rabi* oilseed crop, which is sown during October-November and the harvesting begins from February onwards. Oil content of different forms ranges from 30-48 %. It is self compatible and self pollinated crop. India is one of the major producer in the global oilseeds/vegetable oil economy. There is a severe shortage of edible oil in the country. Thus the availability of energy through oil is word limited. The largest mustard seed producing states in India are Rajasthan (45%), Haryana (13%), Madhya Pradesh (13%) and Uttar Pradesh (11%). The domestic mustard seed production has witnessed a huge fluctuation and marginal growth in the past two decades. In fact, there was a fall in production from 5.8 m tonne to 3.9 m tonne during 1991-2002, but shoot up drastically to a record 8.8 m tonne in 2010-11. Rapeseed-mustard oil is used primarily for edible purposes and is the principal cooking oil in the mustard growing areas of the country. Known for its great taste and subtle flavor, this vegetable oil is the world's

Table-1 : Clustering pattern of 49 genotypes on the basis of non-hierarchical *Euclidean cluster* analysis for 13 characters.

Cluster number	No. of genotypes	Genotypes
I	16	NDYS-07-2, NDYS-107-1, PYS-11-6, Benoy, NDYS-427, PYS-11-15, PYS-9-6, YSK-10-1, YSKM-12-11,YSKM-12-2, NDYS-11-3, RAUDYS-10-7, PYS-07-8, PYS-09-12, NDYS-2, Jagrati
II	6	PYS-2007-10,YSH-0401,YSWB-2014/3, PYS-9-1, PYS-2008-5, NRCYS-05-02
III	5	Pitambari, PYS-10-1, PYS-11-5, PYS-1-9-5, PYS-11-17
IV	2	PYS-09-9, PYS-11-3
V	3	PYS-10-7, PYS-09-11, PYS-10-3
VI	1	PYS-9-3
VII	10	NDYS-116-1,YSWB-2010/8, RAUDYS-10-12,YST-151, NDYS-126, NDYS-425, NDYS-08-4, PYS-11-11, NDYS-117-1, NDYS-424
VIII	6	YSWB-2012/9, PYS-10-2, YSWB-2029/2-12, PYS-11-16, YSWB-2011-10-1, YSWB-2014/3-12

Table-2 : Estimates of average intra and inter-cluster distances for 8 clusters in Yellow sarson genotypes.

S. No.	Clusters	I	II	III	IV	V	VI	VII	VIII
1.	I	11.22	18.492	17.089	38.448	32.573	52.627	20.782	22.273
2.	II		13.641	21.561	54.957	33.141	47.202	31.513	28.891
3.	III			9.369	31.623	35.926	52.819	30.458	33.437
4.	IV				39.433	49.737	69.204	46.806	52.144
5.	V					27.206	49.277	42.755	45.965
6.	VI						0.000	53.933	49.625
7.	VII							18.085	28.456
8.	VIII								12.780

second leading source of protein meal. Beside seeds, it is used as condiments and in preparation of salad, juices, and pickles. The meal cake left after oil extraction forms important cattle feed and may be used as organic manure. A rich source of vitamins and minerals, *Brassica* contains many medicinal properties. They provide high amount of vitamin C, soluble fiber and contain multiple nutrients with potent anti-cancer properties. Conventional breeding programmes coupled with modern agricultural practices resulted in the loss of genetic diversity in most of the cultivated crops. Hence, estimation of the genetic diversity present in the breeding materials is essential before proceeding to the further steps of breeding programs. A plant breeder has to identify the source of favourable genes to incorporate them into breeding population and select for a combination of desirable traits that might result in isolation of productive genotypes and cultivators. Keeping the above facts in view, the present investigation was carried out to study the divergence present among the yellow sarson (brassica rapa) lines.

MATERIALS AND METHODS

The present field experiment was conducted at the Research Farm of Genetics and Plant Breeding, NDUAT, Kumarganj, Faizabad, (U.P.) during Rabi 2012-13. The experiment consisting of 44 germplasm accessions along with 5 checks was laid out in Augmented Block Design. These lines were grown in single row plot of 5 meter length. Each block consisted of 11 entries plus 5 checks. The spacing between row to row and plant to plant was 30cm and 15cm, respectively maintained by thinning. The recommended packages of practices were followed to raise the normal crop.

Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to 50 % flowering and maturity which were recorded on the line basis. The data were recorded for 13 characters i.e. days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seeds per siliqua, length of siliqua (cm), biological Yield (g), seed yield per plant (g), harvest Index (%), 1000-seed weight (g) and oil content (%). The study of genetic divergence among 49 genotypes was done by Non-hierarchical Euclidean cluster analysis. The clustering pattern of 49 genotypes on the basis of Non-hierarchical Euclidean cluster analysis.

RESULTS AND DISCUSSION

Table-1, reveals that 49 genotypes were grouped into eight distinct on-overlapping clusters. The highest number of entries were present in cluster I which contained 16 genotypes represented by NDYS-07-2, NDYS-107-1, PYS-11-6, Benoy, NDYS-427, PYS-11-15, PYS-9-6, YSK-10-1, YSKM-12-11, YSKM-12-2, NDYS-11-3, RAUDYS-10-7, PYS-07-8, PYS-09-12,

Table-3 : Cluster means for different characters of yellow sarson.

Clusters	Days to 50% flower-ing	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Primarybranches / plant	Siliquae on main raceme	Siliqua length	Seeds/ siliqua	Biological yield/plant (g)	Seed yield/ Plant (g)	1000-seed weight (g)	Harvest index (%)	Oil Content (%)
I	47.94	114.65	109.10	44.00	4.80	27.05	3.93	32.31	21.62	5.80	4.99	21.21	43.55
II	57.00**	115.38	105.36*	48.08	5.25	24.08	3.26	27.18	18.52	5.32	4.12	28.10	44.30
III	48.24	115.33	106.83	41.75	5.31	24.28	3.47	34.57**	29.92	8.63**	4.70	28.85	44.50**
IV	45.90	116.25	115.61	35.09*	5.77	19.34*	4.15**	23.41	38.91**	9.54	5.59**	21.13	42.87
V	46.46	120.31	114.75	34.28	2.77*	21.44	3.22	22.95	25.02	4.87*	3.28	20.40*	43.56
VI	52.60	140.45**	108.43	44.27	7.89*	27.92	2.70*	19.52	24.11	6.43	3.87	26.36	42.38
VII	46.29	116.21	123.11**	52.00**	5.15	33.82**	3.88	30.17	24.58	5.96	4.83	24.46	43.02
VIII	39.83*	113.65*	105.95	48.14	7.17	29.05	3.80	18.25*	17.90*	5.65	4.40	31.13**	42.35

*Represent lowest value **Represent highest value

Table-4 : Per cent contribution of different characters towards genetic divergence in 49 yellow sarson genotypes.

Characters	Per cent contribution (%)
Days to 50% flowering	16.75
Days to maturity	5.44
Plant height (cm)	24.40
Primary branches/ plant	0.00
Length of main raceme (cm)	9.35
Siliquae on main raceme	4.85
Siliqua length (cm)	0.00
Seeds/ siliqua	22.53
1000-seed weight (g)	0.00
Biological yield/plant (g)	11.73
Seed yield/ plant(g)	0.00
Harvest index (%)	4.93
Oil content (%)	0.00

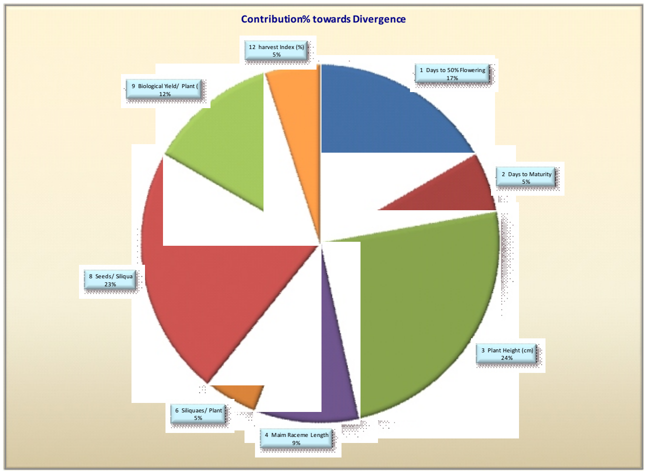

Fig.-1 : Contribution Percent Towards Divergence.

