

A phylogenetic analysis of *Alouatta pigra* inhabiting the Calakmul site of Campeche, Mexico.

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Howler monkey, *Alouatta*, phylogeny is not well understood and researchers have recognized anywhere from six to ten species of *Alouatta*, and up to nineteen subspecies. We analyzed the mitochondrial cytochrome *b* gene sequence of four Yucatan Black Howler individuals (*A. pigra*) and compared them to published sequences from nine of the ten recognized howler species to better understand howler phylogenetic relationships. DNA was extracted from fecal samples collected from two troops of howler monkeys living at the Calakmul site in the Campeche state of southeastern Mexico. We sequenced the first 800 bases of the mitochondrial cytochrome *b* gene. A neighbor-joining tree was constructed to compare the Calakmul sequences with published *Alouatta* sequences, including *A. pigra* samples from two collection sites in Tabasco and Chiapas, Mexico. The Calakmul samples were identical to each other, but did not match the Tabasco and Chiapas samples. We identified four substitutions among the Calakmul howlers. Two substitutions were synonymous, but the other two changes were non-synonymous mutations that resulted in new amino acids. In all, three different sequences were found among the ten *A. pigra* samples collected from the three locations. Although the Calakmul sequences differed from published *A. pigra* sequences, they clustered with them on the neighbor-joining tree and support the identification of *A. pigra* as a separate species. The genetic relationship among the individuals in the two Calakmul howler troops is currently unknown, but these identical sequences suggest the possibility of close maternal relationships that will be further explored in future studies.