

A novel highly expressed plastid protein in chlorarachniophytes

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Chlorarachniophytes are marine unicellular algae that arose by a secondary endosymbiosis in which a cercozoan host engulfed a green alga. Their plastids harbor a relict nucleus of the algal endosymbiont, the so-called nucleomorph, which has disappeared in most cases of secondary endosymbioses. Therefore, chlorarachniophytes are an attractive model to investigate the secondary plastid evolution. In our previous study, we performed a diurnal transcriptome analysis for the chlorarachniophyte *Bigeloviella natans*, and found that 35% (7,700) nuclear genes exhibit diurnal oscillation in their transcript levels. These genes are referred to as differentially expressed genes (DEGs), and we here focused on the highly transcribed DEGs (Hi-DEGs). When we looked at the top 50 of Hi-DEGs, most of them (>80%) were identified as plastid-related protein genes (e.g., RbcS, LHC, GAPDH), whereas there were six hypothetical protein genes, named *hep25*, *hep29*, *hep40*, *hep41*, *hep45*, and *hep48*, that might have important functions like the other Hi-DEGs. Although five of them were specific for chlorarachniophytes, homologs of *hep40* were found in various bacteria and photosynthetic eukaryotes including dinoflagellates, haptophytes, and heterokonts. We found that Hep40 protein was localized in the chlorarachniophyte plastids. In this presentation, we will discuss the function and evolution of this novel plastid protein.