International Conference
FROM SEED TO PASTA III
A SUSTAINABLE DURUM WHEAT CHAIN
FOR FOOD SECURITY AND HEALTHY LIVES
FSTP3
Bologna - Italy, 19-21 September 2018

GENETIC DISSECTION OF FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT (*TRITICUM TURGIDUM SSP. DURUM*)

CONDORELLI G.E.[1], GHIZZONI R.[2], TERZI V.[2], MACCAFERRI M.[1], FRASCAROLI E.[1], SCIARA G.[1], RIGHETTI R.[3], MARTELLI M.[3], RAVAGLIA S.[3], LAIDO' G.[4], MORETTI A.[5], PRODI A.[1], TUMINO G.[2] STEINER B.[6], BUERSTMAYR H.[6], TUBEROSA R.[1], CATTIVELLI L.[2]

1) Department of Agriculture and Food Sciences – DISTAL, University of Bologna, Viale Fanin 44, 40127 (BO), Italy
2) CREA Research Centre for Genomics and Bioinformatics, Via S. Protaso 302, 29017 Fiorenzuola d'Arda (PC), Italy
3) Società Italiana Sementi – S.I.S Spa, Via Mirandola 5, 40068 San Lazzaro di Savena (BO) Italy
4) AGROSERVICE Spa, Loc. Rocchetta, 62027 S. Severino Marche (MC) Italy
5) Institute of Sciences of Food Production (ISPA-CNR), National Research Council, Bari, Italy
6) Department for Agrobiotechnology (IFA-Tulln), Institute for Biotechnology in Plant Production,
University of Natural Resources and Life Sciences, Vienna (BOKU), Konrad-Lorenz-Str. 20, 3430, Tulln, Austria

Fusarium Head Blight (FHB) represents a worldwide threat for many grain crops leading to severe yield and quality losses while threatening human and animal health due to mycotoxin accumulation. *Triticum turgidum* ssp. *durum*, the most important tetraploid wheat in the world, is notoriously highly susceptible to FHB. With the aim to provide a most accurate inventory of Quantitative Trait Loci (QTLs) for FHB in durum wheat, we performed a genetic characterization of 130 elite accessions (Fusarium Panel) and 165 F6 RILs from the population Simeto × Levante. The Fusarium Panel was evaluated in three artificially inoculated nurseries and in three years while the inoculation was carried out with *Fusarium graminearum* and *Fusarium culmorum*. The RIL population was evaluated in greenhouse in Tulln (Austria) in two years and inoculated with *F. graminearum*. Custom R scripts were used to produce best linear unbiased prediction (BLUP) values for the following traits: AUDPC incidence, AUDPC gravity, AUDPC Fusarium index, deoxynivalenol (DON) and Fusarium Damaged Kernels (FDK). A genetic characterization of RILs and Fusarium Panel was carried out using the Infinium wheat SNP 90K iSelect assay and the genotype scores were used to conduct a Genome Wide Association Study (GWAS) in Tassel v.5.2.7 (for Fusarium Panel) and a QTL analysis based on single-marker and multiple interval mapping (MIM) in Windows QTL Cartographer (for RILs). A remarkable number of QTL hotspots were detected in the following chromosomes: 1BL, 2AL, 3AL, 3BS, 3BL, 4AL, 5AL, 5BL and 6AL. Then conserved linkage blocks were investigated in major QTL/gene regions and their related effects. Tag-SNPs and haplotypes identified in this study will be used for marker-assisted selection (MAS) programs in order to accelerate new breeding strategies for FHB-resistant wheat cultivars.