

BROWSING IN THE GLOBAL DURUM PANEL FOR RESISTANCE TO SOIL-BORNE VIRUSES

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Durum wheat (*Triticum turgidum* L. ssp. *Durum* (Desf.)) is among the most important cereals cultivated worldwide with an average production of 40 million tons/year. Empirical and modern breeding has created new high yielding varieties in the last century. A recent effort aiming at exploiting the genetic diversity of wild relatives and landraces and using the results in breeding programs is the Global Durum Panel (GDP), an initiative run by the international durum wheat research community to collect, share and exploit available genetic diversity. GDP is a freely shared wide collection (1033 accessions) composed by modern germplasm and landraces. Our purpose is to use a subset of the collection (214 genotypes), principally landraces, representing most of the genetic diversity present in the GDP, to address resistance to soil-borne viruses. This collection subset has been analysed for population structure and Linkage Disequilibrium Decay.

The soil-borne viruses of wheat present in Italy and other European countries are transmitted by the plasmodiophorid *Polymyxa graminis*, a vector impossible to eradicate, whose resting spores survive for many years in the soil. Once a field is contaminated by the vector carrying the virus, the only strategy to grow cereals is to sow resistant germplasm.

The work we present is carried out in the framework of the SURF project, funded by Regione Lombardia, d.d.s. n. 4403 28/03/2018, grant n° 42, which aims to select and develop durum wheat genetic materials for virus resistance, identifying and utilizing resistance traits through the use of modern experimental approaches and cutting-edge scientific technologies.

Our interest is concentrated on the *Furovirus* named soil-borne cereal mosaic virus (SBCMV), which is becoming more and more widespread in durum wheat, probably because of climatic changes.

Following an initial phase where optimization of detection protocols was carried out, the level of resistance to SBCMV in the subset of 214 genotypes was evaluated using two different approaches. The first approach consisted in the analysis of the susceptibility of wheat seedlings to mechanical inoculation with SBCMV isolates in controlled conditions. This artificial transmission, that is different to the natural transmission of SBCMV through the roots by *P. graminis*, generates data on the direct interaction between the host plant and the virus. The second approach aimed to mimic natural conditions of virus transmission. The genotypes were sown in pots containing soil collected from a SBCMV-contaminated field and grown outdoor under insect-proof net gauze during the winter-spring period. In this experiment, the interaction between the host plant and the virus is mediated by the vector, as happens in natural conditions. As a result of this complex tripartite interaction (plant, virus and vector), the phenotype (susceptibility/resistance) of wheat plants depends not only on the susceptibility to the virus but also on the ability of the vector to infest plant roots.

A subsequent genome-wide association study (GWAS) will be performed using these phenotypic data to identify genomic regions putatively associated to susceptibility/resistance, distinguishing the direct virus/plant interaction from the tripartite one involving the vector.