

2nd International Conference on **Agricultural & Horticultural Sciences**

Radisson Blu Plaza Hotel, Hyderabad, India February 03-05, 2014

Morphological and molecular diversity analysis in Sesame (*Sesamum indicum* L.)

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Twenty three accessions of Sesame (*Sesamum indicum* L.) were collected from local areas of Andhra Pradesh for analyzing diversity in the species using morphological and molecular characterization. Morphological characterization of 13 quantitative and 2 qualitative parameters was carried out by correlation studies. Wide variations were observed in flower color, seed color and capsule bearing capacity. The seed yield is showing positive correlation with capsules per plant. Euclidian similarity matrix for morphological data was computed between observable distances and dendrogram which was observed as $r=0.79$. Cluster analysis revealed two major clusters. Molecular analysis included the study of accessions with 10 SSR markers which revealed 4 polymorphic markers. A total of 14 alleles were detected at the four loci with an average of 3.5 alleles/ locus. The pair wise similarity based on Dice coefficient for all the accessions ranged from 0 to 1 and the correlation coefficient (r) computed between observed distances and dendrogram was 0.77 which indicates a good fit between observed distances and dendrogram. The accessions were genetically and phenotypically found to be diverse. Their genetic distance ranged from 0.1-0.9 which is wider than their phenotypic distance ranged from 0.2-0.7. When MXCOMP was carried out between phenotypic and genotypic data the correlation coefficient value (r)=0.12 which was showing less congruency. Hence the morphological traits were not influenced by molecular variations in *S. indicum*.

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Quality gene introgression for development of quality protein maize hybrid using marker assisted selection

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To improve the nutritional security of maize in India, introgression of the *opaque-2(o2)* trait in to normal maize lines is essential. The *opaque-2* recessive mutant gene is involved in the expression of high tryptophan and lysine content in Quality Protein Maize (QPM). The present investigation deals with conversion of normal elite maize inbred lines of Acharya N. G. Ranga Agricultural University (ANGRAU) to Quality Protein Maize lines using Marker Assisted Backcross breeding (MAB)/MAS. Donor identification was done by the help of three gene specific SSR markers (ϕ 1057, ϕ 112 and ϕ 1066), the identified donor CML181 crossed with elite non QPM inbreds (BML 6 and BML 7) of ANGRAU, marker-based backcross breeding program for incorporation of the *opaque-2* gene along with phenotypic selection for kernel opaqueness and endosperm modification in the background of medium maturing normal maize inbred lines BML 6 and BML 7 was carried out. F_1 generation plants are backcrossed with recurrent parent (non QPM inbreds), BC_1 , BC_2 , BC_3 and BC_3F_2 generation on selfing. Whole genome background selection in the BC_3 generation identified six plants with 94% to 96% recurrent parent genome content. Finally we got double recombinant recessive homozygous *opaque-2* mutant allele in BC_3F_2 generation. Phenotypic selection of recurrent parent characters and amino acid analysis was carried out from BC_3F_1 generation onwards, where more than 80% amino acid increased plants identified in these converted inbred lines are used for development of ruling hybrid of Andhra Pradesh namely DHM 117.

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