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RESEARCH ARTICLE

THE USE OF SHELTERS OF *LONTRA LONGICAUDIS* (OLFERS, 1818) (CARNIVORA: MUSTELIDAE) IN THE LAGOA DO PERI, SANTA CATARINA, BRAZIL

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ABSTRACT

This work aims to analyze the use of shelters by *Lontra longicaudis*, through microsatellite analysis. DNA extraction is performed according to the silica-guanidine methodology. Qui-square test (χ^2) is applied to check sample differences. The similarity of genotypes in the shelters is calculated using the Morisita Index of Similarity and the Jaccard Community Coefficient. Two shelters exhibited high similarities. These preliminary results suggest that the size of the otter population is, at least six individuals, and different otters can use the same shelters.

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INTRODUCTION

Shelters can be used by more than only one individual regarding *Lutra lutra* (Melquist and Hornocker, 1983). In Europe, USA, and Canada, otter shelters can be natural holes between rocks, space between roots, as well as human-made structures (Gorman et al., 2006). At Peri Lake, Santa Catarina Island, south of Brazil, neotropical otter uses natural areas found between rocks and root trees (Carvalho Junior, 2016). This study applies DNA analysis techniques in neotropical otter feces obtained in the wild. Application of techniques based on Polymerase Chain Reaction (PCR) and molecular markers, like microsatellite, allows the identification of individuals in a population of otters (Ralls et al., 2017).

MATERIALS AND METHODS

In total, 18 fresh feces were collected inside neotropical otter shelters, from September to December 2004. Fresh feces were placed in sterilized recipients with silica. Later, feces were separated from silica thanks to a filter paper. DNA was extracted from each faecal sample in at least triplicate by following a silica-guanidine protocol (Hoelzel, 1998). Microsatellite's loci were amplified applying PCR and Primers, described by Dallas & Piertney (1998) for *Lutra lutra*. The allele was compared to each other to define the number of pairs. This comparison helped identify the individual according to the samples. The χ^2 was applied to verify if frequencies of genotypes and alleles, genetically identical, belonged to the same individual with a significant level of 5%. Genotype similarities were calculated by applying the Modified Morisita Index of Similarity. This index reflects the probability of the shelters that are being used by the same individuals (Brower, 1998). Jaccard Index (Ij) was applied to test the similarities between shelters, concerning the groups of genotypes found in each shelter.

RESULTS

Six alleles were identified from the 18 feces. These alleles were separated according to the number of pair bases (pb): Alelo (155pb), Alelo B (151pb), Alelo C (84pb), Alelo D (70pb), Alelo E (65pb) and Alelo F (53pb). The allele A (Fallelic= 0,556) was the most frequent one among the analyzed samples, followed by the allele B (Fallelic= 0,195). Table 1 shows the distribution of genotypes as a function of the shelters in the Peri Lake ecosystem.

Table 1. Distribution of the genotypes found in the shelters.

Genotype	Shelters
AA	1,4 and 7
AB	1, 2, 3 and 7
AC	2 and 6
AE	7
DD	4
FF	1 and 7

Jaccard test, shows that shelters T1 and T7 exhibit higher similarity (0,750) due to the presence of genotypes AA, AB, and FF, but the FF only occurs in shelters T1 and T7. Shelters T2 and T3 represent a second group (0,5), characterized mainly by genotype AB. Genotype AC can be found in shelter T6 (0,125) and T2. Shelter T4 (0,056) is primarily characterized by the presence of genotype AA, also located at shelters T1 and T7. Genotype DD, exclusive to shelter T4, was responsible for the lower similarity between this shelter and the others. Cluster analysis indicates that shelters T1 and T7 still present the highest similarity (0,857) as a result of the genotypes AA, AB, and FF. Genotype FF only occurs at shelters T1 and T7. In descending order of similarity, shelters T2 and T3 also represent a second group, with an index of 0,667, due to the genotype AB. Shelter T4 (0,183), where is found the genotype AA, also present in shelters T1 and T7, resulted in higher similarity with the shelters T1 and T7, and T2 and T3, if compared to shelter T6 (0,083), where it was found the genotype AC, still present in shelter T2.

DISCUSSION

The application of techniques based on PCR and molecular markers (SSR), has allowed the identification of individuals in a population of neotropical otters.

These preliminary results suggest that ecological connectivity among subpopulations of neotropical otters is of extreme importance for the planning and management of conservation units. The presence of outsider individuals also indicates the need for a genetic exchange for keeping a healthy population. The linear density at Peri Lake is 1 otter per 2 kilometers. From seven shelters, six were active during the period of the study, resulting in one otter per active shelter.

CONCLUSION

This study can be important for the conservation of the *Lontra longicaudis*, as well as the planning and management of protected areas, such as the definition of ecological corridors. The results show the importance of more research in the study area, with a greater number of samples.

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