ADDITION OF A NEW LIVING GIANT LIZARD FROM LA GOMERA ISLAND TO THE PHYLOGENY OF THE ENDEMIC GENUS GALLOTIA (CANARIAN ARCHIPELAGO)

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Key words: Phylogeny, Gallotia, La Gomera, Canary Islands

The lacertid lizards of the endemic genus Gallotia (Arnold, 1973) from the Canary Islands represent one of the most important and best studied examples of island reptile radiation and evolution (Klemmer, 1976). Although there have been several attempts to reconstruct their phylogeny and evolution using molecular techniques (Thorpe, McGregor & Cumming, 1993a,b; Thorpe et al., 1994), only the most recent (González et al., 1996; Rando et al., 1997) included all known extant species of the group and could therefore be used to understand the magnitude of this island-lizard radiation. These phylogenies suggested that the ancestor of Gallotia colonized the eastern islands of Lanzarote and Fuerteventura first, moving later to the islands of Gran Canaria, Tenerife, La Gomera, La Palma and El Hierro, following an eastern-western geographic transect (González et al., 1996). Rando et al. (1997) positioned the recently discovered species G. intermedia from Tenerife (Hernández, Nogales & Martin, 2000) in the phylogeny of Gallotia (González et al., 1996) and demonstrated that it was sister to the rediscovered G. simonyi machadoi from El Hierro (Böhme & Bings, 1975; Machado, 1985; Carranza et al., 1999). In total, Rando et al. (1997) recognized five species of Gallotia at the molecular level: G. atlantica from the eastern islands of Lanzarote and Fuerteventura, G. stehlini from the central island of Gran Canaria, G. simonyi from the westernmost island of El Hierro, G. intermedia from Tenerife and G. galloti from Tenerife, La Palma, La Gomera and El Hierro. However, experiments – based on mating, viability of hybrid offspring and allozyme distances – on this last species suggested that the lizards present in La Gomera and El Hierro should be considered as a different species (G. caesaris) (López-Jurado, Mateo & Guillaume, 1997). Genetic distances between G. simonyi machadoi and G. intermedia (belonging to the ‘simonyi group’, which includes all giant lizards from the western islands) were very similar to those between G. galloti and G. caesaris (‘galloti-caesaris group’), suggesting that colonization of the western Canary Islands by each lineage was probably simultaneous.

The casual discovery of this new lizard in Tenerife led to the possibility that other giant lizards could still survive in some remote areas of La Gomera and La Palma islands. Therefore, in June 1999, we started a systematic search mainly focused on the most coastal areas of La Gomera, and fortunately, a new giant lizard was found still living in the westernmost part (Valle Gran Rey) (Valdov et al., 2000).

Hutterer (1985), based on the analysis of subfossil material from La Gomera, described two new subspecies of giant lizards, G. goliath bravoana and G. simonyi gomerana. Morphological studies (Nogales et al. 2001) indicate that this new extant lizard belongs to the ‘simonyi group’ and could correspond with the form described as G. simonyi gomerana, but with enough differences as to be treated as a full species (G. gomerana).

This finding provides an opportunity for further insight into the evolution and radiation of the genus Gallotia in the western Canary Islands. Therefore, in order to establish the phylogenetic position of this new lizard at the molecular level, we amplified and sequenced two enlarged segments of the previously analysed mtDNA gene fragments (500 bp of the 12S ribosomal RNA (rRNA) and 405 bp of the cytochrome b (cytb) using the same methods and conditions as in González et al. (1996) and Rando et al. (1997). Representatives of the Gallotia genus at specific and subspecific levels – as well as the six specimens of the new lizard captured in La Gomera – were analysed. For this, new primers were designed: L14724 (5’ TGACCTGGAAGAACCACCGTTG 3’) and H15149 (5’ AAACCTCGAGCCCTCAATGGA-TATTGTCTCTCA 3’) for cytb and L1064 (5’ TTGACACACGGAAGCTTAGAA 3’) and H1565 (5’ TTCCGGTGACGTTTACCATG 3’) for 12S rRNA fragments. The new lizard sequences were deposited in the GenBank/EMBL with accession numbers AJ272395 and AJ272396 for 12S rRNA and for cytb, respectively.

