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# Abstract Book

## **HPR P43. Identification of pearl millet blast resistant source against different pathotypes**

Rajan Sharma, **N Naresh** and S K Gupta

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.

Email id: r.sharma@cgiar.org

Pearl millet leaf blast caused by *Pyricularia grisea* (teleomorph: *Magnaporthe grisea*), is one of the most important diseases of pearl millet in India. The disease can be best managed by breeding blast resistant hybrid cultivars. For identification of resistance in the elite hybrid parent lines, designated B-lines and R-lines (200 each) were screened under greenhouse conditions against six diverse pathotype-isolates of *M. grisea* (Pg 45, Pg 118, Pg 138, Pg 186, Pg 204 and Pg 232). Of the 200 designated B-lines, 34 lines were found to be resistant to at least one pathotype. Though none of the lines was resistant to all six pathotypes, ICMB 97222 was found resistant to five pathotypes. While three lines [ICMB 94333, ICMB 10999 and advanced B -line ((B x B) F2 S1-109-2-3-3-1-1-4)] were resistant to any four pathotypes. Eleven lines were resistant to three pathotypes and six were resistant to any two pathotypes. Maximum 20 lines were resistant to Pg 45 followed by 17 to Pg 186 and 15 to Pg 118 and 12 to Pg 232. Among designated R-lines, ICMR 08111 and ICMR 10888 exhibited resistance to all the six pathotypes. Whereas, ten lines were resistant to any five pathotypes and 11 lines were resistant to any four pathotypes. Maximum 44 lines were resistant to Pg 204 followed by 39 to Pg 45 and 33 each to Pg 118 and Pg 232. The designated A/B-lines and R-lines having resistance to multiple pathotypes can be used to develop pearl millet hybrids with durable blast resistance.

## **HPR P44. Validation of shoot fly resistance introgression lines using SNP markers in sorghum**

**G Sunita**, J Jayakumar, G Anil, Santosh P Deshpande, B Rajaguru, Jagdish Jaba, H C Sharma and A Ashok Kumar

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.

Email: a.ashokkumar@cgiar.org

Shoot fly is a major pest in sorghum production, globally. Shoot fly management using insecticides is expensive and environmentally un-safe. Therefore, host plant resistance is exploited to develop shoot fly resistance (SFR) lines including transfer of shoot fly resistance QTLs using marker assisted backcrossing. QTLs controlling SFR component traits, glossiness, trichome density, ovipositional non-preference were used for introgression in this study. Three QTLs associated with shoot fly resistance were introgressed into elite cultivars Parbhani Moti and ICSB29004. Crosses were made between recurrent parents and the QTL donors viz., J2658, J2614, and J2714. The SFR QTLs were successfully introgressed using foreground and background selection. Phenotyping of these lines led to the identification of resistant lines for each QTL region present on chromosome SBI-01, SBI-07 and SBI-10 in ICSB 29004 and Parbhani Moti. Validated the introgression lines using single-nucleotide polymorphism (SNP) markers tightly linked to shoot fly resistant QTLs. Ten SNPs linked to shoot fly resistant component traits, glossiness and trichome density on SBI-10 and SBI-05 were used for validation. The results showed the introgression lines with QTL present on chromosome SBI-10 were segregating for four favorable alleles for leaf glossiness and two for trichome density in homozygous condition. Other introgression lines with QTLs on chromosome SBI-01 and SBI-07 for component traits - oviposition non-preference, seedling vigor are segregated for glossiness trait also. This study showed that SNPs can be used to validate introgression lines and can be used as genomic markers for early generation selection of shoot fly resistance lines.