



## COMPARISON OF HALF-SIB AND FULL-SIB PROGENY SELECTION METHODS IN INDIAN MUSTARD (*Brassica juncea* L.) UNDER RAINFED CONDITIONS

V.V. SINGH<sup>1\*</sup>, MAHARAJ SINGH<sup>2</sup>, J.S. CHAUHAN<sup>3</sup>, DHIRAJ SINGH<sup>1</sup> and M.L. MEENA<sup>1</sup>

<sup>1</sup> Directorate of Rapeseed Mustard Research, Sewar, Bharatpur 321303, India

<sup>2</sup> Central Arid Zone Research Institute, Regional Research Station, Jaisalmer, Rajasthan 345001, India

<sup>3</sup> Indian Council of Agricultural Research, Krishi Bhavan, New Delhi, India

\*Corresponding author's email: singhvijayveer71@gmail.com

### SUMMARY

An experiment was carried out to compare half-sib and full-sib progeny selection methods in Indian mustard (*Brassica juncea* L.) under rainfed conditions from 2006-07 to 2009-10 for 14 morpho-physiological characters. Full-sib and half-sib progenies were developed from different populations. The values of genetic parameters were higher in full-sibs compared to half-sibs for a greater number of traits. Estimates of genetic advance (GA expressed as per cent of mean) showed that full-sib progenies had higher GA for most of the traits, except for siliquae /plant. In half-sib progenies, seed yield/plant showed positive and significant correlation only with plant height (0.252) and primary branches per plant, where as in full-sib progenies, seed yield/plant showed positive and significant correlation with plant height (0.256\*), seeds/siliqua (0.258\*), 1000-seed weight (0.335\*\*), oil content (0.311\*\*), protein content (0.286\*), SPAD values at flowering (0.319\*\*), seed filling stage (0.335\*\*) and transpiration at flowering (0.216\*) stage. Full-sib progeny selection yielded significantly more superior progenies (18%) than did half-sib progeny selection (7.7%).

**Keywords:** Full-sib, half-sib, SPAD, genetic advance, *Brassica juncea*

Manuscript received: October 31, 2013; Decision on manuscript: February 7, 2014; Manuscript accepted: March 4, 2014.

© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2014

Communicating Editor: Bertrand Collard

### INTRODUCTION

Indian mustard (*Brassica juncea* L.) is a predominant oilseed crop in India. Belonging to the rapeseed-mustard group of crops, this species is considered self-pollinated, but a fairly high degree of cross-pollination (up to 24%) has been reported (Chauhan *et al.*, 1987). Researchers have shown various ranges of outcrossing, from 7.6 to 18.1% (Labana and Banga, 1984) and from 6.5 to 9.8% (Abraham, 1994) and 16.6% (Ram *et al.*, 1991), indicating a

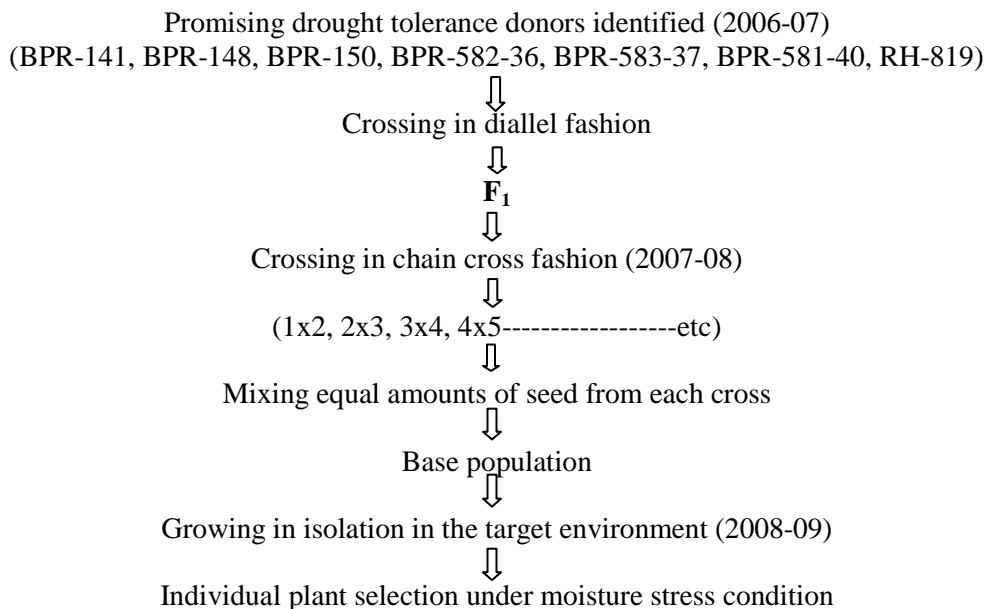
certain level of heterozygosity that can be exploited using population improvement strategies. Efforts to improve crop performance under drought have been initiated following pedigree, bulk, and backcross methods (Singh *et al.*, 2011). In cross-pollinated crops, selection schemes using full-sib, half-sib, and S<sub>1</sub> progenies have been very effective in exposing the hidden variability, thus resulting in effective selection (Sastry *et al.*, 1987). Although, earlier reports in maize (Guei and Wassom, 1993, Bolanos and Edmeades, 1993) and pearl millet

