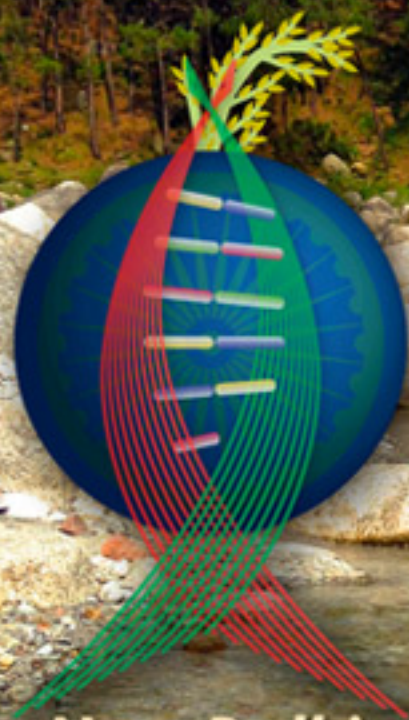


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PVII-191. Allele minning of SKC1 and SOS1 genes for salinity stress tolerance in landraces of riceSingh D¹, Singh AK², Singh NK¹

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Rice (*Oryza sativa* L.) is the principal staple food and over fifty percent of the world's population depends on rice for their food requirements. It is grown under diverse eco-geographical conditions mainly in tropical and subtropical countries. Global climatic changes impose a grave threat to rice production by creating abiotic stress environment of which drought, flood and salinity are considered to be the most serious constraints. Modern high yielding rice varieties are susceptible to such stress environments while the traditional varieties and landraces are very resistant to different types of abiotic stresses as they harbors several stress tolerance genes. So, their proper utilization, conservation and disclosing their hidden genetic potential are of utmost importance. In this study, a total of 75 rice genotypes, including modern high yielding varieties and landraces were screened for salinity tolerance under controlled conditions in hydroponics taking VSR 156 as sensitive; IR74, moderately tolerant, Pokkali and FL 478 as tolerant control. In which Narendra User 1, Narendra User 2 and A-69-1 showed highest tolerance to salt stress, others were either moderately tolerant or susceptible to salt stress. For molecular analysis we plan sequence two well characterized genes responsible for salt tolerance namely SKC1 and SOS1. SKC1 maintained K⁺ homeostasis in the salt-tolerant varieties under salt stress where as SOS1 is involved directly in the transport of sodium ions across the plasma membrane. It contributes to plasma membrane Na⁺/H⁺ exchange, where SOS2 and SOS3 regulate SOS1 transport activity. Primers to amplify SOS1 and SKC1 genes have been designed and amplification is in progress. The amplified product will be used for ion torrent based targeted resequencing and data will be used to get novel alleles of these genes and their possible association with the salt tolerance.

PVII-192. Pyramiding of bacterial blight and blast resistance genes in the Basmati rice variety Pusa Basmati 6 through marker assisted backcross breeding

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Pusa Basmati 6 is a semi-dwarf, superior quality Basmati rice variety with tolerance to lodging, excellent grain, cooking quality and very strong aroma. However, it is highly susceptible to bacterial blight caused by *Xanthomonas oryzae* and blast disease caused by *Magnaporthe oryzae*, which affects both yield as well as grain quality. Marker assisted simultaneous but step-wise backcross breeding (MASS-BB) was used to incorporate the bacterial blight resistance genes xa13 and Xa21 from a common donor Improved Pusa Basmati 1 and two blast resistance genes, Piz5 and Pi54 from Pusa 1602 and Pusa 1603 respectively, into PB6. The isogenic lines carrying individual blast resistance genes were inter-crossed and followed by pedigree selection to develop Pusa 1884 homozygous for both the genes. Gene linked markers were used for foreground selection followed by rigorous phenotypic and background selection to accelerate the recovery of both the recurrent parent phenome and genome. Marker aided selection in combination with phenotypic selection helped in the development of Pusa 1728 (xa13 + Xa21), Pusa 1726 (PB6+ Piz5) and Pusa 1727 (PB6 + Pi54) with RPG recovery of 97.7%, 94.2 % and 93.5% estimated using 19, 54 and 59 STMS markers representing genome wide coverage, respectively. Pusa 1728 (PB6+xa13+Xa21) was found resistant against the virulent BB isolates collected from Basmati growing areas of the country. Similarly, Pusa 1884 (PB6+Piz5+Pi54) exhibited resistance to blast disease under artificial inoculation with respective diagnostic isolates. Further, these lines were also found resistant when evaluated under natural epiphytotic conditions of UBN-Malan. The performance of improved lines was on par with PB6 for agronomic and cooking quality traits. These improved lines will drastically reduce the use of pesticides rendering the produce organic. Further, these lines are invaluable sources for disease resistance genes in Basmati rice improvement program as well as in functional genomics studies.