

Evaluation of sunflower genotypes for phosphorus acquisition and phosphorus partitioning

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ABSTRACT

Field trials were conducted during winter season of 2010 and 2011 to evaluate a total of 111 (52+59) sunflower genotypes for phosphorus (P) acquisition in Vertisols having low status of available phosphorus (9.8 kg/ha). During the study the best genotypes were selected based on the following parameters: shoot drymatter yield, seed yield/plant, shoot P content, seed P content and total P removal. In the first year 22 best performing genotypes out of 52 were selected while, 20 genotypes were selected out of 59 in second year (2011-12). Genotype CMS-42-B had recorded highest P removal (1.71 g/plant) followed by KBSH-44 (1.62 g/plant) > 150-R (1.41 g/plant) > ARM-239-B (1.33 g/plant) > GMU-389 (1.31 g/plant) > KBSH-1 (1.30 g/plant) in first year. The phosphorus acquisition in sunflower genotypes depended on their shoot drymatter, seed yield and their P contents. During 2011-12, the highest P removal was recorded in GMU-38 (2.2 g/plant) followed by GMU-128, KBSH-1, KBSH-44, GMU-3, GMU-5, DRSH-1, GMU-116 and CMS-42-B in descending order. It was noticed that genotype CMS-42-B was found best in acquiring P in both the years of study with 51% of its uptake was partitioned into seeds in 2010-11 and 52.3% in 2011-12. Though, CMS-42-B had removed lower amounts of total phosphorus (1.68 g/plant), it showed high internal distribution of acquired phosphorus towards seed (52.3%) in comparison to genotypes GMU-38, GMU-5 and KBSH-1.

Keywords: Acquisition, Biomass, Genotypes, Phosphorus, Sunflower, Uptake

Among many inorganic nutrients required by plants, phosphorus (P) is one of the most important elements that significantly affect plant growth and metabolism. It plays an important role in photosynthesis, respiration and regulation of a number of enzymes. Phosphorus can be a major limiting factor for plant growth with increasing demand of agricultural production and it is receiving more attention as a non renewable resource (Cordell *et al.*, 2009 and Gilbert, 2009). Availability of P in neutral to calcareous soils is a matter of great concern, as its retention is dominated by precipitation reactions (Lindsay *et al.*, 1989) and it can also be adsorbed on the surface of calcium carbonate and clay minerals (Devau *et al.*, 2010). Phosphate can precipitate with free Ca thereby forming dicalcium phosphate (DCP) that is available to plants. Ultimately, DCP can be transformed into more stable forms (not easily available to crops) such as octocalcium phosphate and hydroxyapatite, which accounts for more than 50% of total inorganic phosphate in calcareous soils. Thus, the availability of P to plants is dominantly determined by interactions among plants, soil and microorganisms in the rhizosphere. On the other hand, P levels in many agricultural soils are building up, because 80-90% of P applied as fertilizer is sorbed by soil particles, rendering it unavailable for plants that lack specific adaptation to access sorbed P. With decreasing global P reserves, P-fertilizer prices are bound to increase. Thus, there is an urgent need to develop crops that are more efficient in acquiring inorganic phosphates from soil and/or in using P

more efficiently. Phosphate acquisition by plants is one of the more thoroughly studied aspects of plant nutrition and there is an extensive literature on the biochemical, morphological, and physiological effects of P deficiency on plants. Successful P management can be achieved by breeding crop cultivars or genotypes more efficient in its acquisition and use. In plants, the integration of root morphological and physiological adaptive strategies can help to maximize the efficiency of plant roots to mobilize and acquire P from the rhizosphere. In this study, an attempt was made to screen sunflower genotypes over a period of two years (2010-12) in field experiment to identify genotypes for high P acquisition capacity in Vertisols under native P conditions without addition through fertilizers.