(Dutt and Nirania, 2005) advocate the use of half-sib and full-sib populations for selection under drought/rainfed conditions, a systematic population improvement program for increasing tolerance for rainfed conditions is scanty in Indian mustard. In 2007, scientists at PAU, Ludhiana, formulated a program on population improvement of Indian mustard. The present study used a set of full- sib and half- sib progenies under rainfed conditions to generate information that would help identify the most effective selection methods.

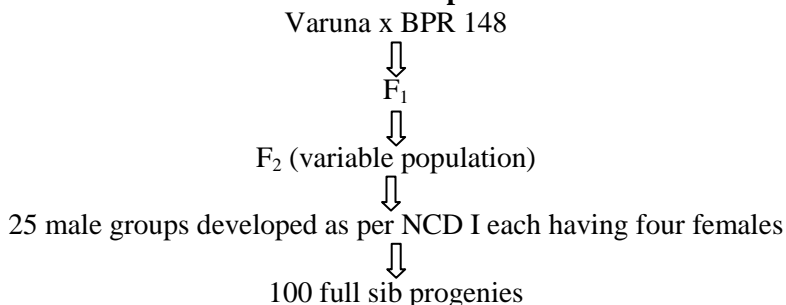
**MATERIALS AND METHODS**

The half-sib and full-sib progeny development program was initiated during rabi 2006-07 at NRCRM (presently the Directorate of Rapeseed Mustard Research [DRMR], Bharatpur). A schematic representation of development scheme is given below:

**Half sib development**



**Full sib development**



## Evaluation of materials

Half-sib (104) and full-sib progenies (100) were evaluated during *rabi* 2009-10 in an augmented block design in 2 separate experiments adjacent to each other at DRMR (77° 27' E, 27° 12' N, 178.37 m above sea level). Fertilizers were applied (40 kg nitrogen/ha and, 20 kg P<sub>2</sub>O<sub>5</sub>/ha) uniformly at the time of sowing. Half-sib and full-sib progenies were sown on conserved moisture received from rainfall. Initial soil moisture content was 11.4%. (The experimental area received 44.1 mm of rainfall during the cropping season.) The material was divided into 5 blocks, each block consisting of 21 progenies (half-sib) and 20 progenies (full-sib). Four rainfed check varieties RH-819, Geeta, RB-50, and PBR-97 were common in both experiments. In each block, progenies and check varieties were sown in a 4 x 0.60 m plot, accommodating 2 rows spaced 30 cm apart with plant-to-plant distance of 10 cm maintained by thinning 15 days after sowing. Observations were recorded on 10 randomly selected plants in both experiments; data on plant height, primary branches/plant, siliquae/plant, seeds/silique, seed yield/plant, 1000-seed weight, oil content and protein content were taken. Data on days to flowering and days to maturity were recorded on a whole plot basis. Data on physiological characters such as SPAD values at flowering and seed formation stages using a SPAD chlorophyll meter (SPAD-502, Minolta Corp., Ramsey, NJ) were gathered; transpiration at flowering and at seed filling was determined using LICOR-LI1600 steady state porometer on the 3<sup>rd</sup> and 4<sup>th</sup> fully expanded leaf from the top of 3 randomly taken plants. The SPAD chlorophyll meter reading (SCMR) is a direct linear relationship with total leaf chlorophyll. Leaves were sampled from nodal positions three and four below the apex on the main axis of three randomly selected plants from each progeny.

