

**New insights on the phylogenetic position and population genetic structure of
the Critically Endangered Karpathos marsh frog *Pelophylax cerigensis***

(Amphibia: Anura: Ranidae)

ELISAVET A. TOLI^{1,*}, SOUZANNA SIARABI¹, ANASTASIOS BOUNAS¹, PANAYIOTIS
PAFILIS², PETROS LYMBERAKIS³, KONSTANTINOS SOTIROPOULOS¹

¹*Molecular Ecology & Conservation Genetics Lab, Department of Biological
Applications & Technology, University of Ioannina, 45110, Ioannina, Greece*

²*Section of Zoology and Marine Biology, Department of Biology, National and
Kapodistrian University of Athens, 15784, Athens, Greece*

³*Natural History Museum of Crete, University of Crete, 71409, Irakleio, Greece*

Running title: Phylogeny and population structure of the Karpathos frog

*Corresponding author: etoli@cc.uoi.gr

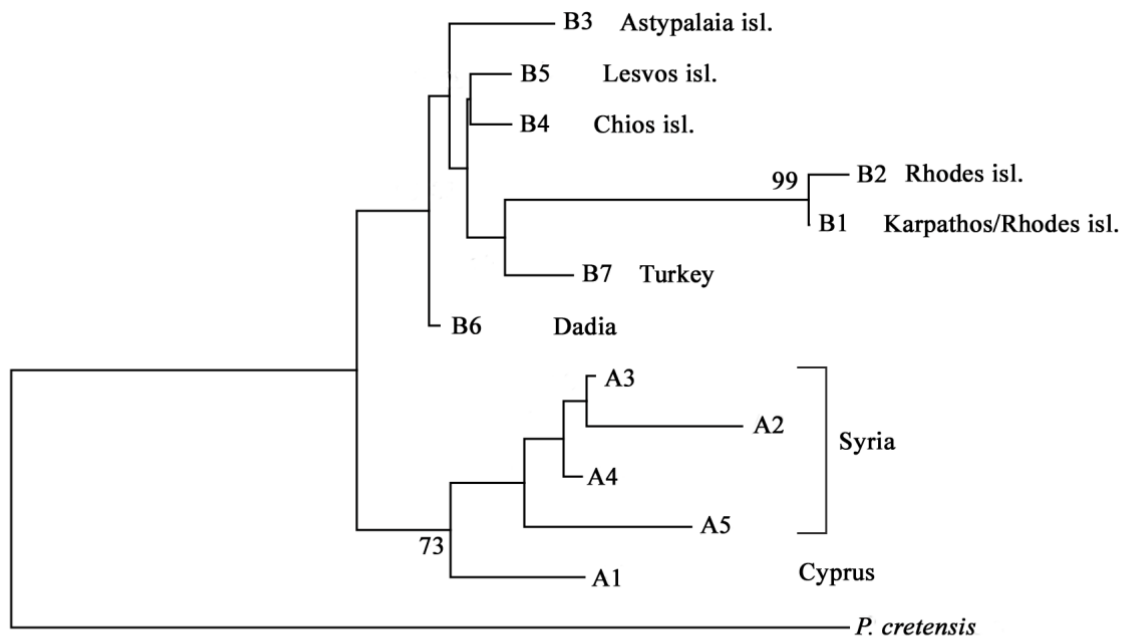
SUPPLEMENTARY MATERIAL

Table A1: Geographic location and sample size (N) of waterfrogs used in the study
(see also Fig. 1).

Locality	Species	N (cytb/AFLPs)	Haplotype	GenBank Accession number
Argoni, Karpathos	<i>P. cerigensis</i>	15/18	B-1	-
Nati, Karpathos	<i>P. cerigensis</i>	8/10	B-1	-
Rhodes isl.	<i>P. bedriagae</i>	3/-	B-1 (2) B-2 (1)	-
Chios isl.	<i>P. bedriagae</i>	1/-	B-4	DQ474138
Lesvos isl.	<i>P. bedriagae</i>	1/-	B-5	DQ474135
Dadia	<i>P. bedriagae</i>	1/-	B-6	DQ474139
Astypalaia isl.	<i>P. bedriagae</i>	2/-	B-3 (2)	DQ474140,DQ474141
Turkey, Marmaris	<i>P. bedriagae</i>	1/-	B-7	AY147957
Turkey, Antalya	<i>P. bedriagae</i>	1/-	B-7	AY014392
Syria	<i>P. bedriagae</i>	6/-	A-2 (1) A-3 (2) A-4 (1) A-5 (2)	DQ474131 DQ474132, DQ474134 DQ474129 DQ474130, DQ474133
Cyprus	<i>P. bedriagae</i>	2/-	A-1 (2)	DQ474136,DQ474137
Crete	<i>P. cretensis</i>	1/-	-	DQ474152

Table A2: Primers used to amplify gene fragments in the current study.

Preselective primers	5'-3'
Prese1Eco	GACTGCGTACCAATTCTC
T01P2	GATGAGTCCTGACCGAAC
T02P2	GATGAGTCCTGACCGACA
Selective primers	5'-3'
EcoR1P4	GACTGCGTACCAATTCTCTA
T105P2	GATGAGTCCTGACCGAACAA
T106P2	GATGAGTCCTGACCGAACAC
T204P2	GATGAGTCCTGACCGACAAT
T205P2	GATGAGTCCTGACCGACAAA



0.01

Fig. A1. Neighbor-Joining tree showing the phylogenetic relationships between the 12 detected waterfrog haplotypes. Only bootstrap values over 70% are shown on nodes. Scale bar represents substitutions per nucleotide position.