PCR reactions designed to amplify the entire small subunit (SSU) ribosomal RNA gene from *Naegleria* species for phylogenetic analyses, demonstrated a single band of approximately 2 kb in most species but a band of approximately 3.2 kb in strains of *Naegleria andersoni*, *Naegieria andersoni* ssp. *andersoni* and *Naegleria australiensis* ssp. *italica*. The extra length in *N. andersoni* ssp. *andersoni* strain PPMFB-6 (1) is due to an insertion of approximately 1277 base pairs in the coding sequence of the rRNA gene. The insertion is sited near the tip of helix 19 immediately prior to the conserved SSU rRNA sequence CC-AG (2). Extraction and sizing of total rRNA by gel electrophoresis revealed that the insertion was removed in vivo to produce a mature SSU rRNA of the same size as strains lacking the insertion in their SSU gene. The insertion in *N. andersoni* ssp. *andersoni* was amplified and directly sequenced using a linear PCR reaction (3, 4). Sequence analysis revealed that it contains motifs which identify it as a group I intron (5). Thus, the short sequences P, Q, R and S, which represent the conserved core structure of group I introns (5), are all present and they occur in that order. The intron also contains a long open reading frame situated between R and S, which codes for a putative protein of unknown function and containing 245 amino acids. Group I introns are rare in nuclear SSU rRNA genes and have hitherto only been reported in *Ustilago maydis* (6), *Pneumocystis carinii* (7) and *Ankistrodesmus stipitatus* (8). The introns in these taxa are all small (394–480 bases), they do not contain long open reading frames, and they are inserted at different positions in the SSU rRNA gene (6). Furthermore, *Naegleria* branches at a point in the eukaryote phylogenetic tree which is much deeper than these taxa (9). Thus, our observation significantly extends the phylogenetic range of group I introns in eukaryote nuclear SSU genes.

REFERENCES