Poster Communication Abstract – 2A.32

THE SPINACH *LHCB1* MULTIGENE FAMILY. WHY MULTIPLE GENES FOR ISOFUNCTIONAL PROTEINS?

LEONI C.*, VOLPICELLA M.*, GALLERANI R.*, CECI L.R.**

*) Department of Biochemistry and Molecular Biology, University of Bari "Aldo Moro", Via Amendola 165/A, 70126 Bari (Italy) **) Institute of Biomembranes and Bioenergetics – CNR, Bari (Italy)

Light harvesting protein, plant adaptation, Spinacia oleracea, multigene family, genome walking

Conversion of light energy in higher plants is carried out by two electrically connected photosystem units, PSI and PSII, containing pigment-protein complexes that act as antennae to harvest solar light energy. The light harvesting complex II (LHCII), associated with PSII, contains three highly homologous chlorophyll-a/b-binding proteins (Lhcb1, Lhcb2 and Lhcb3), which can be assembled in both homotrimers and heterotrimers. Generally Lhcb1 and Lhcb2 are encoded by multigene families, whose members are variable in number from plant to plant, and whose different function is yet to be clarified.

We have identified in spinach leaves the full-length cDNAs corresponding to three isoforms of Lhcb1 polypeptides, whose isoforms appear to be differentially expressed in response to long-term white light exposure (1). The three Lhcb1 mature polypeptides are highly homologous to each other, sharing very high identities (97-98%). Only the Lhcb1.1 polypeptide shows an amino acid substitution having a clear functional meaning. It corresponds to a Thr3>Ser substitution which was found to affect phosphorylation level of Lhcb1 polypeptides, a crucial step in the State Transition process (2).

In order to sequence the regulatory regions of the spinach Lhcb1 genes, we have developed a suitable Genome Walking method which allows the contemporary analysis of members of multigene families (3, 4). By this approach we identified two additional Lhcb1 genes, not previously hypothesised on the basis of cDNA and proteomic analysis. Gel shift assays of identified regulatory motifs showed the different activity that distinct regulatory motifs may have in the expression of members of the gene family (5). These results, together with the phylogenetic analysis of the Lhcb1 families, sustain the hypothesis of a role of members of the multigene families and their regulatory regions in the adaptive response of plants to different light conditions.

REFERENCES

1) Rea et al., 2007, Characterization of three members of the multigene family coding for isoforms of the chlorophyll a/b binding protein Lhcb1 in spinach. Physiologia Plantarum 130: 167-176.

2) Allen and Forsberg, 2001, Molecular recognition in thylakoid structure and function. Trend Plant Sci 6: 317-326.

3) Leoni et al., 2008, A genome walking strategy for the identification of eukaryotic nucleotide sequences adjacent to known regions. BioTechniques 44: 229-235.

4) Leoni et al., 2011, Genome Walking in Eukaryotes. FEBS Journal (Submitted Review).

5) Leoni et al., 2010, Application of a genome walking method for the study of the spinach Lhcb1 multigene family. Plant Physiology 167: 138-143.