Systematic and phylogeographical assessment of the *Acanthodactylus erythrurus* group (Reptilia: Lacertidae) based on mitochondrial and nuclear DNA

M.M. FONSECA[1,2]; J.C. BRITO[1]; O. PAULO[3], M.A. CARRETERO[1] & D.J. HARRIS[1,2]

[1] *CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrário de Vairão, R. Padre Armando Quintas, 4485-661 Vairão, Portugal; mmfonseca@mail.icav.up.pt*

[2] *Departamento de Zoologia e Antropologia, Faculdade de Ciências da Universidade do Porto, 4099-002 Porto, Portugal*

[3] *Centro de Biologia Ambiental/Departamento de Zoologia e Antropologia, Faculdade de Ciências da Universidade de Lisboa, 1749-016 Lisboa, Portugal*

The systematics of the genus *Acanthodactylus* was classically based on external morphological traits, osteological characters and morphology of the hemipenises. Although the identification of species complexes has not been controversial, recognition of species within some groups is complicated by high variability of external morphology. Partial mitochondrial (12S and 16S rRNA) and nuclear (β-fibint7) sequences were analysed from 60 and 22 specimens, respectively, of the *A. erythrurus* group from North and Central Africa, and the Iberian Peninsula including previously described species: *A. blanci*, *A. guineensis*, *A. lineomaculatus*, *A. savignyi* and *A. erythrurus* with three subspecies *A. e. belli*, *A. e. atlanticus* and *A. e. erythrurus*. Several highly distinct genetic units were resolved, but with little support for relationships among them. These units did not coincide with recognised species, but showed geographic structuring. Based on our results, *A. guineensis* and *A. savignyi* should not be included in the *A. erythrurus* group and some forms, such as *A. blanci*, *A. lineomaculatus*, *A. e. atlanticus* and *A. e. belli* do not constitute monophyletic units. Diverse microevolutionary patterns due to the recent contraction/expansion phases of the habitats in North Africa associated with the high dispersal capabilities of these lizards probably are related to the complex phylogenetic patterns observed.