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 – F.07

TOWARD CLONING OF THE APPLE COLUMNAR GENE

BALDI P., KOMJANC M., MALNOY M., MAGNAGO P., COSTA F., VELASCO R., SALVI S.

IASMA Research Centre, Via E. Mach 1, 38010 San Michele all'Adige (Italy)

tree architecture, molecular markers, columnar, Malus domestica

In apple breeding programmes tree architecture is considered an important trait, because it influences fruit quality, planting density, production and labour requirements. Tree architecture can be controlled by pruning and using size-controlling rootstocks, but natural tree forms resulting in small and narrow trees could be desirable to assure a uniform light penetration, high density planting and a reduction of pruning interventions. The columnar growth habit in apple presents all these desirable traits, as it is characterized by short internodes, a thick stem and reduced plant height and branching. The columnar habit seems to be controlled by a single dominant gene (*Co*), even if minor modifier genes can segregate depending of the genetic background. Different apple columnar varieties are currently available such as "McIntosh Wijcik", "Telamon" and "Tuscan" and molecular markers for this character have been developed using segregating population derived from different crosses. The *Co* gene has been reported to map on the apple linkage group 10, and molecular markers associated to the columnar habit include SSR markers, RAPD markers and SCAR markers. At FEM-IASMA three columnar segregating populations of 170, 130 and 70 individuals respectively are currently available, derived from the crosses "Golden x Wijcik", "Goldrush x Wijcik" and "Galaxy x Wijcik". These populations have been phenotypically characterized and tested with some of the available markers in order to associate the columnar habit with the molecular markers. As the final aim of the work is the cloning of the *Co* gene, fine and physical mapping of the columnar region will be necessary. For this purpose, a larger mapping population derived from the cross " Golden x Wijcik" is being produced. FEM-IASMA has been recently funded to sequence the apple genome. This will shortly provide an extremely powerful tool to develop new markers strictly associated to *Co* and directly characterize the corresponding genomic region searching for putative candidate genes.