The mean data were subjected to analysis of variance (Fedrer, 1956) using SPAD (Abhishek *et al.*, 2004) software. Genetic parameters were calculated as per standard procedure (Burton, 1952, Johnson *et al.*, 1955).

## RESULTS AND DISCUSSION

There is observed that the released mustard varieties will not have the desired impact under moisture stress conditions, particularly in the arid and semi-arid zones and this, perhaps, explains the poor adoption of these newly released varieties by resource - poor farmers. The recommended varieties for cultivation should, therefore, possess high yield and stability under adverse set of conditions. Population improvement broadens the genetic base through accumulation of favorable alleles, thereby increasing stability in performance, along with a systematic increase in the mean of the character under consideration (Frey, 1983; Onim, 1981). Further, population approaches expose the hidden variability for selection. Reports are available in cross-pollinated crops such as maize and bajra regarding comparison of different population procedures (Reddy and Agrawal, 1990; Sandhu and Phul, 1984.) developed from the same base population. However, in Indian mustard, as far as review of work is concerned, no such reports exists.

In the present investigation, an analysis of variance revealed significant differences among half-sib progenies for nine morpho-physiological characters, whereas full-sib progenies exhibited significant differences for most of the characters except for days to flowering and transpiration at the seed filling stage. This indicates that half-sib and full-sib progenies have sufficient variability for these traits and response to selection may be expected in the breeding program. The analysis of variance clearly indicated the creation of a greater magnitude of variability through full-sib progeny selection for more traits. The upper range limit was higher for seven traits in the half - sib population, which means that selection for these traits may be more useful, at least for oil content, protein content, and SPAD. However, the mean was greater in bi-parental progenies than in half-sib progenies for nine morpho-physiological characters, including seed yield/plant (Table 1). In general, the magnitude of the PCV was higher than that of GCV for all the characters, indicating a positive effect of the

environment on the expression of character. Again, GCV and PCV in bi-parental progenies were more than those seen in corresponding half-sib progenies for most of the traits, which might be due to a breakage of undesirable linkages and the appearance of new gene combinations.

Heritability expresses the proportion of total variance that is attributable to the average effect of genes and determines the resemblance between relatives (Falconer and Mackay, 1996). Broad sense heritability estimates for all the characters revealed that full-sib progenies had higher values of heritability than half-sib progenies for most of the traits, except for plant height, primary branches/plant, siliquae/plant, and 1000 seed weight. The estimate of GA expressed as a percentage of the mean showed that full-sib progenies had higher GA for most of the traits, except for siliquae/plant. For seed yield/plant, higher values of heritability were accompanied by high GA. For some traits, the higher magnitude of heritability was not accompanied by high GA. This inconsistency may be attributed to the small magnitude of phenotypic standard deviation. Reddy and Agrawal (1990) in maize and Sandhu and Phul (1984) in pearl millet reported that full-sib progenies created more genetic variability than did half-sib progenies. In contrast El Sheikh (1999) reported more gains through the half-sib method in maize.

Simple correlations were worked out for yield and its component characters (Table 2). Full-sib progeny selection exhibited more positive associations than half-sib progeny selection. In half-sib progenies, seed yield/plant showed positive and significant correlation only with plant height and primary branches/plant, whereas in full-sib progenies, seed yield/plant showed positive and significant correlation with plant height, seeds/siliqua, 1000-seed weight, oil content and protein content. No any physiological characters were positively and significantly associated with seed yield/plant in the case of the half-sib progenies. On the other hand, in full-sib progeny selection, seed yield/plant showed positive and significant association with SPAD reading at both flowering and seed-filling stages and transpiration at flowering stage. A positive significant

relationship of SPAD with seed yield was also reported by Fanaei *et al.* (2009) in mustard.

