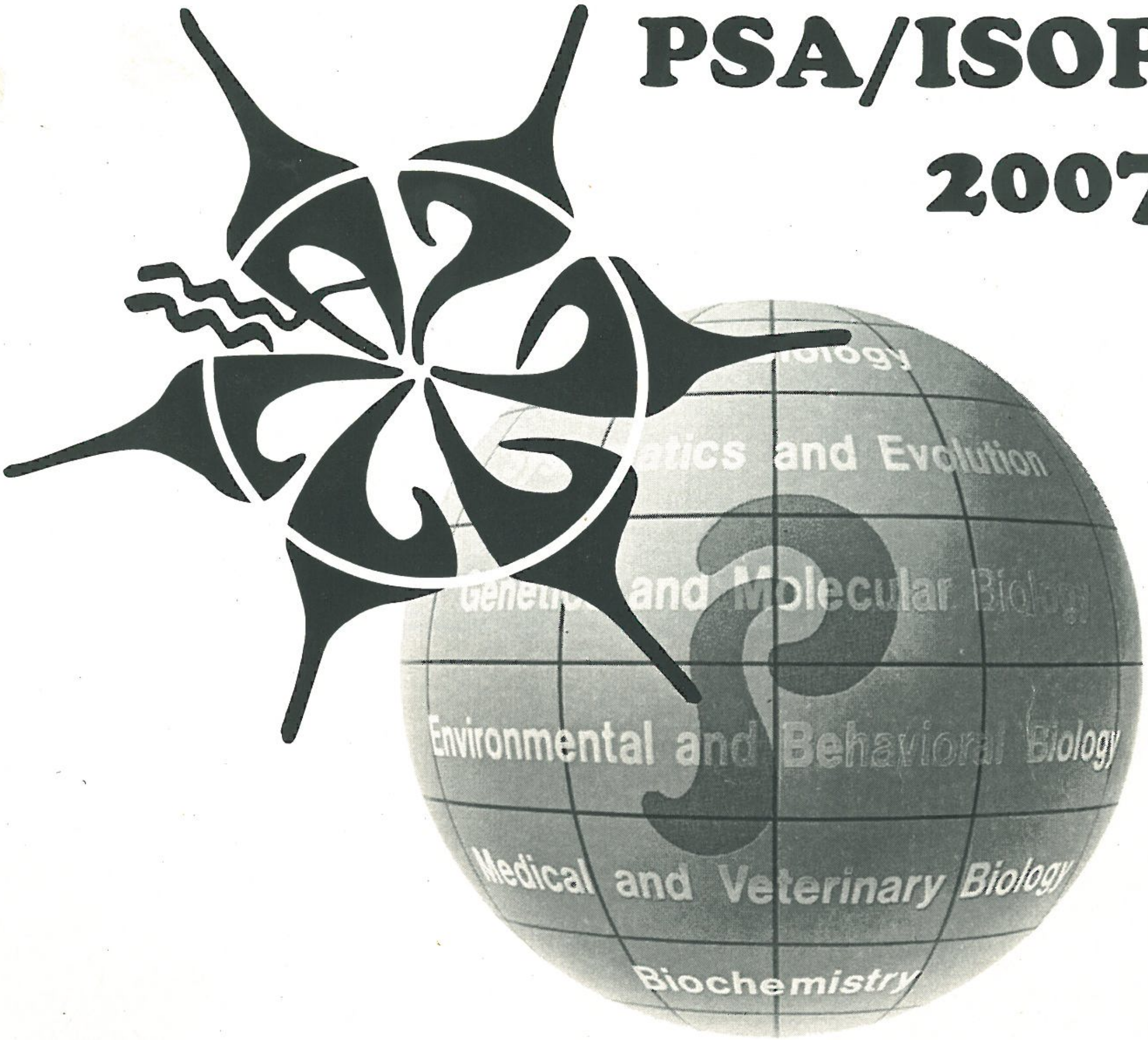
PSA/ISOP 2007



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Meeting Program

cryptic species, which are identical in morphology and possess no or only minimal divergence in their SSrRNA gene and/or the ITS regions.

