Scientists say they have pinpointed genetic changes that allow some Ethiopians to live and work more than a mile and a half above sea level without getting altitude sickness. The specific genes differ from those reported previously for high-altitude Tibetans, even though both groups cope with low-oxygen in similar physiological ways, finds a study in the journal PLOS Genetics.

If confirmed, the results may help scientists understand why some people are more vulnerable to low blood oxygen levels caused by factors other than altitude — such as asthma, sleep apnea, heart problems or anemia — and point to new ways to treat them. The study adds to our understanding of how high-altitude populations worldwide have evolved to be different from their low-altitude ancestors, the researchers say.

Living with less
Lower air pressure at high altitude means fewer oxygen molecules for every breath. “At 4000 meters, every lungful of air only has 60% of the oxygen molecules that people at sea level have,” said NESCent researcher Cynthia Beall of Case Western Reserve University.

To mop up scarce oxygen from thin air,
Uncovering Africa’s oldest known penguins

Africa isn’t the kind of place you might expect to find penguins. But one species lives along Africa’s southern coast today, and newly found fossils confirm that as many as four penguin species coexisted on the continent in the past. Exactly why African penguin diversity plummeted to just one species is still a mystery, but changing sea levels may be to blame, the researchers say.

The fossil findings represent the oldest evidence of these iconic tuxedo-clad seabirds in Africa, predating previously described fossils by 5 to 7 million years.

Co-authors Daniel Thomas of the National Museum of Natural History and Dan Ksepka of the National Evolutionary Synthesis Center happened upon the 10-12 million year old specimens in late 2010, while sifting through rock and sediment excavated from an industrial steel plant near Cape Town, South Africa.

Jumbled together with shark teeth and other fossils were 17 bone fragments the researchers recognized as pieces of backbones, breastbones, wings and legs from several extinct species of penguins.

Based on their bones, these species spanned nearly the full size spectrum for penguins living today, ranging from a runty pint-sized penguin that stood just about a foot tall (0.3 m), to a towering species closer to three feet (0.9 m).

Only one penguin species lives in Africa today — the endangered black-footed penguin, or Spheniscus demersus. But newly found fossils confirm that as many as four penguin species coexisted on the continent in the past. PHOTO BY DANIEL THOMAS.

Humans probably aren’t to blame, the researchers say, because by the time early modern humans arrived in South Africa, all but one of the continent’s penguins had already died out.

A more likely possibility is that rising and falling sea levels did them in by wiping out safe nesting sites.

Although penguins spend most of their lives swimming in the ocean, they rely on offshore islands near the coast to build their nests and raise their young. Land surface...
Beef up your evolutionary toolbox
Register now for summer courses from the NESCent Academy

Interested in hands-on training workshops in evolutionary biology? Act fast: Applications will soon close for the following NESCent Academy courses for summer 2013. Graduate students, postdoctoral fellows and junior faculty members are eligible to apply.

Next-generation sequencing data for phylogenetics and phylogeography
When: June 3-9, 2013
Where: Durham, NC
Application review begins: April 1
The rapid expansion of genomic resources and explosion of new genome sequencing technologies allows researchers to obtain large phylogenomic data sets for any system, rapidly and economically. In this course, students will receive an overview of recent technological advances, learn about data collection using emerging phylogenomic approaches, and analyze data sets using the most recent methods. Areas to be covered include: (1) emerging sequencing technologies, (2) targeted high-throughput sequencing approaches, such as anchored phylogenomics, transcriptome sequencing, reduced-representation library sequencing/RAD sequencing, and high-throughput amplicon sequencing, and (3) data analysis, including phylogenetic and phylogeographic analyses, and species delimitation.

INSTRUCTORS: Alan Lemmon & Emily Moriarty Lemmon (Florida State), Cecilé Ané (U. of Wisconsin-Madison), Jeremy Brown (Louisiana State), Frank Burbrink (College of Staten Island/ CUNY), Seth Bybee (Brigham Young), Laura Kubatko (Ohio State), David Weisrock (U. of Kentucky)
HOW TO APPLY: Application review began April 1. For more info and a link to the application, visit bit.ly/I3KBJT.

