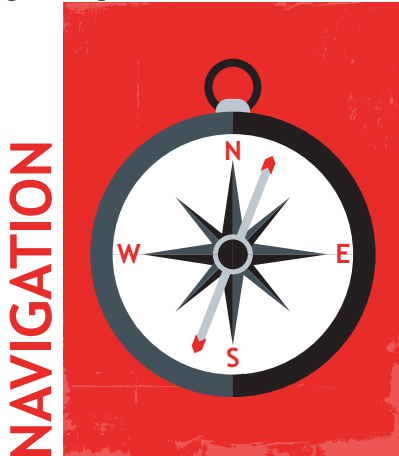


OUTSIDE JEB

Magnetic declination stops migratory birds getting lost at sea



In the 1700s, scientists, sailors, engineers and explorers were trying to work out how to navigate east to west at sea. The stakes were high; many lives were lost because sailors could not reliably measure longitude. Eventually, the invention of accurate timepieces allowed sailors to use the time in their current location, and the time at a fixed reference, to calculate longitude. But how do long-distance migrants navigate longitude at sea without a time-difference clock sense? Nikita Chernetsov of the Zoological Institute of Russian Academy of Sciences and an international team of collaborators suspected that for Eurasian reed warblers, magnetic fields might provide an answer.

Some species navigate east to west using magnetic inclination, which is the angle of magnetic field lines relative to the Earth's surface, and magnetic field intensity. Because these cues vary independently, they can create a bi-coordinate map, which migrants use to get their bearings. The problem is that in many parts of the world, these cues run in parallel and so cannot be used to measure longitude. The research team suspected that if warblers could locate true north using celestial cues, and detect magnetic north, then they could measure magnetic declination – the angle between true north

and magnetic north. Together, magnetic inclination and magnetic declination create a grid that migrants might use to navigate.

To test this idea, the team caught adult migrants flying over Russia. To check whether catching these birds disrupted their flight path, they released them into small, funnel-shaped enclosures where they could hop around; at night, the captive birds became restless and tended to move in the same direction as migrants. The birds were put in the funnels on a clear, starry night, so that they could use the stars to navigate; they moved in a WSW direction. The team then manipulated the magnetic field around the birds' enclosures, holding magnetic inclination and intensity constant but altering magnetic declination. This meant that while the birds were geographically in Russia, they were surrounded by the geomagnetic field found in Dundee, Scotland. This time, when the birds were released into the enclosure on a clear, starry night, they changed their direction of movement by 151 deg and moved in an ESE direction. This enormous change suggests that migratory reed warblers do use magnetic declination to navigate.

The team then repeated this experiment with juvenile birds, reasoning that because these inexperienced migrants had not yet established their functional map, they should be disorientated by a change in magnetic declination if they use magnetic declination to navigate. Juveniles that were caught and released into the same enclosures moved in a WSW direction, just like adult migrants, but when magnetic declination was manipulated around these birds, they moved around randomly. This further supports the idea that magnetic declination is a cue that helps birds chart their course east to west.

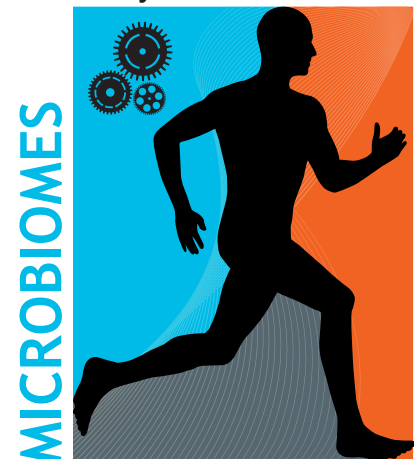
This work reveals an elegant solution used by long-distance migrants to the longstanding challenge of navigating at sea.

10.1242/jeb.147686

Chernetsov, N., Pakhomov, A., Kobylkov, D., Kishkinev, D., Holland, R. A. and Mouritsen, H. (2017). Migratory Eurasian reed warblers can use magnetic declination to solve the longitude problem. *Curr. Biol.* **27**, 2647–2651.

C. Ruth Archer
University of Exeter
c.archer@exeter.ac.uk

Modernity has stripped us of our dynamic bacteria



There is more to us humans than our 30-odd trillion eukaryotic cells. The things that make us *us* – our metabolism, our mental health, our athletic ability, etc. – are dictated not only by our eukaryotic cells but also by the chemical signatures of trillions of prokaryotic cells that inhabit the nooks, crannies and crevices of our bodies. These cells, which are mostly bacterial, congregate at their highest density in the large intestine, and their diversity and composition are heavily influenced by our diet. Samuel Smits and his colleagues at Stanford University were curious about how dietary changes throughout human evolution correspondingly changed the gut microbiome. Because ancestral humans were hunter-gatherers, the team turned to one of the few remaining hunter-gatherer tribes – the Hadza of Tanzania – to approximate an ancestral human diet and, subsequently, the ancestral gut microbiome.

