using space and memory as ways to try to understand that general question. So we started out with a focus on memory and now we are a bit more ambitious, we really want to understand the whole thing. But this is also possible because of all the new methods that are available. You can do things that were very difficult some 10–20 years ago.
May-Britt: But I don't think I agree with you that we stumbled over the network that makes spatial navigation possible. Of course we couldn't know what we would get but it was planned.
Edvard: It definitely came out of ideas that we had about where to search for spatial cells, but still, the grid pattern was a surprise to everyone.
May Britt: Oh, absolutely.

Do you have a favourite paper?
Edvard: I am very much influenced by the early work of Hubel and Wiesel. They had a series of papers in the 1960s, some of which were published before I was born. They showed how individual cells in the visual cortex decompose the visual image, they described how the different cell types of that cortex were organized functionally, and they suggested how those signals could be computed from their inputs, at a time when there was very little computational neuroscience. Their brave and important questions and their approach to solving them is a kind of model for me, and it inspired me when we began with the entorhinal cortex.

What are the other passions in your life?
Edvard: I have one passion and that is volcanoes. Because we have jobs where we travel a lot, I have had a lot of opportunities to visit volcanoes everywhere.
May Britt: And it started on a volcano, we got engaged on Kilimanjaro. But while I also enjoy volcanoes, my own passion is the sea.

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Quick guide

Cheese microbes

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What is cheese? Cheese is a fermented milk product that likely dates back to Neolithic times. Historically serving as a means of preserving milk, today, a fine cheese is viewed as a delicacy rather than a means of survival. Millennia of cheesemaking has led to a diversification of cheese styles and production methods, and more recently, to detailed technical knowledge of the science behind the process. Communities of microbes catalyze the transformation of milk into cheese and remain active participants in the development of a cheese throughout the aging process.

How is cheese made? Cheesemaking occurs in three main stages. In the first stage, milk is transformed into solid curds and liquid whey through the coagulation of the milk protein casein. The coagulation of casein is usually accomplished through two complementary methods, acidification and proteolysis. Acidification occurs when lactic acid bacteria ferment the disaccharide lactose, to produce lactic acid. Originally, cheesemakers relied upon naturally occurring lactic acid bacteria in the milk, but today, the process is usually standardized by the addition of domesticated bacterial 'starter' cultures, including strains of *Lactococcus lactis*, *Streptococcus thermophilus* and *Lactobacillus* sp. The production of acid by these bacteria causes casein to slowly coagulate. This process is often assisted by the addition of the enzyme chymosin, the active ingredient in rennet. Rennet is traditionally made from an extract of the intestinal lining of a milk-fed calf, which produces the protease chymosin to aid in the digestion of milk. Chymosin removes a negatively charged portion of casein, resulting in the rapid aggregation of casein proteins.

In the second stage of cheesemaking, cheesemakers separate the curds, containing the casein and milk fat, from the whey. Depending on the type of cheese, the curds can be heated, salted, pressed, and eventually formed into wheels of various shapes and sizes. Cheese can be eaten fresh at this point, or the wheels can be left to age in a damp, cool place.

It is during the aging stage of cheesemaking that cheese is truly transformed — from fresh cheese into the myriad flavors, aromas, and textures of mature cheese. As a normal part of the aging process, starter cultures and non-starter lactic acid bacteria continue to grow and metabolize the interior of the cheese, while the surface of a cheese is colonized by bacteria and fungi that form a multispecies biofilm, termed the 'rind' of the cheese (Figure 1).

How do microbes impact the flavor, smell, and texture of cheese? Much of the diversity in the flavor, smell, and texture of cheese can be attributed to microbiology. Microbes have a rich assembly of metabolic capacities, and through the production of digestive enzymes and small molecules, microbes contribute to the distinct character of a cheese. However, variations in cheese production can lead to the preferential growth of different groups of microbes. First, the source and treatment (i.e., raw vs. pasteurized) of milk used for cheesemaking can lead to differences in microbial diversity. Subsequently, changes in the pH, salt, moisture, and temperature of a cheese during the initial stages of cheesemaking, or during aging, can dramatically impact the physiology of cheese-associated microbes.

The contribution of certain microbes to cheese has been well characterized, and pure cultures of these microbes are commonly used by cheesemakers. Besides the lactic acid bacterial starter cultures, various species of bacteria and fungi can be added to give a cheese very specific characteristics.

What is the white fuzzy rind on Camembert? Spores of the filamentous fungus *Penicillium camemberti* are inoculated into milk during the production of bloomy rind cheeses such as Brie and Camembert. *P. candidum* is an aerobe and grows preferentially on the surface of the cheese, where it forms a rind made of a dense mat of hyphae (Figure 1A). During growth, proteases are secreted from the hyphae into the cheese. The proteolysis of the casein destroys the structure of the underlying curd, slowly liquefying the cheese and giving Camembert its oozy texture.

