PATHOGEN-DRIVEN EVOLUTION

Coronavirus footprints

Curr. Biol. https://doi.org/10.1016/j.cub.2021.05.067 (2021)

Host–pathogen conflict has driven the rapid evolution of host proteins targeted by pathogens, which mediate interactions between organisms and infectious agents. A third major coronavirus outbreak within the past two decades has motivated extensive research and led to the discovery of hundreds of human proteins that interact with SARS-CoV-2 and other coronaviruses. Souilmi et al. recently examined the genes encoding these virus-interacting proteins (VIPs) and found signatures of past selective sweeps in 42 coronavirus VIPs in three East Asian populations but none of the examined populations outside East Asia. Using the recently developed genealogical reconstruction method RELATE, the authors estimated the time of onset of selection on the VIPs. They found evidence of sustained selection pressure acting between 20,000 and 5,000 years ago, indicating an influential presence of coronaviruses or viruses with similar biology in East Asia within that period. The study represents a novel approach to reconstructing past episodes of adaptation to viral exposure. *OA*

https://doi.org/10.1038/s41588-021-00916-w

PLANT GENOMICS

Hybrid potato genetics

Cell https://doi.org/10.1016/j.cell.2021.06.006 (2021)

Tetrasomic inheritance and clonal propagation in cultivated potatoes have historically been major barriers to genomic improvement. In addition, self-incompatibility in natural populations and landraces of diploid potato has prevented the development of inbred lines, which are of commercial interest because they can enable rapid incorporation of beneficial alleles through backcrossing. Although approaches such as the removal of self-incompatibility through genetic manipulation have seen some success, they have not been able to adequately decrease heterozygosity in the potato genome. A major hurdle in decreasing heterozygosity has been the prevalence of deleterious alleles across the genome that have accumulated over centuries of clonal propagation. Zhang et al. recently provided a new template for the development of diploid hybrid potatoes. Starting with two self-compatible diploid lines with low heterozygosity, the authors identified large-effect deleterious alleles and used genome-assisted selection to remove them, while also stacking beneficial alleles. The resulting highly homozygous inbred diploid lines produced vigorous F1 hybrids, thus possibly paving the way toward a 'green revolution' in potato breeding. *OA*

https://doi.org/10.1038/s41588-021-00917-9

GENE EDITING

Sickle-cell anemia gene therapy

Nature **595**, 295–302 (2021)

The emergence of highly efficient gene-editing technologies has shown promise for developing new therapeutic tools for human genetic disorders. Although past studies using CRISPR–Cas9 have yielded encouraging results, by-products such as chromosomal mutations from Cas9-mediated double-strand breaks hinder clinical translation. Adenine base editors (ABEs) can efficiently convert A–T base pairs to G–T pairs when guided to a site of interest by catalytically impaired CRISPR–Cas9, and were developed through directed evolution of a transfer-RNA adenosine deaminase. Newby et al. have now demonstrated durable editing of the sickle-cell disease allele in the β-globin gene into a non-pathogenic variant in human-patient hematopoietic stem and progenitor cells that were transplanted into mice. Editing successfully mediated phenotypic rescue, thus suggesting a potential one-time ABE treatment for sickle-cell disease. *OA*

https://doi.org/10.1038/s41588-021-00918-8

POPULATION GENETICS

Cultural and genetic interplay

Nat. Commun. **12**, 3581 (2021)

The extent to which culture interacts with genetics is of great interest in understanding human demographic and evolutionary changes over time. López et al. have examined genetic variation in >1,200 Ethiopian individuals belonging to 68 different ethnic groups, and found correlations of genetic distance with language, geographic distance, reported ethnicity and cultural practices, such as wearing lip plates. Although determining causal relationships between correlated genetic and cultural factors can be difficult, estimating the timing of demographic events, such as population splits, alongside archaeological data can provide useful insights. For example, the authors found genetic evidence across different communities of recent isolation along occupational lines. Socially marginalized occupational groups, such as cultivators or weavers, probably diverged from different occupational groups, such as blacksmiths and tanners, ~4,200 years ago, a time corresponding to the start of ironworking in Ethiopia. *OA*

https://doi.org/10.1038/s41588-021-00915-x

SPATIAL TRANSCRIPTOMICS

Single-cell spatial sequencing

Science **373**, 111–117 (2021)

Single-cell sequencing technologies highlight that bulk measurements of gene expression conceal biological complexity, but these methods do not typically provide spatial resolution. Current spatial transcriptomics approaches generally measure the expression of a targeted set of genes or do not resolve single cells, thus resulting in a lack of information about functional heterogeneity across neighboring cells. Srivatsan et al. recently introduced a new spatial transcriptomics method called sci-Space that creates unique combinations of barcoded DNA oligonucleotides arranged in space and transfers them onto permeabilized nuclei on a tissue slide. The DNA oligonucleotides then provide spatial coordinates for each single cell that is subsequently sequenced. The authors applied sci-Space to developing mouse embryos and identified thousands of genes with patterned expression and spatial transcriptomic signatures of neuronal migration. *OA*

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