Proceedings of the 51st Italian Society of Agricultural Genetics Annual Congress
Riva del Garda, Italy – 23/26 September, 2007
ISBN **978-88-900622-7-8**

Poster Abstract – D.43

LINKAGE MAPPING OF ESTS DIFFERENTIALLY EXPRESSED BETWEEN APOMICTIC AND SEXUAL GENOTYPES OF *POA PRATENSIS* L.

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apomixis, linkage mapping, mode of reproduction, EST mapping

Kentucky bluegrass (*Poa pratensis* L.) is a hardy, persistent, attractive forage and turf grass adapted to a wide range of soils and climates. The great adaptive capacity of this species is likely associated with its variable ploidy level and versatile mode of reproduction, ranging from obligate apomixis to complete sexuality. Because different plants may show contrasting modes of reproduction, *P. pratensis* could serve as model species for investigating apomixis and its inheritance.

In the past, data accumulated on *P. pratensis* suggested that apomixis is controlled by a single genetic locus of undetermined size and structure. This implied that the unreduced egg has a built-in tendency to autonomous parthenogenesis, and that apospory and parthenogenesis are pleiotropic. Recently independent works have, instead, demonstrated that apospory and parthenogenesis are controlled by 2 to 5 genes putatively.

Because of these contrasting data we decided to build a genetic map with the aim of finding marker/s co-segregating with the mode of reproduction. The occourence of recombination between apospory and parthenogenesis in this species should guarantee the possibility to map the 2 features independently.

Therefore, we developed a population segregating for the mode of reproduction of 124 progeny plants, by crossing an apomictic and a sexual genotype. For all genotypes, the mode of reproduction (aposporic vs. meiotic and parthenogenetic vs. embryogenetic) was investigated through flow cytometry on an average number of 50 seeds in 5 seeds bulks or single seed analysis. Several PCR-based molecular markers (AFLP, SAMPL, SSR, TRAP) were used to built an adequate framework of markers.

Since, a cDNA-AFLP approach allowed us to isolate 178 ESTs differentially expressed between sexual and apomictic genotypes of *P. pratensis,* our main project aim is to map these ESTs into the PCR-based markers framework to look for ESTs co-segregating with the mode of reproduction (apospory/parthenogenesis). Once one or more ESTs tightly linked to one of the feature of apomixis will be identified, we plan to screen a genomic library (based on cosmidic vectors) to obtain a clone useful for FISH analysis. In this way we could also understand if they are located close to other genes isolated with a different approach and characterized for being differentially expressed (e.g. APOSTART, PpSERK, etc).