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# A DATABASE OF RHODOPHYTE PLASTID PROTEIN FAMILIES AND REGULATION OF *moeB* GENES

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**Key words:** orthology relationship, database of plastid protein families, plastids, algae, transcription regulation, molybdopterin biosynthesis

*Motivation and Aim:* The orthology relationship is not yet decisively formalized, and some of its important features may depend on the taxonomic context. Gene *moeB* is tackled as an example, and is itself an interesting object of research. It encodes an E1-like family enzyme involved in molybdopterin and thiamine biosynthesis. This family includes proteins that catalyze ATP adenylation of the C-terminal glycine carboxyl group in sulfur carrier proteins, e.g., MoaD or ThiS. Gene *moeB* is present in plastids of all sequenced red algae (Rhodophyta), with the exception of *Cyanidioschyzon merolae*.

*Methods and Algorithms:* All plastid proteins of the red algae available in GenBank, NCBI, were considered for the study. Analyses were conducted with original algorithms.

*Results:* We report a first complete database of plastid protein families from the red algae. The families contain proteins with maximal sequence similarity and minimal paralogous content, and were built based on an original definition of paralogy. The database contains 6005 protein entries, 495 families, 286 non-singletons (from which 235 are paralog-free, and other 51 contain at maximum two proteins per species). We will report results of a systematic comparison of the database with biological data and conclusions drawn from analyzing the database. Gene *moeB* exemplifies the results. Candidate bacterial-type promoters in 5'-leader regions of *moeB* distinctly differ from the template. In all sequenced species, except for *Cyanidium caldarium*, these regions contain a conserved 12 nt-long motif. Its high conserved part has the consensus TAGAT. In *Gracilaria tenuistipitata* the motif adjoins the -35 promoter box; in *Grateloupia taiwanensis* it coincides with the -35 box; in *Porphyridium purpureum* and *Chondrus crispus* the motif is distanced from the -35 box; in *Calliarthron tuberculosum*, *Porphyra purpurea*, *Pyropia haitanensis*, and *P. yezoensis* the -35 box is not determined, although the AT-rich region found downstream may represent a functioning -10 promoter box.

*Conclusion:* A notable distinction of the identified promoters from the consensus and presence of a closely located conserved motif suggest this motif to be a putative binding site of a transcription factor activating transcription of *moeB*. In most species, presence of an actively transcribed tRNA gene on the opposite strand precludes *moeB* transcription from a distantly located promoter. Lack of the motif and the bacterial-type promoter upstream *moeB* in *Cyanidium caldarium* suggests a different regulation mechanism for this gene, which comes in agreement with its loss in the close species *Cyanidioschyzon merolae*.

*Availability:* The database of plastid protein families from the red algae, <http://lab6.iitp.ru/ppc/redline45>

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