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'SUPER' PLANT KINGDOM REINSTATED: NONMONOPHYLY OF PRIMARY PHOTOSYNTHETIC EUKARYOTES AS DEDUCED FROM SLOWLY EVOLVING NUCLEAR GENES

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The biodiversity of photosynthetic eukaryotes, traditionally recognized as nine algal divisions or phyla, is attributed to two kinds of endosymbiotic events involving plastids: primary endosymbiosis and secondary endosymbiosis. Therefore, the phylogenetic positions of primary photosynthetic eukaryotes are fundamental for understanding the evolution of eukaryotic cells and establishing higher taxonomic concepts of eukaryotes. Recently, Rodriguez-Ezpeleta et al. (2005, Curr. Biol.) demonstrated the strong monophyly of the three groups of primary phototrophs (green plants, glaucophytes, and red algae) based on 143 nuclear genes (30,113 aa). However, they analyzed only two divisions of the secondary phototrophs belonging to the Stramenopiles-Alveolata (SA) lineage, and their 143 genes included rapidly evolving genes. Since multigene analyses are expected to be increasingly sensitive to long branch attraction, improved taxon sampling and the selection of positions or genes that evolve more slowly have been suggested for resolving deep branching in phylogenies (Philippe & Laurent 1998, Curr. Opin. Genet. Dev.). Here we reexamined the phylogeny of the primary phototrophs based on only 19 slowly evolving nuclear genes (18 genes from the 143 genes, plus hsp90; 5,216 aa) using additional OTUs of Haptophyta and Excavata (Heterolobosea and *Reclinomonas*). The p-distances for each of the 19 genes do not generally exceed 0.4 (based on saturation curves of the distance correction methods [Philippe and Laurent 1998]). Since α- and β-tubulin sequences might be relaxed in eukaryotes lacking flagella (e.g. red algae), and EF-2 sequences might contain unusual phylogenetic information (Stiller et al. 2001, JME), we did not use these three genes. Our phylogenetic results demonstrate the robust non-monophyly of the primary phototrophs and the basal position of red algae within the bikonts, suggesting the loss of plastids in certain eukaryotic lineages under the assumption of the single plastid primary endosymbiosis. Thus the 'super' Plantae (Plant Kingdom) suggested earlier (Nozaki et al. 2003, JME; Nozaki et al. 2003, PSA/SOP meeting) may be reinstated.

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THE RED ALGAL ORDER NEMASTOMATALES: NEW INSIGHTS IN THE LIFE HISTORY, MORPHOLOGY, PHYLOGENY AND BIOGEOGRAPHY OF PERTINENT TAXA

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The order Nemastomatales comprises two families of predominantly gelatinous representatives with heteromorphic life histories, the Nemastomataceae and Schizymeniaceae. New insights in the life history and morphology of pertinent taxa are illustrated with *Platoma cyclocolpum* (Mont.) Schmitz from the Azores, a species in which three modes of thallus development were observed from germinating carpospores. Comparative *rbc*L sequence analysis indicates that species reported as having a wide distribution instead have a restricted distribution. For example. *P. cyclocolpum* may be confined to the Macaronesian islands, and the taxon going under this name in the Indian Ocean (Madagascar) is instead *Platoma chrysymenioides* Gavio et al., a species found throughout the Gulf of Mexico. *Schizymenia dubyi* (Chauvin ex Duby) J. Ag. described from Atlantic France is also present in Japan, but records of this species from the Azores should be referred to *S. apoda* (J. Ag.) J. Ag. described from the Cape Province, S. Africa, and also present in Namibia and Japan. Additionally, new records of recent deepwater collections of *Predaea* and *Titanophora* throughout the Gulf of Mexico, as well as unreported Nemastomatales from the Azores and Japan, are greatly increasing the species diversity of the Order.