

Short Communication

Population genetics analysis of *Podocnemis* sextuberculata (Testudines, Podocnemidae): lack of population structure in the central Amazon Basin

T.J. Silva^{1,2}, L.A.S. Monjeló¹, M.N.S. Viana¹, J.C. Pezzuti³, P.C.M. Andrade⁴, R.C. Vogt⁵ and I.P. Farias¹

¹Laboratório de Evolução e Genética Animal, Departamento de Biologia, Universidade Federal do Amazonas, Manaus, AM, Brasil ²Universidade Federal de Alagoas, Campus Arapiraca-Pólo Penedo, Arapiraca, AL, Brasil ³Universidade Federal do Pará, Belém, PA, Brasil ⁴Faculdade de Ciências Agrárias, Universidade Federal do Amazonas, Manaus, AM, Brasil ⁵Coordenação de Pesquisa em Biologia de Água Doce, Instituto Nacional de Pesquisas da Amazônia, Manaus, AM, Brasil

Corresponding author: T.J. Silva E-mail: themisilva@yahoo.com.br

Genet. Mol. Res. 10 (3): 1393-1402 (2011) Received November 19, 2010 Accepted February 24, 2011 Published July 12, 2011 DOI 10.4238/vol10-3gmr1163

ABSTRACT. The chelonians are, in general, important for the economy of the traditional populations of the Amazon region, especially as a source of animal protein. Furthermore, sub-products, such as eggs and fat, are utilized in the manufacture of cosmetics, and the plastron and carapace are used in the manufacture of adornments. The freshwater turtle species *Podocnemis sextuberculata*, locally known as "iaçá" or "pitiú", is widely distributed in the Amazon Basin in Brazil and

also in Colombia and Peru. This species is on the International Union for Conservation of Nature Red List in the category of vulnerable species. We examined the genetic variability and population structure of three populations represented by 64 individuals sampled from Reserva Federal de Abufari, Tapauá, Amazonas State; Reserva de Desenvolvimento Sustentável Mamirauá, Tefé, Amazonas State, and Terra Santa, Pará State. All of these are over 1000 km from each other. A partial 415-bp sequence of the mitochondrial gene ND1 was utilized as a molecular marker. Seven haplotypes were observed; the most common haplotype was shared by all the areas sampled, while the rarest haplotypes were represented by a single individual and were thus restricted to a single locality. The sharing of the most common haplotype, the high number of migrants (Nm) and the AMOVA results indicate a lack of genetic structure among the sampling localities. The levels of genetic variability observed were homogeneous among the sampling localities. These results (Θ_{sr} and Nm) are compatible with what is known about the ecology of this species, which has a great migratory capacity.

Key words: Chelonians; Iaçá; Amazon basin; Mitochondrial DNA; *Podocnemis sextuberculata*