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Overcoming inter-specific barriers in sorghum

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Crop improvement in sorghum has progressed extensively availing the variation in the primary gene pool of *Sorghum bicolor*, while the wild species of tertiary gene pool remain unexploited.Sorghum wild species are reported to carry resistance genes to biotic and abiotic stresses including for shoot fly and stemborer that prompted us to develop inter-specific hybrid derivatives. Cross incompatible barriers in sorghum were identified to be lack of pollen germination on the stigma and it was overcome in Texas through incorporation of *iap* (inhibition of alien pollen) allele. However, *iap* allele cannot be accessed by Indian programs due to IPR rights. We overcame these barriers of crossing through pollen and floral treatments and developed inter-specific populations. Trait specific pre-breeding lines are identified for use in sorghum crop improvement program in India. Thirteen diverse elite lines of cultivated species were pollinated with eight wild species belonging to tertiary gene pool. Different treatments like pre-treatment of pollen, spray with pollen germination medium and 2, 4-D, and repeated pollinations were used to facilitate crossing. Seed set was observed in 76% crosses, but many seeds were under developed. We raised F_1 hybrids from 10 crosses.F_1 progeny from these eight crosses showed purple leaves, loose panicles and shattering seeds resembling their wild parents. Hybrids were confirmed through PCR analysis in eight crosses. Many (80%) F_1 plants were sterile and 20% of F_1s were advanced to F_2 generation. Wide variation was observed in F_2 progeny and based on the phenotype selections were made and are being evaluated in the field.

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Genetic diversity analysis among advanced breeding lines in pearl millet for grain iron, zinc and agronomic traits

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Evaluation of genetic diversity within breeding populations will help in parents' diversification and identification of trait-specific inbred sources. Total of 294 inbreds were evaluated for grain iron (Fe), zinc (Zn) and agronomic traits in two contrasting seasons using alpha-lattice field design. There was a significant variability observed for all traits. Three-to-four-fold variability noticed for Fe (31-120 mg kg^{-1}), Zn (19-88 mg kg^{-1}), yield (0.6-2.6 tha^{-1}) and 1000-grain weight (6-16 g 1000^{-1}). The magnitude of genetic coefficient of variation explained by traits were varied in the order of Fe (25%)>Zn>TGW>PL>PH>GY>PG>DF (7%) and heritability (broad sense) was very high as >84% for all traits except grain yield (56%). Nine clusters formed at 90% genetic similarity. Clusters I to IV and VII had higher mean value for Fe density (78-100 mg kg^{-1}) and agronomic traits. Highest number of genotypes grouped in cluster I (63) followed by cluster III (54) having higher yield,1000-grain weight, panicle girth, Fe and Zn. Top-10% of high-Fe lines had significantly higher Fe (64%), Zn (49%), grain-weight (29%) and panicle girth (19%) than bottom-10% genotypes. This implies that high-Fe/Zn sources are available with eliteness and can be incorporated into any genetic background without compromising agronomic superiority. Higher heritability and genetic advance as percentage of mean were observed for Fe, Zn and grain-weight suggesting these traits are predominantly determined by additive gene and can be improved through selection.

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Marker assisted selection for bean *anthracnose* resistance in backcross derivatives of French bean

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French bean (*Phaseolus vulgaris* L.) is one of the most important food legumes consumed worldwide including India. Viable production of French bean in the temperate and sub-temperate regions of the north western Himalayas is hampered by anthracnose disease caused by fungus *Collectrotrichum lindemuthianum*. The disease is favoured by cool and humid environment that is prevalent in many parts of Himachal Pradesh. The present study was undertaken on marker assisted selection of bean anthracnose resistant *Co-4* gene positive plants, raised from previously selected BC$_1$F$_2$ seeds. Three previously selected gene positive derivatives of French bean (11-9-1, 11-9-2 and 11-2-2) possessing specific desirable characters like better pod length (11-9-1), higher branch number (11-9-2) and early flowering (11-2-2) were used as donors of anthracnose resistance gene, *Co-4*. The results of the foreground selection in these plants revealed that in cross combination Arka Komal × 11-9-1, out of 20 plants screened for the presence of SY20 marker, 15 were found to be positive for the marker and hence the gene, *Co-4*. Similarly, for cross combination Arka Komal × 11-9-2, the successful amplification was noticed in 30 out of a total of 40 plants. In combination Arka Komal × 11-2-2, out of a total of 18 plants, 8 amplified the