

(P03) **Preliminary multilocus phylogeography of the lacertid lizard genus *Omanosaura* from the Hajar Mountains in Northern Oman**

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A total of 2729 base pairs from three mitochondrial (12S, ND4 and CYTB) and two nuclear (C-MOS, MC1R) genes were used to assess the molecular diversity and phylogenetic structure of the two *Omanosaura* lacertid lizards endemic to the Hajar Mountains in Northern Oman. Sequence data from fifteen samples of *O. jayakari* and five of *O. cyanura* were analyzed using Maximum likelihood and Bayesian inference phylogenetic methods, haplotype networks, and molecular dating. Our divergence time estimates suggest that the two species diverged around 8 million years ago (Mya). Mitochondrial sequence data show that the genetic diversity within *O. jayakari* is very low. Phylogenetic analyses support a partition into two clades without a clear geographic association across the Hajar Mountains, their split dating back to approximately 0.31 Mya. On the other hand, *O. cyanura* presents three relatively deep lineages associated with three geographic regions of the mountains: lineage 1, restricted to the Musandam Peninsula in the extreme north of the mountain range; lineage 2, including only one sample located in the Western Hajars; and lineage 3, including two samples from the Jebel Akhdar, the highest part of the Mountains, situated between the Western and Eastern Hajars. According to our time estimates, lineage 1 diverged from the other two lineages around 3.95 Mya, and lineages 2 and 3 would have diverged approximately 2.44 Mya. Nuclear data confirm the genetic homogeneity of *O. jayakari* and the high genetic diversity within *O. cyanura*. More samples of *O. cyanura* from undersampled areas will be needed to confirm the consistency of this pattern.

Omanosaura, Lacertidae, Oman, phylogeography.