Electronic Journal of Plant Breeding, 8(4): 1236-1239 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00177.6

Research Article

Variability studies in F_3 Populations of Sun flower

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(Received: 17 Nov 2017; Revised: 5 Dec 2017; Accepted: 6 Dec 2017)

Abstract

Two populations in F_3 generation developed from cross between low oleic inbreds (COSF 1B and TNHSF 239-61-2-2-1) and high oleic (HO 5-13) inbred were studied to assess genetic variability among oil yield and its component traits. High PCV and GCV were recorded for oil yield and single plant yield in F_3 population of COSF 1B x HO 5-13. Similarly, high PCV was also noticed for oil yield and single plant yield in F_3 population of TNHSF 239-61-2-4-1 x HO 5-13. This revealed the presence of substantial magnitude of genetic variability in the experimental material and better scope for improvement of these traits. High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was recorded by the traits *viz.* plant height, 100- seed weight, single plant yield, oleic acid content and oil yield in both populations. Non-significant skewness and kurtosis were observed for most of the oil yield contributing traits in both the populations indicating that the genotypes in the population exhibited normal distribution for the traits under study. Highly heritable characters *viz.* plant height, 100- seed weight, volume weight, single plant yield and oil yield could be improved through individual plant selection in subsequent generations. Hence selection based on these characters would contribute for the improvement of oil yield in sunflower.

Keywords: Sunflower, variability, seed yield, oil yield

Introduction

Sunflower (*Helianthus annuus* L.) is an important oilseed crop. It ranks third after soybean and palm oil in worldwide vegetable oil production. It is successfully grown over a widely scattered geographical area and considered as a crop adapted to a wide range of environmental conditions (Ekin *et al., 2005*). Sunflower seeds contain a high amount of oil (40 - 50%) which is an important source of polyunsaturated fatty acid (linoleic acid) of potential health benefits (Monotti, 2004). The understanding and knowledge of genetic variation and genetic similarities present within individuals or populations are useful for the efficient use of genetic resources in breeding programmes. Selection of superior varieties will be possible only when adequate variability exists in the gene pool or segregating population. Therefore, the present research work was carried out to estimate genetic variability in two F_3 populations of sunflowerSunflower (*Helianthus annuus* L.) is an important oilseed crop. It ranks third after soybean and palm oil in worldwide vegetable oil production. It is successfully grown over a widely scattered geographical area and considered as a crop adapted to a wide range of environmental conditions (Ekin *et al., 2005*). Sunflower seeds contain a high amount of oil (40 - 50%) which is an important source of polyunsaturated fatty acid (linoleic acid) of potential health benefits (Monotti, 2004). The understanding and knowledge of genetic variation and genetic similarities present within individuals or populations are useful for the efficient use of genetic resources in breeding programmes. Selection of superior varieties will be possible only when adequate variability exists in the gene pool or segregating population. Therefore, the present research work was carried out to estimate genetic variability in two F_3 populations of sunflower.

Materials and Methods

The experimental material for the present investigation comprised of two populations in F_3 generation *viz.*, COSF 1B x HO 5-13 (CI) and TNHSF239-61-2-4-1 x HO 5-13 (CII) which were developed using COSF 1B (an elite maintainer line with low oleic content) and TNHSF239-61-2-4-1 (a promising restorer with low oleic acid content) as female parents crossed with HO 5-13 (a high oleic inbred line) as male parent. Both the populations were evaluated at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore along with parents during June to September, 2016. Recommended crop production and protection practices for sunflower were followed to ensure good crop health. Observations on ten morphological and yield traits *viz.* days to first flowering, days to 50% flowering, plant height (cm), head diameter (cm), 100- seed weight (g), volume weight (g/100 ml), single plant yield (g/plant), oil content (%), oleic acid content and oil yield (g/plant) were recorded on single plant basis for each cross.

Variability parameters like variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as per cent of mean (GAM) were calculated by adopting the formulae given by Johnson *et al.,* (1955). PCV and GCV were categorized as low, moderate or high following Sivasubramanian and Menon (1973). Heritability (%) percentage was classified as suggested by Robinson *et al.* (1949). Genetic advance as percent of mean (GAM) was categorized as low, moderate or high according to Johnson *et al., (*1955). Skewness and kurtosis were calculated as mentioned by Kapur (1981).

Result and discussion

The success of any breeding programme depends upon the extent of genetic variability in the base population and it is essential to subject a population for selection to achieve improvement for a particular trait. The present study was conducted to assess the presence of variability for desired traits.

Analysis of variation indicated that high PCV was recorded for oil yield (39.27%) and single plant yield (37.67%) and high GCV was also recorded for oil yield (39.17%) and single plant yield (37.60%) in F_3 population of COSF 1B x HO 5-13. High PCV was noticed for oil yield (37.91%) and single plant yield (37.39%) and high GCV was also recorded for oil yield (37.77%) and single plant yield (37.29%) in F_3 population of TNHSF 239-61-2-4-1 x HO 5-13 (Table 1). This revealed the presence of substantial magnitude of genetic variability in the experimental material and better scope for improvement of these traits. This finding was corroborated with the results of Sultana *et al.,* (2005), Rao (2012) and Premnath *et al.,* (2014).

PCV was slightly higher than GCV for all charactersin both the populations A close. correspondence of PCV and GCV values in other characters in both the populations indicated stable expression of the traits and least influence of environment on these traits. Similar reports were given by Janamma *et al.,* (2008), Sutar *et al.,* (2010) and Hassan *et al.,* (2012).

