

有孔虫細胞質構造とタンパク質コード遺伝子の関係解明への挑戦 Can molecular phylogeny of protein-coding genes provide new insights for foraminiferal morphology?

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Multi-gene phylogenetic studies have revealed one of big eukaryotic group, Rhizaria include Foraminifera, Radiolaria, Filosa, and Endomyxa. Foraminifera is known diverse group having two distinct life-styles: planktic and benthic. Recently, molecular phylogeny of foraminifera showed the polyphyletic origins of planktic foraminifera that they were diverged from benthic foraminiferal lineages at least twice (Ujiie et al., 2008). Moreover, high genetic diversity at intra-species level has been inferred based on the SSU rDNA and ITS rDNA sequences (e.g., Darling and Wade, 2008). However, these studies have not been challenged to understand the evolutionary processes according with cell-structures.

This present study shows the foraminiferal phylogenies of two protein-coding genes (actin 2 and b-tubulin 2), which are corresponded to actin granules and microtubules in cell structure. Especially foraminiferal b-tubulin 2 forms a helical filament, which is involved in rapid microtubule assembly/disassembly system resulting in the quick movement of pseudopodia (Habura et al. 2005). Both phylogenies of actin 2 and b-tubulin 2 show two robust clades according with tube- and fan-shaped pseudopodia which are observed in attaching new chamber during their growth processes. Rotaliida including planktic foraminifera have fan-shaped pseudopodia, whereas some of benthic groups have tube-shape one. This preliminary data suggests that the phylogenetic analyses of the protein-coding genes potentially implicate the mechanisms of morphological traits in shell-bearing protozoans. Future assessments are required increasing taxonomic sampling of benthic tube-shaped types.

(References)

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