that would be compatible with the Fermi bump were too conservative. Fresh estimates of the γ-ray 'noise' produced by known sources, provided by the Fermi science team[3] and others[4], allow for much heavier particles. "The excess can be explained with a particle of up to 200 GeV," says Simona Murgia, a physicist at the University of California, Irvine, and a leading scientist in the Fermi team.

BIG-BANG FIT

Armed with this insight, Caron and his collaborators recalculated the predictions of the MSSM theory and found another potential explanation for the excess — an existing dark-matter candidate called a neutralino. The neutralino was heavy enough not to be excluded by previous experiments, yet light enough to potentially be produced in the second run of the LHC.

Caron's model also produces a prediction for the amount of dark matter that should have been created in the Big Bang that is compatible with state-of-the-art observations of the cosmic microwave background — the relic radiation of the Big Bang — performed by the European Space Agency's Planck probe (see *Nature* http://doi.org/38k; 2014). This cannot be a coincidence, he says. "I find this quite amazing."

> ***"This could very well be the single most promising explanation for the Galactic Centre."***

Caron's team is not the only one reanalysing the Fermi bump in light of the new estimates. Similar but less-detailed calculations done by Fermilab physicist Patrick Fox and his colleagues last November[5] also revealed the neutralino as a potential cause of the Fermi γ-rays. And Katherine Freese, director of Nordita, the Nordic Institute for Theoretical Physics in Stockholm, says that she and her collaborators have calculated that the excess could be caused by a type of dark matter that features in a less-popular theory of supersymmetry.

Resolution may be just around the corner. In addition to being produced at the LHC, the neutralino could also be within the shooting range of next-generation underground experiments that are trying to catch dark-matter particles that happen to fly through Earth, says physicist Albert De Roeck, who works on the CMS, one of the two LHC detectors that will hunt for dark matter. If such a particle is indeed the cause of the γ-rays, he says, "it seems that the dark-matter signals should be observed very soon now". ■

1. Achterberg, A. *et al.* Preprint at http://arxiv.org/abs/1502.05703 (2015).
2. Goodenough, D. & Hooper, D. Preprint at http://arxiv.org/abs/0910.2998 (2009).
3. Murgia, S. Talk given at the Fifth Fermi Symposium, Nagoya, 20–24 October 2014; available at go.nature.com/wfwhh6.
4. Calore, F., Cholis, I. & Weniger, C. Preprint at http://arxiv.org/abs/1409.0042 (2014).
5. Agrawal, P., Batell, B., Fox, P. J. & Harnik. R. Preprint at http://arxiv.org/abs/1411.2592 (2014).

PALAEOGENETICS

Mammoth genomes hold recipe for Arctic elephants

Catalogue of genetic differences reveals how ice-age giants braved the cold.

BY EWEN CALLAWAY

Woolly mammoths, unlike their elephant cousins, were creatures of the cold, with long hairy coats, thick layers of fat and small ears that kept heat loss to a minimum. Now, for the first time, scientists have comprehensively catalogued the hundreds of genetic variations that gave rise to these differences.

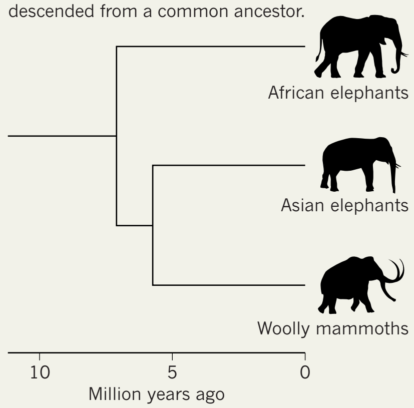
The research reveals how woolly mammoths (*Mammuthus primigenius*) evolved from the ancestor they share with Asian elephants (*Elephas maximus*; see 'Mammoth divergence'). It could even serve as a recipe for engineering elephants to live in Siberia. "These are genes we would need to alter in an elephant genome to create an animal that was mostly an elephant, but actually able to survive somewhere cold," says Beth Shapiro, an evolutionary geneticist at the University of California, Santa Cruz, who was not involved in the latest research. As fanciful as it sounds, such an effort is at a very early stage in a research lab in Boston, Massachusetts.