Before the team could compare the Hadza microbiome with that of other modern populations, they needed to characterize

the seasonality of the Hadza microbiome because the Hadza diet fluctuates over the year: meat in the dry season, berries and honey in the wet season, and fiber-rich tubers the whole year through. The group explored this seasonality by collecting fecal samples from 188 Hadza individuals at five points over a 12 month period, and then used 16S ribosomal RNA to identify the bacterial composition. True to the team's predictions, the bacterial composition cycled over the course of the year, changing as the season progressed from dry to wet and then back again. The dry season saw greater bacterial diversity than the wet season and, looking at the two major gut bacterial groups, the abundance of Firmicutes remained stable throughout the seasons while that of Bacteroidetes declined significantly in the wet season.

The group next hypothesized that these seasonal bacterial changes would manifest in changes at the functional level, specifically a seasonal cycling of bacterial enzymes to complement the Hadza's seasonal cycling of diet. Shotgun metagenomic sequencing and untargeted metabolomics revealed this to be true. The Hadza's dry season microbiomes were rich in enzymes specialized for metabolizing animal-derived carbohydrates, and their wet season microbiomes were rich in enzymes specialized for plant-derived carbohydrates, perfectly complementing the seasonal dietary changes.

With this understanding of how an ancestral-like hunter-gatherer lifestyle influenced the gut microbiome, the group then employed the comparative approach to understand how it differed from that of a modern Western lifestyle. They compared the Hadza with 18 communities from 16 countries of varying lifestyles and found the bacterial families that typified the Hadza microbiome varied significantly from those of the Western microbiome, but were strikingly similar to those of other 'traditional' populations across Asia, Africa and South America, some of which were also hunter-gatherers. These differences were also present at the enzyme level; Hadza guts had more plant carbohydrate-digesting enzymes than Western guts, and Western guts had more animal carbohydrate-digesting enzymes than Hadza guts. Interestingly, the bacterial families that varied most across the seasons in the

Hadza's digestive systems were altogether absent from the Western microbiomes.

To put this evolutionarily, the modern Western microbiome lacks some of the dynamic bacterial species humans co-evolved with – bacteria still possessed by the Hadza. The consequences of this are unknown, but might be understood by identifying the unique metabolites these bacteria produce. While the seasonal cycling of the Hadza microbiome is impressive, it is less than that seen in some non-human animals such as the hibernators, whose diets see even more extreme seasonal fluctuations. How this cycling impacts the host to make a Hadza human different from a Western human, or a hibernating ground squirrel different from an active ground squirrel, is yet to be discovered.

10.1242/jeb.147702

Smits, S. A., Leach, J., Sonnenburg, E. D., Gonzalez, C. G., Lichtman, J. S., Reid, G., Knight, R., Manjurano, A., Chagalucha, J., Elias, J. E. and Dominguez-Bello, M. G. (2017). Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. *Science* 357, 802–806.

Matthew D. Regan

University of Wisconsin-Madison

mdregan@wisc.edu

Swindling cuckoos: hawk-like call tricks hosts



Biological organisms have evolved a plethora of tactics to survive and reproduce in a wide range of habitats. While some species are what you might call 'honest' in their approach to life, many species are rather 'dishonest' and take advantage of other species. In particular, parasites exploit their hosts in a number of ways to cheat their way through

life. Cuckoos are one such parasite: they escape the energetically costly investment of rearing young by laying their eggs in the nests of other birds. This is very detrimental for the hosts, as many, if not all, of their own young do not survive.

While cuckoos are quite adept at sneaking their own eggs into the nests of their apparently unsuspecting hosts, they are not always successful. Many birds actively try to prevent this parasitism, often by attacking the offending cuckoos or by evicting any eggs in their nests that look strange. This enticed Jenny York and Nicholas Davies from the University of Cambridge, UK, to try to discover whether cuckoos have any other clever tricks to enhance the success of their own offspring.