A comparison of both methods was also done on the basis of number of significantly superior progenies (over best check and base population) yielded by each method of selection for seed yield/plant. Selected half-sib and full-sib progenies, along with best check and each base population, were also characterized for other morpho-physiological characters (Table 3). Half-sib progeny selection gave only 8 (7.69%) significantly superior progenies, which is less in comparison with full-sib progeny selection (18%). In terms of individual mean values of selected half-sibs and full-sibs, it was observed that the mean seed yield of full sibs was much higher than that of half sibs. Table 3 clearly indicates non-significant differences between the means of base populations for different characters. This indicated genetic similarity in donors for half-sib and full-sib progeny development. Hence, it can be concluded that full-sib progeny selection can supplement *Brassica* breeding program by way of improving mean performance and creating greater genetic variability because of accumulation of favorable genes. The final outcome is improved selection efficiency.

## REFERENCES

- Abhishek R, Rajendar Prasad and Gupta VK (2004). Computer aided construction and analysis of augmented designs. *Journal of Indian Society of Agricultural Statistics*. 57 (special volume): 320-344.
- Abraham V (1994). Rate of out crossing in Indian mustard (*Brassica juncea* L.). *Eucarpia cruciferae Newsletter*. 16: 69-70.
- Bolanos J and Edmeades GO (1993). Eight cycles of selection for drought tolerance in lowland tropical maize. I. Responses in grain yield, biomass and radiation utilization. *Field Crops Research*. 31: 233-252.
- Burton GW (1952). Quantitative inheritance of grasses. *Proceedings of the 6th International Grassland Congress*. 1: 227-283.
- Chauhan YS, Kumar K and Ram B (1987). Extent of out crossing in Indian mustard (*Brassica juncea* L. Czern & Coss). *Eucarpia Cruciferae Newsletter*. 12: 44.

- Dutt Y and Nirania KS (2005). Efficiency of half sib, full sib and  $S_1$  progeny recurrent selection methods for improvement in grain yield and dry fodder yield in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Indian Journal of Genetics and Plant Breeding*. 65: 257-260.
- El Sheikh MH (1999). Advances from half-sib and full-sib family selection within two maize populations. *Alexandria Journal of Agricultural Research*. 44:195-208.
- Falconer DS and Mackay TFC (1996). Introduction to quantitative genetics 4<sup>th</sup> ed. Longman, England.
- Fanaei HR, Galavi M, Kafi M and Ghanban Bonjar A (2009). Amelioration of water stress by potassium fertilizer in two oilseed species. *International Journal of Plant Production*. 3: 41-54.
- Federer WT (1956). Augmented design. *Hawaiian Planters Record*. 20: 191- 207.
- Frey KJ (1983). Plant population management and breeding. In D. R. wood (Ed.). *Crop Breeding*. pp 55-58. American Society of Agronomy, Madison, WI.
- Guei RB and Wassom CE (1993). Genetics of osmotic adjustment in breeding maize for drought tolerance. *Heredity*. 71: 436-441.
- Johnson HW, Robinson HF and Comstock RE (1955). Estimate of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.
- Labana KS and Banga SS (1984). Floral biology in Indian mustard (*Brassica juncea* L.). *Genetica Agraria*. 38:131-138.
- Onim JFM (1981). Effects of two population improvement methods on grain yield of pigeon pea composite populations in Kenya. *Euphytica*. 30: 271-275.
- Ram B, Chauhan YS and Kumar K (1991). Natural cross pollination in Indian mustard. *Cruciferae New letter*. 14/15: 24-25.
- Reddy KHP and Agrawal BD (1990). Genetic analysis for yield and its components in an improved population of Maize. *Crop Improvement*. 17: 9-12.
- Sandhu SS and Phul PS (1984) Genetic variability and expected response to selection in a pearl millet population. *Indian Journal of Genetics and Plant Breeding*. 44: 73-79.
- Sastry EVD, Narooka DS, Sharma RK and Mathur JR (1987). Efficiency of  $S_1$  method of population improvement in pearl millet. *Current Science*. 56:778-779.
- Singh VV, Singh M, Chauhan JS and Sunil K (2011). Development and evaluation of full sib progenies of Indian mustard (*Brassica juncea* L.) for moisture stress conditions. *Indian Journal of Genetics and Plant Breeding*. 71(1): 78-81.

