Unravelling the mystery of rampant species formation on volcanic islands

How do new species of plants and animals arise? And why do clusters of divergent endemic species evolve so rapidly on remote oceanic archipelagoes such as the Hawaiian and Galápagos Islands? These questions have intrigued biologists since the time of Darwin. For the few chance strays that survive trans-oceanic transport and confront inhospitable volcanic habitats to establish a fledgling population on an actively growing island, extinction is highly likely, given the harsh environment, and low genetic variation in these founding propagules. And yet, rare pioneers have led to astounding levels of biodiversity, with lineages of hundreds, or even a thousand or more, related species stemming from a single introduction a few million years ago. The species richness of terrestrial groups on isolated islands is thus unexpected and paradoxical. How and why are so many new genetic types generated on volcanic islands?

I postulate that stress suffered by colonizers in unstable volcanic habitats triggers “genome shock” that ultimately leads to genomic reorganization and production of novel genetic variants. The key components of the genome activated by stress are mobile or *transposable elements* (TEs), sometimes referred to as “jumping genes.” These DNA sequences (earlier thought of as selfish or parasitic DNA), are ubiquitous in genomes, comprising >50% of the human genome, for example. Upon active mobilization, their random insertion into gene coding regions disrupts functioning and is typically deleterious. Thus, TEs are usually tightly controlled and kept dormant by a variety of processes to protect genomes from excessive damage.

Previous considerations of mechanisms underlying the rapid evolution and adaptive divergence observed on volcanic islands have overlooked the high levels of physiological and genomic stress experienced by founder populations colonizing newly available but still unstable volcanic habitats. Stress results from both environmental (abiotic) and genetic (biotic) factors. Organisms close to molten lava flows suffer heat stress that unravels their proteins and DNA, among other effects. Chemicals in volcanic gas plumes are toxic, and induce cellular and oxidative stress. The initially small population sizes force inbreeding, the main source of biotic stress incurred by colonizing populations.

Over the tens of thousands of years of volcanism that builds up an island above the ocean’s surface, lava flows repeatedly cause local extinction and fragmentation of populations, forcing population isolates through recurrent genetic bottlenecks and repetitive cycles of biotic and abiotic stress. Each episode of genomic stress disrupts the mechanisms that suppress TE activity, unleashing them to proliferate in a burst of transposition (TE mobilization), with replicated copies spreading to new chromosomal locations within the genome. Each stress-induced period of genomic instability is limited, once silencing mechanisms come into action to restore genome stability. Nonetheless, the recurring transposition bursts of hundreds of different TEs in the genome leave a lasting imprint, generating a host of novel mutations in both coding and noncoding regions.

Because TEs possess regulatory sequences, expression of genes near their insertion sites is affected. Such regulatory mutations can be harmful, neutral, or beneficial. These provide the fodder for accelerated evolution via natural selection, sexual selection, and genetic drift, a chance process likely in small populations.

My hypothesis proposes that a central driver of the rapid evolutionary diversification and speciation on volcanic islands is the reactivation of TEs in genomes of new arrivals to unstable volcanic habitats. Repeated waves of stress-induced transposition bursts generate innumerable mutations and rewire genomic regulatory systems, setting the stage for formation of evolutionarily novel species with dramatically altered morphologies, ecologies, and behaviors. Currently available data are consistent with predictions of the hypothesis, but it remains to be tested empirically via whole genome sequencing and bioinformatic analyses of test organisms.

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Publication

Profuse evolutionary diversification and speciation on volcanic islands: transposon instability and amplification bursts explain the genetic paradox.
Craddock EM
Biol Direct. 2016 Sep 6