Poster Communication Abstract – 2A.15

MITOCHONDRIAL GENOME OF *ASPLENIUM NIDUS* REVEALS FEATURES HIGHLY SIMILAR TO THOSE OF SEED PLANT mtDNAs

RAINALDI G.*, PANARESE S.*, MIACOLA C.**, LOTTI C.**

*) Department of Biochemistry and Molecular Biology University of Bari "Aldo Moro", Via Orabona 4, 70125 Bari (Italy)

**) Department of Agroforestry, Environmental Biology and Chemistry, Section of Genetics and Plant Breeding, University of Bari "Aldo Moro", Via Orabona 4, 70125 Bari (Italy)

Plant Mitochondria, Monilophytes, Asplenium nidus

Mitochondrial genomes of land plants have been fully sequenced and characterized in several species belonging to the Briophytes (*Marchantia polymorpha* and *Physcomitrella patens*) and Spermatophytes (*Arabidopsis thaliana*, *Beta vulgaris*, *Oryza sativa*, *Brassica napus*, *Zea mays*, *Nicotiana tabacum* and *Triticum aestivum*).

To gain more knowledge on the mitochondrial biogenesis of Monilophytes, we chose plants of a filicale family, the fern *Asplenium nidus*, available at the Botanical Garden of the University of Bari.

The comparison of organization, structure and expression between Spermatophyte mitochondrial genomes reveals several homogeneous features which can be summarized as follows:

- i) the presence of repeated sequences,
- ii) a heterogeneous structure,

iii) the presence of DNA segments of extra mitochondrial origin (mainly chloroplastic) carrying in some cases active genes (usually for tRNAs),

- iv) the editing of transcription products of structural genes,
- v) an incomplete set of tRNA genes.

On the contrary not all of these features can be considered peculiar properties of Briophyte mitochondrial genomes, in particular: RNA editing, active in some species but not in all, absence of homologous recombination events; absence of incorporation of foreign genetic information; absence of chloroplast DNA insertions.

Using two differents approach - RAPD PCR and an unusual PCR procedure, we were able to obtain several sequences of the *A. nidus* mitochondrial genome.

The main results obtained from our investigation are the following:

i) the detection of DNA segments of chloroplast origin (*trnA*, *rps11*, *rpoB*, *psbA*, *rrn16S*)

ii) the identification of complete genes for proteins, rRNA and tRNAs (*nad4L*, *nad9*, *atp9*, *coxIII*,*rrn26*, *rrn 5S*, *trnN*, *trnR*, *trnK*, , *trnP*, *trnW*);

- iii) a couple of inverted repeats although of small size.
- iv) Higher transcription editing level respect Spermatophytes