*S7.1 Cytb tree and network reconstruction*

Our *cytb* database was supplemented with 74 *P. leo* *cytb* sequences from previous studies (GenBank accession numbers: GU131164-GU131185, AY781195-AY781210, DQ018993-DQ018996, DQ022291-DQ022301, AF384809-AF384818, KC495048- KC495058) [1–3]. Three *cytb* sequences of *Panthera tigris* were included as outgroup (KC495059, AF053051, AF053047). Haplotypes were determined using DNaSP v5.10.01 [4]. A maximum-likelihood (ML) haplotype tree was constructed using the HKY85 substitution model with PhyML v3.0 [5]. The nucleotide substitution model that best fit the data was identified with the web application FindModel ([www.hiv.lanl.gov](http://www.hiv.lanl.gov)) [6]. Bootstrap analysis (1,000 replicates) was used to estimate the robustness of the tree branches. A haplotype minimum spanning network was then reconstructed using the Minspnet algorithm implemented in Arlequin v3.5, using default settings [7]. At our study scale, networks were considered preferable to trees because they did not force haplotypes to occupy tip positions and allowed for multifurcations in the topology.

*S7.2 Cytb genetic diversities*

*Cytb* nucleotide (*π*) and haplotype (*h*) diversities and their standard deviations, as well as the net distance between lineages, were calculated using DNaSP v5.10.01 [4]. The demographic history was also inferred by testing the departure from neutrality using Fu’s *Fs* and Tajima’s *D* statistics in DNaSP. An exact test of population differentiation of pairwise weighted mean *FST* [8] was performed using the same software (10,000 permutations for significance).

Cytochrome *b* haplotype diversity was shown to be greater in the East-Southern lineage (*h* = 0.809) as compared to the West-Central lineage (*h* = 0.588) (Table 1). The fixation index between both lineages was of 0.670 (*p*-value < 0.05), indicating that they were well differentiated. The net genetic divergence between the two groups was 0.7%.

**Table 1. Haplotype (*h*) and nucleotide (*π*) diversities computed for the two main lineages based on the *cytb* sequences.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | | | **GENETIC DIVERSITY** | |
| **LINEAGE** | N | Nh | *h* (SD) | *π* (SD) |
| **WEST-CENTRAL** | 49 | 4 | 0.588 (0.061) | 0.002 (0.001) |
| **EAST-SOUTHERN** | 79 | 13 | 0.809 (0.034) | 0.004 (0.002) |

N: sample size, Nh: haplotype number.

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