MATERIALS AND METHODS

A total of 111 sunflower genotypes were evaluated in two years (i.e., 52 in first year and 59 in second) in deep black soils belonging to Vertisol soil order at DOR-ICRISAT research farm located at Patancheru, Hyderabad. A fixed plot of 50m x 60m size in BM-3 block was selected for conducting this trial. However, the site for genotypes was not fixed as it is difficult to maintain fixed rows (for each genotype). The soils of experimental site was alkaline in reaction (pH=8.3), with low electrical conductivity (0.35 dS/m) and organic carbon content (5.38 g/kg soil). The soils had low available nitrogen (233 kg/ha) and phosphorus (9.8

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kg P/ha) but had high levels of potash (816 kg/ha). Before growing sunflower, in every rainy season maize was grown as preceding crop for exhaust without the application of phosphorus in order to create P stress in experiment site. Screening experiment was conducted during the winter season of 2010 and 2011. Sunflower genotypes were sown in last week of November and harvested in second week of March in both the years. To all the sunflower genotypes 12.5 kg N/ha and 15.0 kg K₂O/ha was uniformly applied at the time of sowing, remaining 12.5 kg N/ha was applied as top dress at 30 day after sowing. Phosphorus was not applied to genotypes so as to evaluate them for P acquisition under native fertility. Rest of the package of practices was uniformly followed in all the genotypes. The genotypes comprised elite germplasm, inbred lines, CMS and R-lines and released hybrids KBSH-1 and KBSH-44. Each genotype was planted in three rows with spacing of 60 cm between rows and 30 cm between plants. Ten plants were maintained in each row. Three random plants (as three replications) were labelled in the middle row for recording biometric observations at physiological maturity stage and yield parameters at the time of harvest. Soil samples were collected at harvest and analyzed for available P. Biometric observations (plant height, number of leaves and head diameter) were recorded at the physiological maturity of genotypes. At harvest, the shoot drymatter (stem+leaves+thalamus) and seed yield were recorded for all genotypes. Processed plant sample (leaves, stem, thalamus and seed) for each genotype was digested in diacid (nitric acid + perchloric acid 9:4) and the P content in the digest was estimated with yellow colour method as described by Dhyan Singh *et al.* (2005). Available P in soil samples was extracted with 0.5M sodium bicarbonate extracting solution and the P concentration in extracts was measured by blue colour method described by Watanabe and Olsen (1965). The data generated were statistically analyzed adopting single factor randomized block design with three replications with M-STATC.

RESULTS AND DISCUSSION

Shoot drymatter, seed yield and phosphorus content in genotypes: During the year 2010-11, 52 sunflower genotypes were screened to study the P acquisition capacity in black soils belonging to Vertisol soil order. The data presented in table 1 showed variation in the shoot dry matter (SDM), seed yield and the P content in SDM and seed of different sunflower genotypes.

It was noticed that genotype KBHS-44 produced significantly highest shoot drymatter yield (218 g/plant), followed by KBSH-1 (206 g/plant) > CMS 42 B (203 g/plant) > 150-R (179 g/plant) > GMU-389 (162 g/plant) > PS-1047 (155 g/plant). The highest seed yield was recorded in KBSH-44 (30.8 g/plant). However, the seed yield of

KBSH-1 (28.5 g/plant), CMS-42 B (27.6 g/plant) and PS-1047 (27.6 g/plant) were found to be statistically at par with released hybrid KBSH-44. The P concentration in the shoot biomass varied significantly. The highest P content was noticed in the genotype 150-R (0.97%) followed by CMS-42 B (0.88%) and ARM 239 B (0.79%). However, it was noticed that P content in the shoots of genotypes CMS-17 B (0.71%), GMU-389 (0.71), NDR-71 (0.71%), GMU-310 (0.70%), KBSH-44 (0.66%) and PS-2016 (0.64%) were at par. The P content in the seeds of genotypes GMU-420, CMS-42 B and CMS-17 B was 0.99, 0.93 and 0.93%, respectively was at par to each other but significant over rest of the genotypes. The results presented in table 1 showed that genotype CMS 42 B had recorded highest P removal (1.84 g/plant) followed by KBSH-44 (1.62 g/plant) > 150-R (1.41 g/plant) > ARM-239-B (1.33 g/plant) > GMU-389 (1.31 g/plant) > KBSH-1 (1.30 g/plant). The greater amount of P removal or uptake by these genotypes might be due to their high shoot biomass yield, seed yield and their respective P contents. The results showed that among all the genotypes screened for P acquisition during the year 2010-11, RHA-214 had lowest values for SDM yield (81.3 g/plant), seed yield (14 g/plant) and removal of phosphorus (0.6 g/plant) from the soil.

