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Abstract – SY03

PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF QGNS.UBO2A, A MAJOR LOCUS RESPONSIBLE FOR SPIKE FERTILITY ON *TRITICUM TURGIDUM* SSP *DURUM*

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Wheat is one of the major world staple crop. Increasing grain yield potential is a central target for developing future wheat. QGns.ubo2A, a major QTL on chr2AS (s.i. 84.6-87.6 cM), governs grain number per spikelet (GNS) in the 4-way durum cross population derived from Neodur, Colosseo, Claudio and Rascon-Tarro (NCCR) (Milner et al., 2016, PBJ, 14(2):735-48). The Rascon Tarro haplotype (derived from Altar84 variety) showed a 0.55 grain increase per spikelet. Based on Triticum turgidum cv. Svevo reference sequence, the pericentromeric interval contains approximately a hundred genes, whose sequence and position are strongly conserved across Bread Wheat cv. Chinese Spring, wild emmer wheat accession Zavitan and durum wheat cv. Svevo reference genomes. The genetic interval was explored by a BLAST analysis pointing out a possible candidate for GNS with a 4 kbp chromosome deletion in the Rascon-Tarro haplotype, absent in other parents of the 4-way cross population NCCR. Six KASP markers developed from the 90K SNP chip showed that modern varieties most frequently had the low-fertility haplotype and the gene of interest is located in a 5 Mbp interval between markers K44 and K49. During 2019, a phenotypic assay was carried out on 1500 lines from the F4 Iride (Rascon-Tarro haplotype) x Relief population (R x I) and Global Tetraploid Collection (TGC) including 1856 tetraploid wheat (Maccaferri et al., 2019, Nature Genetics, 51:885–895): fertile florets per central spikelets were counted in six spikes per accession homogenously harvested. Furthermore, a PCR assay was developed on the gene deletion to detect presence of the 4 kbp INDEL showing a good discrimination capacity among NCCR parental lines. The PCR assay together with KASP markers analysis were used to genotype 700 lines of RxI population, 200 lines showed the Iride haplotype which was correlated with highly fertile spikelets by the phenotypic analysis. As regards the TGC collection, 1000 lines were genotyped, but the fertility haplotype was not detected among ancient wheat varieties hypothesizing a recent origin for the mutation in the QGns.ubo2A QTL. As to future experiments, the PCR and KASP analysis will be carried out on the Global Durum Panel from the DW-expert working group of the Wheat Initiative (GDP, 700 lines) Moreover, 2000 M4 Svevo and Kronos mutants will be screened for mutations. In conclusion, we report herein the identification of a major locus for spikelet fertility and seed number per spike in tetraploid wheat, potentially valuable for improving

the grain yield potential of both tetraploid and hexaploid wheat. The locus deserves a further and deep characterization towards the fine mapping and eventually cloning.