

Category	: 8th Rice Genetics Symposium
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	: Comparative genomics
Genome biology Structure Function and Comparison Keyword 2	: Genome evolution
Genome biology Structure Function and Comparison Keyword 3	:
Title of Entry	: Research activities on wild rice species and its applications in International Rice Research Institute (IRRI)
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Crop improvement by breeding process is highly dependent on genetic variations. Domestication process and repeated use of elite germplasms in breeding program narrow-downed the genetic variations. Wild relatives of rice have been regarded as a genetic reservoir for rice improvement. The <i>Oryza</i> genus consists of two cultivated species (<i>O. sativa</i> and <i>O. glaberrima</i>) and 22 wild species. More than 4,000 accessions are maintained in the International Rice Genebank of IRRI. Constant efforts for development of introgression lines using wild species, screening of the developed lines, and genetic analysis identified many valuable genes, especially biotic stress resistance genes. These isolated genes significantly contribute rice breeding program and rice improvement. Still many research groups are exploring the wild rice species to isolate the genes controlling valuable traits. In this presentation, current research activities on wild rice species and its applications in IRRI including transferring high-out crossing trait from <i>O. longistaminata</i> to <i>O. sativa</i> , screening of new salt tolerant wild species, development of monosomic alien additional lines (MAALs) from <i>O. rhizomatis</i> , and an initial intergeneric cross between <i>O. sativa</i> and <i>Leersia perrieri</i> will be introduced. Furthermore, an idea ‘Building a genome-indexed wild rice library for a future rice’ will be proposed.

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