

## In this issue . . .

### Genetic basis of convergent evolution in pandas

Despite being classified as carnivores, giant pandas and red pandas, which separately evolved from meat-eating ancestors and diverged from each other around 47.5 million years ago, subsist almost entirely on bamboo—a phenomenon termed phenotypic convergence, which is observed in distantly related species. Additionally, both species possess a false thumb, which enables the animals to adroitly grasp bamboo. To uncover the genetic basis of such convergence, Yibo Hu et al. (pp. 1081–



Wild giant panda.

1086) sequenced the genome of a wild male red panda and compared it with the reassembled genome of the giant panda. Genome analysis revealed signs of adaptive convergence in 70 genes, including convergent amino acid replacements in two genes—*DYNC2H1* and *PCNT*—implicated in false-thumb development. Further, enzymes involved in dietary protein digestion and amino acid utilization as well as proteins involved in vitamin metabolism and absorption showed signs of adaptive convergence, suggesting that these genes may have similarly evolved to support and supplement a bamboo-based diet. Giant and red panda genomes share 10 pseudogenes, which are versions of genes decommissioned over evolutionary time. Notably, the *TAS1R1* gene, which enables carnivores to taste meat's umami flavor, was rendered a pseudogene in both species, reflecting the animals' shift from carnivory to omnivory and, ultimately, herbivory. According to the authors, comparative genomic analysis can illuminate the genetic basis of phenotypic convergence. — P.N.

### Improving vaccine design

Many promising vaccine candidates for bacterial, parasitic, and viral diseases are unstable and expensive to produce for clinical use. For instance, the malaria vaccine candidate, *Plasmodium falciparum* reticulocyte-binding protein homolog 5 (PfRH5), has shown effectiveness in animal models, but the protein exhibits only moderate temperature tolerance and is expensive to produce, limiting the vaccine's usefulness in many malaria-endemic countries. Ivan Campeotto et al. (pp. 998–1002) developed a computational one-step design strategy to improve the design of a PfRH5-based malaria vaccine. Using phylogenetic analysis and simulations, the authors identified mutations likely to occur in the PfRH5 protein, and subsequently developed three optimized



Improving vaccine design for *P. falciparum*, transmitted by mosquitoes. Image courtesy of CDC/James Gathany.

PfRH5 variants that were experimentally tested in *Escherichia coli*. Compared with the wild-type PfRH5, the PfRH5 variants were more easily produced and exhibited improved stability in the bacteria; the most improved PfRH5 variant, bearing 18 mutations, had a thermal tolerance 10–15 °C higher than wild type, and retained the wild-type bacterium's immunogenic properties. According to the authors, the computational method might help to enhance the design of vaccines for many diseases. — C.S.

### Educational attainment, genetics, and fertility

Educational attainment is associated with genetic variation as well as having fewer children, suggesting that the average genetic propensity for education in a population should decline over time. To test this idea, Augustine Kong et al. (pp. E727–E732) developed a polygenic score of a person's genetic propensity for educational attainment based on the results of a recent genome-wide association study. The authors calculated this score for more than 100,000 Icelanders born between 1910 and 1975; the reproductive history of the same individuals was obtained from the deCODE genetics genealogical database. Individuals with a high genetic propensity for education tended to have children later in life, and consequently fewer children overall, than those with low propensity for education. The associations

remained significant even after adjusting for the individuals' education levels, suggesting that the association between the polygenic score and reproduction was mostly independent of education. Analysis of more than 120,000 Icelanders born between 1910 and 1990 revealed a significant decline in polygenic score with year of birth. According to the authors, the results suggest that the tendency for individuals with high polygenic scores to have few children leads to selection against genetic variants associated with educational attainment. — B.D.



The University of Birmingham. Genetic propensity for educational attainment may have declined over time. Image courtesy of Wikimedia Commons/GavinWarrins.