Community Assembly Through Adaptive Radiation in Hawaiian Spiders

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Community assembly arising through adaptive radiation are generally regarded as unique, with speciation and adaptation being quite different from immigration and ecological assortment. Here, I use the chronological arrangement of the Hawaiian Islands to visualize snapshots of evolutionary history and stages of community assembly. Analysis of an adaptive radiation of habitat-associated, polychromatic spiders shows that (i) species assembly is not random; (ii) within any community, similar sets of ecomorphs arise through both dispersal and evolution; and (iii) species assembly is dynamic with maximum species numbers in communities of intermediate age. The similar patterns of species accumulation through evolutionary and ecological processes suggest universal principles underlie community assembly.

Community assembly has intrigued biologists for decades (1), leading to a sophisticated understanding of the ecological parameters that dictate community membership (2). The role of evolution in shaping communities is also well appreciated (3, 4), although the steps through which communities are assembled as a result of evolutionary processes have been enigmatic. Adaptive radiations on remote islands provide opportunities to study multiple communities, each comprising closely related organisms—a feature that has produced insights into evolutionary patterns of species composition and number (5). In particular, two patterns have emerged: (i) A predictable number of species can exist for a given area on remote islands, apparently driven by higher rates of speciation on larger islands (6); and (ii) the end-product of adaptive radiation is often a nonrandom set of species, with lineages diversified in such a way that the same set of ecomorph types occur on each island (7, 8). These findings suggest that evolution on more remote islands can act in a manner analogous to immigration on less remote islands, giving rise to similar spe-
cies numbers and communities. What has been missing is knowledge of the historical processes that underlie these present-day patterns. Volcanic “hot spot” archipelagos provide a natural experiment for observing processes of adaptive radiation. In the Hawaiian Islands, the extreme isolation, topographical diversity, and chronological series of islands [from Kauai, formed 5 million years ago (Ma), to Hawaii, formed <1 Ma], illustrate different stages in an adaptive radiation, thus revealing the historical series of events that lead to the present.

The largest spider radiation in the Hawaiian Islands belongs to the genus *Tetragnatha* (Tetragnathidae), which includes several closely related lineages. The best known lineage is the monophyletic “spiny leg” clade of 16 species that have abandoned web-building, developed long spines along their legs, and hunt through active pursuit of prey (9, 10). Species of spiny leg *Tetragnatha* spiders exhibit four distinct types (ecomorphs) of different color and size that can be mapped directly to one of four ecological roles (Fig. 1) (11). The “green” ecomorph is an actively moving, leaf-dwelling spider that feeds mostly on small flying insects.

The “maroon” ecomorph is mostly moss-dwelling and feeds on weakly flying insects. The “large brown” ecomorph is slow-moving, associated with tree bark, and feeds largely on Lepidoptera larvae. The “small brown” ecomorph is actively moving, inhabits twigs, and feeds on very small flying insects. I investigated first the ecological roles of different spider species, then the evolutionary origins of the ecomorphs, and finally the dynamics of community assembly, using a phylogenetic hypothesis of relationships in the context of the chronological history of the Hawaiian Islands.

Within any single community, two to four different ecomorphs co-occur (9, 10). Similar sets of the different ecomorphs occur in most native habitats, regardless of volcano age, and the assemblage of species on each island is highly significantly nonrandom (Fig. 2). Not all localities have all ecomorphs, but at any given site, there is never more than one species representing a given ecomorph, and different species of the same ecomorphs have distinct parapatric distributions. The finding that similar ecomorphs never co-occur is most apparent on East Maui. Here, each of the ecomorphs is represented across most of the northeast slope, yet the species composition of the array of four ecomorphs changes markedly between locations.

Historical hypotheses were generated to determine whether ecomorphs evolved once and spread among volcanoes and islands by dispersal, or whether ecomorphs evolved multiple times and converged on similar morphologies and ecological functions. I compiled two data sets consisting of DNA sequences (from three mitochondrial gene regions) and allozymes. Analyses of both showed that species clustered within islands, indicating multiple independent evolutionary origins of ecomorphs (Fig. 3). The most ubiquitous green ecomorph may have evolved either (i) once at the base of the clade with multiple (at least four) losses, or (ii) at least three times, once on each of the other islands, Kauai (*Tetragnatha kauaiensis*) and Oahu (*T. tantalus* and *T. polychromata*), as well as on the Maui, Molokai, and Lanai complex of islands, referred to as Maui Nui (*T. brevignatha*, *T. macracantha*, and *T. waikamoi*). Likewise, the maroon ecomorph has evolved independently on Oahu (*T. perreirai*) and Maui Nui (*T. kamakou*); both species are closely related to a green ecomorph with which they co-occur. One of the small brown ecomorphs (*T. restricta*) has also evolved independently on Maui. Yet, species formation is not always associated with change in ecological role, because some species with the same ecomorph have dispersed between islands. For example, the small brown species are mostly related to species of the same ecomorph on other islands. The large brown ecomorph is unusual in that,
island. This is a common feature of most of the oldest (Kauai) to the youngest (Hawaii) shows progression down the island chain from 12S ribosomal DNA, and 16S ribosomal DNA, and multiple nuclear loci (allozymes) (Phylogeny of the spiny leg clade based on combined mitochondrial cytochrome oxidase I, Fig. 3.

Tetragnatha leg in the Caribbean (different localities has occurred in cichlid fish and repeated evolution of similar ecomorphs in extinctions. Extensive within-locality proliferation without speciation. Ecomorph from one locality to another with or without speciation.

