

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Biotic stress tolerance
Keyword 2	: Marker-assisted selection
Keyword 3	: Germplasm Enhancement
Title of Entry	: Marker-assisted breeding for sheath blight resistance in rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Rice sheath blight (ShB) is an economically important disease of rice caused by <i>Rhizoctonia solani</i> . <i>R. solani</i> . Infected rice sheaths collected from Kota Baharu, Kelantan, Malaysia were used to isolate the pathogen. Identification and virulence test of the pathogen were done using three rice cultivars i.e., MR219, UKMRC9, and O. rufipogon in greenhouse inoculation. Nine rice cultivars including six moderately resistant to ShB, namely Teqing, Jasmine85, Tetep, Pecos, Azucena and Taducan; one susceptible local cultivar MR219; and two new advanced breeding lines UKMRC2 and UKMRC9 were screened in greenhouse using micro-chamber and mist-chamber methods for selection of donors. ShB infestation was evaluated as disease severity index (DSI) based on 0 to 9 scale with relative lesion height (RLH) and visual rating (VRT). Results indicated that Tetep was the most resistant cultivar followed by Teqing among the tested materials with the lowest DSI 3.0 (VRT) and 4.0 (VRT and RLH), respectively. On the other hand, UKMRC2 showed the highest level of susceptibility with a DSI of 6.67, while MR 219 was at 7.22. Identified donors Teqing and Tetep were used to cross with the susceptible cultivar UKMRC2 to introgress resistance QTLs. Two BC1F1 populations were developed between UKMRC2 and Teqing, and UKMRC2 and Tetep. Field evaluations were performed using both BC1F1 progenies. Results showed sufficient segregations in plant height, days to heading, tiller numbers and in pathogenicity. A total 13 out of 414 BC1F1 progenies were detected as 'resistant' to 'moderately resistant' genotype with ShB score 0 to 3. QTL analysis was also performed using composite interval mapping (CIM) at 15 cM fixed window with cofactor-

dropping method. The analysis revealed that the QTL qSB-9Teqing located between SSR markers RM3787 and RM24772 with LOD values 3.13 and 3.66 had the phenotypic variance 14.1 from 16.2 %, respectively. Another QTL qSBR11-1Tetep was also detected as a major QTL. These two QTLs could be used for further study to confirmation and use in marker assisted breeding programs to improve of ShB resistance in rice.

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