Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – B.04

FUNCTIONAL MARKERS FOR AMYLOSE CONTENT IN MOLECULAR BREEDING FOR RICE QUALITY

BRUSCHI G.*,**, LANZANOVA C.*, GREPPI D.*, CAVIGIOLO S.*, PIFFANELLI P.**, LUPOTTO E.*

*) CRA – Unità di Ricerca per la Risicoltura, s.s.11 per Torino km 2,5, 13100 Vercelli
**) Parco Tecnologico Padano, CERSA, Via Einstein, Lodi

Oryza sativa, amylose content, granule bound starch synthase, SNPs, SSR

Rice is the staple food for about half of the world's population, and is consumed cooked in a wide aray of ways. Improvement of rice quality is among the major goals in current breeding programs, as tradition and sensorial evaluation are among the main determinants of the eating and cooking quality for consumers.

Rice eating, cooking and processing qualities are mainly influenced by physicochemical properties of its starch, that accounts for about 90% of milled rice. Starch is composed of amylose and amylopectin, and apparent amylose content (AAC) has been well recognized as one of the most important determinants of various rice products. Amylose content is primarily controlled by the *waxy* gene encoding a granule bound starch synthase (GBSS).

The present study is addressed to the exploitation of functional molecular markers for molecular breeding in the amylose content: a (CT)n microsatellite and a G/T single nucleotide polymorfism (SNP) have been well characterized with different alleles differing in AAC. The polymorphic microsatellite (CT) in the *waxy* gene which encodes for GBSS, explains a large portion of the variation of amylose content in non-glutinous cultivars, and it is currently used as aid in selection (MAS). We have chosen a panel of 59 rice varieties (with different amylose content) to be analyzed for the relationship of the microsatellite (CT)n (a total of 5 class) and the SNP (AGGTATA/AGTTATA) polymorphism, with the starch physicochemical properties on the rice germplasm. Of the 59 accession, 33 had (CT)18 allele, indicating that this is the most frequent; the three glutinous accessions had only the (CT)17 allele. All the glutinous lines studied had the AGTTATA sequence at the putative leader intron 5' splice site. All the non-glutinous rice with an allelic frequencies of (CT)17 and (CT)18 had the polimorphism AGTTATA.

This study acknowledges the financial support of the project VALORYZA (D.M. 301/7303/06, date 05.12.2006, MIPAAF).