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1: Mol Ecol 1999 Dec;8(12 Suppl 1):S79-94

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Disparate phylogeographic patterns of molecular genetic variation in four closely related South American small cat species.

Johnson WE, Slattery JP, Eizirik E, Kim JH, Raymond MM, Bonacic C, Cambre R, Crawshaw P, Nunes A, Seuanez HN, Moreira MA, Seymour KL, Simon F, Swanson W, O'Brien SJ.

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Tissue specimens from four species of Neotropical small cats (*Oncifelis geoffroyi*, N = 38; *O. guigna*, N = 6; *Leopardus tigrinus*, N = 32; *Lynchailurus colocolo*, N = 22) collected from throughout their distribution were examined for patterns of DNA sequence variation using three mitochondrial genes, 16S rRNA, ATP8, and NADH-5. Patterns between and among *O. guigna* and *O. geoffroyi* individuals were assessed further from size variation at 20 microsatellite loci. Phylogenetic analyses using mitochondrial DNA sequences revealed monophyletic clustering of the four species, plus evidence of natural hybridization between *L. tigrinus* and *L. colocolo* in areas of range overlap and discrete population subdivisions reflecting geographical isolation. Several commonly accepted subspecies partitions were affirmed for *L. colocolo*, but not for *O. geoffroyi*. The lack of geographical substructure in *O. geoffroyi* was recapitulated with the microsatellite data, as was the monophyletic clustering of *O. guigna* and *O. geoffroyi* individuals. *L. tigrinus* forms two phylogeographic clusters which correspond to *L.t. oncilla* (from Costa Rica) and *L.t. guttula* (from Brazil) and which have mitochondrial DNA (mtDNA) genetic distance estimates comparable to interspecific values between other ocelot lineage species.

Using feline-specific calibration rates for mitochondrial DNA mutation rates, we estimated that extant lineages of *O. guigna* diverged 0.4 million years ago (Ma), compared with 1.7 Ma for *L. colocolo*, 2.0 Ma for *O. geoffroyi*, and 3.7 Ma for *L. tigrinus*.

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