Generic Model Organism Database (GMOD) Summer School
When: July 19-23, 2013
Where: Durham, NC
Application review begins: June 10
The Generic Model Organism Database (GMOD) project provides free, open-source, interoperable software packages for visualization, storage, and dissemination of genetic and genomic data. The GMOD Summer School is a five-day course that covers the installation and usage of a number of widely used GMOD components, including the configuration of tools for different server and data types, and setting up a database with a Chado schema. The course is taught by members of the software development teams, who are all experienced developers, and GMOD project staff. The course comprises a set of hands-on tutorials; most sessions are four hours long (a half day), and the evenings feature work sessions where the instructors are available to answer questions and help participants use the tools with their data.

INSTRUCTORS: Scott Cain (GMOD, GBrowse, Chado), Dave Clements (Galaxy), Sheldon Mackay (GBrowse synteny browser), Rob Buels (JBrowse), Barry Moore (MAKER), Stephen Ficklin (Tripal), Ed Lee (Web Apollo)
HOW TO APPLY: Application review begins June 10. For more info and a link to the application, visit bit.ly/Yhpz1F.

Ontologies for evolutionary biology
When: July 29-August 3, 2013
Where: Durham, NC
Application review begins: June 1
Evolutionary research has been revolutionized by the explosion of genetic information available, and ontologies must play a central role in relating this knowledge to observable diversity. Ontologies provide scaffolding that interconnects many kinds of observations; across species, they provide evolutionary, developmental, and mechanistic insights. In this course, we will discuss the integration points between ontologies including anatomy, phenotype, ecology, and biodiversity efforts; on partnerships between domain experts and expert ontologists; and on descriptions of various tools and tricks to handle ontologies and ontology-annotated data in the context of evolutionary biology.

INSTRUCTORS: Melissa Haendel, Matt Yoder, Jim Balhoff, Erik Segerdell
HOW TO APPLY: Application review begins June 1. For more info and a link to the application, visit bit.ly/ZAQ6Dt.

Evolutionary quantitative genetics
When: August 5-10, 2013
Where: Durham, NC
Application review begins: May 20
Quantitative genetics deals with the inheritance of measurements of traits that are affected by many genes. Developments in the field are not reflected in textbooks and available courses aimed at evolutionary biologists. This workshop will review the basics of theory in the field of evolutionary quantitative genetics, its connections to evolution that is observed at various time scales and illustrate how that theory can be tested with data. Participants will learn to use R, an open-source statistical programming language, to build and test evolutionary models.

INSTRUCTORS: Steve Arnold, Joe Felsenstein, Thomas Hansen, Trudy Mackay, Brian O’Meara, Patrick Phillips, Liam Revell, Josef Uyeda
HOW TO APPLY: Application review begins May 20. For more info and a link to the application, visit bit.ly/ngFq5y.

Proposing a course
Got an idea for an evolution-related course that you want to teach? NESCent welcomes proposals for short 1-2 week courses at the postgraduate level. NESCent provides the venue, budget and logistics support, allowing PIs to focus on the syllabus and format. The deadline for course proposals is July 10 of each year: bit.ly/MASFBP.
THE PREMIER INTERNATIONAL CONFERENCE OF EVOLUTIONARY BIOLOGISTS

Sign up for a workshop on teaching evolution to undergrads
WHERE: Snowbird Conference Center
WHEN: Friday, June 21
8:30 a.m. - 5 p.m.
Evolution is a key biological concept, but it is also a very challenging topic to teach. Join us for a day focused on effective methods and tools for teaching evolution. Designed for future and current faculty, this workshop will cover national movements to improve undergraduate biology education, evolution resources to use in the classroom, information on how students learn evolutionary concepts, and more. $25 registration fee includes lunch, as well as a collection of materials for teaching evolution. Sign up for the workshop by paying the $25 fee when you register for Evolution 2013 on the main conference registration site. Limited to 30 participants. For more information visit bit.ly/154unuC or contact Louise Mead (lsmead@msu.edu), Jamie Jensen (jamie.jensen@byu.edu) or Kristin Jenkins (kjenkins@nescent.org).

