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MITOGENOME ANNOUNCEMENT

Otters (Lutrinae) belong to the largest family of carnivores: Mustelidae (Koepfli et al. 2008). In South Africa, there are two species of otter; spotted-necked (Hydrictis maculicollis) and African clawless (Aonyx capensis). The International Union for Conservation of Nature (IUCN) list these otters as Near Threatened (Jacques et al. 2015; Reed-Smith et al. 2015). In this study, we present novel full mitochondrial genomes of these otter species. The comparable mitogenomes consist of 36 genes including 13 protein-coding genes, 2 ribosomal RNAs, and 22 tRNAs including a hypervariable region. Only 19 out of the 36 genes showed some level of variation between species with the smallest being trnV (68 bp difference) and the biggest being nad5 (1830 bp difference). Such variations may provide guidance in selecting gene regions during marker development for phylogenetic assessments.

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KEYWORDS
Mitogenomes; otter; Illumina sequencing; phylogenetic analysis

ABSTRACT
Otters are flagship species for pristine habitats and their southernmost distribution in Africa includes two species; Aonyx capensis and Hydrictis maculicollis. Here, we present novel full mitochondrial genomes of these otter species. The comparable mitogenomes consist of 36 genes including 13 protein-coding genes, 2 ribosomal RNAs, and 22 tRNAs including a hypervariable region. Only 19 out of the 36 genes showed some level of variation between species with the smallest being trnV (68 bp difference) and the biggest being nad5 (1830 bp difference). Such variations may provide guidance in selecting gene regions during marker development for phylogenetic assessments.

The complete mitochondrial genomes of A. capensis (16,188 bp) and H. maculicollis (16,308 bp) are comparable in length to other otter species. The arrangement of genes is also similar to otters and other mustelid species, 36 genes including 13 protein-coding genes, 2 ribosomal RNAs, and 22 for tRNAs including a hypervariable region. Of these, 27 are codons on the sense (+) strand with the remaining nine on the antisense (−) strand for both species. The 13 protein-coding genes share similar start/stop codons between species with variations only observed at gene nad2 (start codon), cox2 (stop), and nad3 (start) where the codons are ATT, TAA, and ATT for H. maculicolis and ATC, TAG, and ATA for A. capensis, respectively. Only 19 out of the 36 genes showed some level of variation between the two species with the smallest being trnV with a 68 bp difference and the biggest being nad5 with an 1830 bp difference. Individual GC content calculations for both A. capensis and H. maculicollis gave 42.7 and 41.3%, respectively which are comparable to a variety of mammals, such as brown bears (41.3%), Eurasian otter (42.1%), and sea otter (41.1%) (Ki et al. 2010). To explore phylogenetic relationships, a maximum likelihood (ML) tree was constructed using available mitogenomes from mustelid species. This phylogenetic reconstruction was performed using the Molecular Evolutionary Genetics Analysis (MEGA) phylogenetic software version 7.0.9 (Pennsylvania State University, State College, PA) (Kumar et al. 2016). The topological structure strongly supports the
published taxonomy (Koepfli et al. 2008) of the Lutrinae family of mustelids with a bootstrap probability of 100% in almost all clades (Figure 1). The two mitogenomes will provide invaluable genetic resources for further studies.

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Disclosure statement

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References


Figure 1. Phylogenetic reconstruction of full mitogenomes from mustelid species. Mitogenomes from this are provided in Genbank with accession numbers MK 309841 (*A. capensis*) and MK 309842 (*H. maculicollis*).