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RESPONSE TO MASS AND S_I SELECTION FOR AUTOGAMY, SEED YIELD AND OIL CONTENT IN SUNFLOWER POPULATIONS (*Helianthus annuus* L.)

Gowda, J.*, and Seetharam, A.

Project Coordinating Unit (Small Millets) University of Agricultural Sciences,
Bangalore 560 065, India

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SUMMARY

Two population improvement methods, mass selection (two cycles) and S_I selection (one cycle) were imposed on a base population to study the response to selection by comparing their efficiency in improving autogamy, seed yield and oil content in sunflower. Mass selection was adopted for developing two distinct populations regarding maturity, one early (80-85 days) and one medium (95-100 days). The derived populations MSE -2 (early) and MSM - 2 (medium) retained substantial variability for most of the characters even after two cycles of mass selection. As compared with the base population, these derived populations showed substantial improvements in seed yield, to an extent of 40 to 65%, oil content (38%) and oil yield (83 to 97%). However, the response to S_I selection was effective only in improving oil content. For other characters including seed yield, the derived populations were inferior compared with the base population.

Key words: **sunflower, mass selection, S_I selection, autogamy, response to selection**

INTRODUCTION

Superior source population is a pre-requisite for sunflower improvement, either through hybrids or open-pollinated varieties. So, systematic population improvement programs are required to develop superior source populations. The end product of a population improvement program can be either a commercial cultivar or a source population for deriving inbred lines. The superior open-pollinated cultivars so derived must have high self-fertility and oil content, medium plant height, certain level of uniformity for morphological characters, disease and insect resistance and high seed yield.

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* Corresponding author: e-mail: jg_gene@rediffmail.com

Mass selection has been used for cultivar improvement in sunflower for many years and it was effective in developing cultivars with early maturity, higher oil percentage and resistance to diseases. Pustovoit's "method of seed reserves" (Pustovoit, 1964) has been widely used in Russia and other east European countries for developing new cultivars and it has been reported to be highly successful in improving oil content. According to Borojević (1981), the efficiency of mass selection depends on gene effects for the characters selected for their heritability, sample size and the genotype-environment interaction. Mass selection is effective for characters controlled by additive genes.

The S_I progeny selection is regarded as the quickest method of intra-population improvement (Moll and Smith, 1981) and it has been widely used in maize. The method capitalizes on genes with additive effects and it also eliminates deleterious recessive alleles. An attempt was made in the present investigation to study the response of two population improvement methods, mass selection (two cycles of phenotypic selection) and S_I selection (one cycle of genotypic selection) by comparing their efficiency in improving autogamy, seed yield and oil content in sunflower.

MATERIALS AND METHODS

Prior to employing the selection methods, a highly heterogeneous base population was generated by intermating eleven inbreds/populations with diverse geographic origins and agronomic characteristics over three seasons, from 1998 to 2000. As expected, the base population was highly variable for all agronomic attributes including flowering and maturity. The two selection methods applied in the study, mass and S_I, took advantage of the variability available for flowering and maturity to produce populations distinctly differing in maturity. In order to provide equal opportunity for each plant during selection, the plot was divided into 12 grids.

The base population was subjected to two cycles of mass selection and one cycle of S_1 selection. Mass selection was exercised in the base population during the rainy season of 2001, on both maturity (early and medium) groups. Observations on seven quantitative characters, plant height, head diameter, percent seed set, 100-seed weight, seed yield per plant, oil content and oil yield per plant, were recorded for all the selected plants. Phenotypically superior early and medium maturing plants were selected separately and initial base populations were designated as MSE-0 and MSM-0 populations, respectively. Considering oil yield per plant, equal quantities of seed from best plants were bulked and intermated during the rainy season of 2002. The derived populations were designated as MSE-1 and MSM-1 for early and medium maturity, respectively. The second cycle of mass selection initiated during the rainy season of 2003 on the population derived from the first cycle of mass selection on both maturity groups and selected plants, based on oil yield per plant (> mean + 1 standard deviation), were intermated during summer 2004. The derived populations were designated as MSE-2 and MSM-2 (Table 1).

