**Experiment-I: Screening sunflower genotypes for phosphorus acquisition in Vertisols- Field study**

**Results**

*Shoot dry matter, seed yield and phosphorus content in genotypes*

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genotypes** | **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** | **-** | **-** |

It was noticed that genotype KBHS-44 produced significantly highest shoot dry matter yield (218 g/plant), followed by KBSH-1 (206g/plant)> CMS 42 B (203g/plant)> 150-R (179 g/plant) >GMU-389 (162g/plant) > PS-1047 (155g/plant). The highest seed yield was recorded in KBSH-44 (30.8g/plant). However, the seed yield of KBSH-1 (28.5g/plant), CMS-42 B (27.6g/plant) and PS-1047 (27.6g/plant) were found to be statistically at par with released hybrid KBSH-44. The phosphorus 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 (.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 percent, 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 (1.84g/plant) followed by KBSH-44 (1.62g/plant)> 150-R (1.41g/plant) >ARM-239-B (1.33g/plant) > GMU-389 (1.31g/plant) > KBSH-1 (1.30g/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 (81.3g/plant), seed yield (14g/plant) and removal of phosphorus (0.6g/plant) from the soil.

In the year 2011-12, a total of 59 sunflower genotypes were screened for acquisition of native phosphorus 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.

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genotypes** | **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** | **-** | **-** |

Highest SDM yield was recorded in KBSH-1(275g/plant) followed by genotypes GMU-136 (268g/plant), GMU-128 (253g/plant) and GMU-38 (241g/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 (35.1g/plant) and KBSH-44 (35.0g/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 namely 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 phosphorus removal by sunflower genotypes depended on their shoot dry matter, seed yield and their P contents. The highest P removal was recorded in GMU-38 (2.2g/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). The available phosphorus 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 phosphorus.

*Partitioning of phosphorus in sunflower genotypes*

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

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

*Year 2011-12*: The ability of genotypes to internally distribute the phosphorus 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.

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

About 24 P solubilizing bacteria were isolated in efficient sunflower genotypes (Fig.3)

