

Primer Information & Laboratory Protocols

Standard PCR amplification protocols were performed using AmpliTaq Gold reagents (Perkin Elmer/Applied Biosystems). Reaction mixtures and thermal cycling parameters differed between taxa. RAG-1 light and heavy strand primers were G396 (R13) 5'-TCT GAA TGG AAA TTC AAG CTG TT-3' (Groth and Barrowclough 1999) and G884 5'-GCA TTA TGA GCG TTC ATG AAY TTY TG-3' (Townsend et al. 2004), respectively. *C-mos* primers were light strand G303 5'-ATT ATG CCA TCM CCT MTT CC-3' and G73 5'-GCG GTA AAG CAG GTG AAG AAA-3'; and heavy strand G74 5'-TGA GCA TCC AAA GTC TCC AAT C-3' and G708 5'-GCT ACA TCA GCT CTC CAR CA-3' (Saint et al. 1998; Hugall et al., in review). PCR products were sequenced using the ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit and an ABI 3700 automated sequencer. Some additional sequencing was outsourced to a commercial firm (Macrogen, Seoul, South Korea). Sequences were edited manually and aligned by eye using reading frame and the BioEdit Sequence Alignment Editor (Hall 1999).

Groth, J.G., Barrowclough, G.F. 1999. Basal divergences in birds and the phylogenetic utility of the nuclear RAG-1 gene. *Mol. Phylogenet. Evol.* **12**(2), 115-123.

Hall, T. A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucl. Acids Symp. Ser.* **41**, 95-98.

Saint, K. M., Austin, C. C., Donnellan, S. C., Hutchinson, M. N. 1998. *C-mos*, A nuclear marker useful in squamate phylogenetic analysis. *Mol. Phylogenet. Evol.* **10**(2), 259-263.