FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



Contribution ID: 98

Type: Oral

NATIONAL REPOSITORY OF RICE EMS MUTANTS OF AN UPLAND RICE CULTIVAR NAGINA 22: PROGRESS UPDATE ON CHARACTERIZATION AND UTILIZATION

The Indian initiative for creating a mutant genetic resource in rice has generated 87000 mutants in the background of a popular drought and heat tolerant upland cultivar, Nagina 22 (N22) through EMS mutagenesis. To enable mapping of the mutants, high quality sequence resources of the wild type (WT), N22, has been created with less than 5 % gaps in the total of 113 Mb genic sequences. So far, 541 macro-mutants from this resource have been identified and are being maintained in the mutant garden. Detailed characterization of these 541 mutants based on 44 descriptors pertaining to distinctness, uniformity and stability (DUS) of rice and their morphological characterization, organic (chlorophyll and epicuticular wax content) and inorganic constituents (phosphorous, silicon and chlorine) are hosted in a database named 'EMSgardeN22'. High throughput capillary based SSR genotyping of these mutants with 57 genome-wide markers revealed that more than 93% of the mutants were identical to the WT with less than one change in SSR repeat motifs. Further, similarity index of the mutants was more than 0.6 for nearly 90% of the mutants with respect to DUS descriptors establishing the validity of the mutants. Recently, a novel herbicide (Imazethapyr) tolerant mutant has been identified and characterized from this resource and is now being used in introgressing the herbicide tolerant trait in 10 major rice varieties of India. One mutant which can grow well in low phosphorous shows monogenic recessive inheritance while two functional stay green mutants show monogenic dominance inheritance were also indetified. Mapping populations of these three mutants have been generated, the mutant type plants have been pooled in each population separately and subjected to whole genome sequencing to enable mapping of the mutants. Further, mutants have been identified for tolerance to sheath blight, blast, drought, higher photosynthetic efficiency and root traits from this resource.

Country or International Organization

India

Author: Dr SV, Amitha CR Mithra (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India)

Co-authors: Dr SINGH, Ashok K (ICAR-Indian Agricultural Research Institute, New Delhi, India); Dr PRAKASH, Chandra (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Dr S, Gopalakrishnan (ICAR-Indian Agricultural Research Institute, New Delhi, India); Dr P, Jeyaprakash (Tamil Nadu Agricultural University, Coimbatore, India); Dr KAR, Meera Kumari (ICAR-National Rice Research Institute, Cuttack, India); Dr SINGH, Nagendar K (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Ms YADAV, Neera (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Dr SWAIN, Padmini (ICAR-National Rice Research Institute, Cuttack, India); Dr KALE, Prashant (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Dr SHARMA, Rameshwar P (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Mr MK, Ramkumar (ICANational Research Centre on Plant Biotechnology, New Raveendran (Tamil Nadu Agricultural University, Coimbatore, India); Dr N, Sarla (ICAR-Indian Institute of Rice Research, Hyderabad, India); Dr MANGRAUTHIA, Satendra Kumar (ICAR-Indian Institute of Rice Research, Hyderabad, India); Dr MS, Sheshashayee (University of Agricultural Sciences, Bengaluru, India); Mr V, Sureshkumar (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India); Dr MOHAPATRA, Trilochan (Indian Council of Agriculture Research, New Delhi, India)

Presenter: Dr SV, Amitha CR Mithra (ICAR-National Research Centre on Plant Biotechnology, New Delhi, India)

Track Classification: Enhancing agricultural biodiversity through new mutation induction techniques