



International Conference

FROM SEED TO PASTA III

A SUSTAINABLE DURUM WHEAT CHAIN
FOR FOOD SECURITY AND HEALTHY LIVES

Bologna - Italy, 19-21 September 2018



A WIDE COLLECTION OF WILD EMMER ACCESSIONS TO RECOVER DIVERSITY FOR YELLOW RUST RESISTANCE

Elisabetta Mazzucotelli¹, Oadi Matny², Matthew Martin², Brian Steffenson², Pablo Roncallo³,
Viviana Echenique³, Francesca Desiderio¹, Delfina Barabaschi¹, Raffaella Battaglia¹, Esra Cakir⁴,
Hakan Ozkan⁴, Luigi Cattivelli¹, Anna Maria Mastrangelo⁵

1) Council for Agricultural Research and Economics (CREA), Research Centre for Genomics and Bioinformatics,
Fiorenzuola d'Arda (PC), Italy

2) Department of Plant Pathology, University of Minnesota, St Paul, Minnesota

3) Depto. de Agronomía, Universidad Nacional del Sur and Centro de Recursos Naturales Renovables
de la Zona Semiárida (CERZOS-CONICET), Bahía Blanca, Argentina

4) University of Çukurova, Faculty of Agriculture, Department of Field Crops, Adana, Turkey

5) Council for Agricultural Research and Economics (CREA), Research Centre for Cereal and Industrial Crops,
Bergamo (BG), Italy

The stripe or yellow rust (YR) disease, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), severely threatens grain yield. Unusual and severe epidemics of YR were observed on several continents in 2017 and years before, including not endemic geographic area, as a consequence of climate changes. Urgent is the exploration of new genetic variability to discover novel resistance genes. Alleles of the wild emmer wheat (*T. dicoccoides*), progenitor of the domesticated durum wheat, have been introgressed in cultivated wheat and showed to positively contribute to biotic and abiotic stress tolerance, yield components and quality. Among a wide collection of wild emmer accessions established c/o CREA-Genomics and Bioinformatics Research Centre, 285 lines have been genotyped using the Axiom 35k array, obtaining about 12000 poly-high resolution SNPs. The collection includes accessions originated from all Fertile Crescent countries, thus it represents all environments where wild emmer naturally occurs. The assessment of genetic diversity and population structure identified two well-defined groups, mostly corresponding to the two known races, as well as subgroups, according to the originating geographic area. A genome-wide critical distance around 0.5Mb was found for LD decay (r^2). The collection has been evaluated in controlled conditions for reaction to three YR isolates (Pstv14, Pstv37, Pstv40), and in open field in Southern Italy. The GWAS identified a number of resistance loci widespread into the genome. These QTLs, together with those identified in other tetraploid wheat panels, were projected on the durum reference genome (cv Svevo) thus evidencing the overlapping with known genes as well as novel resistance loci to be introgressed in durum varieties. The QTLs were also projected to the wild emmer reference genome (Zavitan) to identify candidate genes.

This study was supported by the Italian Ministry of Foreign Affairs and International Cooperation (special grant RES-WHEAT).

ABSTRACT