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| Category | : 8th Rice Genetics Symposium |
| Select Theme | : Genetic improvement |
| Endorsement email | : |
| Keyword 1 | : Pre-breeding |
| Keyword 2 | : Genomics-assisted breeding |
| Keyword 3 | : Abiotic stress tolerance |
| Title of Entry | : Genetic improvement of adapted US rice cultivars through introgression of salt tolerance genes/traits |
| Presenting author | : Prasanta Subudhi |
| Presenting author email | : psubudhi@agcenter.lsu.edu |
| Co author 1 | : Teresa De Leon |
| Co author 2 | : John Ontoy |
| Affiliation presenting author | : Louisiana State University Agricultural Center |
| Affiliation 1 | : Louisiana State University Agricultural Center |
| Affiliation 2 | : Louisiana State University Agricultural Center |
| Select only one type of presentation | : 15 minute oral presentation |
| Abstract | : Soil and water salinity is a major climate-related threat for global food security. Rice is a staple food for the world population, but it is highly sensitive to salinity at both seedling and reproductive stages. Therefore, the development of salt tolerant cultivars is necessary for sustainable rice production under future climatic uncertainties. The major bottleneck for genetic improvement of US varieties for salt tolerance is its narrow genetic base. However, abundant natural genetic variation existing in the world rice germplasm provides us opportunity for making progress on this front. The improvement in seedling stage salinity tolerance is crucial for better crop establishment. Multiple mapping populations such as recombinant inbred lines (RILs) and introgression lines (ILs) developed from crosses involving elite US rice cultivars and well-known salt tolerant donors such as Pokkali and Nona Bokra were genotyped using genotyping by sequencing (GBS) and SSR markers. Phenotyping of these populations for seedling stage salt tolerance was conducted in hydroponics. Quantitative trait loci (QTL) for both morphological and physiological attributes conferring salt tolerance were discovered and validated. A high density consensus was constructed for meta-analysis of QTLs for salt tolerance traits at the seedling stage using multiple mapping populations. Advanced breeding lines with enhanced tolerance to salt stress were developed through introgression of salt tolerance genes/traits from exotic donors. Our results on identified candidate genes in the QTL regions indicated that possible mechanisms of tolerance could be Na+ |

dilution in leaves, vacuolar Na⁺ compartmentation, homeostasis between Na⁺ and K⁺, and possibly synthesis of compatible solutes. The increased resolution of QTL mapping in the GBS-based linkage map led to identification of candidate genes for further validation and use in marker-assisted gene pyramiding to develop climate resilient rice varieties. Moreover, the genomic and germplasm resources generated in this project will accelerate discovery of genes involved in salt tolerance mechanisms using functional genomics strategies in future.

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