

Category	: International Rice Research Conference
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Keyword 2	: Salinity tolerance
Keyword 3	: Photosynthesis
Title of Entry	: Integrated analysis of the gas exchange traits and chlorophyll fluorescence in the introgression lines of KMR3 X O. rufipogon and Swarna X O. nivara for salt tolerance
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: High yielding introgression lines derived from KMR3 x <i>O. rufipogon</i> and Swarna x <i>O. nivara</i> (BC2F6-7) were screened at reproductive stage in pot/soil for salinity tolerance. The most salt tolerant ILs, K478, K463 and K50-13 and most sensitive, K198 (ILs of KMR3 x <i>O. rufipogon</i>) and moderately tolerant S166 and S3-1 (ILs of Swarna x <i>O. nivara</i>) were analyzed for their yield under salt stress pot conditions. The physiological experiments were conducted with 17 diverse rice genotypes including popular rice varieties, <i>O. sativa</i> (KMR3) X <i>O. rufipogon</i> (BC2F6-7) introgression lines under two different concentrations (100 mM and 150 mM) of salt. We studied salinity induced changes in leaf photosynthetic traits by measuring gas-exchange and chlorophyll fluorescence traits, under continuously maintained salinity stress conditions at reproductive stage. The data on fluorescence characteristics indicated that salinity treatments had no significant influence on Fv/Fm ratio (maximum efficiency of PSII) and yield, indicating that salinity stress did not influence the primary photochemical efficiency of the leaves. However, Imposition of salt stress had significantly reduced photosynthesis rate (Pn), stomatal conductance (gs), transpiration rate (E) and intercellular CO ₂ concentration in all the tested genotypes. The reduction in Pn was highest in KMR3 introgression line K198 where as the reduction was minimum in ILs K458, K463, K50-13 and K478 indicating relative tolerance to salinity stress in these ILs. Interestingly, these ILs performed better in terms of grain yield under moderate salinity treatments than the other popular varieties. Further, the whole genome transcriptomic analysis was performed to compare differential expression of genes in the most-tolerant K478 and the most-sensitive K198. The K478 showed 281 up-regulated and 1832 down regulated genes while K198 showed 125 up-regulated and 1918 down-regulated genes. Thus, the mechanism for salt tolerance recorded through data of photosynthetic rate was directly correlated to the genes up-regulated. Thus, our results on gas-exchange traits and chlorophyll fluorescence characteristics indicate that introgressions of KMR3 (<i>O. sativa</i>) with wild rice <i>O. rufipogon</i> has the potential to improve tolerance and can be used to develop salinity tolerant rice varieties and hybrids.

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