In the year 2011-12, a total of 59 sunflower genotypes were screened for acquisition of native P in Vertisols. The results of 20 best performing genotypes for selective biometric parameters like shoot dry matter (SDM) yield, seed yield, phosphorus concentration in SDM and seed has been presented in table 2.

Highest SDM yield was recorded in KBSH-1 (275 g/plant) followed by genotypes GMU-136 (268 g/plant), GMU-128 (253 g/plant) and GMU-38 (241 g/plant). The SDM of genotypes KBSH-44, GMU-5 and CMS-42-B were 224.3, 222.4 and 221.3 g/plant, respectively, were at par to each other. The highest seed yield was noticed in GMU-116 (35.1 g/plant) and KBSH-44 (35.0 g/plant). However, genotypes GMU-116, KBSH-44, GMU-136, KBSH-1 and GMU-13 were statistically at par to each other in seed yield. The results also showed that genotypes CMS-42-B, GMU-9, DRSH-1, GMU-20 and GMU-38 had produced at par seed yield within this group. Significant highest SDM P content was recorded in the genotype GMU-3 (1.06%) followed by DRSH-1, GMU-38 and GMU-116 which had similar amounts of P (0.83%). These genotypes were significantly superior in SDM P content over GMU-5 (0.75%), KBSH-44 (0.72%), CMS-42-B (0.66%) and KBSH-1 (0.65). For seed P content, among all the genotypes only two genotypes viz., KBSH-1 and CMS-339-B recorded P content below 0.7%. The highest seed P content was noticed in GMU-142 (0.95%) which was at par with GMU-9 (0.90%) followed by GMU-3= GMU-38> GMU-11> GMU-51> GMU-116= GMU-136= CMS-42-B> GMU-32=GMU-16> KBSH-44= DRSH-1>KBSH-1. The P removal by sunflower genotypes

depended on their shoot drymatter, seed yield and their P contents. The highest P removal was recorded in GMU-38 (2.2 g/plant) followed by GMU-128, KBSH-1, KBSH-44,

GMU-3, GMU-5, DRSH-1, GMU-116 and CMS-42-B in descending order (Table 2).

Table 1 Shoot drymatter (SDM), seed yield, SDM-P and seed P contents of sunflower genotypes screened during 2010-11

Genotype	SDM (g/plant)	Seed yield (g/plant)	SDM- P (%)	Seed P (%)	Total P removal (g/plant)	Available P after harvest (kg/ha)
RHA 214	81.3	13.9	0.63	0.70	0.61	09.7
CMS 17 B	113.1	22.5	0.71	0.93	1.01	10.8
R 649	107.2	24.3	0.57	0.74	0.79	10.2
KBSH 1	206.7	28.5	0.56	0.46	1.30	10.3
KBSH 44	218.2	30.8	0.66	0.60	1.62	09.8
CMS 335 B	129.5	15.6	0.61	0.75	0.91	09.0
GMU 389	162.0	23.9	0.71	0.66	1.31	11.8
GMU 420	129.8	20.9	0.62	0.99	1.02	09.4
GMU 302	148.5	26.3	0.64	0.62	1.11	08.3
GMU 310	147.7	21.9	0.70	0.54	1.15	09.2
ARM 239 B	152.9	21.7	0.79	0.59	1.33	10.2
CMS 42 B	203.4	27.5	0.78	0.93	1.71	09.7
PS 1040	128.8	21.9	0.72	0.65	1.07	11.2
150-R	178.8	16.8	0.97	0.74	1.41	11.7
PS 1047	155.0	27.5	0.45	0.43	0.82	14.5
L 33-1	134.2	18.2	0.54	0.52	0.82	16.1
LDM 02	146.0	26.5	0.62	0.51	1.04	10.9
NDR 71	145.6	22.6	0.71	0.53	1.15	12.6
PS 2016	154.9	22.6	0.64	0.88	1.19	10.2
CMS 40 B	147.5	25.4	0.48	0.74	0.90	11.7
ARM 242 B	114.5	14.5	0.60	0.60	0.77	09.9
EC 5126-79	128.2	20.5	0.51	0.63	0.78	12.1
LSD (0.05)	6.0	3.2	0.07	0.09	--	--
C.V (%)	2.5	8.7	6.2	8.4	-	-

