

6th World Congress on **Biotechnology**

October 05-07, 2015 New Delhi, India

Genetic diversity and phylogenetic analysis of Indian wild rice germplasm based on 50K genotyping chip

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Wild rice are distinct with elite cultivated rice varieties as they are survived for thousands of years in the nature and are adapted to extreme habitat. Hence, they are expected to harbor genes for resistance to various kinds of biotic and abiotic stresses and provide tremendous potential for global food security. Knowledge on diversity and population structure is expected to help plant breeders in the selection of parents for crossing, providing a more rational basis for expanding the gene pool and for identifying materials that harbor alleles of value for crop improvement. To overcome these challenges functional genomics tools particularly SNP marker can play a significant role in very less time frame. Here, we report haplotype based phylogenetic analysis of Indian wild rice germplasm using single-copy gene based 50K genotyping chip. Phylogenetic analysis unravels the origin of mutations and provides clues to the evolution of genetic diversity in populations. The single-copy gene based 50K rice SNP chip was used to study the genetic diversity and phylogenetic relationship among 192 diverse rice germplasm including wild rice accessions, traditional rice varieties and genetically improved rice cultivars. Genotypes were separated into four major groups. Group-1 comprised entirely of wild rice accessions including both *O. rufipogon* and *O. nivara*. Group-2 comprised wild rice accessions along with landraces, including well-known Aus varieties, Group-3 comprised mainly of well-known *indica* rice varieties. Group-4 was of *japonica* rice cultivars. Several wild rice accessions showing proximity with the Aus group of cultivated rice which may have been domesticated from this wild rice group. Wild rice could play a major role in future breeding programs that would improve biotic and abiotic tolerance capacity and enhance the food security to meet the projected demands of global population.

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Review on advances in forest biotechnology

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Extension of land under forest cover for meeting demands of swelling population is some how inhibited in the current scenario of strong competition between different land uses. Biotechnology when accompanied with traditional tree improvement programs can be considered as a possible option to meet growing human demands for forest produce earlier when compared to traditional tree improvement programs alone and also biotechnology open doors for understanding to a vast range of complex biological problems. Forest biotechnology is related with a wide array of modern tools and methodologies covering aspects of genetic engineering, genomics, metabolomics, proteomics, molecular markers, marker assisted selection, marker assisted breeding. In past few years considerable developed has been achieved in this regard. These advanced biotechnological tools creating new vistas for understanding the populations for forest tree species and their genetic structure, identifying factors of biotic and abiotic stress tolerance and link some of the important traits and genetic markers making possible accelerated selection and further breeding programs. These advanced technologies make possible to utilize genetic material not only from the same species but also from other creatures such as viruses, plants and animals etc., to create novel traits for increased resistance and productivity in short time intervals.

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