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NMR TECHNIQUES COUPLED WITH MULTIVARIATE STATISTICAL ANALYSIS: TOOLS TO ANALYZE *ORYZA SATIVA* METABOLIC CONTENT UNDER STRESSES

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Rice (*Oryza sativa* L.), one of the most important crops in the world, is the staple food for over half the world’s population. Among European countries, Italy is the largest rice producer and exporter, with cultivated areas extending over 228,000 ha and production of 1,430,000 tons during 2006.

Even if rice growth on the most productive irrigated lands in the world has reached almost the maximum potential production, the achievement of the optimum yield is made difficult by environmental stresses, such as water deficiency, soil salinity and pathogens attack. The development of new rice varieties with a higher tolerance/resistance to both abiotic and biotic stresses is of great interest also in our country, for the adaptation of rice to suboptimal climate and soil conditions.

Metabolomics is considered an emerging tool for metabolic pattern studies and, together with transcriptomics and proteomics, for gene function identification, under normal and stress conditions. One strategy to identify more suitable varieties might be to compare the metabolic profile of different cultivars and verify a possible correlation between the accumulation of specific metabolites and the level of stress tolerance/sensitivity.

In this work, we have first investigated the metabolic profile in shoots and roots of two rice cultivars (Arborio and Nipponbare) through solid state ^{1}H HR MAS and liquid state NMR experiments. Drought and salt stress experiments on shoots and roots growth showed a higher sensitivity of Arborio seedlings than those of Nipponbare to these abiotic stresses. Moreover, the metabolic content of the same samples was analysed by liquid state NMR coupled with multivariate statistical analysis. Principal Component Analysis highlighted a significant accumulation of amino acids and sugars in shoots and roots under stress conditions and the existence of clear differences between the two analyzed rice cultivars. In particular, Arborio seedlings accumulated a higher concentration of amino acids and sugars than Nipponbare ones. Furthermore, we also obtained preliminary data about rice metabolic changes following infection with the fungus *Magnaporthe grisea*.

This work indicates that NMR technique coupled with multivariate statistical analysis is a powerful tool to assess a possible correlation between differences in metabolic profile and in tolerance/sensitivity phenotype in rice cultivars.