

FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



Contribution ID: 130

Type: Oral

HIGH-RESOLUTION MAPPING OF WHEAT CHROMOSOME ARM 5AS HARBOURING THE FUSARIUM HEAD BLIGHT RESISTANCE QTL *Qfhs.ifa-5A*

Fusarium head blight (FHB) is a severe fungal disease of wheat affecting yield and grain quality. One major QTL for FHB resistance in wheat is *Qfhs.ifa-5A*, which is located on the centromeric region of the wheat chromosome arm 5A. Genetic mapping of *Qfhs.ifa-5A* resulted in a low resolution in the *Qfhs.ifa-5A* region: In a near-isogenic RIL population, segregating for the *Qfhs.ifa-5A* resistance allele, four out of 3650 lines recombined within the pericentromeric C-5AS1-0.40 bin, yielding only a single recombination point. To further increase the map resolution a radiation induced deletion mapping approach was performed. Two gamma irradiated wheat deletion panels were created: (i) radiation selfing (RS) panel: seeds of line NIL3 carrying the *Qfhs.ifa-5A* resistance allele in a susceptible background were irradiated and plants thereof were selfed to obtain deletions in homozygous state and (ii) a radiation hybrid (RH) panel: irradiated pollen of the wheat line Chinese Spring (CS) was used for pollinating the CS-nullisomic5Atetrasomic5B. Overall, 5125 RS and 276 RH plants were pre-screened for deletions on 5AS. Plants having one or more markers deleted were analysed using 102 5AS-specific markers. A consensus map derived from both deletion panels results in a 380-fold map improvement (cR/cM) of the 5AS chromosome compared to the genetic mapping approach, with an average map resolution of 0.77 Mb/cR. This striking improvement in map resolution underlines the superiority of radiation induced deletion mapping over genetic linkage mapping for low recombining regions. Phenotyping the RS deletion lines can help to narrow down the QTL-interval for gene cloning.

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Track Classification: New challenges and technologies in plant genomics and breeding