

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetic improvement
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Keyword 1	: Genetic gain
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Keyword 3	: Pre-breeding
Title of Entry	: Development of mapping populations from stable backcross introgression lines (<i>Oryza nivara</i> ./ <i>Oryza sativa</i> L.) to identify QTLs for yield
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Identification of the stable back cross introgression lines derived from Swarna x <i>Oryza nivara</i> cross and detection of novel QTLs from crossing these lines was the major focus of this study. Swarna x <i>Oryza nivara</i> BILs were phenotyped for five seasons in normal irrigated conditions especially for yield, photosynthesis and vigour traits. Stability analysis was conducted using the data on yield traits from different seasons and locations using AMMI analysis and GGE biplot (Yan and Kang, 2003). Among the BILs tested 14s was identified as the most stable genotype across the locations and seasons followed by 166s and 248s. 14s and 166s showed yield stability across the seasons along with high mean yield performance. 14s is early in flowering with high yield and has good grain quality and medium height, hence could be recommended for most of the irrigated locations. 166s is a late duration genotype, with strong culm strength, high grain number and panicle weight. 166s has higher yield and stability than Swarna with Swarna grain type. Selected Swarna x <i>Oryza nivara</i> BILs were crossed and advanced to F2 and F3 population. 817 SSR markers screened for parental polymorphism and F1s were confirmed using 42 polymorphic markers. F2:3 populations derived from the cross 166s x 14s (181 lines) were phenotyped for 17 yield traits and subjected to QTL mapping. Linkage map was constructed using MAP functionality of QTL IciMapping v4.1 (www.isbreeding.net) with Kosambi mapping method. QTL detection was carried out by Inclusive Composite Interval Mapping (ICIM) method. In 166s x 14s population, among 181 derived lines 73 lines were better than the best parent for various yield traits. 21 major QTLs were identified for grain yield and contributing traits in F2 and 14 QTLs in F3 of the 166S x 148S population. Out of these, 3 QTLs for plant height, days to flowering and culm length were found stable over the generations. QTL

hotspot regions with pleiotropic effect for grain yield and contributing traits were identified at chromosome 6 (RM8213 to RM16649) and 12(RM3431 to RM276).

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