The first woolly mammoth genome[1] was published in 2008, but contained too many errors to reliably pinpoint how it differs from the elephant genome. Other studies singled out variations in mammoth genes that would have led to light-coloured coats[2] and oxygen-carrying haemoglobin proteins that work in the cold[3].

In the latest study, a team led by Vincent Lynch, an evolutionary geneticist at the University of Chicago in Illinois, describe how they sequenced the genomes of three Asian elephants and two woolly mammoths (one died 20,000 years ago, another 60,000 years ago). They found that about 1.4 million DNA letters differ between mammoths and elephants, which altered the sequence of more than 1,600 protein-coding genes. The study[4] was posted on the biology preprint server bioRxiv.org on 23 April.

MAMMOTH DIVERGENCE

Woolly mammoths and elephants are descended from a common ancestor.



SOURCE: ADAPTED FROM REF. 4

A search for what those proteins do in other organisms revealed genes that could be relevant to life in the Arctic. Several were involved in setting the circadian clock, a potential adaptation to living in a world with dark winters and 24 hours of daylight in summer. The mammoth genomes also contained extra copies of a gene that controls the production of fat cells, and some of the genes that differ between the two species are involved in sensing heat and transmitting that information to the brain.

In the case of one heat-sensing gene, which encodes a skin protein called TRPV3 that also regulates hair growth, the team 'resurrected' the mammoth version. They inserted the gene sequence into human cells in the lab, which then made the protein. Exposing the mammoth TRPV3 to different temperatures revealed that it is less responsive to heat than the elephant version is. The next step, says Lynch, is to insert the same gene into elephant cells that have

NAT. HIST. MUS., LONDON/SPL

been programmed to behave like embryonic cells, and so can be turned into various cell types. These could then be used to examine how mammoth proteins work different tissues. Lynch's team also plans to test the effects of other mammoth variations in this way.

MAMMOTH TASK

Similar work is already under way in the lab of geneticist George Church at Harvard Medical School in Boston. Using a technology known as CRISPR/Cas9 that allows genes to be edited, his team claims to have engineered elephant cells that contain the mammoth version of 14 genes potentially involved in cold tolerance.

The work, says Church, is a preamble to potentially editing into the elephant genome all the variations that differentiate it from the woolly mammoth genome — and perhaps, one day, even resurrecting the woolly mammoth, or at least giving an Asian elephant enough mammoth genes to survive in the Arctic. A reserve in north Siberia, dubbed Pleistocene Park, has even been proposed as a home for such a population of cold-tolerant elephants.

It is not clear whether this would ever be feasible, however. Such a venture could allow endangered Asian elephant populations to thrive, but innumerable hurdles stand in the way of breeding genetically modified 'woolly elephants'. Shapiro outlines these in her book *How to Clone a Mammoth* (Princeton University Press, 2015; see review on page 30), charting the ethics of using reproductive technologies for an endangered species and the fact that the field of elephant reproductive biology is still immature. "I probably should have called the book *How One Might Go About Cloning a Mammoth (Should It Become Technically Possible, And If It Were, In Fact, a Good Idea, Which It's Probably Not),*" Shapiro says. "But that was a much less compelling title." ■

Woolly mammoths (artist's impression) evolved from a shared elephant ancestor to survive the cold.

1. Miller, W. *et al. Nature* **456,** 387–390 (2008).
2. Römpler, H. *et al. Science* **313,** 62 (2006).
3. Campbell, K. L. *et al. Nature Genet.* **42,** 536–540 (2010).
4. Lynch, V. *et al.* Preprint at bioRxiv http://dx.doi.org/10.1101/018366 (2015).