High heritability values were observed for all the characters *viz.* single plant yield (99.62%), oil yield (99.49%), oleic acid content (97.45%), 100-seed weight (94.86%) and plant height (94.49%) in F_3 population of COSF 1B x HO 5-13. The traits *viz.* head diameter and oleic acid content showed moderate heritability. Similarly, high heritability values were recorded for the characters *viz.* single plant yield (99.47%), oil yield (99.25%), oleic acid content (98.57%), plant height (95.29%), volume weight (92.83%) and 100- seed weight (92.69%) in F_3 population of TNHSF 239-61-2-4-1 x HO 5-13 (Table 1) indicating the dependence of phenotypic expression reflecting the genotypic ability to transmit genes to their offsprings and less influence of environmental effects on these traits.

High genetic advance as per cent of mean was observed for the characters *viz.*, oil yield (80.48%), single plant yield (77.30%), 100- seed weight (37.9%) and oleic acid content (33.82%) in F_3 population of COSF 1B x HO 5-13. Similarly, high genetic advance as percent of mean values of 77.50% and 76.61% were observed for the characters *viz.* oil yield and single plant yield respectively and high genetic advance as per cent of mean values were recorded for the traits *viz.* plant height (24.40%), 100- seed weight (30.53%) and oleic acid content (46.13%) in F_3 population of TNHSF 239-61-2-4-1 x HO 5-13 (Table 1).

Johnson *et al.,* (1955) suggested that heritability considered together with genetic advance is more reliable in predicting the effect of selection than heritability alone. High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was recorded by the traits *viz.,* 100-seed weight, single plant yield, oleic acid content and oil yield in both the populations. Ashok *et al.,* (2000), Sutar *et al.*, (2010) and Premnath *et al.,* (2014) also reported high heritability coupled with high genetic advance as per cent of mean for single plant yield and oil yield. High heritability coupled with high genetic advance as per cent of mean indicated that most likely heritability is due to additive gene effects (Panse, 1957) and these characters were least influenced by environmental effects and selection based on such characters would be rewarding.

The traits such as days to first flowering and days to 50% flowering recorded significant positive skewness and leptokurtic nature whereas all the other traits exhibited normal distribution and mesokurtosis in F_3 population of TNHSF 239-61-2-4-1 x HO 5-13 (Table 1). This revealed that larger number of individuals possessed low mean values for the flowering traits indicating the presence of more number of early flowering genotypes in the population. Non-significant skewness and kurtosis were observed for all the traits in F_3 population of COSF 1B x HO 5-13 indicating that the genotypes in the population exhibited normal distribution for those traits.

It is concluded that wider genetic variability for yield contributing characters among the progenies of both the populations could be useful for selecting genotypes in terms of better oil yield for investigation of oil quality in further generations and highly heritable characters *viz.,* 100- seed weight, volume weight, single plant yield and oil yield with high heritability and high genetic advance as per cent of mean could be improved through individual plant selection in subsequent generations. Hence selection based on these characters would contribute for the improvement of oil yield in sunflower.

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Table 1. Variability parameters in F_3 population of crosses, COSF 1B x HO 5-13 (CI) and TNHSF 239-61-2-4-1 x HO 5-13 (CII)

Traits	Cross	Mean	PCV (%)	GCV (%)	h^2 (%)	GAM (%)	Skewness	Kurtosis
Days to first flowering	CI	59.42	5.37	5.10	90.18	9.97	0.17	-0.50
	CII	55.71	4.83	4.48	86.16	8.57	0.69**	0.83*
Days to 50% flowering	CI	62.40	5.10	4.71	85.21	8.96	0.18	-0.47
	CII	58.68	4.55	4.04	78.94	7.40	0.71**	0.96*
Plant height (cm)	CI	160.01	10.21	9.92	94.49	19.87	0.44	0.41
	CII	142.09	12.43	12.13	95.29	24.40	-0.11	0.11
Head diameter (cm)	CI	13.63	9.15	6.79	55.11	10.39	0.20	-0.65
	CII	13.76	10.49	8.55	66.48	14.36	-0.28	0.22
100- seed weight (g)	CI	4.93	19.40	18.89	94.86	37.9	-0.09	-0.75
	CII	5.02	15.99	15.39	92.69	30.53	0.27	0.42
Volume weight (g/100 ml)	CI	33.93	9.59	9.17	91.45	18.07	-0.21	-0.10
	CII	32.12	11.07	10.66	92.83	21.16	0.24	-0.15
Single plant yield (g/plant)	CI	27.72	37.67	37.60	99.62	77.30	0.38	-0.31
	CII	23.74	37.39	37.29	99.47	76.61	0.19	-0.35
Oleic acid content (%)	CI	66.81	16.85	16.63	97.45	33.82	0.41	-0.25
	CII	66.27	22.72	22.55	98.57	46.13	-0.14	-1.07
Oil content (%)	CI	39.34	4.74	3.59	57.37	5.61	-0.13	0.83
	CII	39.35	3.81	2.22	34.05	2.67	-0.22	2.14
Oil yield (g/plant)	CI	10.95	39.27	39.17	99.49	80.48	0.52	-0.07
	CII	9.34	37.91	37.77	99.25	77.50	0.25	-0.35

* , ** Significant at 5% and 1% level respectively