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Poster Abstract – A.17

YIELD PERFORMANCE OF NAKED BARLEY NILs AND QTL ANALYSIS OF YIELD TRAITS IN A NAKED X HULLED DH POPULATION

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In order to determine the physiological effects of the naked/hulled caryopsis character upon barley grain yield components, a NIL population (32 lines BC5F2) developed by backcrossing five times the naked cultivar 'Iabo' (donor parent) to the hulled cultivar 'Arda' (recurrent parent) was employed. Naked NILs, that possess the same (about 80%) genetic background respect to the cultivar 'Arda', but only differ at the locus controlling the kernel type character, were developed as reference lines to remove the interaction that the other genetic background of the naked cultivar 'Iabo' might have on yield. In this context we conducted a comparison and systematic evaluation of agronomic performances and yield components among these NILs and their hulled counterpart, together with recurrent and donor parents in replicated yield trials, at Fiorenzuola d'Arda (Italy), in two years (2005 and 2006).

The naked near-isogenic lines resulted to have the potential to return an equal grain yield compared to hulled genotypes only if they were adjusted by the weight loss of the hull. The interaction between the naked/hulled trait and the different yield components has been studied, and results are here presented.

To further analyze the effect of the *nud* gene, (located on chromosome 7H), in a different genetic background by means of a genetic (QTL) analysis, we analysed data of grain yield and other agronomical traits in a barley doubled haploid (DH) population, derived from the cross 'Proctor' (hulled) x 'Nudinka' (naked). A total of 101 PN lines were evaluated in 1998 for yield, plant architecture, seed weight, biotic and abiotic resistances in yield replicated trials in four contrasting environments in Italy. The software MapQTL v5.0 was used to determine the genomic regions (QTL) controlling the described traits and the overall QTL picture is here presented and discussed.