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 limited to the CaMV 35S RNA promoter sequence. CaMV infection suppressed GUS expression in T3 transgenic plants with the same symptomatic pattern as that in T1 transgenic plants (Fig. 1C). However, silencing in T3 transgenic plants was not likely mediated by posttranscriptional mechanisms because the construct lacked viral RNA homology. Nuclear run-on experiments revealed that transcription of the T3 GUS transgene was inhibited in infected plants, despite concurrent transcription of the CaMV minichromosome (Fig. 4A). We suggest that transcriptional silencing of the 35S RNA promoter in the CaMV minichromosome does not occur in the presence of posttranscriptional silencing. However, transcriptional suppression of the CaMV 35S RNA promoter in the T3 construct suggests that viral transcription could potentially be down-regulated in those infections that do not result in recovery from symptoms as in B. napus. Such regulation could explain the differential accumulation of CaMV in chlorotic and dark green tissue observed in the absence of posttranscriptional silencing (15).

Thus, plants respond to pathogen invasion by regulating pathogen gene expression, apparently at both transcriptional and posttranscriptional levels. Posttranscriptional suppression of viral genes results in posttranscriptional cosuppression of transgenes that share sequence homology with the virus. Sequences homologous to the viral promoter can be silenced at the transcriptional level. Posttranscriptional suppression of gene expression appears to take precedence over transcriptional regulation, possibly by preventing transcriptional suppression of the same gene, thereby linking cytoplasmic and nuclear gene regulatory mechanisms.

Most gene silencing phenomena that have been described in plants occur as a result of transformation with transgenes (5, 9). Gene silencing can also be elicited by viruses in the absence of transgenes (3, 4). It is not clear whether this response is antipathogenic or whether it is more broadly related to regulation of highly expressed genetic elements.

REFERENCES AND NOTES

8. Infection of B. napus was established by mechanical inoculation of seedlings (second true leaf) with 1 μg of CaMV virus (isolate Cabb B-JI) in 10 μl of 10 mM sodium phosphate buffer (pH 7.0) containing Celite (Celite Corp.) abrasive. Plants were propagated in a containment greenhouse supplemented with illumination to 16 hours per day at 18° to 22°C.
10. Total nucleic acid was extracted as described (17). CaMV DNA and RNA were analyzed by Southern and Northern blotting, respectively, with the appropriate probes.
13. Nuclei were isolated as described (3). Incorporation of uridine 5′-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).
16. Leaf disks (12 mm in diameter) were collected and treated as described [R. A. Jefferson, T. A. Ka

17. In situ hybridization to detect CaMV was performed as described (15) with the same leaf disks as those used for histochemical detection of GUS activity.
18. We thank N. Owen and C. Jones for producing transgenic lines. J. Jones for transformation constructs, and A. Langara for advice on nuclear run-on assays. This work was supported by the U.K. Biotechnology and Biological Sciences Research Council and covered by license PHF 1491/982/34 of the Ministry of Agriculture, Fisheries and Food.

Contingency and Determinism in Replicated Adaptive Radiations of Island Lizards

Jonathan B. Losos,* Todd R. Jackman, Allan Larson, Kevin de Queiroz, Lourdes Rodrı́guez-Schettino

The vagaries of history lead to the prediction that repeated instances of evolutionary diversification will lead to disparate outcomes even if starting conditions are similar. We tested this proposition by examining the evolutionary radiation of Anolis lizards on the four islands of the Greater Antilles. Morphometric analysis indicates that the same set of habitat specialists, termed ecomorphs, occurs on all four islands. Although these similar assemblages could result from a single evolutionary origin of each ecomorph, followed by dispersal or vicariance, phylogenetic analysis indicates that the ecomorphs originated independently on each island. Thus, adaptive radiation in similar environments can overcome historical contingencies to produce strikingly similar evolutionary outcomes.

