Proceedings of the LXII SIGA Annual Congress
Verona, Italy – 25/28 September, 2018
ISBN **978-88-904570-8-1**

Poster Communication Abstract – 2.15

FINE-MAPPING OF *QSbm.ubo-2BS, A* MAJOR QTL FOR RESISTANCE TO SOIL-BORNE CEREAL MOSAIC VIRUS (SBCMV)

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

*) DIPSA, University of Bologna, Viale 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 Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, Erwin-Baur-Str. 27, 06484 Quedlinburg (Germany)
****) Department of Agricultural and Environmental Sciences, Research Unit of "Genetics and Plant Biotechnology", University of Bari Aldo Moro, Bari (Italy)

durum wheat, SBCMV, resistant QTL, Sbm2 fine mapping, KASP ™markers

QSbm.ubo-2BS = Sbm2, a major QTL controlling the response to SBCMV (Soil-borne cereal mosaic virus) in durum wheat, was characterized in Meridiano (resistant, R) x Claudio (moderately susceptible, MS) Recombinant Inbred Lines (RILs). By means of QTL analysis, *QSbm.ubo-2BS* was mapped as a unique major QTL (R^2 = 88.5%) within a 2 cM-wide interval (LOD-2) in the distal region of chromosome arm 2BS, with the nearest marker represented by *wPt-2106* (DArT®) . The addition of the Illumina 90K SNPs array to the durum linkage maps allowed to map 36 gene-associated SNP markers in a 4.5 cM-long segment containing the mendelized QTL . Five SNPs from the Illumina 90K and seven SNPs from the Affimetrix 420K wheat array were converted to KASP™ markers, which provided fluorescent high-throughput PCR assays spanning the QTL region. In order to narrow down the QTL interval, high resolution mapping was constructed using KASP™ markers flanking the QTL confidence interval (*KUBO 9* and *KUBO 13*) on ~2000 RILs Svevo (R) x Ciccio (MS) developed by UNIBA. Screening procedure resulted in the identification of 330 recombinant RILs, which were characterized for SBCMV response in an inoculated field under severe and uniform SBCMV infection. Symptom severity (SS) was scored on a 0 to 5 scale and screened with five KASP™ markers distributed along the QTL interval. Phenotyping results confirmed the presence of the QTL in the *KUBO 13 – KUBO 9* interval. Fine mapping results allowed to narrow down the interval between the flanking markers. Basing on the markers physical position on the available wheat genome assemblies, we were able to identify the gene space of *Qsbm.ubo-2BS.* On a total of 43 genes, 12 could be described as candidates because either receptors or other resistance genes. As regards to future perspectives, exome capture analysis will be conducted to identify allelic variants among the candidate resistant genes. Moreover, an RNAseq experiment was performed on two groups of five susceptible and resistant haplotypes each. Two large recombinant populations obtained by crossing resistant and susceptible parents, produced and advanced at F_4 generation, are being analyzed to identify new informative recombinants and heterozygotes to obtain $F_{4:6}$ contrasting genetic stocks. The research was supported by FSOV (Le Fonds de soutien à l'obtention végétale): Développement d'outils phénotipyque et génotypique pour améliorer la sélection de la résistance du blé dur à deux virus des mosaïques du blé.