

Molecular phylogeography of the smooth-coated otter (*Lutrogale perspicillata*, Mustelidae) for its conservation in the Mesopotamian marshes of Iraq

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The smooth-coated otter (*Lutrogale perspicillata*) (SCO) includes *perspicillata* (SE Asia), *sindica* (SE Pakistan, W India) and endemic-to-Iraq *maxwelli* morphological subspecies. Classified as vulnerable by IUCN, the SCO is threatened by habitat transformation, illegal trade and poaching. Non-invasively collected samples in Iraq (10), central and E Asia (nine countries, 46) were sequenced at the entire mtDNA Cytochrome-*b* gene and genotyped (ongoing) at the microsatellite DNA. We also obtained 307 bp-long gene fragments from 16 SCOs resident to US and European museums. We used 19 Lutrinae GenBank entries. In Iraq, we provided genetic evidence for endemism of *maxwelli* to Mesopotamia (private haplotype, mostly from Al-Hawizeh Marsh, S Iraq), while we could not confirm the occurrence of the SCO in N Iraq (Kurdistan). We found reciprocally monophyletic mtDNA lineages across the SCO range each corresponding to a subspecies. Preliminary microsatellite DNA results confirmed this mtDNA picture, overall pointing to three Evolutionarily Significant Units. Looking-like SCOs from Singapore showed oriental small-clawed otter (*Aonyx cinerea*) mtDNA. We will investigate *A. cinerea*-mtDNA introgressed SCOs at the microsatellite DNA to assess if they are descendant of *L. perspicillata* x *A. cinerea* otters (i.e., first hybrid record in the wild for Lutrinae). Several museum specimens were genetically identified as other than the SCO (even an African otter), indicating that morphology can be not sufficient to reliably catalogue otter study skins. In Iraq, genetic and fieldwork (not shown) data will help establishing a National Single Species Action Plan for the SCO. [National Geographic Society Conservation Trust grant #C261-13 to F.B.].