

ects at risk. NSF says it will have more to say in the coming months on how it will choose between the TMT and the GMT. “Neither is a slam dunk. Both have risks,” Turner says. “I don’t envy the NSF.”

Made up of 492 segments, the TMT’s 30-meter mirror makes for the larger, more sharp-eyed instrument. But its chosen site, the summit of Mauna Kea on Hawaii’s Big Island, is opposed by some Native Hawaiian groups who consider the summit sacred. They have blocked any construction work since 2015. TMT officials hope work will be able to proceed under the aegis of a new state-appointed authority that governs the mountaintop and includes both astronomers and Native Hawaiians. “We’re working on our relationships in Hawaii,” says TMT Executive Director Robert Kirshner. “We’re learning how to do that in a humble and straight-forward way.” Turner says the impasse may not be solved anytime soon. “I’m sure a solution will be found, but it may take longer than people like,” he says.

The GMT, smaller and cheaper, is a lower risk choice. Its foundations are being laid on a mountaintop at Las Campanas in Chile, while support structures for its mirrors are taking shape in the United States. Three of its seven 8.4-meter mirrors, the equivalent of a 25.4-meter-wide mirror, are already finished; the other four are being polished.

Because of the risks attached to the TMT, Monnier and Ellis suspect NSF will probably back the GMT. But with a mirror less than 40% of the size of its 39-meter European rival, the GMT “is no match for ELT,” says Ellis, a former TMT board member. Monnier thinks the GMT will probably be good enough in key astronomy areas, but NSF will need to judge whether those areas are important for U.S. astronomers.

Abandoning either of these very capable telescopes will harm U.S. astronomy, says Wendy Freedman at Chicago, one of the GMT’s partner organizations. “The science that will come out really does justify two telescopes.” Upcoming survey telescopes such as the 8.4-meter Vera C. Rubin Observatory in Chile will identify a wealth of interesting objects in need of follow-up observations by instruments on the GMT and the TMT that can split the light into information-rich spectra. “That’s what these big telescopes give you,” she says.

Language in a spending bill passed by Congress this week “strongly encourages” NSF to build both telescopes, even though lawmakers cut NSF’s 2024 funding by more than \$800 million, to \$9 billion (see story, p. 1043). Freedman hopes the congressional direction will prompt a rethink. “The United States will sit out the future of astronomy if we don’t get these telescopes,” she says. ■

BIOLOGY

Surprise RNA paints colorful patterns on butterfly wings

Understudied means of regulating genes is likely widespread in butterflies—and perhaps other animals

By Elizabeth Pennisi

A mutant butterfly for sale on eBay has helped upend naturalists’ picture of how butterfly wings acquire their intricate variety of red, yellow, white, and black stripes. It and recent research into other butterflies show how visible traits in many animals may be controlled by an underexplored genetic regulatory mechanism, based not on proteins, but on RNA.

In 2016, geneticists thought they had pinned much of the wing-pattern variation on a protein-encoding gene called *cortex*. But three teams have now proved that a different gene, previously missed because it overlaps with *cortex*, is the key. Its final product is not protein, but RNA that regulates genes responsible for the pigmentation patterns of black and other hues on the wings. One team also showed the RNA is broken down into a smaller RNA that fine-tunes the production of the colors. “They solved a puzzle that had left everyone in the community wondering,” says Nicolas Gompel, a developmental biologist at the University of Bonn.

The discovery, detailed in three preprints this month, also represents the first time long noncoding RNA (lncRNA), so-called because it does not code for proteins, has been linked to the evolution of a visible trait in animals. “Now we have to pay more attention to noncoding RNA,” says Ilik Saccheri, an evolutionary biologist at the University of Liverpool and a member of one of the teams that had focused on *cortex*.

For evolutionary developmental biologist Luca Livraghi, now at George Washington University, the key break came when a colleague told him and Joseph Hanly, a bioinformatician at Duke University, about completely white *Heliconius* butterflies

being sold on eBay. When they sequenced dozens of these so-called ivory mutants, they found a deletion in the region of the *cortex* gene. They then realized the missing DNA included a sequence encoding an lncRNA that no one had ever closely examined. Working with painted lady butterflies (*Vanessa cardui*), which have colorful wings and are easy to breed in the lab, they used the gene editor CRISPR to disable just the lncRNA’s gene. The edit yielded white-winged painted ladies, just like the ivory *Heliconius*, they reported on 12 February in a preprint on bioRxiv. Disabling *cortex* had no effect.

Moreover, Livraghi’s team found this same lncRNA also controls black and other



A gene edit affecting one wing (right) of this *Heliconius erato* radically changed its normal color pattern.

pigmentation in the scales of other butterfly species, some distantly related. “We have to conclude now that the key regulator is an RNA, not a protein,” says Peter Holland, an evolutionary biologist at the University of Oxford who was not part of any of the new work.

At a conference midway through these studies, Livraghi learned that a Cornell University group studying wing color patterns in the buckeye butterfly (*Junonia coenia*), common throughout North America, was homing in on this same lncRNA. The two teams decided to coordinate their efforts.