Table 2 Shoot drymatter (SDM), seed yield, SDM-P and seed P contents of sunflower genotypes screened during 2011-12

Genotype	SDM (g/plant)	Seed yield (g/plant)	SDM-P content (%)	Seed P (% P)	Total P removal (g/plant)	Available P after harvest (kg/ha)
GMU-38	241.5	27.3	0.83	0.83	2.23	06.5
GMU-20	106.3	27.8	0.60	0.72	0.84	09.0
GMU-142	198.0	22.5	0.70	0.95	1.60	18.9
GMU-5	222.4	24.9	0.74	0.70	1.83	10.8
GMU-32	168.7	21.8	0.51	0.78	1.03	09.3
GMU-128	253.0	24.9	0.72	0.70	1.99	08.3
R-649	107.9	15.6	0.68	0.74	0.85	09.2
KBSH-1	275.2	32.5	0.65	0.62	1.98	09.6
CMS-42B	221.3	29.2	0.66	0.79	1.68	09.8
KBSH-44	224.2	35.0	0.72	0.72	1.86	09.2
CMS-339B	186.9	24.4	0.51	0.67	1.11	08.6
DRSH-1	193.8	28.4	0.83	0.72	1.80	10.0
GMU-136	268.2	34.4	0.61	0.79	1.06	12.2
GMU-116	209.6	35.1	0.83	0.79	1.71	11.6
GMU-9	150.0	28.8	0.70	0.90	1.31	16.4
GMU-3	154.3	25.9	1.06	0.84	1.85	08.2
GMU-13	219.4	33.2	0.54	0.72	1.27	09.4
GMU-11	226.8	27.6	0.59	0.82	1.51	09.9
GMU-51	144.8	26.4	0.48	0.80	0.91	13.6
GMU-16	171.5	26.2	0.57	0.78	1.18	10.3
LSD (0.05)	9.2	3.1	0.07	0.07	-	-
C.V (%)	3.1	5.6	6.1	6.3	-	-

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The available P status in soil after the harvest of sunflower genotypes showed variations and the values were within the range of low to medium in both the years (Table 1 and 2). The site for genotypes was not fixed and therefore, the data on available P after harvest of genotypes depicts the actual P fertility condition of soils in which they were evaluated. Thus, most of the genotypes including CMS-42-B and released hybrids KBSH-1 and KBSH-44 were screened for P acquisition under marginal conditions of available P.

Partitioning of phosphorus in sunflower genotypes:

Year 2010-11: The internal distribution of P content in the plants during its stress is very essential in determining the yield and quality parameters of crop. Based on P content in plant parts and its partitioning (percent distribution) in to different parts for the total uptake was worked out for the genotypes. Partitioning of P was done in genotypes whose seed yield was at par with checks *viz.*, KBSH-1 and KBSH-44 in both the years. The data presented in figure 1 depicts the partitioning of P content into different plant parts for sunflower genotypes screened during the year 2010-11.

Genotype CMS-42-B had distributed 51.7% of total P content into seeds and the rest 48.3% was left in the biomass of the plants compared to check KBSH-44 with 47.6% of total P content was partitioned into seeds and the rest 52.4% was left back in the biomass. Hence, in the year 2010-11, genotype CMS-42 B was found to be superior in acquiring phosphorus in the plant and efficient in its internal distribution towards the economic produce (seed) when compared to checks KBSH-44 and KBSH-1. This was followed by GMU-302 (50%) > CMS-40 B = LDM-02 (48.7%).

Year 2011-12: The ability of genotypes to internally distribute the P of the total P absorbed into different plant parts has been depicted in figure 2 for the promising sunflower genotypes screened during year 2011-12.

