The authors note that more research is required before the technique can be safely applied to hives outside the laboratory environment. In particular, bee-to-bee transmission of microbiota both within and between hives needs to be better understood. While within-hive transmission of engineered *S. alvi* may prove beneficial by promoting the persistence and spread of pathogen resistance, between-hive transmission may not be desirable.

Nonetheless, beyond their commercial and ecological value, honey bees are also an important model organism. Thus, in addition to its application to bee health, the symbiont-mediated RNAi system offers a useful new research tool for analysing the functions of genes involved in myriad biological processes.

Dorothy Clyde

ORIGINAL ARTICLE Leonard, S. P. et al. Engineered symbionts activate honey bee immunity and limit pathogens. *Science* **367**, 573–576 (2020)
RELATED ARTICLE Grozinger, C. M. & Zayed, A. Improving bee health through genomics. *Nat. Rev. Genet.* https://doi.org/10.1038/s41576-020-0216-1 (2020)

Credit: PaulPaladin/Alamy

of the protein structures and normalization of migration rates. Expression of exogenous β-actin mRNA, in the presence of trapped endogenous β-actin mRNA, was also able to restore cell migration to normal levels.

The optogenetic control afforded by mRNA-LARIAT will help to dissect the roles of specific mRNAs and RNA–protein interactions at the single-cell level.

Linda Koch

ORIGINAL ARTICLE Kim, N. Y. et al. Optogenetic control of mRNA localization and translation in live cells. *Nat. Cell Biol.* https://doi.org/10.1038/s41556-020-0468-1 (2020)

Credit: Klaus Vedfelt/DigitalVision/Getty

POPULATION GENOMICS

There and back again — ancient genes reveal early migrations

Previous studies have shown that modern Europeans, Asians and Americans carry Neanderthal DNA in their genome as a result of interbreeding between *Homo neanderthalensis* and *Homo sapiens*. Now, a study in *Cell* suggests that these sequences may also be present in modern Africans, owing to previously undescribed migratory events.

Using a novel technique called IBDmix, Chen et al. compared a genome obtained from Neanderthal remains from the Altai mountains with those of 2,504 modern individuals worldwide. The technique assessed the probabilities that sections of DNA are shared between the modern and archaic genomes. The length of the identified genes could be used to differentiate whether genes were from a common ancestor in the distant past or introduced via interbreeding events approximately 50,000 years ago. Previous studies investigating Neanderthal genes used a modern African reference genome as a negative control to differentiate admixing from common shared ancestry, under the assumption that there was little admixing between Neanderthals and populations from Africa owing to their geographical isolation. In these studies, African genomes were shown to have less than 1 Mb of sequence homology with Neanderthals. However, using the 'reference-free' IBDmix method, the team found a much larger Neanderthal sequence in African populations, with an average of 17 Mb per individual.

To understand how these genes could be present in Africans, given that Neanderthals were localized to Europe and Asia, the authors simulated characteristics such as the length and frequency of introgressed archaic segments in the modern African genomes and the amount of sequence shared between African and non-African populations based on different historical demographic situations. They then compared these predictions with their empirical data. The authors found that the most probable model of admixture with Neanderthals was not due to a single interbreeding event between Neanderthals and African ancestors, but through back-migration of non-African ancestors carrying Neanderthal genes into Africa. Their model also supported the introduction of *H. sapiens* DNA into the Neanderthal genome through early migration events from Africa.

By comparing data from chromosome 1 for all of the African samples and identifying tracks of European and East Asian ancestry, the authors found that the rate of overlap with Europeans, but not East Asians, was significant, suggesting not only that back-migration occurred after the split of Europeans and East Asians but also that migration of Europeans to Africa specifically contributed to African Neanderthal ancestry. Of the European Neanderthal sequence, 7.2% was shared exclusively with Africans, which is substantially higher than the 2% of East Asian sequences shared with Africans. The authors note that this increased homology between European and African Neanderthal sequences may have contributed to the bias seen in previous methods, which identified an enrichment of more than 20% of Neanderthal DNA in East Asians compared with Europeans. Using IBDmix, this number was found to be closer to 8%, indicating that Neanderthal ancestry among non-African populations is more uniform than previously described.

The data therefore show that back-migration and gene flow events led to the introgression of Neanderthal genes into the genome of early Africans and that Neanderthal genes are universal across modern human populations. "We often imagine there was a single dispersal out of Africa," says senior author Joshua Akey (Princeton University, USA). "Our results show … there were many waves of dispersal out of Africa, some of which led to admixture between modern humans and Neanderthals that we see in the genomes of all living individuals today."

Joseph Willson

ORIGINAL ARTICLE Chen, L. et al. Identifying and interpreting apparent Neanderthal ancestry in African individuals. *Cell* https://doi.org/10.1016/j.cell.2020.01.012 (2020)