Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 6A.21

USING WILD SPECIES OF THINOPYRUM GENUS IN BREEDING WHEAT RESISTANT TO FUSARIUM HEAD BLIGHT

FORTE P., KUZMANOVIC L., GENNARO A., BITTI A., CEOLONI C.

Dip. Scienze e Tecnologie per l'Agricoltura, le Foreste, la Natura e l'Energia **(**DAFNE), Università della Tuscia, Via S. Camillo de Lellis snc, 01100 Viterbo (Italy)

Chromosome engineering, Triticum aestivum, Triticum durum, FHB resistance, scab

In recent years, climatic changes have favoured the spreading of previously uncommon fungal diseases, including Fusarium Head Blight (FHB), in several wheat growing areas worldwide. Because of the relevant economic damages to wheat production and quality caused by FHB, and the scarcity of resistant sources among cultivated *Triticum* species, we have looked outside the primary gene pool and targeted wild wheat relatives of the *Thinopyrum* genus as promising sources of effective resistance. Two such species are the decaploid *Thinopyrum ponticum* (carrier of an *el*-type genome) and the diploid *Thinopyrum elongatum* (carrier of an E-type genome). In both species, one or more genes/QTLs for FHB resistance are located on the long arm of a homoeologous chromosome to those of wheat group 7 (named 7el_2L and 7EL, respectively). Resorting to chromosome engineering, i.e. aiming at the recombination-based transfer into wheat of small, 7el_2L or 7EL chromosomal segments carrying the desired gene(s), we were aware of the different cytogenetic affinity relating the donor and the recipient chromosomes. In fact, bread wheat substitution lines for the 7el_2L arm or the complete 7E chromosome for the wheat 7D counterparts were employed as donor lines, while durum and bread wheat recombinant lines, already carrying *Th. ponticum* 7el_1L portions, have been chosen as recipient lines. These contain the 7el_1L-derived *Lr19+Yp+Sr25* genes but lack any effective FHB resistance gene. Almost complete homology has been verified to exist between 7el_1L and 7el_2L (presumably originating from different *Th. ponticum* accessions), whereas that between the former and 7EL of *Th. elongatum* is only partial (around 20% pairing as from our records). Thus, homologous recombination is expected to allow pyramiding of all the desired 7el_1L + 7el_2L traits with relative ease, while the use of wheat homoeologous pairing mutants (*ph1* and *ph2* mutations) is being included in the transfer schemes to enhance 7el_1L-7EL recombination frequency. The multi-targeted and multi-genomic transfers are being aided by development of suitable polymorphic markers along the 7L arms and application of GISH (Genomic In Situ Hybridization) in somatic and meiotic cells. As a result, the first recombinants with the desired gene combinations are being isolated.