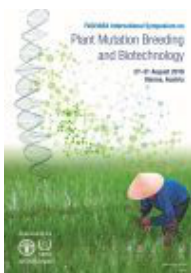


FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



Contribution ID: 195

Type: Oral

GENERATION AND CHARACTERIZATION OF NOVEL GENETIC VARIATION IN RICE FOR THE ENHANCEMENT OF GRAIN QUALITY AND AGRONOMIC PERFORMANCE

Induced plant mutants are important resources for the breeding of improved varieties to provide food, feed and fibre to an ever-increasing global population. Furthermore, the development of powerful, high throughput sequencing-based strategies for mutation detection has increased the value of these resources, enabling functional genomics of agriculturally important traits. The major goals of our research are to identify novel mutations and traits to further the understanding of agronomic performance and grain quality in rice and to develop novel genetic resources for breeding new and improved varieties. Towards these ends, chemical mutagenesis has been used to generate mutant populations in the japonica rice varieties Nipponbare, Kitaake, and Sabine. Using the reverse genetics method Targeting of Induced Local Lesions in Genomes (TILLING) by sequencing, mutations in genes involved in seed phytic acid content, silicon/arsenic uptake and accumulation, and starch biosynthesis have been identified. Forward genetics has also been employed to complement the TILLING by sequencing approach and to identify morphological and developmental mutants. Characterization of the phenotypic effects of mutations identified via TILLING and progress towards isolating the genes underlying mutant phenotypes obtained by forward genetics screens will be presented using examples involving silicon/arsenic uptake and cuticular wax synthesis and accumulation.

Country or International Organization

USA

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Track Classification: Enhancing agricultural biodiversity through new mutation induction techniques