

not only promote stability, but also allow the proteins to incorporate diverse signals and communicate these signals across domains. These signals may include cellular ligands, disease-related mutations and post-translational modifications. The authors' solving of the HIF- $\alpha$ -ARNT structures provides exciting opportunities to explore previously uncharacterized cell-regulatory pathways and to advance drug discovery. ■

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## BIODIVERSITY

# Multiple origins of mountain life

A study of DNA sequences from more than 1,800 organisms on Mount Kinabalu in Borneo reveals the evolutionary mechanisms that led to the mountain's high and unique biodiversity. [SEE LETTER P.347](#)

ALEXANDRE ANTONELLI

Mountains occupy only about one-eighth of the world's land surface outside Antarctica, yet they are home to around one-third of all terrestrial species<sup>1</sup>. However, little is known about when, where and how this mountain biodiversity developed. In a paper on page 347, Merckx *et al.*<sup>2</sup> investigate the origins of species on a highly diverse tropical mountain, Mount Kinabalu on the island of Borneo. They find that most endemic species — those found nowhere else — arose relatively recently on the mountain, deriving from both local ancestors and distant

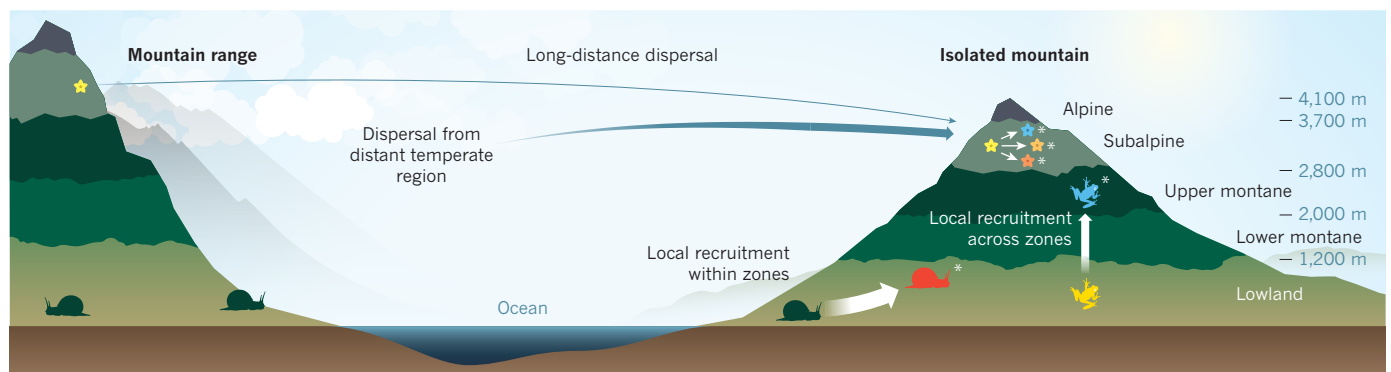
immigrants that were pre-adapted to cool environments. These observations have direct implications for our understanding of montane biodiversity, and may offer clues on how to protect both the unique organisms found there and the habitats that provide the stage for speciation.

Ever since the first botanical documentation of a tropical mountain by Alexander von Humboldt more than two centuries ago<sup>3</sup>, naturalists have been fascinated by the diverse and unusual variety of life forms found on mountains. But we still lack answers to fundamental questions about the evolution of mountain biodiversity. Did the species living

on mountains originate in the surrounding lowlands, where their ancestors became successively adapted to higher altitudes? Or are montane species mostly pre-adapted immigrants from far-away mountains? And are the mountain-dwelling species ancient or recent?

Merckx and colleagues got to the root of these questions by using a new comparative approach. Rather than studying the formation of species in a single group of organisms and extrapolating from there, which has been the standard approach so far, the researchers collected a large variety of organisms — from frogs and snails to insects, plants and fungi — that inhabit the iconic Mount Kinabalu and its surroundings. They then sequenced DNA from the approximately 1,850 collected specimens, compared these sequences with others in their own collections and public databases, and calculated their relationships, ages, geographical origins and ancestral environments.

The first striking result is that most of the montane organisms examined are relatively young. They started to speciate during the past 6 million years, after, or at the same time as, the rise of the mountain they inhabit. Unlike the ancient creatures found on a remote tropical mountain in Arthur Conan Doyle's novel *The Lost World*, this finding suggests a recent origin



**Figure 1 | Routes to mountain biodiversity.** Isolated tropical mountains generally contain high levels of species richness and endemism (species uniqueness). Merckx *et al.*<sup>2</sup> show that a large proportion of endemic species (indicated by asterisks) on Mount Kinabalu in Borneo derive from lineages that were previously present on the island (arrow widths reflect the relative number of identified cases; organisms depicted are indicative only). Only some of these locally recruited species have adapted to different vegetation zones. By contrast, some species, especially those found at high altitudes, have

their origins in similar vegetation zones on other mountain ranges outside Borneo, or at lower altitudes in temperate regions, and have arrived by means of long-distance dispersal. (Note that vegetation zones on mountain ranges are usually at higher elevations than on isolated mountains, owing to heat retention and wind shadowing.) Most of these immigrant lineages have then undergone local speciation. The evolutionary history of Mount Kinabalu's biodiversity exemplifies the interactions among dispersal, adaptation and speciation in generating mountain biodiversity.

for montane species across the domains of life, and supports the recent speciation documented for alpine plants on several continents<sup>4</sup>.

