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Poster Communication Abstract – 3.23

A MAJOR QTL FOR RESISTANCE TO FUSARIUM HEAD BLIGHT AND CROWN ROT OF WHEAT ON *THINOPYRUM ELONGATUM* CHROMOSOME 7E: CYTOGENETIC MAPPING AND ASSEMBLING INTO BREAD WHEAT WITH VALUABLE GENES FROM *TH. PONTICUM*

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Among wheat relatives, the *Thinopyrum* genus represents one of the richest sources of valuable genes/QTL for wheat improvement. One notable and still unexploited trait is the exceptionally effective resistance to Fusarium Head Blight (FHB) originating from a diploid member of the genus, Thinopyrum elongatum. Up to date, the resistance was only associated to the long arm of Th. elongatum chromosome 7E (7EL), while detailed genetic mapping of the responsible gene/QTL was still lacking. We targeted the transfer of the temporarily designated Fhb-7EL locus into bread wheat, by pyramiding it with other valuable genes/QTL (Lr19 for leaf rust resistance, yield-related traits) and included in a Th. ponticum 7el₁L segment, stably inserted into the wheat 7DL arm of line T4. Mapping of the Fhb-7EL QTL was here based on a bioassay with Fusarium graminearum, the main causal agent of FHB, of different 7EL-7el₁L bread wheat recombinant lines. Nine such recombinant types were successfully obtained without resorting to any genetic pairing promotion, but relying on the 7EL-7el₁L close homoeology. Pairing between the two critical arms was in fact observed by Genomic In Situ Hybridization (GISH) at meiotic metaphase I of F₁ plants between the 7E(7D) substitution line and the translocation line T4 (70% distal 7el₁L on 7DL), which resulted in 14% 7EL-7el₁L recombination frequency. The Fhb-7EL locus was mapped to the telomeric portion of 7EL, associated with marker loci XBE405003 Xsdauk66 and Xcfa2240. FHB resistant recombinants, with useful combinations of more proximally located 7el₁L genes/QTL, could be selected. The transferred *Fhb-7EL* locus was shown to reduce disease severity at the spike level and fungal biomass in the grains of infected recombinants by over 95%. The same Fhb-7EL QTL was, for the first time, proved to be effective also against F. culmorum and F. pseudograminearum, predominant agents of Fusarium Crown Rot (FCR). Yield performance in preliminary field tests of the pre-breeding lines possessing a suitable 7EL-7el₁L gene/QTL assembly showed to be very promising. Given the expected inheritance as a unit of the composite Thinopyrum segment in cross progeny with wheat, either of the several co-dominant PCR-based markers identified in the course of the work will enable easy tracking of the novel gene/QTL assembly in transfer programs into adapted cultivars.