**Table 1.** Mean, range, genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance in half-sib and full- sib progenies of Indian mustard.

Character	Mean		Range		GCV		PCV		h <sup>2</sup>		GA	
	HS	FS	HS	FS	HS	FS	HS	FS	HS	FS	HS	FS
Days to flowering	50.07	47.77	40.05-60.3	39.2-54.8	NS	NS	NS	NS	NS	NS	NS	NS
Days to maturity	129.08	138.37	119.05- 139.3	114-176	NS	9.25	NS	9.70	NS	90.83	NS	18.15
Plant height (cm)	160.00	167.74	121.9.- 188.97	128.8- 202.1	6.32	4.9	7.38	6.3	73.46	61.43	1.34	7.9
Primary branches/plant	3.86	3.84	2.44-5.69	2.55-5.2	14.88	13.27	15.96	16.26	86.84	66.66	12.48	22.31
Siliquae/plant	41.76	42.15	27.39-56.39	18.3-62.2	9.27	9.9	11.55	13.09	64.44	56.96	30.38	15.34
Seeds/siliquea	14.47	14.79	12.24-16.60	9.4-17.7	NS	7.37	NS	9.32	NS	62.63	NS	12.02
1000-seed weight (g)	4.44	4.93	3.07-6.68	3.7-6.4	9.81	14.76	11.91	19.56	67.85	56.98	6.73	22.93
Seed yield/plant (g)	7.62	9.72	1.83-17.52	1.1-20.8	33.45	28.58	40.97	36.03	66.66	77.77	19.13	57.16
Oil content (%)	42.47	40.14	39.27-44.51	38.9-44.2	NS	18.75	NS	19.05	NS	96.88	NS	37.99
Protein content (%)	2.02	19.58	18.01-21.62	14.9-21.6	3.16	19.31	3.52	19.49	80.39	98.08	1.46	39.35
SPAD (FS)	45.05	45.85	34.02-55.9	3.54-53.94	NS	18.25	NS	19.20	NS	90.38	NS	35.72
SPAD (GFS)	40.17	38.59	24.26-50.86	27.19- 49.84	9.26	17.44	12.06	22	59.00	62.85	17.41	28.46
Transpiration (FS)	4.99	5.75	1.03-10.19	0.20-11.97	24.62	34.65	31.74	40.37	60.15	73.65	46.4	61.21
Transpiration (GFS)	1.58	0.92	0.09-3.95	-0.06-2.67	35.23	NS	45.19	NS	60.78	NS	66.68	NS

HS=half sib, FS=full Sib

**Table 2.** Correlation coefficients between different characters in the half-sib and full - sib progenies of Indian mustard.

