

W622 Use of EcoTILLING to Find Genes Related to Salt Tolerance in Rice

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Sónia Negrão, ITQB-Universidade Nova de Lisboa, Oeiras, Portugal

M. Cecilia Almadanim, ITQB-UNL, Oeiras, Portugal

Inês Pires, ITQB-UNL, Oeiras, Portugal

João P. Maroco, ISPA, Lisbon, Portugal

Brigitte Courtois, CIRAD, Montpellier Cedex 5, France

Glenn Gregorio, International Rice Research Institute

Kenneth L. McNally, Int'l Rice Research Institute, Metro Manila, Philippines

M. Margarida Oliveira, ITQB-UNL, Oeiras, Portugal

Salinity is considered one of important physical factors influencing rice (*Oryza sativa* L.) production. Roots are the first parts of the plant to experience any soil-based salt stress and it is at the roots that the entry of Na⁺ and Cl⁻ is determined. Rice as other plants, have several strategies to cope with salinity including minimizing the entry of toxic ions through roots, and/or maintaining low Na⁺/K⁺ ratios at shoot level, etc...A tremendous variation for salt tolerance within genotypes provides opportunities to improve rice salt-stress tolerance through genetic means. Aiming to find alleles associated with salinity tolerance we used the EcoTILLING technique to explore the natural variability existing in 390 rice germplasm accessions at key genes related to salt stress. This working collection is representative of the large morphological, physiological, and ecological variation available in domesticated rice. All targets genes, namely *OsNHX1*, *OsHKT1;5*, *SalT*, *OsRMC* and *OsCPK17*, have been previously described and characterized as related to salt-tolerance enhancement in rice, through different mechanisms such as Na⁺/K⁺ equilibrium, signaling cascade and stress protection. Sequence results showed hundreds of SNPs (Single Nucleotides Polymorphisms) and small INDELS, resulting in a total of 40 allelic variants, thus coding 31 different proteins. After phenotypic characterization of the allelic variants at CDS level, we found significant statistical associations between some particular gene haplotypes and phenotypic parameters under salt stress. We will discuss the utility of EcoTILLING and SNP discovery in breeding efforts for salt tolerance, with particular emphasis to the mechanisms related to root genomics.

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