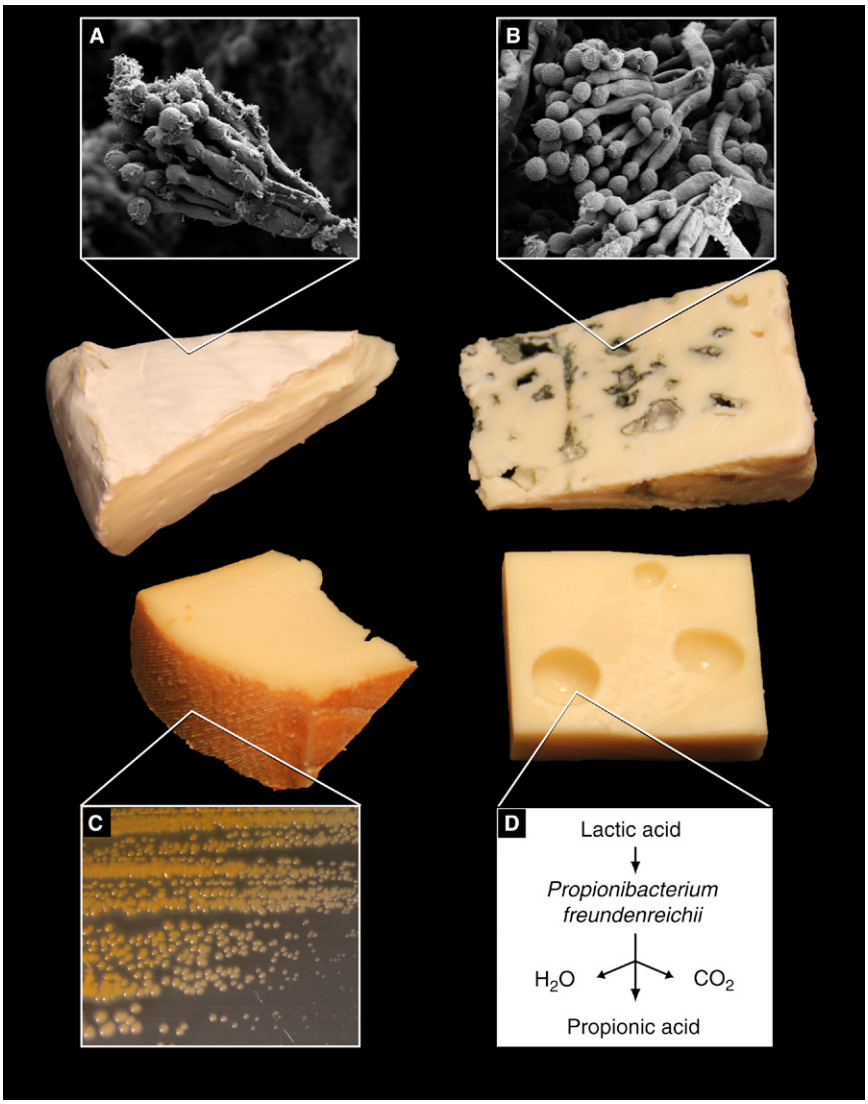

Figure 1. The microbiology of cheese aging.
The surfaces of bloomy rind cheeses are colonized by the filamentous fungus *Penicillium camemberti* (A: Fungal structures visualized by scanning electron microscopy, magnified 12,850X), whereas *Penicillium roqueforti* (B) grows inside crevices of blue cheeses. The orange-pigmented bacterium *Brevibacterium linens* (C: colonies of *B. linens* growing in isolation) contributes to the distinctive color and aroma of washed rind cheeses. Fermentation of lactic acid by *Propionibacterium freundenreichii* (D) produces CO_2, causing the typical holes found in Swiss cheeses.

What is the blue in blue cheese?
A related fungus, *Penicillium roqueforti,* is the key microbe in blue cheese (Figure 1B). While this fungus can be found growing naturally in the limestone caves of southwestern France where the classic cheese, Roquefort, is produced, it can also be inoculated into milk destined to become blue cheese. Because *P. roqueforti* is a microaerophile, it prefers to grow in crevices created by puncturing a cheese with metal spikes after the wheels are formed. *P. roqueforti* produces lipases that convert the fats in cheese to peppery free fatty acids and the methyl ketone 2-heptanone, which gives the characteristic blue aroma. The blue pigment seen in blue cheese is produced by *P. roqueforti* during sporulation.

Why are some cheeses so stinky?
Washed rind cheeses, such as Epoisses and Limburger, are regularly washed with a brine solution during the aging process. This creates a moist, salty environment on the surface of the cheese in which certain species of fungi and bacteria thrive. One of the best-known species is the actinomycete bacterium *Brevibacterium linens* (Figure 1C). *B. linens* contributes to the reddish-orange color typical of these cheeses through the production of carotenoid pigments. Additionally, *B. linens* metabolizes the casein proteins to a variety of volatile compounds, including amines and sulfur compounds, giving these cheeses their funky, sweaty aromas. The related bacterium *B. epidermidis* can be found growing on human skin and, not surprisingly, is thought to contribute to body odor.

What causes the holes in Swiss cheese? The holes in Swiss cheese result from the growth of the bacterium *Propionibacterium freundenreichii* (Figure 1D). *P. freundenreichii* ferments the lactic acid present after the growth of the lactic acid bacteria. The products of this fermentation include propionic acid, which is one of the characteristic flavors of Swiss cheese, and CO_2. Because *P. freundenreichii* prefers anaerobic conditions, growth occurs inside the wheel of cheese, and the CO_2 produced during fermentation is trapped and forms the typical bubbles, or holes, found in Swiss cheese.

What other microbes are found in cheese? The microbial components of cheese are only partially dictated by the pure cultures inoculated by cheesemakers. A wheel of cheese is home to a whole community of microbes, and the rind in particular may be colonized and dominated by species derived from the local environment rather than by starter cultures. Although the identity and function of these additional species is only beginning to be uncovered, cheesemakers have learned, through trial and error, how to reproducibly cultivate specific communities by manipulating the conditions to which a cheese is subjected during the aging process. Each variety of cheese represents the output of a slightly different microbial community. Because the metabolism of cheese-associated microbes greatly impacts the sensory attributes of cheese, differences in microbial diversity result in tangible changes in flavor, odor, texture, and color that are tracked (and often influenced) by the cheesemaker. Conditions that produce distinct microbial communities have been documented and passed down by generations of cheesemakers.

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?

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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 (tepuis) 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 Kukenan-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