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Poster Abstract - C.06

FINGERPRINTING WHEAT VARIETIES FOR BREEDING PURPOSES

G. BARCACCIA*, E. ALBERTINI**, L. PALLOTTINI**, S. ANCILLOTTI**, R. TORRICELLI**, C. INVERNIZZI***, L. MAZZA****, M. FALCINELLI**

*) Dipartimento di Agronomia Ambientale e Produzioni Vegetali, Facoltà di Agraria - Università degli Studi di Padova, Viale dell'Università 16, 35020 Legnaro, Padova
**) Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali e Zootecniche - Facoltà di Agraria, Università degli Studi di Perugia, Borgo XX Giugno 74, 06121 Perugia - falcinel@unipg.it
***) APSOV Sementi S.p.a. - Associazione Produttori Sementi Oltrepo Vogherese, Strada Torremenapace 40, 27058 Voghera, Pavia
****) CO.NA.SE. - Consorzio Nazionale Sementi Soc. Coop. Agr., Via Selice 301, 48017 Conselice, Ravenna

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Modern wheat varieties are thought to display quite low levels of gene pool variation because of the high selective pressure applied in breeding programs. The genetic diversity of durum wheat and bread wheat elite germplasm has been traditionally estimated on the basis of morphological and quantitative traits, disease resistances, gliadin proteins and only recently by molecular markers. In the last decade, RFLP and PCR-derived markers have been extensively applied in wheat genetics, not only for the construction of linkage maps, but also for gene tagging and QTL mapping. The information acquired is now being exploited to transfer different traits, including biotic stress resistances and improved quality traits, to important wheat varieties by means of marker-assisted selection (MAS) programs. In wheat, the most widely exploited techniques include AFLP and SSR markers which offer an almost unlimited supply of molecular traits for distinctive plant DNA fingerprinting and genotyping. A total of 38 durum wheat and 26 bread wheat DNA samples isolated from commercial varieties and experimental lines were investigated by fluorescent AFLP markers using five primer combinations previously selected on the basis of their ability of detecting polymorphisms. As many as 267 clearly detectable markers were scored, of which 59 (41.6%) and 73 (51.4%) proved to be polymorphic among varieties within and between species, respectively. Dice's (1945) genetic similarity (GS) estimates among the 64 pure lines were calculated in all possible pair-wise comparisons and the correspondent matrix was used for the construction of UPGMA dendrograms and the definition of centroids according to PCA analysis. Mean genetic similarity estimates within durum wheat and bread wheat were 92% and 89%, respectively. In each species, a few multi-locus genotypes showing almost full identity were found. Several species-specific and variety-specific DNA markers were also scored: the latter types will be cloned, sequenced and converted into easily detectable single-locus markers. On the whole, more than 68% of the total genetic variation found in wheat materials was explained by the first two principal coordinates. The observed number (na) and the effective number (ne) of alleles were equal to 1.416 and 1.163 in durum wheat and to 1.514 and 1.184 in bread wheat, respectively. Nei's (1973) genetic diversity (H) estimates over all genomic loci were also comparable for the two species (0.102 and 0.119, respectively). Linkage disequilibrium (LD) tests were performed for all pair-wise comparisons of marker alleles. The number of significant LD was 78 over 142 loci (0.78%) in durum wheat and 139 over 142 loci (1.42%) in bread wheat. Preliminary data suggest the finding of a few AFLP markers displaying highly significant linkage disequilibrium ($P<0.01$) with a number of wheat resistance genes, including yellow and brown rust, powdery mildew, Fusarium head blight and Septoria leaf spot diseases. The final aim is that of assembling a database of DNA polymorphisms for the durum and bread wheat germplasm. This

information is potentially useful not only for tracing single pure lines through genetic fingerprints, but also for planning experimental crosses between pure lines on the basis of their genetic distances.