Out of the 405 bp analysed for the cytb, 144 were variable and 108 parsimony-informative. For the 12S rRNA fragment, 122 out of 500 bp were variable and 69 parsimony-informative. Parsimony analyses were performed using PAUP, version 3.1.1 (Swofford, 1993). Confidence in the nodes was determined by 1000 bootstrap replications using Branch-and-Bound searches. Phylogenetic relationships were also determined with the neighbour-joining algorithm as implemented in MEGA version 1.01 (Kumar, Tamura & Nei, 1993) using the Kimura 2N-parameters distance (Kimura, 1980). Since both methods gave similar topologies, only the results from the parsimony analysis are reported.

Phylogenetic relationships among the different representatives of the genus Gallotia based on the cytb and 12S rRNA sequences are shown in Figs. 1A and 1B respectively. Discrepancies at the specific level between both phylogenies commented upon in our previous arti-
The number of differences between taxa within the group (20 and 9 substitutions for cytb and 12S rRNA, respectively) or by the Kimura 2N-parameters distance (Kimura, 1980) (0.052 ± 0.011 and 0.023 ± 0.006 for cytb and 12S rRNA, respectively), is always lower than that found among subspecies of the ‘galloti-caesaris’ group (33 and 25 substitutions; 0.092 ± 0.017 and 0.053 ± 0.011, for cytb and 12S rRNA, respectively), suggesting that the ‘galloti-caesaris’ radiation could predate that of simonyi. Nevertheless, the existence of a common ancestor of the ‘simonyi’ and galloti-caesaris groups,’ suggested by Rando et al. (1997), is supported by the fact that both conform to a monophyletic group (Fig. 1B).

Finally, the null variation observed for both fragments among the only six individuals of G. gomerana captured after four months of intensive trapping, seems to indicate that this lizard is in danger of extinction. In the last twenty-five years, living giant lizards from the ‘simonyi’ group have been found in El Hierro, Tenerife and La Gomera; La Palma is currently the only western Canary Island where their presence is unknown. In this island giant fossil bones have been recorded (see Bischoff, 1998) but, after prospecting 57 suitable localities for its presence, we have not yet succeeded in finding living animals.

Acknowledgements. We would like to thank G. M. Hewitt for his critical reading of the manuscript and our colleagues from the Departments of Genetics and Zoology, particularly V. M. Cabrera and A. Martin. We also thank an anonymous referee for his useful comments and suggestions.

REFERENCES

FIG. 1. Phylogenetic relationships among the Canary endemic lizard genus Gallotia and one outgroup, based on cytochrome b (A) and 12S rRNA (B) partial sequences. Numbers on branches indicate the percentage of bootstrap support. The new branch is highlighted with bold lines. Psammomodromus sequences for cytb and 12S rRNA have been taken from GenBank (Accession numbers: AF206535 and AF206588, respectively) (Fu, 2000).

G. gomerana

G. steinhil

Psammomodromus

G. atlantica

G. galloti palmae

G. galloti esenrauti

G. galloti galloti

G. caesaris gomerae

G. caesaris caesaris

G. intermedia

G. simonyi

G. gomerana

A

B

12S rRNA, measured as the maximum number of differences between taxa within the ‘simonyi group’ (20 and 9 substitutions for cytb and 12S rRNA, respectively) or by the Kimura 2N-parameters distance (Kimura, 1980) (0.052 ± 0.011 and 0.023 ± 0.006 for cytb and 12S rRNA, respectively), is always lower than that found among subspecies of the ‘galloti-caesaris’ group (33 and 25 substitutions; 0.092 ± 0.017 and 0.053 ± 0.011, for cytb and 12S rRNA, respectively), suggesting that the ‘galloti-caesaris’ radiation could predate that of simonyi. Nevertheless, the existence of a common ancestor of the ‘simonyi’ and galloti-caesaris groups,’ suggested by Rando et al. (1997), is supported by the fact that both conform to a monophyletic group (Fig. 1B).

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Accepted: 6.7.01


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Page 171, left column, line 23: Rando et al. (1997) recognised four species and not five.

Page 171, left column, lines 35-36: *Gallotia simonyi* not *Gallotia simonyi machadoi*. 