Character	Progeny	Day to flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Siliquae/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant(g)	Oil content (%)	Protein content (%)	SPAD reading at FS	SPAD reading at GFS	Transpiration at FS	Transpiration at GFS
Days to flowering	HS	1													
	FS	1													
Day to maturity	HS	0.999**	1												
	FS	0.205*	1												
Plant height (cm)	HS	0.244*	0.238*	1											
	FS	-0.082	-0.035	1											
Primary branches/plant	HS	0.041	0.040	0.139	1										
	FS	0.040	-0.169	0.475**	1										
Siliquae/plant	HS	0.041	0.163	0.255**	0.136	1									
	FS	-0.192	-0.04	0.452**	0.294**	1									
Seeds/siliqua	HS	-0.098	-0.096	0.205*	0.133	0.166	1								
	FS	-0.094	-0.164	0.106	-0.044	0.124	1								
1000-seed weight (g)	HS	0.147	0.148	0.123	0.050	0.089	-0.083	1							
	FS	-0.168	0.009	0.235*	0.013	0.156	0.098	1							
Seed yield/plant (g)	HS	-0.055	-0.054	0.252*	0.218*	-0.014	0.102	0.024	1						
	FS	-0.179	0.018	0.256**	-0.027	0.06	0.258**	0.335**	1						
Oil content (%)	HS	-0.195*	-0.196*	0.153	0.056	0.132	0.081	-0.076	0.021	1					
	FS	-0.222*	-0.024	0.484**	0.142	0.34**	0.101	0.749**	0.311**	1					
Protein content (%)	HS	0.268**	0.269**	-0.070	-0.054	0.066	-0.295**	-0.110	-0.090	-0.214*	1				
	FS	0.189	-0.011	0.427**	0.171	0.34**	0.036	0.762**	0.286**	0.962**	1				
SPAD reading at FS	HS	-0.162	-0.163	-0.32**	-0.019	-0.112	-0.083	0.088	0.029	0.135	0.068	1			
	FS	-0.141	0.051	0.339**	0.076	0.26**	0.068	0.730**	0.319**	0.947**	0.95**	1			
SPAD reading at GFS	HS	0.012	0.009	0.029	0.099	-0.112	0.022	0.218*	-0.130	-0.064	-0.059	0.482**	1		
	FS	-0.117	0.064	0.270**	0.023	0.24**	0.039	0.622**	0.335**	0.817**	0.833**	0.914**	1		
Transpiration at FS	HS	-0.017	-0.020	0.182	0.036	0.040	-0.177	-0.035	0.028	-0.198*	0.049	-0.102	-0.077	1	
	FS	-0.284**	-0.100	0.323**	0.105	0.146	0.139	0.322**	0.216*	0.461**	0.428**	0.384**	0.312**	1	
Transpiration at GFS	HS	0.063	0.066	0.025	-0.28**	-0.012	-0.051	-0.191	0.050	0.226*	0.0129	-0.065	-0.374**	0.042	1
	FS	-0.025	-0.114	0.034	-0.059	0.115	0.272**	0.191	0.108	0.219*	0.193	0.196*	0.124	0.673**	1

HS= half sib, FS=full sib

**Table 3.** Characterization of selected half-sib and full-sib progenies of Indian mustard for morpho-physiological characters along with best check and base population.