The second major finding is the dual origin of montane organisms (Fig. 1). Some of the species, in particular those found at the highest elevations of Mount Kinabalu, have their closest relatives outside of Borneo. Their ancestors were often good at dispersing, such as plants or fungi that produced large quantities of light seeds or spores that could be transported with the wind. Other species — about twice as many — derive from local ancestors at lower altitudes on the same island. The location of Mount Kinabalu, surrounded by an exceedingly diverse tropical forest at the crossroads of Asia and Oceania, two regions that have their own distinct fauna and flora, apparently provided the mountain with a rich initial stock for the evolution of its unique biodiversity.

Finally, the authors' analysis shows an overarching role for niche conservatism — the tendency for organisms to maintain their environmental preferences over evolutionary time. This result is evident both from the immigrant and the local lineages that gave rise to Mount Kinabalu's biodiversity. Most of the ancestral species were already adapted to cool conditions, either in temperate regions or in other montane habitats. Even the lineages that 'climbed up' Mount Kinabalu often remained in the same broadly defined vegetation zone. The niche conservatism and pre-adaptation shown for the inhabitants of this tropical mountain are in line with previous findings across the Southern Hemisphere<sup>5</sup> and with observed patterns of plant movement into cold environments around the world<sup>6</sup>.

Merckx and colleagues' study thus provides a textbook example of how biodiversity originates from the interplay between long-distance dispersal and local recruitment, followed by adaptation and speciation through interaction with changes in the landscape, climate and environment<sup>7</sup>. Its limitations are shared with other studies that are based on living organisms and current species distributions. Biological surveys sample only a fraction of the total biodiversity of an ecosystem, and large organisms found in easily accessible sites are typically over-represented. Furthermore, estimates of speciation events, geographical history and niche conservatism obtained from phylogenetic trees are prone to large error intervals and many assumptions, and largely disregard the confounding effects of extinction. The integration of recent and past data — from DNA, fossils and environmental and geological proxies — could remedy these shortcomings<sup>8</sup>, but such data are still scarce or not readily available.

Much could be gained by applying Merckx and colleagues' whole-community approach to other systems around the world. As well as increasing our fundamental knowledge of the diversity and distribution patterns of species, such eco-evolutionary studies would shed light

on why some regions are much more biodiverse than others. A better understanding of the past may also, at least to some extent, help scientists to manage the present and predict the future. Taking climate changes as an example, evolutionary studies may help to inform us about the resilience of species and ecosystems<sup>9</sup>. They may also help to ascertain the role of mountains as potential reservoirs of biodiversity, because montane species need to move only short distances to keep their preferred niche<sup>10</sup>. Finally, we may need to devote more resources to preserving the natural corridors that link vegetation zones along altitudinal slopes if we are to safeguard the biotic interchange reported by Merckx *et al.*, and thus enhance our protection of the world's unique and rich mountain biodiversity. ■

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#### ASTROPHYSICS

# Mystery survivor of a supermassive black hole

**The G2 cloud in our Galaxy's core has survived an encounter with the central black hole and failed to trigger a major flare-up in the black hole's activity. A promising theory endeavours to explain the cloud's nature.**

JOHN BALLY

The centre of the Milky Way hosts a supermassive black hole (SMBH) weighing approximately 3.6 million solar masses. In 2012 a faint, dusty object of cloudy appearance was discovered<sup>1</sup>, accelerating towards the SMBH on an eccentric orbit with a predicted closest approach (periape) of only about 200 times the mean Earth–Sun separation (Fig. 1). During its encounter with the SMBH, the object, known as G2, avoided complete tidal disruption by the black hole's gravity, implying that it is gravitationally bound (held together by gravity). But what is the nature of G2? Various early searches failed to find an ordinary or an evolved giant star lurking in the cloud. Writing in the *Astrophysical Journal*, Mapelli and Ripamonti<sup>2</sup> propose that the central object might be a planetary embryo that was dynamically ejected from its parent system and is nearly as large as the distance between Earth and the Sun.

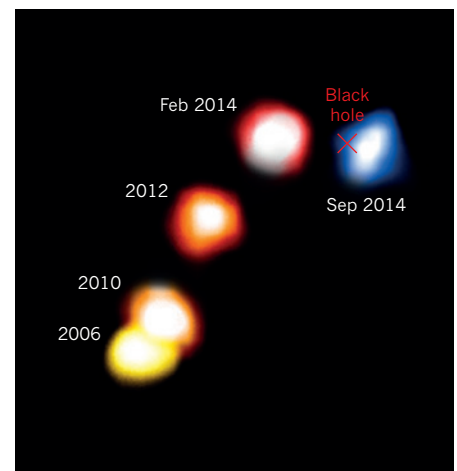
The central few light years of the Milky Way encompass a dense stellar field containing more than 10 million low-mass stars (Fig. 2); a comparable volume near the Sun typically only contains one star. Among these dim, ancient stars, there is a swarm of luminous massive

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**Figure 1 | At close quarters to Sagittarius A\*.** The G2 cloud is shown at different times along an orbit that took it perilously close to Sagittarius A\*, the supermassive black hole in our Galaxy's centre (red cross). These observations show that G2 was on a course towards the black hole from 2006 to early 2014 (reddish colours indicate that the object is receding from the observer). Its closest approach to Sagittarius A\* was in May 2014 and observations in September 2014 (blue indicates that G2 is approaching) show that the object survived being ripped apart by the black hole.