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Molecular evolution of foraminiferal tubulins

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Foraminiferans are known to be highly divergent in several normally conserved genes. Although the best-understood example of this phenomenon is the ribosomal small subunit (Pawlowski, 2000; Habura *et al.*, 2004), other genes also show evidence of strong modifications. These modifications are generally conserved within the Foraminifera but are found in no other organism, which presents several opportunities for foraminiferal molecular research. From a phylogenetic standpoint, these genes are useful for estimating relationships between different groups of foraminiferans. In addition, the identification of close relatives of the Foraminifera (particularly *Gromia*, but also other members of the Rhizaria; Adl *et al.*, 2005) should permit identification of some of the particular evolutionary changes that resulted in the emergence of morphologically-distinctive foraminiferans by the early Cambrian. Study of the physical implications of changes in conserved genes will also result in enhanced understanding of foraminiferal cell biology.

Foraminiferal beta-tubulins are a case in point. These genes are highly useful for phylogeny, and can be used to test ideas about foraminiferal relationships that are hard to resolve using SSU rDNA data (Habura *et al.*, 2006). In addition, foraminiferal beta-tubulins are highly modified compared to those from other organisms, in ways which have implications for foraminiferal microtubule assembly (Habura *et al.*, 2005). Because these genes are so unusual, specific primers can be used to identify foraminiferal tubulins in environmental DNA samples. This approach allows rapid testing of hypotheses about environmental influences on tubulin assembly, such as low temperatures.

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