The theory of historical contingency proposes that unique past events have a large influence on subsequent evolution (1–3). A corollary is that repeated occurrences of an evolutionary event would result in radically different outcomes (4). Indeed, faunas and floras that have evolved in similar environments often exhibit more differences than similarities (5–7). These differences in evolutionary outcome probably result from clade-specific factors that cause taxa to respond to similar selective factors in different ways, as well as from unique historical events and subtle environmental differences in the different areas (2, 8). Here we show that such factors will not always lead to disparate outcomes. Anolis lizards are a dominant element of the Caribbean fauna. On each of the islands of the Greater Antilles (Cuba, Hispaniola, Jamaica, and Puerto Rico), lizard assemblages are composed of species that differ in

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2115

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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 characteristics that are closely linked to habitat use (10, 11) for members of each ecomorph class from each island to investigate whether the ecomorphs constitute objectively recognizable classes (12). Our analyses reveal distinct ecomorph classes; members of an ecomorph class are more similar to other members of that class from different islands than they are to members of different ecomorph classes from their own island (Fig. 1A) (13).

The presence of the same set of ecomorphs on each island suggests that either ecomorphs evolved only once and then, by colonization or vicariance, occupied all four islands, or that each ecomorph evolved independently on all four islands. Because six ecomorph classes exist (crown-giant, grass-bush, trunk, trunk-crown, trunk-ground, and twig; the classes are named for the microhabitat that constituent species normally use), the single-evolution hypothesis predicts that only five instances of the evolution of new ecomorphs have occurred (assuming that one ecomorph is ancestral). By contrast, the recurring evolution hypothesis (9) predicts that none of the ecomorph classes form a monophyletic group and that 17 to 19 evolutionary transitions between 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).

Phylogenetic analysis based on mitochondrial DNA sequences (15, 16) for 55 species (17) indicates that, with two exceptions, members of the same ecomorph class from different islands are not closely related (Fig. 1B). Statistical analyses (18) indicate that none of the ecomorph classes constitutes a monophyletic group relative to members of the other classes and that at least 17 evolutionary transitions among 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).

![Fig. 1.](image)

**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.

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>$D$</th>
<th>$T_s$</th>
<th>$n$</th>
<th>$Z$</th>
<th>Parsimony $P$ value</th>
<th>Likelihood difference</th>
<th>$t$</th>
<th>Likelihood $P$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monophyly of ecomorph class</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Crown-giant</td>
<td>120</td>
<td>5,350</td>
<td>229</td>
<td>7.8</td>
<td>$&lt;0.001$</td>
<td>424.2</td>
<td>7.5</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Grass-bush</td>
<td>165</td>
<td>17,647</td>
<td>339</td>
<td>6.2</td>
<td>$&lt;0.001$</td>
<td>633.8</td>
<td>8.5</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Trunk</td>
<td>42</td>
<td>2,016</td>
<td>113</td>
<td>3.4</td>
<td>$&lt;0.001$</td>
<td>110.0</td>
<td>2.5</td>
<td>0.014</td>
</tr>
<tr>
<td>Trunk-crown</td>
<td>201</td>
<td>7,921</td>
<td>289</td>
<td>9.1</td>
<td>$&lt;0.001$</td>
<td>771.0</td>
<td>11.6</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Trunk-ground</td>
<td>175</td>
<td>22,927</td>
<td>382</td>
<td>6.3</td>
<td>$&lt;0.001$</td>
<td>546.5</td>
<td>11.4</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Twig</td>
<td>99</td>
<td>12,882</td>
<td>270</td>
<td>4.2</td>
<td>$&lt;0.001$</td>
<td>384.0</td>
<td>6.6</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Shortest tree with 16 ecomorph transitions</td>
<td>5</td>
<td>2,706</td>
<td>106</td>
<td>0.4</td>
<td>0.683</td>
<td>51.1</td>
<td>1.4</td>
<td>0.171</td>
</tr>
<tr>
<td>15 ecomorph transitions</td>
<td>25</td>
<td>6,444</td>
<td>172</td>
<td>1.5</td>
<td>0.128</td>
<td>103.1</td>
<td>2.7</td>
<td>0.007</td>
</tr>
<tr>
<td>14 ecomorph transitions</td>
<td>48</td>
<td>7,803</td>
<td>198</td>
<td>2.5</td>
<td>0.011</td>
<td>212.3</td>
<td>4.5</td>
<td>$&lt;0.001$</td>
</tr>
</tbody>
</table>
One hypothesis to explain the repeated evolution of the same ecomorph types is that the diversity of morphological variants that can be produced by anoles is constrained to these ecomorphs. However, the existence of several Greater Antillean species, usually restricted to montane areas (9), and many mainland species (22) that are not members of any of the ecomorph classes shows that morphological diversification among anoles is not constrained to produce only members of these ecomorph classes. Rather, the recurring evolution of ecologically and morphologically similar species in these replicate adaptive radiations suggests that adaptation, rather than constraint, is responsible for the predictable evolutionary responses of Anolis lizards.

