Proceedings of the LXIV SIGA Annual Congress
Online, 14/16 September, 2021
ISBN: **978-88-944843-2-8**

Poster Communication Abstract – 7.38

CHARACTERIZATION OF SBM2, A LOCUS FOR SOIL-BORNE CEREAL MOSAIC VIRUS (SBCMV) RESISTANCE IN DURUM AND BREAD WHEAT

BRUSCHI M.*, BOZZOLI M.*, SCIARA G.*, ORMANBEKOVA D.*, FORESTAN C.*, GOUNDEMAND E.**, DEVAUX P.**, PEROVIC D.***, PANKOVIC D.***, CORNETI S.*, STEFANELLI S.*, RATTI C.*, RUBIES-AUTONELL C.*, GADALETA A.****, TUBEROSA R.*, MACCAFERRI M.*

*) Department of Agricultural and Food Sciences, University of Bologna, Viale G. Fanin, 44, 40127 Bologna, Italy
**) S.A.S. Florimond-Desprez Veuve and Fils, BP41, 59242, Cappelle-en-Pévèle, France
***) Julius Kühn-Institut JKI, Federal Research Institute for Cultivated Plants, Erwin-Baur-Str. 27, 06484, Quedlinburg, Germany
****) Department of Agricultural and Environmental Science, University of Bari 'Aldo Moro', Via G. Amendola 165/A, 70126 Bari, Italy

fine mapping, KASP, candidate genes, RNA-seq, GWAS

QSbm.ubo-2BS is a major QTL controlling the response towards Soil-Borne Cereal Mosaic Virus in durum wheat that we initially mapped within a 2 cM-wide interval in the distal region of chromosome arm 2BS. A GWAS was conducted on a panel of 244 durum wheat elite varieties with Illumina 90K iSelect wheat SNPs array. Phenotypic traits investigated involved visual score data from three year observations and ELISA data from two years collected in a field nursery under severe and uniform SBCMV infection. Results evidenced a peak on chromosome 2B of ~22 –Log10(P-value) for visual score and of ~18 –Log10(P-value) for ELISA values corresponding to *Sbm2*. At the same time, fine mapping was performed by means of a combination of: 1. search for polymorphic SNP mapped in the region and sampled from the Illumina 90K iSelect wheat and the 420 K Affymetrix Axiom arrays, 2. Development of genome- and SNP-specific KASP® markers, 3. extensive screening for recombinants in three RIL populations (Svevo x Ciccio, Iride x Relief, Monastir x Odisseo) and a BC1F2 Meridiano (resistant) x Meridiano/Claudio110 using KASP® developed from SNP. SNP and KASP markers allowed to robustly and consistently classify modern cultivars based on two

resistant and susceptible common haplotypes, with only rare recombinants. Nine functional KASP® were developed spanning the relevant locus region and well defining the resistant and susceptible haplotypes. Fine mapping allowed to narrow down the QTL interval to 1.0 Mb including 12 high confidence and 24 low confidence genes. Interestingly, the region included two clusters of potential candidate genes all involved in the disease resistance response (Serine protease inhibitor family protein, receptor-like protein kinase, NBS-LRR class, NBS-LRR like proteins and defensins). RNA-Seq atlas of gene expression from 13 diverse cultivars of durum wheat and diverse tissues/ organs including non-infected roots at seedling stage evidenced a differential constitutive expression for some of those genes involved in signal transduction and plant-pathogen interaction that matched with the resistant/susceptible haplotype classification. Two further dedicated transcriptomic experiment are being performed. In the first experiment, parental lines and critical recombinants have been grown in a SBCMV-uniformly infected field nursery in Cadriano farm station in 2020/2021 wheat growing season and a time course transcriptomic investigation was performed from late fall to early Spring. In a second experiment, a growth-chamber controlled environment experiment including infected and non-infected soil has been performed at JKI, Germany, using the same genetic materials. Best performing markers were optimized for specificity towards bread wheat by means of a KASP® primer design pipeline based on the Wheat Ten Genome Project sequences. Further validation of these markers is being carried out in collections of both durum and bread wheat. The KASP® are also being used to elucidate the resistance and susceptible haplotype distribution in a world-wide comprehensive collection of ca. 3,000 tetraploids including modern cultivars, landraces, domesticated and wild emmer. This work paves the way to the positional cloning of *QSbm.ubo-2BS* and provides KASP markers useful for marker-assisted selection in breeding programs. Moreover, optimized KASP markers aim at leveraging durum wheat as a bridge between tetraploid and hexaploid wheat. The research was in part supported by FSOV: Développement d’outils phénotipyque et génotypique pour améliorer la sélection de la résistance du blé dur à deux virus des mosaïques du blé and by INNOVAR (Next-generation variety testing for improved cropping on European farmland), a Horizon 2020 project under the topic SFS-29-2018.