

IDENTIFICATION OF RESISTANCE FACTORS TO SEPTORIA TRITICI BLOTCH IN DURUM WHEAT LANDRACE GERMPLASM

NOVI J. B.*, SCIARA G.*, CONDORELLI G.*, JANNI M.**, PIGNONE D.**, MARCEL T.***,
YAHYAOU A.****, M'BAREK S. B.****, INVERNIZZI C.*****, VIOLA P.*****, OLIVERI F.*****,
TUBEROSA R.*, MACCAFERRI M.*

*) Alma Mater Studiorum - Università di Bologna

**) Institute of Bioscience and Bioresources (IBBR) - National Research Council (CNR)

***) INRA UMR BIOGER

*****) CRP Wheat Septoria Precision Phenotyping Platform

*****) APSOVsementi S.P.A.

durum wheat, Septoria Tritici Blotch, landraces, Zymoseptoria tritici, STB

Wheat is the second most important cereal crop in the world, second only to maize, and overall, one of the major food staples. Among wheat, durum is mostly cultivated in semi-arid areas of Mediterranean Basin where it is used mainly for human consumption. *Zymoseptoria tritici*, agent of STB (Septoria Tritici Blotch), is a foliar pathogen that yearly causes high damages in wheat if not controlled. The use of very strong and unsustainable fungicides, linked to the fact that modern varieties lack resistance genes, are the reasons why recent years research in durum wheat breeding is focused on the identification of novel, underexploited resistance genes. This work aims at characterization and selection of a collection of durum wheat landraces mainly derived from the Mediterranean basin with the aim of identifying valuable Quantitative Trait Loci (QTLs) for breeding for *Z. tritici* resistance. We characterized a panel of 236 landraces from the Institute of Biosciences and Bioresources, IBBR, Bari, Italy. The complete collection was subjected to Single Seed Descent (SSD) purification and genotyped with the Illumina *iSelect* 90K wheat SNP array. The genetic structure analysis of the collection pointed out the presence of seven main groups of distinct origins as follows: South-Eastern Europe, Eastern North Africa, Western North Africa, Greece-Balkans, Western Asia, Italy and Ethiopia. A further group included into the genetic and phenotypic analysis included modern cultivars. The phenotypic evaluation was carried out at seedling stage (artificial inoculation) in growth chamber and under field conditions. At INRAE BIOGER the collection was inoculated at seedling stage with three different isolates, respectively from Italy, Greece and Tunisia. For each isolate the experiment was replicated (three plants per rep and two reps). Based on single leaf inoculation Area under progressive curve (AUDPC) data were obtained for percentage of green, necrotic and sporulating (picnidia) leaf area. Phenotyping identified 26 genotypes resistant to all isolates, 14 resistant to Italian and Tunisian strain, 11 resistant to Italian and French isolates, and 7 resistant to both French and Tunisian strain. The panel was field-tested in Tunisia at two locations (Beja and Koudja) and in Grosseto, Italy. 16 of the landraces that were found resistant at the seedling stage at INRAE were also classified as resistant at adult stages in field. The durum collection was then subjected to a Genome-Wide Association Study (GWAS). The "Modern" group was found to be the most susceptible, on average, and the Greece-Balkans being the most resistant landraces, indicating the presence of under-utilized resistance sources. QTLs for STB response were found in several chromosomes. The best prospect is to validate QTLs in bi-parental populations (in progress) that

can be used for both fine mapping of the QTLs and the introgression of resistant alleles into modern germplasm at the same time.