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Identifying sloth species at a genetic level

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Identifying species, separating out closely related species and managing each type on its own, is an important part of any animal management system. Some species, like the two types of two-toed sloth, are so close in appearance and behavior that differentiation can be challenging. Conservation researchers at San Diego Zoo Global's Institute of Conservation Research have developed a mechanism for identifying these reclusive species from each other.

"Species identification of two-toed sloths has always been problematic in the wild and captivity due to their large overlap in external morphology. " said Oliver Ryder Ph.D., Director of Genetics for San Diego Zoo Global's Institute of Conservation Research. "Through this effort we have described a low-cost easy-to-use molecular tool for species identification that will help to improve management of two-toed sloth species so that we can ensure that they are properly represented on the ark of rare and endangered species."

The study, published in the December 2011 issue of *Zoo Biology*, describes a PCR-based technique that allows species identification of two-toed sloths without requiring sequencing, by using a mitochondrial marker (COI gene) and restriction enzyme assay. It also reports intra- and inter-specific patterns of chromosome variation in captive two-toed sloths. The chromosome number in Hoffman's two-toed sloths showed low variation ranging only between 50 and 51. In contrast, Linnaeus's two-toed sloths appeared to vary widely, with diploid numbers ranging from 53 to 67, suggesting distinct geographic groups.

Provided by Zoological Society of San Diego

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