



Genetic diversity in populations of the viper *Bothrops moojeni* Hoge, 1966 in Central Brazil using RAPD markers

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ABSTRACT. *Bothrops moojeni* is an abundant venomous snake responsible for most of the snakebite cases in the Central region of Brazil and as a result of the anthropogenic habitat disturbance, such as the increase in extensive farming, the range of *B. moojeni* has been greatly fragmented. Here, we obtained genomic DNA from a total of 75 snakes belonging to four populations. Genetic variability evaluated for five RAPD primers was low ($H_e = 0.20$) and was not spatially structured. We found evidence of significant genetic divergence among *B. moojeni* populations that were isolated (Φ_{ST} values of 0.21 and 0.25), while populations more proximal exhibited less divergence (Φ_{ST} values of 0.04 and 0.08). We found only moderate divergence (Φ_{ST} value of 0.12) between two populations greatly isolated (851.83 km apart) along with great differentiation (0.24) between two proximal populations (290 km apart). Even though these populations are close to each other, they occur in an urbanized area that is almost completely covered by extensive crops, representing an obstruc-

tion to the mobility of this viper. Molecular variance analysis (AMOVA) showed some degree of subdivision in these populations, with a Φ_{ST} value of 0.16, significant to the level of 1% by 1000 random permutations. We also performed a Bayesian analysis that confirmed the AMOVA results and found a value of $\theta^B = 0.14$ and an $f = 0.27$, suggesting a high level of endogamy. This is the first study that characterizes genetic variability for this important species of the *Bothrops* genus, and our data are of significant importance in terms of classifying populations in relation to their conservational value and management strategies. Thus, given the high levels of population structure found in this case, we recommend sampling as many populations as possible to maximize the genetic variability to be preserved when aiming for *in situ* conservation. The same should be done to perform samplings toward *ex situ* conservation.

Key words: *Bothrops moojeni*; Vipers; Genetic variability; RAPD; Conservation genetics; Genetic structure