The similarity of ecomorphs, often with independent origins on different islands, parallels similar observations of other adaptive radiations. Extensive within-locality proliferation and repeated evolution of similar ecomorphs in different localities has occurred in cichlid fish in the African Great Lakes (sticklebacks in Canadian glacial lakes (Anolis lizards in the Caribbean (7). For the lineage of spiny leg Tetragnatha, the phylogenetic analysis also shows progression down the island chain from the oldest (Kauai) to the youngest (Hawaii) island. This is a common feature of most of the Hawaiian taxa that initially colonized the islands ≥5 Ma (14, 15). Because the spiders have diversified within islands, each island displays a series of small adaptive radiations of spiders that reflect time periods dating from 5 Ma to the present. These historical snapshots provide insight into the assembly of species in a community over evolutionary time.

Comparison of patterns of species composition on the youngest Hawaiian island to the oldest shows that the adaptive radiation is dynamic. The most recent stage, as exemplified on the youngest island, is not representative, with only three species of spiny leg Tetragnatha endemic to Hawaii Island; the remaining three are shared with East Maui. This distribution might suggest that, over time, these Hawaii Island populations would diverge in allopatry from conspecifics on Maui, with each ecomorph on Hawaii unchanged from its closest relative on Maui. However, this prediction is not supported by observations from older islands, where single colonizations resulted in species proliferation (e.g., one colonization event gave rise to at least five species on Maui and three species on Oahu), and ecomorphs have evolved largely independently within islands (Fig. 3).

After Hawaii Island, East Maui illustrates the next stage in the chronology of adaptive radiation. Here, a large number of species (multiples of the same ecomorph) exist in allopatry on this relatively young (formed 0.8 Ma) volcano, suggesting that, at least initially, there may be no limit to the number of species that can form subsequent to successful colonization of a given land mass. Considering the situation on Hawaii and Maui together, species accumulation in the initial stages of adaptive radiation seems to involve a “race” between in situ evolution of species, coupled with change in ecomorph type, and dispersal from older islands and subsequent speciation in allopatry without change in ecomorph type. This scenario implies that when population numbers are low (as they are during colonization of new habitats), competition among species is minimal, and there is little impediment to the accumulation of more species. The different older islands each have similar numbers and ecological sets of species, perhaps because of competition after accrual of species. In other words, the community may undergo fine tuning after initial species proliferation, as a result of inter- and intraspecific competition for resources (16). Such a process has also been proposed to explain numbers of species in a radiation of weevils in an isolated sub-Antarctic archipelago (17).

A markedly similar pattern of species buildup and subsequent decline was observed in ecological studies of mangrove islets off the Florida
Defining the Epithelial Stem Cell Niche in Skin

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Many adult regenerative cells divide infrequently but have high proliferative capacity. We developed a strategy to fluorescently label slow-cycling cells in a cell type-specific fashion. We used this method to purify the label-retaining cells (LRCs) that mark the skin stem cell (SC) niche. We found that these cells rarely divide within their niche but change properties abruptly when stimulated to exit. We determined their transcriptional profile, which, when compared to progeny and other SCs, defines the niche. Many of the 100 messenger RNAs preferentially expressed in the niche encode surface receptors and secreted proteins, enabling LRCs to signal and respond to their environment.

Epidermis and its appendages undergo continuous renewal and maintain reservoirs of multipotent SCs whose descendants are organized spatially and temporally. The epidermal basal layer (BL) contains putative SCs in addition to the transiently amplifying (TA) cells, which give rise to terminally differentiating suprabasal layers. The BL and the hair follicle outer root sheath (ORS) are contiguous and biochemically similar. In the hair bulb, the dermal papilla maintains contact with matrix TA cells until they differentiate to form the inner root sheath and hair shaft. Follicles periodically undergo cycles of growth (anagen), destruction (catagen), and rest (telogen). The zone between noncycling and cycling segments is a SC niche, the ORS bullying (4, 5).

Multipotent epithelial SCs with high proliferative potential reside in the bulge (6, 7). The bulge contains the majority of infrequently cycling, label-retaining cells (LRCs), which can respond to anagen DP signals to regenerate the follicle. After wounding or transplantation, bulge cells give rise to epidermis, follicles, and sebaceous glands. Additionally, when dissected from rat whiskers and cultured, bulge cells yield more colonies than other follicle segments.

It is not known what features define this specialized SC niche, what its interactions with bulge LRCs are, and whether all LRCs are SCs. To begin to address these issues, we devised a strategy based on the prediction that bulge SCs are uniquely both slow-cycling and active for a keratinocyte-specific promoter. With this strategy, we purified and characterized bulge LRCs and related keratinocyte progeny in the BL and ORS. Analyses of their transcriptional profiles reveal the skin LRC mRNAome; some of these mRNAs are found in SCs of other tissues, whereas others specify the unique environment of the skin SC niche.

To mark infrequently cycling cells of adult skin epithelium, we engineered transgenic mice to express histone H2B–green fluorescent protein (GFP) controlled by a tetracycline-responsive regulatory element (TRE). A tightly regulated TRE-mCMV-H2B-GFP founder animal was crossed with mice harboring a keratin 5 (K5) promoter-driven tet repressor–VP16 transgene (9), and offspring were selected for doxycycline-controlled regulation restricted to skin epithelium (Fig. 1A). Without Tet, backskin