Tracking the trail of big data
Join us for the 4th annual iEvoBio conference on evolutionary informatics
WHERE: Snowbird Conference Center
WHEN: Tues.-Wed. June 25-26
8 a.m. - 5 p.m.
Are you interested in the intersection of biology, software, and mathematics? Come to the iEvoBio Meeting on June 25-26, in conjunction with Evolution 2013 in Snowbird, Utah!
The iEvoBio Meeting brings together biologists working in evolution, systematics and biodiversity with software developers and mathematicians. You can participate by giving a 5-minute lightning talk on a method, idea, or software product about bioinformatics, by demonstrating your open-source software product, or by joining a “birds of feather” group, an informal group of meeting participants with a common interest.
You’ll also see talks by two fabulous keynote speakers, Drs. Holly Bik (hollybik.com/) and Heather Piwowar (researchremix.org/)
You can register for iEvoBio alone or together with the main meeting. Get the latest program details, find answers to frequently asked questions, and more at ievobio.org/

NEW AWARDS

Grad students win travel awards to attend the “World Congress on Evolution III”

Congratulations to the two outstanding graduate students who were selected for travel awards to attend the third “World Congress on Evolution,” to be held June 1-5, 2013, on the Galapagos Island of San Cristobal.

Melissa Kemp is a third-year PhD student in Elizabeth Hadly’s lab at Stanford University, and Aide Macias Muñoz is a first-year PhD student from Adriana Briscoe’s lab at UC Irvine.
The awards will cover conference registration, travel, food and lodging. As part of NESCent’s efforts to serve members of groups that are under-represented or under-served in evolutionary science, the awards were restricted to graduate students who identify as American Indian/Alaska Native, Asian, Black/African American, Hispanic/Latino/Latina, and/or Native Hawaiian/Other Pacific Islander.
Forty-two students applied. Our only regret is that we have funds to send just two of them. Congrats again to Melissa and Aide!
Congratulations to the newest award recipients for 2013

NESCent is pleased to announce the following new awards:

WORKING GROUPS
Michael Gavin (Colorado State University)
Explaining cultural diversity: a new evolutionary synthesis

Susan Kalisz (University of Pittsburgh)
Linking self-fertilization, dispersal and distribution traits of species: Is Baker’s law an exception to the rule?

Cynthia Riginos (The University of Queensland)
Advancing genetic diversity research in the Indian and Pacific Oceans

Mary Shenk (University of Missouri)
Integrating evolutionary models of human fertility change

LONG-TERM SABBATICAL SCHOLARS
Jeffrey Conner (Michigan State University)
Synthesizing data on natural selection and genetics across multiple scales

Uri Gophna (Tel-Aviv University)
Do microbial immune systems reduce lateral gene transfer in prokaryotic genomes?

SHORT-TERM VISITORS
Christina Caruso (University of Guelph)
Gynodioecy and the evolution of separate sexes in the flowering plants

Jeremy Chase Crawford (University of California, Berkeley)
Bridging ontogeny, mechanism, and function in the study of complex animal signals

Lynn Fellman (Fellman Studio)
Visions of Neanderkin: comparing ancient and modern genomes through art and narrative

Hafiz Maherali (University of Guelph)
Exploring ecological and evolutionary causes of the plant-fungal symbiosis

C. Tristan Stayton (Bucknell University)
Tools for measuring the magnitude and significance of convergent evolution

Brandon Routman
Explaining the framing effect through evolutionary analysis

GRADUATE FELLOWS
Meghan Balk (University of New Mexico)
Predator-prey interactions: drivers of mammalian body size evolution

Heath Blackmon (University of Texas, Arlington)
Comprehensive analysis of the rates and patterns of sex chromosome evolution in arthropods

