

SL207 Cyclophilin of a red alga *Griffithsia japonica* : Differential expression and phylogenetic analysis

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Cyclophilin (Cyp) was first identified as a cytosolic binding protein for the immunosuppressive drug cyclosporinA (CsA), and it was subsequently identified as a peptidyl-prolyl *cis-trans* isomerase (PPIase). As an immunophilin, Cyp-CsA complex suppresses the immune response through binding with the calcineurin and blocking Ca^{2+} -dependent T-cell activation pathway. Cyp-CsA complex plays a role as an inhibitor of protein phosphatase and blocks Ca^{2+} -induced inactivation of K^+ channels in plant guard cells. As an isomerase, Cyp is suggested to accelerate folding and refolding of various proteins. Cyp is a family gene which has been isolated from animals, fungi, plants, protozoan and bacteria. Cyps are abundant in cytosol, but the others can be either secreted into the extracellular medium or transported into subcellular organelles such as ER, mitochondria and chloroplast. Five or six isoforms have been suggested in the Cyp family, but there are discordance among those classification and nomenclature system. And these groupings are based on the size, so do not necessarily reflect the relationship among the groups. During a differential screening of the gametophyte-specific cDNA library of a red alga *Griffithsia japonica*, a cDNA clone for cyclophilin was isolated. The transcript corresponding to Cyp was abundant in male and tetrasporangial thalli, but only basal level of transcript was detected in female gametophyte. Therefore, it was designated GjFW-2 (*G. japonica* Female Weak-2). GjFW-2 may be involved in folding of proteins which are exceedingly produced during spermatogenesis and sporogenesis in male gametophyte and tetrasporophyte of *G. japonica*. In young gametophyte of which sexual reproductive structures yet developed, GjFW-2 transcript was detected rather strongly. The high level of GjFW-2 transcript in young gametophyte might reflect a generally high level of gene expression in this state. Currently available amino acid sequences of eukaryotic Cyps were compared and analyzed to place GjFW-2 at a proper phylogenetic relation. Phylogenetic trees derived from the alignment showed a clustering of two distinct groups: cyclophilinA (CypA) and cyclophilinB (CypB). CypA included cytosolic and mitochondrial Cyp, and could be again subdivided into 5 subgroups: mammal, invertebrate, protozoan, fungal and plant CypA. Group CypB possessed ER targeted or secreted Cyps and chloroplast Cyps. GjFW-2 was analyzed to correlated mostly with CypA and to be independent from 5 subgroups. The phylogenetic relationship among CypA will be discussed.