CP3

**From wild emmer to durum wheat: the genomic history of pasta**

Luigi Cattivelli.

The International Durum Wheat Genome Sequencing Consortium

Durum wheat (Triticum turgidum L. subsp. durum (Desf.) Husn) is the most widely grown tetraploid wheat and represents a main component of the worldwide recognized Mediterranean diet. Durum wheat was domesticated from wild emmer (T. turgidum subsp. dicoccoides) through an intermediate step represented by cultivated emmer (T. turgidum subsp. dicoccum) and then subjected to further genetic modifications during the selection of the modern cultivars. We have generated a high quality reference sequence of the modern durum wheat cultivar Svevo. The Illumina reads were assembled with the NR-Gene DeNovoMAGICTM pipeline into 10.5 Gb of sequence with an L50 and L90 length of 6 and 1 Mb, respectively (N50: 493; N90: 2019). The assembly scaffolds have been anchored to a high-density genetic map and merged into super-scaffolds using Hi-C data; 95% of the scaffolds have been anchored along the chromosomes and 90% oriented.

The annotation of the assembled genome implemented with extensive transcriptomic data has identified 66,559 high confidence genes, 774 miRNA coding loci and 8.4 Gb (82%) of transposons and their deteriorated remnants. The availability of the durum wheat genome allows to highlight the suite of genetic modifications imposed by ancient empirical selection and modern breeding. An indication of the overall modifications imposed by the selection process from wild emmer to modern durum wheat was achieved by comparing the genome of Svevo with the genome of the wild emmer wheat accession Zavitan (Avni et al., 2017).

Beyond enabling genome-wide comparisons, a highly contiguous durum assembly also makes possible an extended analysis of the genetic diversity. A high density SNP genotyping applied to an extensive collection of tetraploid wheats has highlighted the strong reduction in overall diversity associated to the transition from cultivated emmer to durum landraces as well as the relatively limited overlap between the whole T. dicoccum and T. durum gene pools. Furthermore the genomic data were used for the dissection of a locus associated to cadmium accumulation in durum wheat seeds, a trait of significant human health concern. We identify a 17 bp insertion in metal transporter gene HMA3-B1 which causes high dietary cadmium accumulation. The fast and precise dissection of this trait demonstrates the utility of this new genomic resource to the durum wheat improvement community.