INTRODUCTION:
Although durum wheat represents less than 10% of the global wheat production, durum wheat is the main cereal crop in some regions of the Mediterranean Basin. North American Great Plains as well as the South-western part of USA, Mexico, Australia and India. Previous genetic mapping studies conducted in durum wheat included the development of a dense map of simple sequence repeat (SSR) and single-nucleotide polymorphism (SNP), reported by Trebill (et al., 2011). Mapping the available data and marker combination for marker-assisted selection (i.e. SSR) marker order and haplotyping in association mapping studies, (ii) mapping novel SNP markers, (v) genome selection and (vi) studying the evolution of the A and B wheat genomes.

MATERIALS and METHODS:
Mapping populations: Twelve RILs from a cross between Carthage (de Giary et al., 2005) (Bicentennio 21) and IWB70389 (1703-1704), using a common mapping protocol including Maximum Likelihood (ML) marker order and extensive use of marker order optimization tools. The frequency distribution of crossover events in component populations were also incorporated in order to further check marker density of the segregating lines.

CONSENSUS MAP:
Sets of common (\textit{v} anchor) markers across RIL populations (with genotypic scores in two or more RILs) have been obtained for each chromosome and used to assemble framework consensus maps in Carthage (by merging anchor data-sets).

Backward projection of single map maker distances onto the consensus order was used to highlight non-monotonic changes of marker orders due to:
- illumina SNP assays that recognised duplicated/paralogous loci across different mapping populations,
- markers with low quality segregation data,
- presence of true physical rearrangements and/or emerently adopted alternative marker orders in the original map.

Markers showing breaks of monotony over distances \( d \geq 5 \) cM in the back projections across maps were then removed and accordingly the mapping process was repeated.
Markers uniquely mapped in single maps and in the DH map population, were projected onto the consensus framework by interpolation (Cona et al., 2002, Plant Physiol 130: 1598-1605).

RESULTS A: A preliminary consensus framework map of anchor markers was built for all chromosomes with mixed parameters for binning of closely linked markers. Two to three rounds of consensus mapping, inspection of results and marker re-naming has been carried out. For each chromosome, a small number of markers (10-20) on average for which the illumina assay clearly recognized duplications/paralogous loci mapped in different positions across maps and identified re-named (spotted).

Anchors markers were mapped in 2.9 ± 1.2 mapping populations on average. Details of mapping results are reported in Figure 1.

Figure 1. Details of the consensus framework constructed with anchor markers scored in two or more populations.

Figure 2. Consensus framework for chromosome 6B (taken as a representative) and component maps.

A. Single component maps align to the consensus framework of anchor markers. Anchor markers are highlighted by colors according to the number of segregating mapping populations.

B. Projection-plot of chromosome 6B single component linkage maps onto the consensus framework. Only common markers have been considered.

CONCLUSIONS/PERSPECTIVES:
Our preliminary results indicate that it is possible to successfully develop accurate consensus linkage maps in durum wheat. It is expected that this map will include as many as 30,000 gene-centered SNP markers. This resource will help future genomic studies as well as genetic-assisted genetic improvement in tetraploid wheat, including easy selection of highly informative markers sets at global or local genomic levels, more accurate ancestry-based mapping analysis, association mapping and haplotype-based mapping. More in general, this consensus map will provide robust anchor points to compare mapping results obtained in tetraploid and hexaploid wheat and to link the genetic to the physical map of wheat for genome sequencing initiatives.

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