Table 1: Selection protocols for each selection method

Selection method	Cycle	No. of plants initially selected	No. of plants used for intercrossing	Selection intensity
Mass selection (early group)	Cycle I	450	106	24
	Cycle II	374	54	14
Mass selection (medium group)	Cycle I	375	67	18
	Cycle II	397	50	13
S_1 Selection	Cycle	No. of plants selfed	No. of progenies evaluated	No. of plants selected for intermating
	Cycle I	650	59	20

S_1 selection was initiated simultaneously on the base population during the rainy season of 2001. Considering both the percent seed set on selfing and oil content, the selected plants were evaluated in plant to row progeny evaluation with three checks in two replications following a randomized complete block design. Three plants from each progeny were selfed for autogamy estimation. Based on percent autogamy, seed and oil yields, the remaining seeds of superior progenies were bulked. The selected bulk was grown in isolation and crossed *inter se* during the rainy season of 2002 (Table 1).

Evaluation of derived populations

To compare the efficacy of mass and S_I selection in the derived superior populations, the six populations including the base population were evaluated along with four diverse checks during the rainy season of 2004. The trial was laid out in a randomized complete block design with three replications. Each entry was grown in seven rows each 4.2 m in length, with the spacing of 60 cm between rows and 30 cm between plants.

RESULTS AND DISCUSSION

The grain yield, oil yield and the extent of autogamy were the three selection criteria used in the present study. Therefore, the selection responses in terms of mean and variances for these traits were considered as direct whereas the responses to the other traits were regarded as indirect and correlated response.

Response to mass selection - early group

Cycle I: All plants from the base population that matured in 80 to 85 days were selected based on oil yield per plant. Equal quantities of seed of the selected plants were sown in isolation and crossed *inter se* to form MSE-1 population which was the base population for the second cycle of mass selection. The original base population from the first cycle of mass selection exhibited substantial variability as could be seen from the wide ranges and phenotypic coefficients of variability (PCV) for all the characters studied. At the end of the first cycle of mass selection, relatively higher ranges were observed in MSE-1 (derived population) as compared with the base population for oil content and 100-seed weight. The minimum values were higher in MSE-1 than that in MSE-0 for all characters except plant height and head diameter indicating modest improvement due to one cycle of mass selection. However, the same was not reflected in terms of genetic gain for the characters except 100-seed weight, oil content and oil yield per plant. The genetic gains realized for 100-seed weight and oil yield were marginal. A meager difference was seen in the estimates of PCV between MSE-0 and MSE-1. The poor response of the population to one cycle of mass selection could be attributed to low heritability of characters. Nevertheless, the response to mass selection was significant as genetic gain of 8.88% for oil content was observed in the derived population (Table 2).

Table 2: Mean, variance for different agronomic characters in derived populations (MSE-1 and MSE-2) from first and second cycle of mass selection as compared with the base populations (MSE-0 and MSE-1 -early group)

Character	Population	Range	Mean	SD*	PCV
Plant height (cm)	MSE–0	119-220	175.89 ± 1.03	-38.06	10.91
	MSE-1	87-177	137.83 ± 0.88	11.45	12.41
	MSE–2	100-181	149.27 ± 2.01	-26.62	9.92
Head diameter (cm)	MSE–0	9-24	16.65 ± 0.15	-3.52	16.87
	MSE–1	9-19	13.13 ± 0.10	2.37	15.00
	MSE–2	12-29	15.50 ± 0.22	-1.15	10.46
Seed yield / plant (g)	MSE–0	2.34-117.32	41.58 ± 1.00	-5.79	45.02
	MSE–1	8.07-90.50	35.79 ± 0.71	24.17	38.53
	MSE–2	18.77-91.7	59.96 ± 1.24	18.38	15.24
100-seed weight (g)	MSE–0	1.7-9.06	4.56 ± 0.06	0.57	24.56
	MSE–1	1.92-11.63	5.13 ± 0.06	1.50	24.95
	MSE–2	2.24-10.35	6.63 ± 0.18	2.07	20.09
Seed filling percentage (%)	MSE–0	18.67-100	82.64 ± 0.61	-6.85	13.80
	MSE–1	38.8-98.2	75.79 ± 0.60	3.73	15.29
	MSE–2	55.30-94.10	79.52 ± 1.24	-3.32	11.51
Oil content (%)	MSE–0	18.36-40.16	29.52 ± 0.22	8.88	15.88
	MSE–1	22.40-46.90	38.40 ± 0.24	2.37	11.19
	MSE–2	29.55-46.86	40.76 ± 0.33	11.24	5.87
Oil yield / plant (g)	MSE–0	2.73-39.43	13.21 ± 0.33	1.73	45.06
	MSE–1	3.09-34.83	14.94 ± 0.37	9.48	38.15
	MSE–2	6.45-37.35	24.14 ± 0.52	10.93	15.83

* Selection differential

Cycle II: The second cycle of mass selection also retained substantial variability for all characters except seed yield and oil content as evident from the estimates of PCV and the range values in MSE-2 as compared with the first cycle (MSE-l) (Table 2). In the cases of seed yield and oil content, PCVs were reduced by almost fifty percent in MSE-2 compared with MSE-l. The observed reduction in variability due to selection is indicative of positive response to selection in these two characters. In fact, this was well reflected through selection differential. It is also of interest to note that the selection for seed yield, oil content and autogamy brought a correlated response in plant height also. This is not surprising because, it is a well established fact that there is a strong positive correlation between plant height and seed yield in sunflower. The second cycle of mass selection was effective in shifting the mean values of all characters of the population towards the positive side.