Progeny	Seed yield/plant(g)	Days to flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Siliquae on main shoot	Seeds/siliqua	1000-seed weight(g)	Oil content (%)	Protein content (%)	SPAD reading at FS	SPAD reading at GFS	Transpiration at FS	Transpiration at GFS
<b>Half sib</b>														
DHS-14	17.52	50.55	129.55	167.50	5.64	42.49	15.3	4.00	42.99	20.09	45.80	30.37	3.40	1.97
DHS-54	16.72	50.05	129.05	172.27	5.69	46.86	15.4	3.98	42.39	20.41	45.62	35.96	5.20	0.82
DHS-51	16.55	49.05	128.05	182.67	3.69	38.86	13.7	5.31	42.13	20.41	46.42	36.56	5.55	1.16
DHS-48	15.44	45.05	124.05	159.47	4.69	43.66	13.8	4.26	42.54	20.34	44.92	38.16	5.24	0.45
DHS-11	15.37	51.55	130.55	150.90	3.24	40.09	14.5	4.12	42.93	20.17	50.20	41.37	3.68	2.86
DHS-67	15.16	54.30	133.30	170.37	4.79	40.19	14.7	4.68	41.58	20.39	47.97	48.21	9.13	0.69
DHS-25	14.39	46.05	125.05	163.47	3.24	35.64	13.8	3.93	43.66	19.79	46.70	27.66	6.44	2.31
DHS-33	13.87	45.05	124.05	142.87	4.24	39.84	13.9	3.80	43.13	21.01	51.80	42.06	6.52	1.66
RB-50 (best check)	8.69	54.00	133.00	171.88	3.40	36.40	14.7	4.88	40.644	20.274	38.08	43.04	5.00	1.38
Population	4.45	49.05	128.05	174.20	3.44	37.42	14.4	4.21	42.02	20.351	45.6	42.29	3.238	0.85
<b>CD ( 5 %)</b>	<b>4.64</b>	<b>6.6</b>	<b>6.6</b>	<b>15.6</b>	<b>0.59</b>	<b>7.4</b>	<b>1.45</b>	<b>0.81</b>	<b>1.94</b>	<b>0.83</b>	<b>8.17</b>	<b>8.00</b>	<b>2.59</b>	<b>1.18</b>
<b>Full sib</b>														
DFS-45	20.85	44.95	136.3	156.9	3.2	49.7	16.3	4.78	41.39	21.26	49.14	41.3	3.84	0.75
DFS-77	20.25	47.20	139.5	165.3	3.5	39.06	15.8	5.57	39.99	20.62	46.94	42.3	8.19	1.30
DFS-35	18.32	47.45	130.3	182.1	5.0	43.16	13.9	5.76	40.44	21.37	46.09	41.8	8.23	1.39
DFS-34	15.72	51.45	129.3	194.9	5.1	46.76	15.4	5.34	42.52	20.76	46.99	37.8	4.49	1.31
DFS-5	15.45	48.70	141.0	172.4	4.8	46.81	17.7	5.32	41.47	19.72	46.47	42.1	2.74	0.49
DFS-11	15.45	44.70	133.0	148.8	3.4	30.41	14.4	5.61	40.68	19.28	43.07	27.9	9.39	1.79
DFS-78	14.95	49.20	142.5	165.7	3.5	39.66	14.3	5.06	41.26	14.95	45.74	40.1	5.77	0.84
DFS-66	14.65	41.20	129.5	202.1	4.1	51.46	16.8	4.92	41.35	19.11	43.84	28.4	8.61	1.46
DFS-85	14.64	44.70	137.0	172.6	4.8	44.66	13.6	5.35	41.94	20.78	46.47	39.8	4.62	0.09
DFS-8	14.45	51.70	141.0	176.4	4.8	47.21	17.1	4.78	40.99	20.07	45.77	37.3	3.96	0.74
DFS-23	14.22	46.45	133.3	155.3	3.8	42.96	13.9	5.1	41.20	20.50	47.69	43.3	11.97	1.33
DFS-58	14.15	48.95	153.3	163.5	3.2	43.10	14.2	5.18	41.79	20.90	49.54	40.8	4.34	0.84
DFS-2	14.05	50.70	143.0	165.2	3.4	33.01	14.4	5.37	39.12	20.39	50.77	43.4	1.84	0.47
DFS-61	13.75	41.20	132.5	182.5	4.5	38.86	16.0	5.00	39.92	20.67	47.54	43.6	8.71	0.85
DFS-29	13.72	45.45	131.3	163.9	3.6	47.56	14.1	5.94	41.73	21.04	47.19	40.7	8.05	1.44
DFS-40	13.72	47.45	132.3	160.5	3.6	40.37	15.8	4.94	42.42	21.18	52.49	47.0	5.61	0.67
DFS-63	13.65	41.20	131.5	178.9	4.1	44.46	15.7	4.97	41.63	20.74	45.64	38.9	6.71	1.01
DFS-13	13.55	52.70	140.0	162.6	3.4	37.81	17.3	4.99	39.99	20.42	50.67	44.6	8.06	1.58
Best check	8.05	54.8	144.4	177.8	3.76	38.6	15.1	5.15	40.57	20.01	49.58	42.76	6.41	0.79
Base population	4.37	49.21	128.21	174.20	3.47	37.64	14.4	4.26	41.94	20.35	45.35	42.30	3.30	0.85
<b>CD ( 5 %)</b>	<b>5.5</b>	<b>9.16</b>	<b>10.48</b>	<b>16.9</b>	<b>0.96</b>	<b>9.33</b>	<b>2.18</b>	<b>1.64</b>	<b>3.48</b>	<b>1.36</b>	<b>7.04</b>	<b>13.34</b>	<b>3.06</b>	<b>1.66</b>