Come fall, especially in the U.S. East, the light brown wings of buckeyes darken to a deep red, enabling them to absorb heat more efficiently. When Cornell evolutionary biologists Robert Reed and Richard Fandino used CRISPR to knock out different parts of the lncRNA in these butterflies, they were born with little or no color and their fall reddening was altered, the team reported on 19 February on bioRxiv.

A white butterfly mutant posted on the social media platform X (formerly Twitter) alerted Livraghi to the team behind the third new preprint: evolutionary developmental biologists Antónia Monteiro and Shen Tian at the National University of Singapore. They were focused on short RNA sequences, microRNAs, known to regulate gene activity in plants, animals, and other eukaryotes—organisms that pack their DNA in a nucleus. In the squinting bush brown butterfly (*Bicyclus anynana*), a well-studied tropical species, they found that a microRNA was active in the black wing pattern, just as Livraghi had found for the ivory lncRNA.

When the Singapore team disabled the DNA encoding this microRNA, mir-193, bush brown wings became lighter, the team reported on 12 February in a bioRxiv preprint. Knocking out mir-193 also had dramatic effects in a distant relative, the Indian cabbage white (*Pieris canidia*), changing its black-patterned wings to completely white. After learning about the lncRNA identified by the two other groups, Monteiro and Tian concluded that the longer RNA is broken down to produce these microRNAs.

“A lot is happening within this small part of the genome,” says Violaine Llaurens, an evolutionary biologist at the College of France. She cautions that other regulatory elements probably play a role in butterfly wing patterns. But the fact that the same microRNA fine-tunes coloration in very distantly related species is “amazing,” says Anyi Mazo-Vargas, an evolutionary biologist at Duke who worked with Reed. She suspects similar RNAs color wings in most, if not all, of the 180,000 species of moths and butterflies. And because mir-193 is conserved across the animal kingdom, Monteiro and Tian think noninsects may also make use of these regulatory RNAs.

Small RNAs derived from parent lncRNAs affect traits in plants, too, says Yaowu Yuan, an evolutionary biologist at the University of Connecticut whose team last year reported that so-called siRNAs determine color in monkeyflowers. The RNA realm is expanding, Yuan says. “I am quite positive that many more similar studies will come soon.” ■

MUSEUM COLLECTIONS

Smithsonian urged to speed repatriation of human remains

Task force says museum should return many of its 30,000 remains and seek descendants’ consent for research

By **Rodrigo Pérez Ortega**

Since the 19th century, scientists at the Smithsonian Institution have obtained, studied, and stored more than 30,000 human remains, one of the largest such collections in the United States. In the past, many remains were studied in order to justify scientific racism. Now, the institution should rapidly offer to return most of these remains to lineal descendants or descendant communities, according to a report released last month by an institutional task force.

“It’s important to face this past and try to repair the harms caused by our institution and so many others,” says Sabrina Sholts, curator of biological anthropology at the Smithsonian’s National Museum of Natural History and member of the task force.

Most of the Smithsonian’s human remains were collected without proper consent in the early 20th century, and many acquisitions were part of an attempt to prove now-debunked notions of white superiority. “It’s a collection that should have never been amassed, and we’re committed to dismantling as much of it as possible,” wrote Secretary of the Smithsonian Lonnie Bunch III last year in an editorial.

The Smithsonian already has a process for repatriating its 15,000 Native American remains, as a 1989 federal law requires; it has returned more than 5000. Now, the report urges that the collection’s Indigenous remains be returned more quickly and that the effort extend to all human remains. It also suggests prioritizing the remains of other marginalized groups, such as the collection’s 2100 African American remains, as well as the nearly 6000 remains of people whose names are at least partially known.

The task force applies a bedrock principle of research on living humans—the need for informed consent—to the remains, a

first for the Smithsonian. It advises that no research should be done without consent from the deceased or their descendants. Research would be permitted without consent on ancient remains that cannot be linked to any of today’s communities, which are a small percentage of the total.

Other new recommendations include returning as many remains as possible by 2030 and barring destructive sampling—to analyze DNA, for example—to identify descendants.

Studies of the remains, such as DNA analysis of dental calculus to study pathogens, might be harder to carry out under the new recommendations. Although there’s no official moratorium, no new human remains research has been approved in recent years

because of stricter requirements, Sholts says. She expects a pause on approvals while the new policy is established, but notes the report anticipates positive outcomes from future research.

The 15-member task force, including both Smithsonian staff and outsiders, says the insti-

tution should ramp up its efforts to identify both lineal descendants and communities of descent and then initiate contact, rather than waiting for repatriation requests. The report recommends the Smithsonian request new funds and staff for the massive repatriation effort, but does not say how much would be needed.

“I’m impressed,” says Carlina de la Cova, a biological anthropologist at the University of South Carolina who is not on the task force. The recommendations “will force scholars working with the dead to think about how they engage with [remains] and what that means for the living.” She adds that it’s the first time a museum has made such recommendations public, and she expects other institutions to follow the Smithsonian’s steps.

Sholts agrees: “This first step towards a long-overdue reckoning makes it more likely that others will do the same.” ■

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National Museum of Natural History