When the base population (MSE-0) and the derived population after two cycles of mass selection were compared, it was observed that MSE-2 retained large variability with respect to plant height, head diameter, percent seed filling and 100-seed weight. However, reduction in range values was observed in seed yield per plant, oil content and oil yield per plant indicating a positive response of the population to the two cycles of mass selection (Table 2). Obviously, this was reflected through positive selection differential and upward shift of mean performance for these traits. Thus, the two cycles of mass selection effectively agglomerated favorable genes and genotypes for the three most important characters. Pandey *et al.* (1988) also observed a significant shift in mean seed yield after imposing two cycles of mass selection on sunflower.

Response to mass selection - medium group

Plants that matured in 95 to 100 days were selected from the base population, bulked and designated as medium group. The population thus established was advanced through two cycles of mass selection and the obtained results are discussed hereunder.

Cycle I: When the derived population (MSM-1) was compared with the base population (MSM-0) at the end of the first cycle of mass selection, reductions in mean values for all characters except oil content and oil yield per plant were observed contrary to the expectations based on the response to mass selection of the previously discussed early group. The derived population also retained substantial variability and the differences in the estimates of PCV between MSM-1 and MSM-0 were marginal for all characters except oil content and oil yield (Table 3).

Cycle II: The selection imposed on MSM-1 resulted in MSM-2 showing shift in mean values towards the positive side for all characters, but with noted shifts for seed yield followed by oil yield. The positive response for seed and oil yield also brought about a correlated response for plant height. The positive correlated response observed in the derived population (MSM-2) is the consequence of gene shuffling in MSM-l due to selective random mating which might have helped in breaking closely linked genes or gene complexes. The derived population MSM-2 also retained a substantial variability for all traits, as evident from the estimates of PCV and range values in relation to the initial population MSM-l.

The two cycles of mass selection resulted in significant improvements in mean seed yield, oil content and oil yield in MSM-2 compared with the base population (Table 3).

Table 3: Means and variances for different agronomic characters in MSM-1 and MSM–2, populations derived from first and second cycles of mass selection as compared with the base populations (MSM-0 and MSM-1 -medium group)

Character	Population	Range	Mean	SD*	PCV
Plant height (cm)	MSM–0	120-235	193.02 ± 1.26	-32.2	8.41
	MSM-1	95-275	160.82 ± 0.79	8.26	9.79
	MSM-2	130-190	169.08 ± 1.86	3.01	7.67
Head diameter (cm)	MSM-0	9-23	16.50 ± 0.28	-2.28	17.81
	MSM-1	9-23	14.22 ± 0.11	3.26	16.52
	MSM-2	10-24	17.48 ± 0.34	0.98	13.73
Seed yield / plant (g)	MSM-0	2.51-121.66	44.79 ± 1.76	-1.58	50.32
	MSM-1	7.97-129.84	43.21 ± 0.82	30.82	37.97
	MSM-2	19.31-132.64	74.03 ± 1.90	29.24	18.19
100-seed weight (g)	MSM-0	1.9-8.48	5.08 ± 0.09	-0.07	24.21
	MSM-1	2.38-8.10	5.01 ± 0.05	1.23	20.55
	MSM-2	4.44-8.90	6.28 ± 0.13	1.15	15.06
Seed filling percentage (%)	MSM-0	1.49-99.13	83.64 ± 1.05	-2.94	16.16
	MSM-1	21.5-99.70	80.70 ± 0.58	4.47	14.46
	MSM-2	54.6-99.7	85.17 ± 1.27	1.53	10.58
Oil content (%)	MSM-0	20.17-41.51	30.52 ± 0.31	9.76	13.79
	MSM-1	27.61-47.7	40.28 ± 0.17	1.68	8.39
	MSM-2	36.08-45.57	41.96 ± 0.30	11.44	5.15
Oil yield / plant (g)	MSM-0	5.05-41.25	16.05 ± 0.61	1.75	45.01
	MSM-1	3.67-53.35	17.80 ± 0.36	13.82	39.55
	MSM-2	23.6-52.23	31.62 ± 1.05	15.57	23.33

