

What can we learn from the microbial communities on cheese?

Very little is known about how microbes behave in the context of a community. Since studies have recently demonstrated that microbial communities living in and on the human body greatly impact our health, the importance of understanding how microbial communities function and how we can manipulate them is now widely recognized. By studying microbial communities that we already know how to manipulate, like those on cheese, we may readily find answers to questions about which forces are most important in determining succession of species within a microbial community, how species cooperate or compete within a community, and how whole communities respond to perturbations, like invasion by pathogenic species. The adaptation of cheese communities into a laboratory model system can help to delineate the principles that govern microbial communities.

Why will cheese be such a good model system for studying microbial communities? A good model system must be simple, easily cultivated in the lab, and reproducible. The rind communities that form a biofilm on the surface of an aged cheese exhibit all of these properties. Because cheese communities have relatively few members, linking species to function will be experimentally practical. Since these communities grow on cheese, a defined substrate, their natural habitat is easily reproduced, and member species may be isolated in the lab. This will make it possible to reconstruct whole communities and observe their development. The simplicity, culturability, and reproducibility of cheese microbial communities will provide a unique, experimentally practical system that will help us understand how microbes live together.

Where can I find out more?

Kinstead, P. (2012). *Cheese and Culture: A History of Cheese and its Place in Western Civilization*. (White River Junction, VT: Chelsea Green Publishers.)

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Low genetic diversity in tepui summit vertebrates

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The Pantepui region of South America, located in southern Venezuela, northern Brazil, and western Guyana, is characterized by table mountains (tepui) made of Proterozoic (> 1.5 billion years old) sandstone — the highest reaching nearly 3 km — that are isolated from their surroundings by up to 1000 m high vertical cliffs (Figure 1A). Tepuis are among the most inaccessible places on earth (Supplemental information), and the majority of their summits have been visited less than the moon. Due to its age and topography [1,2], this region has been assumed to be an ideal nursery of speciation and a potential inland counterpart to oceanic islands [3,4]. High endemism has been reported for the flora (25% in vascular plants) and fauna (68.5% in amphibians and reptiles) of single tepuis [5,6], and an ancient origin has been postulated for some of these organisms. But, it has also been suggested that a few taxa living in habitats extending from lowlands to summits (e.g., savannah) invaded some of the more accessible tepuis only recently [6–8]. Taken at face value, the overall timing and extent of biotic interchange between tepui summits has remained unstudied. Here, we show that recent faunal interchange among currently isolated tepui summits has been extensive, and affected even taxa living in some of the most tepui-specific habitats and on the most inaccessible summits.

We used a comprehensive sampling of five Pantepui amphibian genera (*Anomaloglossus*, *Oreophrynella*, *Pristimantis*, *Stefania* and *Tepuihyla*) and one reptile family (Gymnophthalmidae) — the most conspicuous vertebrates on tepui summits — from 17 tepuis in

the Eastern Pantepui region and surrounding uplands. If individual tepui summits were indeed reservoirs of ancient endemism, phylogenetic analyses of these taxa would identify genetically distinct populations on each tepui without close relatives elsewhere. Instead, analyses of two mitochondrial gene fragments evolving at different rates (16S rDNA and ND1 mtDNA; see Supplemental information) indicate that populations of a given species on individual summits are often closely related to those on other summits (e.g., *Oreophrynella*), or to those from the surrounding uplands (e.g., *Tepuihyla*). Uncorrected pairwise distances in both genes indicate unexpectedly low genetic divergence — as low as zero — among multiple tepui summit species or populations in five of the six groups (*Stefania* being the only exception), as well as among some summit species or populations and uplands populations described as distinct species (Figure 1B; Supplemental information). Some of the lowest genetic distances are observed for populations that are currently recognized as distinct species and show striking phenotypic differences. For instance, the inconspicuously black ventral coloration in the toad *Oreophrynella nigra* (Yuruani-tepui and Kukanan-tepui) differs markedly from the potentially aposematic yellow–orange–black color contrasts in *O. quelchii* (Mt. Roraima and Wei Assipu-tepui), despite pairwise distances of 0.63–0.95% in ND1 and zero in 16S between both taxa. The absence of genetic uniqueness suggests that the majority of these summit populations were only recently isolated. To provide an approximate estimate of the timing of their isolation, we used a nonlinear regression analysis that corrects for substitutional saturation and the systematic underestimation of evolutionary rates in recent divergences (Supplemental information). Our analyses suggest that 10 of the 11 most inaccessible tepuis studied show evidence for one or multiple instances of gene flow with other summits or with surrounding areas as recent as the late Pleistocene–Holocene (<1.8 mya; Figure 1B).

