

## INTRA-SPECIFIC MAP OF DURUM WHEAT BASED ON SSR MARKERS

YOUSEFI JAVAN I.\*, MONDINI L.\*, NACHIT M.\*\*, PAGNOTTA M.A.\*

\*) Department of Science and Technologies for Agriculture, Forestry, Nature and Energy (DAFNE), Tuscia University, Via S. C. de Lellis, 01100 Viterbo (Italy)

\*\*) ICARDA P.O. Box 5466 Aleppo (Syria)

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Now a day several technologies are available to increase the abundance of DNA markers and to contribute in developing high resolution genetic maps suitable for genetic analysis. Among those simple sequence repeats (SSRs), highly dispersed in the genomes, were used for designing genetic maps and, in turn, estimating the genetic relationship between the A and B genome. A genetic linkage map of tetraploid wheat (*Triticum turgidum* L. ssp. *durum* (Desf.) Husn.) will construct based on a intraspecific cross between two recombinant inbred lines (RILs): one deriving from the cross of Jennah Khetifa x ChamI, the other from the cross [Omrabi x Dicoccoides] x Omrabi.

The aim of this study is to expand the number of simple sequence repeat (SSR) and single-nucleotide polymorphism (SNP) markers on the wheat array that can be mapped in the wheat genome, and to determine their chromosomal location.

The 190 single-seed descent lines derived F8 RILs were analyzed with a total of 204 loci SSR and 20 loci SNP. After 7 generations of selfing looking at two genes in the F8, we will get a percentage of 98.45% homozygosity and 1.55% heterozygosity. It was also variable the number and location of SSR on chromosomes. The total number of markers and the density was higher in homoeologous groups 2 and 4 (with respect of a total of 73 and 35). Here are presented the ongoing results. After analyzing a total of 204 markers, 113 markers SSR revealed polymorphism between parents, while the rest were monomorphic. These markers were previously located on chromosome arms in ditelosomic and nullitetrasonic aneuploid lines of *T. aestivum* cv. Chinese Spring. The SSR markers were distributed on all chromosomes of the two genomes in durum wheat (A and B), with the highest percentage of polymorphism in the A-genome (64%) comparing with the B-genome (57%). It was also variable, the percentage of polymorphism, both between chromosomes and between genomes of the seven homologues in this of tetraploid wheat species, The homology groups 1, 4 and 6 in the A-genome showed a highest level of polymorphism (54%, 21%, 38%, respectively).

We are going to built a genetic linkage map. The total number of markers and its density is higher in homoeologous groups 2 and 4 (84 and 39 SSR). Each marker corresponds to one locus. We are also looking for specific molecular markers on the LOX and DREB genes, among some markers we have chosen and selection four markers (WMS251, WMS149, WMC349 and WMC47), because the literature shows that these markers were highly associated with genes that are interested. This map will provide useful groundwork for further genetic analyses of important quantitative traits, positional cloning, and marker-assisted selection, as well as for genome comparative genomics and genome organization studies in wheat and other cereals.