Michael Landis (University of California, Berkeley)
Bayesian model testing of Bergmann’s Rule on mammalian biogeography

Matthew Wilkins (University of Colorado, Boulder)
Factors shaping acoustic signal evolution and implications for decision-making contexts

JOURNALISTS-IN-RESIDENCE
Rebecca Searles (The Huffington Post)
Applied evolutionary psychology and the future of human evolution

Lynn Fellman (Fellman Studio)
I am a Multi. An iBook about human genetic ancestry

Carrie Arnold (freelance)
Our microbial minds: how microbes make us human

TRIANGLE SCHOLARS
Kathleen Donohue (Duke University)
How genetics pathways influence organismal responses to climate change

Andrea Taylor (Duke University)
Big mouths or strong bites: what drives the evolution of the feeding apparatus in primates?

EVOLUTION 2013 TRAVEL AWARDS FOR FACULTY FROM MINORITY-SERVING INSTITUTIONS
Yonas Tekle (Spelman College)
Elizabeth Torres (California State University, Los Angeles)

UNDERGRADUATE DIVERSITY AT EVOLUTION TRAVEL AWARDS
Bianca Brown (CUNY York College)
Jason Bundy (Pennsylvania State University)
Joseph Caucuglia (University of Utah)
PangKou Chang (University of California, Merced)
Jessica Coates (Spelman College)
Nena Cole (Portland State University)
Emily Geest (University of Missouri- St. Louis)

DOMONIQUE HATTON (SPELMAN)
Devon Humphreys (University of Georgia)
Cierra Keith (Oklahoma State University)

Karoline Lake (Barnard College)

SHEHNA NEWTON (CALIFORNIA STATE UNIVERSITY, LONG BEACH)

Devin O’Brien (University of Connecticut)
Julio Ramirez (University of Kansas)

Victoria Rodriguez (Texas A&M University)

Riley Smith (San Francisco State University)

Jonathan Sullivan (University of Alabama, Huntsville)

Carrie Tribble (Williams College)

Madhvi Venkatraman (Occidental College)

Randee Young (Louisiana State University)

For more information about these scholars and their research projects, please visit nescent.org/science/awards.php.
“Uncovering Africa’s oldest known penguins” (NBC News) Africa isn’t the kind of place you might expect to find penguins. But one species lives along Africa’s southern coast today, and newly found fossils confirm that as many as four penguin species coexisted on the continent in the past. Exactly why African penguin diversity plummeted to the one species that lives there today is still a mystery, but changing sea levels may be to blame. The fossil findings represent the oldest evidence of these iconic tuxedo-clad seabirds in Africa, predating previously described fossils by 5 to 7 million years, says NESCent postdoc Dan Ksepka. Also picked up by Discovery, the Huffington Post, the UK Daily Mail and Scientific American. Read the full story at bit.ly/14qKT7J.

“Text-mining spat heats up: scientists and publishers clash over licenses that would let machines read research papers” (Nature) It is seen as the future of computer-based research — if only the gatekeepers would let scientists in. Fearful that their content might be freely redistributed, publishers tend to block computer programs that they find crawling across the full text of research articles, a methodology known as text mining that can reveal large-scale patterns in the studies. NESCent postdoc Heather Piwowar says that it is unfair that large firms such as Google are allowed to crawl across content to index it — yet scientists are restricted: bit.ly/147X2qg.

Call for proposals
Looking for support for a graduate student, faculty sabbatical, short-term visit or meeting? NESCent welcomes your proposals. We are looking to support innovative approaches to outstanding problems in evolutionary biology. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students.

Proposals for short-term visits are two weeks to three months. Proposals for sabbaticals may be for up to a full year. The next deadline for short-term visitors and graduate fellowships is July 1. For sabbaticals, catalysis meetings and course proposals, the next deadline is July 10:

• Apply to be a short-term visitor at NESCent. Next deadlines July 1, Sept. 1: bit.ly/3X1icKb.
• Graduate students are invited to apply for one-semester research fellowships in NC. Next deadline July 1: bit.ly/chaOcr.
• Evolution researchers of all nationalities are welcome to apply for sabbatical fellowships at NESCent. Next deadline July 10: bit.ly/4beg6U.
• Apply for meeting funds to bring 30 scientists together to tackle the research question of your choice. Next deadline July 10: bit.ly/qKdzrX.

