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Abstract: Nucleotide sequences from the c-mos proto-oncogene have previously been used to reconstruct the phylogenetic relationships between distantly related vertebrate taxa. To explore c-mos variation at shallower levels of avian divergence, we compared c-mos sequences from representative passerine taxa that span a range of evolutionary differentiation, from basal passerine lineages to closely allied genera. Phylogenetic reconstructions based on these c-mos sequences recovered topologies congruent with previous DNA-DNA hybridization-based reconstructions, with many nodes receiving high support, as indicated by bootstrap and reliability values. One exception was the relationship of Acanthisitta to the remaining passerines, where the c-mos-based searches indicated a three-way polytomy involving the Acanthisitta lineage and the suboscine and oscine passerine clades. We also compared levels of c-mos and mitochondrial differentiation across eight oscine passerine taxa and found that c-mos nucleotide substitutions accumulate at a rate similar to that of transversion substitutions in mitochondrial protein-coding genes. These comparisons suggest that nuclear-encoded loci such as c-mos provide a temporal window of phylogenetic resolution that overlaps the temporal range where mitochondrial protein-coding sequences have their greatest utility and that c-mos substitutions and mtDNA transversions can serve as complementary, informative, and independent phylogenetic markers for the study of avian relationships.