TRANSCRIPTOMICS

EVOLUTION OF EUSOCIALITY

Eusocial insects of the order Hymenoptera display reproductive division of labour, whereby offspring are born to reproductive individuals but cared for by others ('workers') in a colony. A new transcriptomics study implicates insulin signalling as a mechanism underlying the evolution and regulation of this social behaviour.

Looking at seven different ant species, including queen-less species, the authors compared gene expression in whole brains or heads of reproductive ants with those of worker ants. The expression of one gene, *insulin-like peptide 2* (*ilp2*), was consistently upregulated in reproductive animals.

To investigate the role of ILP2, the team used the clonal raider ant *Ooceraea biroi*, a queen-less species in which workers reproduce asexually and whose colonies alternate between brood-care and reproductive stages. The brood-care phase begins when larvae hatch from eggs, as the larvae suppress reproduction and induce brood care in adults. The reproductive phase begins when the larvae pupate, upon which all workers produce eggs through a type of parthenogenesis.

ILP2 protein was found exclusively in the brain of *O. biroi*. Removing larvae from colonies in the brood-care phase increased *ilp2* expression, whereas adding larvae in the reproductive phase decreased *ilp2* expression, in brains of adults. Injecting synthetic ILP2 into adults in the presence of larvae strongly activated ovaries, thus overriding inhibitory larval signals.

These findings, as well as previously reported functions of ILP2 in larval growth, metabolism and reproduction in other organisms, strongly support a role for this protein in reproductive potential.

Linda Koch

ORIGINAL ARTICLE Chandra, V. et al. Social regulation of insulin signalling and the evolution of eusociality in ants. *Science* **361**, 398–402 (2018)
FURTHER READING Yan, H. et al. Eusocial insects as emerging models for behavioural epigenetics. *Nat. Rev. Genet.* **15**, 677–688 (2014)

HUMAN EVOLUTION

FOXP2 tells a cautionary tale

The forkhead box transcription factor encoded by *FOXP2* has a role in human speech and language, and has long been suggested to be an important factor in the evolution of these traits. Atkinson et al. now show that previous conclusions about recent selection at this locus may have been artefacts of the data set used.

Complex spoken language is a uniquely human attribute, and *FOXP2* is heralded as a key gene in this trait. Mutations are associated with language disorders, and FOXP2 has a role in fetal brain development, as well as in communication in other animals. In 2002, a study by Enard et al. found that this gene is highly conserved in primates, but two non-synonymous mutations seemed to be fixed in the small sample of humans tested. A likelihood-based analysis detected positive selection at this locus on the human lineage, and population genetic approaches (Tajima's D) implied a recent selective sweep. This finding led to suggestions that the locus has a causal role in the evolution of human speech, although this hypothesis was questioned when the same mutations were found in Neanderthal and Denisovan genomes. In light of improvements in sequencing, Atkinson et al. now re-examined the evidence for selection at this locus.

Calculating Tajima's D for genomic data from the Human Genome Diversity Panel and the 1000 Genomes Project, the authors replicated the signal of positive selection at *FOXP2*. However, population substructure can influence this test. Indeed, when African individuals were considered separately from populations which had been through the out-of-Africa bottleneck, the significant signal disappeared. Other tests of selection corroborated this observation, and the authors concluded that the previous finding of a selective sweep on the early human lineage may have been due to skewed

> "the previous finding of a selective sweep on the early human lineage may have been due to skewed population sampling"

COMPLEX TRAITS

Lessons from 1 million genomes

A person's educational attainment is a model behavioural phenotype for genetic analysis owing to the very large available sample sizes. A study published in *Nature Genetics* now reports a genome-wide association study (GWAS) for educational attainment in more than 1 million individuals and identifies 1,271 independent lead single-nucleotide polymorphisms (SNPs) associated with this phenotype.

In total, 71 independent cohorts were brought together in a sample-size-weighted meta-analysis to increase the number of analysed individuals from the previous 405,072 to now 1,131,881. The 162 SNPs known from the hitherto largest study showed good reproducibility in the newly added data sets. Analysis of the X chromosome in a subset of 694,894 individuals uncovered 10 lead SNPs, and the SNP heritability due to the X chromosome was estimated at 0.3%, which is lower than what would be expected for a comparable autosome. A separate analysis of the X chromosome in women and men (including only data from the UK Biobank) demonstrated almost identical SNP heritability estimates between sexes.

Using a Bayesian statistical framework, posterior probabilities of

Credit: Ellen Isaacs/Alamy