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Evolution of the SEC1 gene in New World monkey lineages (Primates, Platyrrhini)

B.N. Borges[1], T.S. Paiva[2] and M.L. Harada[1]

[1]Laboratório de Biologia Molecular “Francisco Mauro Salzano”,
Instituto de Ciências Biológicas, Universidade Federal do Pará,
Cidade Universitária Prof. José da Silveira Netto, Belém, PA, Brasil
[2]Departamento de Zoologia, Laboratório de Protistologia,
Instituto de Biologia, CCS, Universidade Federal do Rio de Janeiro,
Ilha do Fundão, Rio de Janeiro, RJ, Brasil

Corresponding author: B.N. Borges
E-mail: bnborges@ufpa.br

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ABSTRACT. The structure and evolution of the SEC1 gene were examined for the first time in New World primates of the genera *Alouatta*, *Aotus*, *Ateles*, *Brachyteles*, *Callicebus*, *Callithrix*, *Cebus*, *Chiropotes*, *Lagothrix*, *Leontopithecus*, *Pithecia*, *Saguinus*, and *Saimiri*. This gene has a high CG content (63.8%) and an estimated heterogeneous size ranging from 795 (*Callithrix*) to 1041 bp (*Pithecia*), due to numerous indel events. Similar to other fucosyltransferases, three conserved regions are shared by these primates, except for the callitrichines, *Aotus* and *Pithecia*, in which indel events resulted in premature stop codons that are related to the production of a supposedly non-functional protein. Phylogenetic analysis of the SEC1 gene, transition/transversion rates, and nucleotide sequence alignment support the hypothesis that primate SEC1 evolved by divergent evolution, and that the lack of activity in some lineages occurred independently at least twice in New World primates, once in the *Aotus*-*Cebus*-Callitrichinae group and again in *Pithecia*. Likelihood-based inference of ancestral states for the activity of SEC1 leads us to suppose that inactivation of SEC1 in the Callitrichinae was a result of a more complex series of events than in *Pithecia*.

Key words: Fucosyltransferases; Divergent evolution;
Molecular inactivation; New World monkeys