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Czech J. Genet. Plant Breed.

**E., Tondelli A.,
Gianinetti A., Stanca
A.M., Pecchioni N.:**

Effect of the *nud* gene on grain yield in barley

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Naked barleys are less yielding than the hulled ones while the reason for this difference has not been definitely clarified. To investigate the effect of the *nud* gene on yield, a barley doubled haploid (DH, Proctor × Nudinka) population was initially tested in three environments and a QTL study was run on the entire population as well as on two *nud*/*NUD* DH subpopulations. Among the agronomic traits studied, a QTL effect was found at *nud* locus on chromosome 7H only for yield and thousand grain weight (TGW), while a second QTL was found on 6H, although contributed by the naked parent. Other QTLs for TGW were identified on 2H, 3H and 5H. Most QTLs

found in the entire population were confirmed by the study on the two groups. No interaction was observed between QTLs. To provide a more accurate evaluation of the effects of the *nud* gene upon grain yield, its components and other agronomic traits, sixteen naked advanced backcross (AB) BC5F2 lines in the hulled background of cultivar Arda were prepared and evaluated in a replicated yield trial for two years. The only differences found between AB lines and Arda in grain yield and TGW were due to hull weight (11.97% of kernel weight). No differences were observed in other traits such as grains/m², grains per spike, plant height, heading date and mildew resistance. In conclusion, we think to have clarified that the effect of the *nud* gene on yield is due to hulls, and we did not find any pleiotropic effect of *nud* on other traits. This suggests, together with the finding of a QTL contributed by the naked parent, that there is a great potential to improve naked barley up to the yield levels of hulled barley.

Keywords:

advanced backcross lines; doubled haploids; naked barley; *nud* gene; QTL

mapping; yield

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