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Title of Entry	: Development of Bacterial blight resistance pyramiding rice lines through MAS
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Development of Bacterial blight resistance pyramiding rice lines through MAS *Presenting Author:priyalal.biswas@yahoo.com Abstract Bacterial blight disease of rice (BB), caused by <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> , is one of the most economically destructive plant diseases limiting rice production of the world. BB can cause damage at any stages of rice plant but it is more severe at vegetative and reproductive stages of the rice plant. It causes significant yield losses in severely infected fields ranging from 10% to 30%, but this can reach as high as 80% depends on location, season, weather, crop growth stage and cultivar (Mew et al. 1992; Noh et al. 2007; Reddy, 1989; Shin et al. 1992). Several management practices like biological and chemical control methods are not well accepted by farmers due to lack of suitable biological agents with changeable pathogenic races and, scarcity of economically viable and environment-friendly chemicals (Schantz et al. 2001). So, development of host plant resistance cultivars having major resistance gene(s) is the most effective and economic strategy for controlling this disease with management practices which have a less effect on the environment (Huang et al. 1997; Jena and Mackill, 2008; Singh et al. 2001). Pyramiding of effective BB resistance genes (Xa genes) into susceptible varieties is the most economical approach to manage the disease. Four BB resistance genes, Xa4, xa5, xa13, and Xa21, were pyramided into RIL populations derived by a cross between Ciherang with IRBB60 (a pyramid line having Xa4, xa5, xa13, and Xa21). Ciherang rice variety is widely grown in Indonesia which is susceptible to bacterial blight. To select for BB resistance lines, phenotyping against selected three virulent strains, C5, P6, and V were done until F6. Marker-aided selection for confirmation of BB genes was done at F6 and F7 generations using gene linked and gene-based primers. Eleven promising lines with

four BB resistance genes, thirty lines containing three BB resistance genes and twenty-five lines possessed two resistance genes were identified in 265 RILs through foreground and strong phenotypic selection. Most of the pyramided lines showed significant variation in the nine yield and yield contributing traits

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