

International Conference

FROM SEED TO PASTA III A Sustainable Durum Wheat Chain for Food Security and Healthy Lives



Bologna - Italy, 19-21 September 2018

SELECTION SWEEP SIGNATURES IN THE TETRAPLOID WHEAT GERMPLASM

Marco Maccaferri,

in behalf of The International Durum Wheat Genome Sequencing Consortium

DISTAL, Department of Agricultural and Food Sciences, Viale G. Fanin 44, 40127 – Bologna, Italy

Modern durum wheat suffers from limited diversity. Nevertheless, Triticum turgidum genetic resources including Wild Emmer Wheat (WEW) Domesticated Emmer Wheat (DEW) and Durum Wheat Landraces (DWL) are a wide reservoir of diversity, also valuable for common wheat as highlighted by the success of synthetic wheats. We assembled a comprehensive Global Tetraploid wheat Collection (GTC) of 1,856 accessions representing 11 tetraploid wheat taxa. Based on the iSelect 90K SNP array we carried out an inclusive genetic relationship study. The results (i) highlight the most probable origin of DEW from North-eastern Fertile Crescent (Turkey) WEW and (ii) confirm the radial dispersal pattern occurred first for DEW and, then, for DWL, most probably originated from Southern-levant DEW. Ethiopian emmer and durum, T. turanicum and T. carthlicum were the most differentiated with minimal contribution to modern durum. WEW and DEW germplasm were highly structured while DWL showed a high admixture rate already at low K values. WEW showed the highest genome-wide diversity, a reference for assessing the diversity reductions associated to domestication and breeding. WEW-to-DEW, DEW-to-DWL and DWL-to-modern DW transitions are characterized by several region-specific diversity depletions arised independently and progressively consolidated through domestication and breeding. We searched these signatures by means of diversity reduction index (DRI), Fst, haplotype-based XP-EHH and hapFLK and spatial pattern of site frequency spectrum (XP-CLR). Frequently, two or more indexes occurred in overlapping regions. In total, 104 pericentromeric (average size 107.7 Mb) and 350 non-pericentromeric (average size 11.4 Mb) regions were identified, some of which co-localized with QTLs or Mendelian loci. WEW-to-DEW and DEW-to-DWL transitions mostly involved extended pericentromeric regions tagged by DRI and Fst, while the DEW-to-DWL DWL-to-DWC transitions were also associated to numerous XP-EHH and XP-CLR signals. Data and results from this study provide a useful basis to more effectively characterize and leverage the tetraploid wheat germplasm.

ABSTRACT