## Phenotypic and physiological tolerance of rice genotypes to saline and sodic soil environments.

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## Abstract:

Globally around 1000 m ha land is afflicted with soil salinity problems and this menace is likely to expand in more areas. Development of salt tolerant genotypes as identified through reliable and representative screening methods can increase rice productivity of these problem areas with minimum input costs. The overall biological tolerance to salinity being a polygenically governed trait is a multitude of several physiological mechanisms. With an aim to identify better salt tolerant genotypes and donors, a total of 121 diverse and elite genotypes received from IRRI, Philippines were screened in 2 sets (set I and set II consisting of 53 and 68 genotypes, respectively). The genotypes were tested under nearly homogeneous salt stress conditions of the micro-plots, which is often a lacking feature under natural field conditions.

Single row of a genotype under each set was transplanted in a thrice replicated RBD in 3 soil stress environments *i.e.* sodic (soil  $pH_2 \sim 9.6$ ) and 2 saline ( $EC_2 \sim 6.0$  and 8.0 dSm<sup>-1</sup>) environments in the micro-plots. Recommended agronomic practices were followed to raise the crop. At maturity grain yield and associated characters were recorded.In a separate experiment, seedlings of these genotypes were exposed to 125mM concentration of NaCl under timer controlled saline culture solution screening facility under controlled glass house conditions at CSSRI, Karnal. After 10 days of treatment, 3<sup>rd</sup> leaf of these genotypes was sampled for their relative uptake of Na and K ions.

Significant differences were found among genotypes for grain yield in each set under all stresses. In set I, on overall basis when genotypic performance was averaged across 3 stresses, entry IR61919-3B-14-3 gave highest yield (3.71 t ha<sup>-1</sup>) followed by IR51500-

AC11-1 (2.97 t ha<sup>-1</sup>), IR63311-B-3R-B-24(2.70 t ha<sup>-1</sup>), IR64197-3B-14-2 (2.68 t ha<sup>-1</sup>) and CSR23 (2.42 t ha<sup>-1</sup>). As regards physiological mechanisms, IR64197-3B-14-2, CSR23 and IR61919-3B-14-3 gave higher yields despite higher Na uptake ( >1.08mM per dry weight in g) thus indicating the mechanism of tissue tolerance in these entries. The line IR63311-B-3R-B-24 in addition to having higher Na content also exhibited greater uptake of K (~1.23 mM per dry wt.in g). Similarly evaluation of set II across 3 salinity regimes revealed that entry IR61925-3B-1-1 exhibited maximum yield performance( 2.60 t ha<sup>-1</sup> ) followed by IR 63731-1-1-4-3-2 (2.27 t ha<sup>-1</sup> ), BW267-3 (2.15 t ha<sup>-1</sup>) and IR 71656-5R-B-12P(2.06 t ha<sup>-1</sup>). Regarding the ionic uptake of stressed plants, IR 63731-1-1-4-3-2 and BW267-3 showed very little presence of Na content (  $\leq 0.60$  mM per dry wt.in g) and therefore could be termed as Na excluding genotypes. The highest yielding line IR61925-3B-1-1 also exhibited higher Na content (~ 1.25 mM per dry wt.in g), therefore showing better tissue tolerance to Na. IR 63731-1-1-4-3-2 besides showing Na exclusion trait exhibited quite high K mining ability (1.90 mM per dry wt.in g) both of which are desirable traits for enhancing the overall tolerance. These promising lines are being used in our breeding programs to harness the potential of enhanced limits of tolerance.