* Selection differential

However, the improvements in mean performance of head diameter, number of leaves, 100-seed weight and percent seed filling were marginal. The significant improvements in seed yield, oil content and oil yield could be due to accumulation of favorable genes and appearance of new favorable genotypes. Thus, performing two cycles of mass selection was quite effective in bringing desired changes in these three economically important characters. Harinarayana *et al.* (1980) and Luduena *et al.* (1992) observed a similar response of seed yield after three cycles of mass selection. For oil content, however, the rate of increase was noticed up to the second cycle, thereafter the rate of increase was slow. In contrast to this, Giriraj *et al.* (1985) reported a positive response of seed oil content after five cycles of Pustovoit's method of reserves whereas, for seed yield, the response was non-significant and the derived population still retained large variability for oil content. The most immediate and obvious consequence of the upward shift in mean performances of these three characters was a significant reduction in variability (in terms of PCV or range) in the present study.

Table 4: Estimation of mean and genetic parameters for different agronomic characters in S_1 progenies as compared with the base population

Character	Population	Range	Mean	PCV	GCV	Heritability (%) (Broad sense)
Plant height (cm)	BP (S_0)	119-235	184.45	8.66	-	-
	S_1 progenies	88-177	142.64	16.96	11.02	42.17
	S_1 population	121-178	153.20	8.56	-	-
Head diameter (cm)	BP (S_0)	9-24	16.57	17.34	-	-
	S_1 progenies	8.6-16.5	12.40	15.84	6.85	18.71
	S_1 population	11.8-16.5	13.57	9.21	-	
Autogamy (%)	BP (S_0)	-	-	-	-	-
	S_1 progenies	7.65-98.3	54.89	50.63	43.42	75.29
	S_1 population	-	-	-	-	-
100-seed weight (g)	BP (S_0)	-	-	-	-	-
	S_1 progenies	3.81-7.25	5.81	20.24	2.73	11.8
	S_1 population	-	-	-	-	-
Seed yield / plant (g)	BP (S_0)	2.51-121.66	43.18	47.67	-	-
	S_1 progenies	9.53-48.73	29.71	34.93	21.52	37.94
	S_1 population	26.89-49.65	38.02	15.28	-	-
Oil content (%)	BP (S_0)	18.36-41.51	30.02	14.83	-	-
	S_1 progenies	31.71-46.22	39.14	9.63	3.69	14.70
	S_1 population	36.24-47.2	40.66	5.83	-	-
Oil yield/ plant (g)	BP (S_0)	2.73-41.25	14.63	45.03	-	-
	S_1 progenies	3.98-19.23	11.65	34.98	24.24	48.04
	S_1 population	10.5-21.25	16.32	14.29	-	-

Response to S_I selection

The response to one cycle of S_I selection in terms of means and variances for different characters is discussed hereunder.

Mean and variance of S_I population in comparison with base population

After estimating the mean, variability and genetic parameters in S_0 and S_I progenies, the top 20 progenies were selected and bulked to constitute the derived population. The response to one cycle of S_I selection was assessed by comparing the mean and variance of the derived population with those of the base population. One cycle of S_I selection was able to improve oil content and oil yield over the base population, as evident from the values of genetic gain. The response was apparent for oil content for which genetic gain as high as 10.64% was achieved and the same was reflected through drastic reduction in the estimates of PCV from the base population. This means that further cycles of S_I selection may not be as effective for improving the oil content. For other characters, S_I selection response was not encouraging and in fact the mean of the derived population was found to be reduced in relation to the base population. The possible reason for this negative response could be due to inbreeding depression as a result of genetic drift as a smaller number of S_I progenies (20) was selected and bulked to constitute the derived population. Garay *et al.* (1996) observed a negative response to S_I selection for lodging resistance in maize as a result of selecting only few S_I progenies for *inter se* crossing to make up the derived population. Therefore, a sufficiently high number of S_I progenies should be selected from a large base population.

