Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 2A.85

GENOMIC STABILITY OF ANDROGENETIC HAPLOIDS DERIVED FROM *SOLANUM TUBEROSUM (+) S. BULBOCASTANUM* SOMATIC HYBRIDS

SCARANO M.-T.*, CRISTIANO L.**, TAVANO R.**, FRUSCIANTE L.**, AVERSANO R.**

*) Institute of Plant Genetics – CNR, Research Division Portici, Via Università 133, 80055 Portici (Italy)
**) Department of Soil, Plant, Environmental and Animal Production Sciences, University of Naples Federico II

Potato, molecular markers, nuclear DNA, cytoplasmic DNA

Somatic hybridization via protoplast fusion provides a powerful tool to overcome crossing barriers in potato (4x=48), allowing the integration of parental nuclear and cytoplasmic genomes. Previously, we used protoplast fusion to produce hybrids between incongruent 2x *S. bulbocastanum* and haploids of the cultivated potato *S. tuberosum*. Due to somatic hybrid sterility, we engineered haploidization as strategy to overcome such a drawback. The aim of this study was to establish the extent of genetic variation of somato haploids obtained through anther culture. The assessment was carried out at mitochondrial (*mt*) and chloroplast (*cp*) level by 13 (4 *mt* and 9 *cp*) ‘‘universal primers’’ homologous to conserved sequences, and at nuclear level by 8 Inter Simple Sequence Repeats (ISSRs) markers. As for the cytoplasm, the analysis revealed a very low rate of polymorphism in our haploids both for *cp*- and *mt*-DNA. This result is likely due to the very strong stability of such genomes. By contrast, a high degree of polymorphism was detected at nuclear DNA level, ranging from 17% to 38%. Pair-wise comparisons between the banding patterns of haploids and somatic hybrids they derived from allowed detecting two types of changes: disappearance of parental ISSR fragments (termed “loss”) and appearance of novel ISSR fragments (termed “gain”). The most frequent event occurring in the haploids was the loss of fragments (16% on average). Cluster analysis revealed that haploids were genetically distant from the parental somatic hybrids as well as among them. Implications of our findings from a breeding standpoint will be discussed.