If the tepuis are indeed as ancient as often stated, the young age of

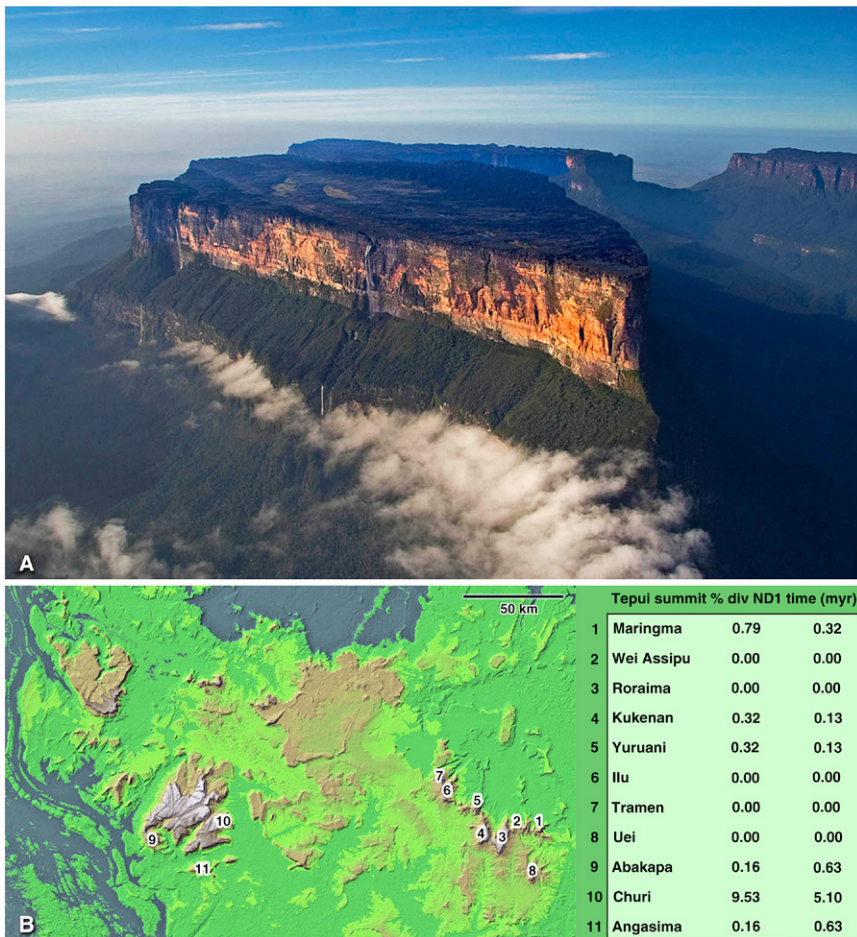


Figure 1. The tepui ecosystems. (A) Mount Roraima, an emblematic tepui. (B) Map showing part of the Eastern Pantepui region, highlighting the highest and most isolated tepuis sampled in this study (numbered from 1 to 11), and table indicating estimates of divergence time among these tepuis, or between these tepuis and the surrounding uplands, based on genetic divergences in ND1 (see Supplemental information for details).

extant summit fauna can only be explained by active dispersal among summits with subsequent extinction in the intervening uplands, e.g., during ice ages, or by passive dispersal, e.g., by birds or storms. The highly specific ecological niche preferences of some taxa restricted to tepui summits are likely to have limited active dispersal. Most *Oreophrynella* species, for example, exclusively occupy rocky habitats with extremely impoverished flora, which are absent in the intervening areas. Time estimates for the isolation of individual tepuis range from the Cretaceous [7,8] to the Quaternary [2,9]. The youngest estimates, although widely neglected in biological studies, could be compatible with the low genetic diversity and leave

vicariance as a possible mechanism for speciation.

Regardless of the mechanism, our study shows that, even in small vertebrates restricted to summit-specific habitats, gene flow has been maintained until recently, making single-tepui endemism an exception rather than a rule. Nevertheless, as several of the taxa studied here (e.g., *Oreophrynella* and *Stefania*; Supplemental information) represent phylogenetically distinct lineages restricted to the Pantepui region, this area as a whole may still act as a reservoir of high-level endemism.

Supplemental Information

Supplemental Information includes experimental procedures and supplemental tables and can be found with this

article online at <http://dx.doi.org/10.1016/j.cub.2012.06.034>.

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