York and Davies chose to focus on reed warblers as the host species, as their nests are often the preferred choice of cuckoos. Firstly, they played four different calls to nesting reed warblers, including a female cuckoo, a male cuckoo, a Eurasian sparrowhawk and a collared dove. Theoretically, the reed warblers should not treat the calls of the male cuckoo or the dove as threats; the female cuckoo, while a threat to their clutch, should not pose an immediate threat to the adults; whereas the sparrowhawk would necessitate instantaneous vigilance. Indeed, the reed warblers did not react to the male cuckoo and the dove calls; however, they responded with increased alertness to the female cuckoo and the sparrowhawk calls.

However, York and Davies wanted to confirm whether this similarity in response was due to similarities between the calls or whether they are individually perceived as threats. Therefore, they repeated the same experiment on tits, birds which are often preyed upon by sparrowhawks, yet are not typically used as hosts by cuckoos. So, one could expect that the tits' response to the calls of female cuckoos and sparrowhawks would vary if they do indeed sound different. However, their responses to all four calls were identical to those of the reed warblers, suggesting that while the calls of the female cuckoos and sparrowhawks sound different to us, they sound similar enough to birds.

But how does having a similar call to a sparrowhawk help female cuckoos? Well it's the perfect distraction, of course. York and Davies conducted one final experiment where they painted one of the eggs in a reed warbler nest solid brown,

ensuring it looked different to their usual splotchy eggs, and then presented the parents with the four varying bird calls. The reed warbler parents that were distracted by either the sparrowhawk or the female cuckoo calls were less likely to reject the odd egg, in contrast to the parents presented with the male cuckoo or dove calls, which often removed the foreign-looking egg from their nest.

By diverting the attention of the hosts with a false predatory call, female cuckoos increase the chance of their own offspring being accepted and surviving. While this may be a rather 'dishonest' way of ensuring your genes live on, we have to admit that it is a very clever tactic.

10.1242/jeb.147694

York, J. E. and Davies, N. B. (2017). Female cuckoo calls misdirect host defences towards the wrong enemy. *Nat. Ecol. Evol.* **1**, 1520-1525.

Clare Stawski
Norwegian University of Science and
Technology
clare.stawski@ntnu.no

White-nose syndrome dehydrates bats



Over the past decade, millions of North American bats have perished from a fungal infection known as white-nose syndrome. As its name suggests, the most conspicuous manifestation of the disease is the development of fuzzy white fungus on the muzzle, which strikes during hibernation. Beyond this superficial symptom, the fungus causes nasty lesions on the wings and disrupts blood chemistry prior to death. The disease also causes bats to wake up more frequently during hibernation and the increased energy expenditure causes the animals to wither away.

Whilst it is clear that the fungus wreaks physiological havoc, exactly how the pathology progresses is unclear. To investigate how the initially innocuous-looking infection causes death and population demise, Liam McGuire and his colleagues, then at the University of Winnipeg (Canada), devised a series of experiments on wild-caught little brown bats. Half of the (initially healthy) animals were inoculated with the fungus that causes white-nose syndrome before hibernating in captivity.

Over the initial 4 months, the hibernating bats were filmed with an infrared camera, and the team observed that infected bats woke up considerably more often than healthy animals. After this period, the authors moved the bats into chambers in which they could record the animals' metabolic rate (by measuring carbon dioxide excretion) and water loss. Even whilst dormant, the infected bats were spending more energy. The researchers also measured evaporative water loss when the bats were exposed to either humidified or dry air. The bats inoculated with the fungus lost more water than healthy animals in both circumstances, and they were especially vulnerable to desiccation in dry air.

At the end of their experiment, McGuire and colleagues measured the severity of the infection by taking photographs of the bats' wings under UV light. The fluorescent fungus covered up to almost half the wing surface area in inoculated animals (but was confirmed to be absent in uninfected animals). The authors then looked for correlations between the extent of the individuals' infection and their metabolic rate or water loss. There was a clear relationship between water loss and wing damage; the individuals with extensive wing lesions became most dehydrated. This indicates that water probably seeps directly through the wounds. However, there was no correlation between torpid metabolic rate and severity of wing lesions, which suggests that factors other than water loss are elevating metabolic rate.

This timely study demonstrates that increased evaporative water loss and elevated metabolic rate independently endanger bats infected with white-nose syndrome. The finding that dry air exacerbates the dehydration is particularly pertinent and may influence how infected animals are treated. Thus, this study neatly exemplifies how a mechanistic understanding of how emerging pathogens disrupt animal physiology may provide a key bedrock to developing successful conservation programmes.

10.1242/jeb.147710

McGuire, L. P., Mayberry, H. W. and Willis, C. K. R. (2017). White-nose syndrome increases torpid metabolic rate and evaporative water loss in hibernating bats. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **ajpregu.00058.2017**.

William Joyce
Aarhus University
william.joyce@bios.au.dk