Table 5: Mean performance of derived populations

Population	Days to 50% flowering	Head diameter	100-seed weight	Auto-gamy	Seed yield	Oil content	Oil yield
	days	(cm)	(g)	(%)	(q/ha)	(%)	(q/ha)
BP	59.00	15.80	6.54	32.05	16.16	38.61	6.24
MSE-1	58.00	15.87	6.77	20.90	19.74	40.39	7.97
MSM-1	66.00	15.13	6.73	29.94	16.79	39.85	6.72
MSE–2	58.00	15.10	6.97	23.85	20.33	40.60	8.26
MSM-2	67.00	15.93	6.71	28.08	19.64	39.86	8.16
S_1	65.00	15.33	6.85	30.64	17.72	39.33	6.97
MORDEN	56.00	15.87	6.22	4.43	13.23	39.45	5.22
GAU –SUF-15	69.00	14.00	6.00	18.73	14.42	35.63	5.14
TNAU-SUF-7	64.00	16.00	6.02	17.11	14.99	39.55	5.92
KBSH-1	64.00	14.50	6.16	43.19	17.77	37.14	6.58
Mean	63.00	15.35	6.49	24.89	17.08	39.04	6.72
CD @ 5 %	1.12	NS	NS	NS	2.54	1.46	1.05
CV (%)	1.05	8.5	1.02	19.77	8.67	2.18	9.12

EVALUATION OF DERIVED POPULATIONS

The two cycles of mass selection resulted in the development of four new population, MSE-I and MSE-2 with early maturity and MSM-I and MSM-2 with medium maturity. Similarly, one cycle of S_I selection resulted in the development of one new population, S_I. These newly derived populations, along with four checks consisting of three open pollinated varieties (Morden, GAU-SUF-15, TNAU-SUF-7) one hybrid (KBSH-I), were evaluated against base population. The analysis of variance indicated significant differences among the populations for the following characters: days to 50% flowering, seed yield, oil content and oil yield. MSE-2 and MSM-2, derivatives of the second cycle of mass selection, had higher seed and oil yields, respectively, than the hybrid check KBSH -I and the other open pollinated checks (Table 5). Tt was inferred from these results that the populations obtained after two cycle of mass selection are superior for most of their characters in respect to the other derivatives and the commercial checks.

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RESPUESTA A LA SELECCIÓN MASAL Y S_1 POR AUTOGAMIA, RENDIMIENTO DE SEMILLA Y CONTENIDO DE ACEITE EN UNA POBLACIÓN DE GIRASOL (*Helianthus annuus* L.)

RESUMEN

Se impusieron dos métodos de mejoramiento de poblaciones: dos ciclos de selección masal y un ciclo de selección S_1, a una población base para estudiar la respuesta a la selección a través de la comparación de su eficiencia para mejorar autogamia, rendimiento de semilla y contenido de aceite en girasol. Se adoptó selección masal para el desarrollo de dos poblaciones diferentes, a saber, precoz (80-85 días) e intermedia (95-100 días), sobre la base de la duración del ciclo. Las poblaciones derivadas, llamadas MSE-2 (precoz) y MSM-2 (intermedia), retuvieron sustancial variabilidad, aún luego de dos ciclos de selección masal, para la mayoría de los caracteres. Comparando con la población base, estas poblaciones derivadas mostraron una mejora sustancial para rendimiento de semilla hasta un nivel del 40 al 65%, contenido de aceite hasta un nivel del 38% y rendimiento de aceite hasta un nivel del 83 al 97%. Sin embargo, la respuesta a la selección S_1 sólo fue efectiva para mejorar contenido de aceite, mientras que para los otros caracteres, incluyendo rendimiento de semilla, la población derivada fue inferior en comparación a la población base.

RÉPONSES ENTRE LA SÉLECTION MASSALE ET LA SÉLECTION S_1 POUR L'AUTOGAMIE, LE RENDEMENT GRAINIER ET LA TENEUR EN HUILE DANS UN POPULATION DE TOURNESOL (*Helianthus annuus* L.)

RÉSUMÉ

Deux méthodes d'amélioration de population: la sélection de masse (deux cycles) et la sélection S_1 (un cycle) ont été imposées sur une population de base pour étudier la réponse de la sélection en comparant leur efficacité en amélioration d'autogamie, la production de semences et le contenu d'huile dans le tournesol. Une selection de masse a été adopté pour développer deux populations distinctes à savoir, précoce (80-85 jours) et medium (95-100 jours) basé sur la durée de la maturité. Les populations dérivées MSE-2 (précoce) et MSM-2 (medium) ont conservé une variabilité substantielle même après deux cycles de sélection massive pour la plupart des caractères. Ainsi, comparées aux populations de base, ces populations dérivées ont montré une amélioration substantielle du rendement jusqu'à une mesure de 83 à 97 pour cent. Cependant, la réponse à la sélection S_1 n'a été efficace qu'au niveau de l'amélioration du contenu oléique et d'autre caractéristiques, incluant le rendement de graine, la population dérivée était inférieur comparée à la population de base.