

Contingency and Determinism in Replicated Adaptive Radiations of Island Lizards



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Science, New Series, Vol. 279, No. 5359 (Mar. 27, 1998), 2115-2118.

Stable URL:

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Science is currently published by American Association for the Advancement of Science

both T1 and T2 transgenic plants (Fig. 4C). The amount of NPTII protein was not affected by infection in T3 plants, in which the *NPTII* transgene does not share homology with the CaMV promoter. The distribution of NPTII protein between dark green island and chlorotic vein border tissue of T1 transgenic plants (Fig. 4C) reflected that of GUS activity (Fig. 2B).

Suppression of the *NPTII* gene might have occurred through interference from the adjacent *GUS* gene. Alternatively, CaMV infection might result in host regulation of the 35S RNA promoter. Therefore, we tested the effects of CaMV infection on expression of the *GUS* transgene of the T3 construct (Fig. 1A), for which viral homology is

tipathogenic or whether it is more broadly related to regulation of highly expressed genetic elements.

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10. Total nucleic acid was extracted as described (11). CaMV DNA and RNA were analyzed by Southern and Northern blotting, respectively, with the appropriate probes.
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13. Nuclei were isolated as described (3). Incorporation of uridine 5'-[³²P]triphosphate (DuPont Biotechnology Systems) was determined by probing 1 μg of the appropriate DNA samples immobilized as slots on Hybond-N⁺ membranes (Amersham).
14. Plant protein was extracted and NPTII was measured with an enzyme-linked immunosorbent assay (CP Laboratories).
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16. Leaf disks (12 mm in diameter) were collected and treated as described (12). A. Jefferson, T. A. Ke...

Table 1. Hypotheses tested with DNA sequence data. A significant result denotes rejection of the stated hypothesis. *D* is the difference in length between the most parsimonious tree (8889 steps) and the tree constrained to conform to the stated hypothesis. *T_s* is the test statistic for the Wilcoxon signed-ranks test. *n* is the number of characters that differed

in numbers of changes on the two trees. *Z* is the normal approximation when *n* > 100 (25). "Difference" is the difference in negative log likelihoods between the maximum likelihood tree (-ln *L* = 41,059.9) and the tree constrained to conform to the stated hypothesis. *t* is the Student's *t* test statistic.

Hypothesis	<i>D</i>	<i>T_s</i>	<i>n</i>	<i>Z</i>	Parsimony <i>P</i> value	Likelihood difference	<i>t</i>	Likelihood <i>P</i> value
Monophyly of ecomorph class								
Crown-giant	120	5,350	229	7.8	<0.001	424.2	7.5	<0.001
Grass-bush	165	17,647	339	6.2	<0.001	633.8	8.5	<0.001
Trunk	42	2,016	113	3.4	<0.001	110.0	2.5	0.014
Trunk-crown	201	7,921	289	9.1	<0.001	771.0	11.6	<0.001
Trunk-ground	175	22,927	382	6.3	<0.001	546.5	11.4	<0.001
Twig	99	12,882	270	4.2	<0.001	384.0	6.6	<0.001
Shortest tree with								
16 ecomorph transitions	5	2,706	106	0.4	0.683	51.1	1.4	0.171
15 ecomorph transitions	25	6,444	172	1.5	0.128	103.1	2.7	0.007
14 ecomorph transitions	48	7,803	198	2.5	0.011	212.3	4.5	<0.001

habitat use. The same set of "ecomorphs"—species specialized to use particular structural microhabitats—occurs on each island, except that two ecomorphs are absent from Jamaica and one from Puerto Rico (9).

We measured six morphometric charac-

teristics of ecomorph classes have occurred (Table 1) (19, 20). Although similar sets of ecomorphs have evolved independently on

each island, the sequence by which they have evolved differs among islands (Fig. 1C) (21).

A

One hypothesis to explain the repeated evolution of the same ecomorph types is that the diversity of morphological variants

mass; number of subdigital lamellae on the second and third phalanges of pedal digit IV; and snout-to-vent length (svl), forelimb length, hindlimb length, and tail length. Mean values were used for each species. To remove the effects of body size, interspecific covari-

Hedges, *Caribb. J. Sci.* **26**, 7 (1990)]. Hence, depending on the phylogenetic relationships of these two species, we may underestimate by two both the number of evolutionary origins of ecomorphs and the instances in which the same ecomorph evolved.

parsimonious tree conforming to each of the 15 possible phylogenetic topologies for the four ecomorphs (in the case of the two twig anoles on Hispaniola, we used *A. insolitus* because *A. sheplani* is the sister taxon of Cuban twig anoles and is nested within a clade of Cuban species) using the "backbone constraints" option in PAUP*, which constrains the relationships of a subset of the taxa but allows the remaining taxa to occur anywhere on the tree (that is, the subset of constrained taxa does not necessarily form a monophyletic group, but the relationships among these taxa must conform to the

constraint). We compared each of these trees to the most parsimonious tree (Fig. 1B) using the Wilcoxon signed-ranks test. In addition, we compared the maximum-likelihood tree with each constraint tree using the Kishino-Hasegawa test. Each of the 15 possible ecomorph topologies was rejected for at least one island. Hence, we conclude that the topology of ecomorph evolution differed among islands. In addition, when ancestral ecomorph states were reconstructed with parsimony, each island exhibited a different order of ecomorph evolution.

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26. This work was supported by NSF, the National Geographic Society, and the David and Lucile Packard Foundation.

2 September 1997; accepted 10 February 1998