For more information, please visit bit.ly/cfJUJx.

Job openings
Interested in employment opportunities at NESCent? Our center runs with the help of a dynamic team of programmers, financial experts, event planners, and other specialists. To find out about job openings as they become available, visit nescent.org/about/employment.php.
In the Miocene, when sea levels were much lower, Madagascar and other islands may have been connected to the African mainland by land bridges. This allowed penguins, which are typically Associated kernels, to breed while staying safe from mainland predators. However, as sea levels rose, these land bridges were submerged, isolating populations on different islands. This isolated environment may have allowed for the evolution of unique subspecies that are not found in the African penguin population today.

But sea levels in the region are lower today. Once-isolated islands have been reconnected to the continent by newly exposed land bridges, which may have wiped out beach nesting sites and provided access to predators. Although humans didn’t do previous penguins in Africa in, we’ll play a key role in shaping the fate of the one species that remains, the researchers add. Numbers of black-footed penguins have declined by 80% in the last 50 years, and in 2010 the species was classified as endangered. The drop is largely due to oil spills and overfishing of sardines and anchovies — the black-footed penguin’s favorite food.

“There’s only one species left today, and it’s up to us to keep it safe,” Thomas said.

travelers to high altitude compensate by making more hemoglobin, the oxygen-carrying component of human blood. But high hemoglobin comes with a cost. Over the long term, excessive hemoglobin can increase the risk of blood clots, stroke, and chronic mountain sickness, a disease characterized by thick and viscous blood.

“Altitude affects your thinking, your breathing, and your ability to sleep. But high-altitude natives don’t have these problems,” said Beall, who has studied high altitude adaptation in different populations in Ethiopia, Peru and Tibet for more than 20 years. “They don’t wheeze like we do. Their thinking is fine. They sleep fine. They don’t complain of headaches. They’re able to live a healthy life, and they do it completely comfortably,” she added.

How do they do it?

Research over the last four decades has revealed that people born and raised in mountainous regions cope with altitude in different ways. Native highlanders in Tibet and some in Ethiopia, for example, are able to maintain relatively low blood hemoglobin concentrations at high altitude compared to their counterparts in the Andes, a trait that makes them less susceptible to chronic mountain sickness.

Tibetans and some Ethiopians have both evolved a dampened response to low oxygen, explained study co-authors Anna Di Rienzo and Gorka Alkorta-Aranburu of the University of Chicago.

The researchers wanted to pinpoint the genetic changes that enable Ethiopians to thrive in thin air, and to see if the same genes play a role for Ethiopians as found in recent studies for Tibetans. When they scanned the villagers’ DNA, the researchers found a genetic variant associated with low hemoglobin levels in the Amhara. This variant was located in a different region of the genome than those previously found to be associated with low hemoglobin in Tibetans. In other words, the physiological coping mechanisms shared by Amhara and Tibetans in response to life at high altitude — ie., dampened hemoglobin levels — are due to different underlying genes.

It is still unclear whether the first settlers of high altitude regions in Ethiopia and Tibet carried different genetic variants with them when they arrived, or whether different mutations occurred in these populations after they got there. But it’s clear that each group followed a different evolutionary pathway.

“They have a similar physiologic solution, but that doesn’t necessarily amount to a similar genetic solution,” Di Rienzo said.

For the Omoro — who are relative newcomers to high altitudes — the researchers also found differences between highlanders and lowlanders in DNA methylation, a chemical process that causes changes in gene activity, but doesn’t necessarily alter the genetic code. While the differences aren’t linked to hemoglobin levels, the results suggest that such changes may play a role in the early stages of high altitude adaptation, the researchers say.