

TESTING A SUBSET OF THE GLOBAL DURUM WHEAT PANEL COLLECTION FOR RESISTANCE TO SOIL-BORNE CEREAL MOSAIC VIRUS

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Durum wheat (*Triticum turgidum* L. ssp. *durum* (Desf.)) contributes to 14% of total European wheat production, with Italy representing the major producer among European countries. This crop is extremely important for the Mediterranean area, where it was originally domesticated. In Italy, durum wheat is historically cultivated in central-southern regions but, with temperatures arising for the effect of climate change, the cultivation of this cereal could increase also in northern regions. Viral diseases are a growing problem for durum wheat cultivation in Italy, and soil-borne cereal mosaic virus (SBCMV) is one of the most common viruses, that causes severe crop losses. This virus is transmitted to plants through a vector that lives in the soil, the plasmodiophoromycota *Polymyxa graminis* Led. There are no methods to eradicate *P. graminis* whose resting spores survive in infested soil for several years. Thus, the only strategy to reduce the damage caused by this virus is to develop and use resistant wheat varieties. To this aim, the genetic study of traditional genotypes and landraces is very important for the identification of new resistance traits.

The SURF project, funded by Regione Lombardia (d.d.s. n. 4403 28/03/2018, grant n° 42), aims to select and develop genetic materials of durum wheat for resistance to virus diseases. To this purpose, a subset of 215 genotypes, mostly landraces, were selected from the international Global

Durum Wheat Panel (GDP) collection. Genetic analysis of the population showed that the selected genotypes retained a high level of genetic variability.

The response to SBCMV infection (susceptibility or resistance) of the 215 genotypes was evaluated by carrying out a test in a screenhouse at IPSP-CNR in Turin (Italy). The plants were sown in the autumn-winter period in pots with SBCMV-infested soil. Sampling was carried out in the spring and the plants were tested for virus quantification by qRT-PCR. The obtained data have been used to perform a genome-wide association study (GWAS) to identify genomic regions putatively involved in SBCMV resistance.