NDYS-2, Jagrati. Cluster II having 6 genotypes was represented by PYS-2007-10, YSH-0401, YSWB-2014/3, PYS-9-1, PYS-2008-5, NRCYS-05-02. Cluster III possessing 5 genotypes represented by Pitambari, PYS-10-1, PYS-11-5, PYS-1-9-5, PYS-11-17. Two genotypes were in Cluster IV represented by PYS-09-9, PYS-11-13. Cluster V having 3 genotypes (PYS-10-7, PYS-09-11 and PYS-10-3). Cluster VI was having single genotype (PYS-9-3). Cluster VII possessing 10 genotypes represented by 116-1, YSWB-2010/8, RAUDYS-10-12, YST-151, NDYS-126, NDYS-08-4, PYS-11-11, NDYS-117-1, NDYS-424. Cluster VIII having 6 genotypes represented by YSWB-2012/9, PYS-10-2, YSWB-2029/2-12, PYS-11-16, YSWB-2011-10-1, YSWB-2014/3-12. The estimates of intra and inter-cluster distance for eight clusters have been presented in Table-2, the maximum intra-cluster distance was recorded for cluster IV (39.433) followed by cluster V (27.206), VII (18.085), II(13.641), VIII (12.780), I (11.22), III (9.369). The remaining one cluster VI had minimum intra-cluster value (0.000). The maximum inter-cluster distance was found between cluster IV and VI(69.204) followed by cluster II and IV (54.957), I and VI (52.627),III and VI (52.819) and cluster V and VI(49.277). The minimum inter-cluster distance was observed between cluster I and III(17.089) followed by I and II(18.492), which indicated that the genotypes in these clusters were less divergent.

The cluster means for 13 characters are presented in Table-3, obvious that the genotypes of cluster- II took maximum days to 50%flowering (57.00) followed by cluster-VI (52.60) and III (47.94). The genotypes with early days to 50% flowering were concentrated in cluster-VIII (39.83). The genotypes of cluster-VI showed highest mean for days to maturity (140.45) followed by cluster V (120.3), cluster-IV (116.25) , cluster-III (116.21) and cluster-II (115.38). The genotypes with early days to maturity were grouped in cluster-VIII(113.65). The highest cluster mean for plant height was observed in cluster-VII (123.11), followed by cluster-IV (115.61), cluster-V (114.75) and cluster-I (109.10). The cluster-VIII (7.898) showed highest cluster mean for primary branches per plant followed by cluster-VIII (7.170). However, cluster-V (2.774) had lowest value for this trait. The genotypes occurring in cluster-VII (52.00) produced highest cluster mean for length of main raceme followed by cluster-VIII (48.14), cluster-II (48.08), cluster-VI (44.27) and cluster- I (44.00) while, lowest mean was recorded in cluster-V(34.28 cm). Highest cluster mean for siliquae on main raceme was exhibited by cluster-VII (33.82), followed by cluster-VIII (29.05) and VI (27.92), while, lowest mean was noted in cluster-IV (19.34). The cluster mean for siliqua length was exhibited by cluster-IV (4.15) followed by cluster- I (3.93), cluster VII (3.88) and cluster VIII (3.80) while, it was lowest for cluster VI-(2.70).The highest cluster mean for seeds per siliqua was observed in case of cluster-III (34.57), followed by cluster-I (32.31) while, it was lowest for entries occurring in cluster-VIII(18.25). The highest cluster mean for 1000-seed weight (g) was observed in case of cluster-IV (5.59), while, it was lowest for entries occurring in cluster-V (3.28 g).

The highest cluster mean for biological yield (g) was observed in case of cluster–IV (38.91g) while, it was lowest for entries occurring in cluster-VIII (17.90 g). The cluster mean for oil content (%) was highest in the genotypes of the cluster-III (44.50) followed by cluster-II (44.30). The lowest value for this trait was observed in cluster-VIII (42.35%). The highest cluster mean for seed yield per plant (g) was observed in case of cluster-IV (9.54), followed by cluster-III (8.63) and cluster-6 (6.43), which indicated that, lines having very high seed yield were concentrated in these clusters. The genotypes which had very low seed yield were grouped in cluster-V (4.87). Remaining clusters had medium seed yield per plant. The highest cluster mean for harvest index (%) was observed in cluster –VIII (31.13), followed by cluster III (28.85), cluster II (28.10), cluster I (27.21) and VI (26.36). The genotypes which had low harvest index were grouped in cluster V (20.4).