The results showed that highest internal distribution towards seed was recorded in GMU-136 with a value of 56.8% out of total P absorbed, followed by CMS-42-B (52.3%). It has been noticed that though genotypes GMU-3 and GMU-38 had absorbed maximum P (i.e., total plant P was 1.90 and 1.66%, respectively) but their internal distribution of P towards seeds was low compared to GMU-136 and CMS-42-B. Among the 22 genotypes, the lowest distribution of P towards seed was noticed in GMU-5 (45.1). During second year study though genotype CMS-42-B had removed lower amounts of total P 1.68 g/plant with a seed yield of 29.2 g/plant had showed profound distribution of absorbed P towards seed with 52.3% as compared to genotypes GMU-38 (49.0%), GMU-5 (45.1%) and KBSH-1 (50.0%). The integration of genetically improved P-efficient crops with advanced P management in the soil-plant system is important for

improving nutrient-use efficiency and sustainable crop production. Successful P management can be achieved by breeding crop cultivars or genotypes which are more efficient in P acquisition and internal distribution. Great progress has been made in traditional plant breeding programs in China toward selecting crop varieties for high P-use efficiency. Phosphorus efficient wheat variety 'Xiaoyan54' was identified, which secreted more carboxylates (e.g. malate and citrate) into the rhizosphere than P-inefficient genotypes (Li *et al.*, 1995).

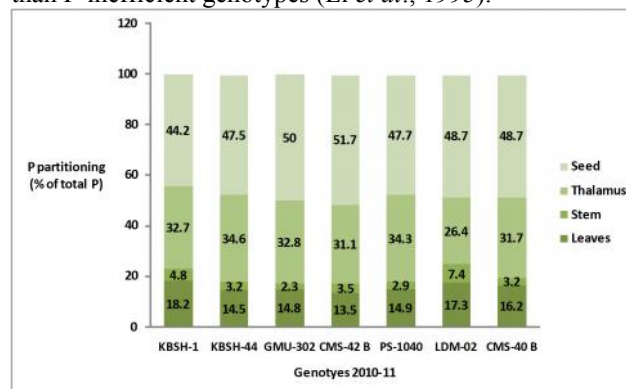


Fig. 1. Internal distribution of phosphorus of promising sunflower genotypes during 2010-11

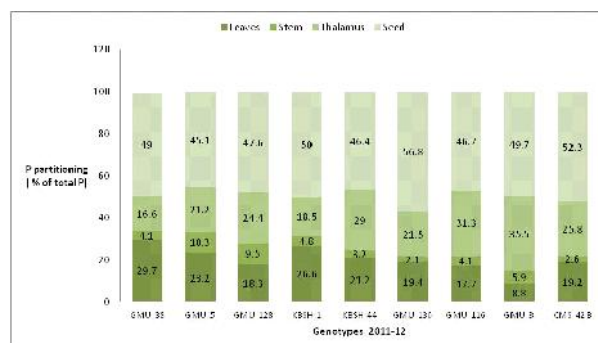


Fig. 2. Partitioning of phosphorus in different plant parts of promising sunflower genotypes during 2011-12

In soybean, genotype 'BX10' had superior root traits showing better adaptation to low-P soils (Yan *et al.*, 2006). Some important root genetic traits have been identified with potential utility in breeding P-efficient crops, including root exudates, root hair traits, topsoil foraging through basal, or adventitious rooting (Gahoonia and Nielsen, 2004; Lynch and Brown, 2008). In addition, the ability to use insoluble P compounds in soils can be enhanced by engineering crops to exude more phytase, which results from over expression of a fungal phytase gene (George *et al.*, 2005).

Among the 52 sunflower genotypes screened for P acquisition during 2010-11, four genotypes *viz.*, GMU-420,

CMS-335-B, PS-2016 and CMS-42-B had showed better P acquisition for the total P removed from soil. During 2011-12, seven genotypes viz., GMU-136, GMU-13, GMU-38, CMS-42-B and KBSH-1 showed better P acquisition from native soil P. It was noticed that genotype CMS-42-B was best in P acquisition during 2010-11 with 51% of its uptake was partitioned into seeds and 52.3% during 2011-12. This genotype had removed lower amounts of total P 1.68 g/plant however; it had showed high internal distribution of acquired P towards seed (52.3%) in comparison genotypes GMU-38, GMU-5 and KBSH-1. To conclude, genotype CMS-42-B showed repeated performance for P acquisition and the acquired P was better distributed towards seeds in black soils with low phosphorus fertility.

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