Poster Abstract - F.08

SURVEY OF MOLECULAR DIVERSITY AT nud LOCUS IN BARLEY

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The naked caryopsis trait in barley is controlled by a single recessive gene, called *nud*, located on chromosome 1 (7H); it prevents adhesion of the lemma and palea to the caryopsis and permits free threshing at maturity (hulless barley).

It was performed a Bulked Segregant Analysis (BSA) on the barley Proctor x Nudinka mapping population, to identify new PCR-based markers closely linked to the nud gene in order to facilitate marker-assisted selection (MAS) of the naked trait. Six RAPDs out of 392 tested were found to be associated to the naked bulk, and five mapped on barley chromosome 1; only the most tightly linked RAPD OP-J14 was successfully converted into the SCAR sJ14. This new SCAR marker developed would provide an alternative approach to conventional methods of selection for naked barley in breeding programs.

Moreover, using doubled haploid (DH) barley lines derived by the anther culture from the F1 of the cross between Proctor (hulled parent) and Nudinka (naked parent), sJ14 together with other 3 SCAR, one RAPD and two SSR markers were mapped onto the reference map (Heun et al. 1991) in an interval of 3.7 cM surrounding the *nud* gene.

In order to individuate the haplotype structure surrounding the *nud* locus in barley, the markers found to be the most tightly linked to *nud* gene, were evaluated for the level of allelic polymorphism they displayed within a phenotypically differentiated barley germplasm (184 genotypes), including both hulled and naked forms.

Furthermore the resistance-susceptibility phenotype of 130 (naked/hulled) accessions of the same germplasm collection was verified by artificial inoculation with the highly virulent monoconidial isolate Dg2 of the pathogen *Pyrenophora graminea* (the causal agent of the barley leaf stripe disease) in order to investigate any possible associations between incidence to this seed-borne fungal disease and other traits, as naked trait, height, row-type, growth habit and origin.