The analysis of character contribution towards divergence between 49 genotypes of yellow sarson are given in (Table-4). The maximum contribution was recorded by plant height followed by seeds/siliqua, days to 50% flowering, biological yield/ plant, length of main raceme, days to maturity, harvest-index and siliquae on main raceme. The lowest contribution was made by primary branches per plant, 1000-seed weight, siliqua length, seed yield/plant and oil content towards total genetic divergence. Other characters showed low contribution towards total genetic divergence.

REFERENCES

1. Murty, B.R. andArunachalam, V (1966). The nature and divergence in relation tobreeding system in some crop plants. Indian *J. Genet. 26 :* 188-198.
2. Somayajulu, P.L.N.;Joshi, A.B. and Murty, B.R. (1970). Genetic divergence in wheat.*Indian J. Genet*., *30 :* 47-58.
3. Maurya, D.M. andSingh, D.P., (1977). Genetic divergence in rice. *Indian J. Genet., 37:* 395-402.
4. Jatasara, D.S. andParoda, R.S. (1983). Genetic divergence in wheat. *IndianJ. Genet. 43 (1):* 63-67.
5. Swamy Gowda (1993).Variability and genetic divergence in Mustard *(Brassica juncea*L. Czern and Coss) and Rapeseed *(Brassica campestris* L.). *Ph.D. Thesis, Univ. Agric. Sci,* Bangalore.
5. Sandhu, S.K. andGupta, N.P. (1996). Genetic divergence and correlation studies in *Brassica* species. *Crop Improv., 23(2) :* 253-256.
6. Jiban–Mitraand Saini, H.C. (1998) . Genetic divergence for yield and itscomponents in toria (*Brassica campestris* var. toria).*International Journal of Tropical Agriculture*, *16(1-4) :* 243-246.
7. Shalini, T.S. (1998). Genetic divergence in Indian mustard *[Brassica juncea* L. (*Czern* and *Coss*)]. *M.Sc. Thesis, Univ. Agric. Sci.,* Bangalore.
8. Das, S.P., harver, P.M. and Briadar, A.B.(2000). Genetic divergence and selection of genotypes in soyabean. *Journal of Maharashtra Agriculture University 25(3) :* 272-277.
9. Jeena, A.S. and Sheikh, F.A. (2003). Genetic divergence analysis in gobhi *sarson,Brassica napus L. Journal of oilseeds Research; 20*(2) : 210-212.
10. Aunwinithul; ShantiPatil; Charjan; S.U., Thakare, P.G. and Wankhade, M. (2004). Geneticdivergence studies in Indian mustard. *Soil and Crops, 14 (2) :* 297-304.
11. Singh, R.V., Chaudhary, S.P.S., Singh, J. and Singh, N.P., (2005), Genetic Divergence in cluster bean (*Cyanmopsistetragonoloda* (L.) Taub.), *Journal Arid legummes, 2(1):* 102-105.
12. Dalsaniya, S.B., Poshiya, V.K., Savaliya, J.J., Pansuriya, A.G. and Davada, B.K. (2009). Genetic divergence in Cowpea (*Vigna Ungiculata* (L.) Walp.) *Legume Research., 32(4) :* 250-254.
13. Kushwaha, R.K., Nandan, R. and Reddy, G.E. (2013). Genetic Divergence for Morphological and Qualitative Characters in Winged bean, *Progressive Research 8(2) :* 200-202.
14. Reddy, P.A., Lavanya, G.R., Suresh, B.G., Ravichandra, K., Reddy, G.E. and Sravan, T. (2015). Genetic divergence in Mung beans (*Vigna Radiata* (L.), Wilczek). *Progressive Research 10(1) :* 43-45.

Received : September-2017 Revised : October-2017 Accepted : October-2017