The phylogenetic analysis reveals only two cases in which an ecomorph has evolved more than once on a single island. Interspecific competition, which is intense among anoles (23) and may drive their adaptive radiation (9, 24), is probably responsible; once an ecomorph niche is filled on an island, other species are excluded from utilizing that niche. Thus, the importance of historical contingency depends on the frame of reference: Among islands, it has little discernible effect in that the same ecomorphs evolve on each island, whereas within each island, prior evolutionary events limit the options available to particular species and thus determine the directions in which evolution can proceed.

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Monoallelic Expression of the Interleukin-2 Locus

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The lymphokine interleukin-2 (IL-2) is responsible for autocrine cell cycle progression and regulation of immune responses. Uncontrolled secretion of IL-2 results in adverse reactions ranging from anergy, to aberrant T cell activation, to autoimmunity. With the use of fluorescent in situ hybridization and single-cell polymerase chain reaction in cells with different IL-2 alleles, IL-2 expression in mature thymocytes and T cells was found to be tightly controlled by monoallelic expression. Because IL-2 is encoded at a nonimprinted autosomal locus, this result represents an unusual regulatory mode for controlling the precise expression of a single gene.

IL-2 is a growth factor important in the regulation and differentiation of lymphocytes and natural killer cells (1). Produced by a subpopulation of activated T cells, IL-2 also plays a pivotal role in the generation of an adoptive immune response. Decreased secretion or the complete absence of IL-2 in humans is associated with primary and secondary immunodeficiencies (2). Mice homozygous for an IL-2 null mutation (IL-2–/–) have a compromised immune system with alterations of both cellular and humoral functions (3). Overproduction of IL-2 results in an impaired immune response to autoimmunity, breaking of clonal anergy, and suppression of certain T cell functions (4). IL-2 expression, therefore, is firmly controlled by multiple signaling pathways emanating from the T cell receptor and antigen-independent coreceptors (5). These signals regulate the transcriptional control of ubiquitous and T cell-specific factors, which transactivate transcription of the gene encoding IL-2 in vivo through binding to the promoter and enhancer sequences using an all-or-nothing mechanism (5). Coreceptors also transduce signals that stabilize IL-2 mRNA (6).

The number of functional IL-2 alleles may also determine the amount of IL-2 produced. Therefore, we investigated whether T cells heterozygous for the IL-2 null mutation produce less IL-2 than wild-type T cells. We stimulated CD4+ T cells purified from wild-type and heterozygous mice. The amount of IL-2 produced by concanavalin A (Con A)-treated IL-2–/– T cells was decreased by half when compared with that produced by T cells from wild-type mice (Fig. 1). As expected, Con A stimulation of IL-2–/– T cells did not result in detectable IL-2 secretion.

Was each heterozygous CD4+ T cell producing only half of the amount of IL-2 produced by wild-type cells, or were only half of the CD4+ T cells secreting amounts of IL-2 comparable to that secreted by wild-type T cells? Concurrent transcription from both (that is, the mutant and the wild-type) alleles of the IL-2 gene would lead to the first result, whereas the latter result would be obtained if allele-specific expression occurred from only one of the two copies of the IL-2 gene. To distinguish between these two mutually exclusive models, we determined IL-2 secretion at the single-cell level. Mature CD4+ thymocytes and CD4+ peripheral T cells were stimulated with Con A and subsequently stained for the presence of IL-2 (7). About half of the CD4+ T cells from 3- to 4-week-old heterozygous mice stained positively for IL-2 (Fig. 2, A and B, left). In agreement with these data, limiting dilution assays showed that the relative frequency of IL-2–secreting CD4+ T cells was diminished by a third to a half in heterozygous mice in comparison with...