related synchronization issue — how to delay the witness bunch behind the drive bunch with sub-picosecond accuracy so that it interacts properly with the wakefield — would have to be investigated. It will also be important to understand and mitigate possible beam-quality degradation during the acceleration process as particles in the accelerated bunches scatter against the plasma electrons (and ions). Several groups are already vigorously investigating these issues; Corde and colleagues' results provide further impetus to these studies. ■

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EVOLUTION

Gene transfer in complex cells

A comparative genomic study shows that, during evolution, nucleus-containing cells acquired DNA from bacteria primarily by endosymbiosis — the uptake and integration of one cell by another. SEE ARTICLE P.427

JOHN M. ARCHIBALD

Once controversial, the idea that genetic material can be transferred laterally between organisms is now known to be a key factor in the evolution of the prokaryotes (bacteria and archaea), whose DNA is not enclosed in a nucleus[1]. However, it is unclear to what extent such transfer affects eukaryotic (nucleus-bearing) cells, which are typically thought to transmit their genes vertically from parent to offspring. In this issue, Ku *et al.*[2] (page 427) assess the contribution of lateral gene transfer (LGT) to the eukaryotic nuclear genome, and conclude that, although prokaryote-to-eukaryote LGT has happened, it has not extensively affected the eukaryotic cell over long evolutionary timescales.

The nuclear genome is an ever-evolving mosaic of DNA acquired from different sources (Fig. 1). For instance, mitochondria and chloroplasts are eukaryotic organelles derived from prokaryotic cells that were assimilated by another cell through a process called endosymbiosis. Although these organelles usually retain some DNA, most of their original genome has moved to the host nucleus through endosymbiotic gene transfer (EGT)[3]. In the case of chloroplasts, subsequent eukaryote–eukaryote endosymbioses have spread the organelle and its associated genes laterally across the evolutionary tree[4]. But, endosymbiosis aside, how web-like is eukaryotic genome evolution?

In multicellular eukaryotes, the separation of the sex cells from the rest of the organism is often assumed to be a strong barrier to the stable acquisition of foreign DNA. However, the strength of this assumption has been questioned[5], and there are compelling examples of recent, lineage-specific LGT in both animals[6] and plants[7]. Viruses can serve as gene-transfer vectors[8] and might facilitate LGT in eukaryotes as they do in prokaryotes[1]. Single-celled eukaryotes might acquire DNA simply by ingesting and digesting prey[9]. Most eukaryotic LGT has been inferred solely on the basis of phylogenetic incongruence — genes whose evolutionary histories are at odds with known or predicted organismal relationships. But phylogenetic trees are prone to artefacts and open to interpretation. As such, the true impact of LGT in eukaryotes is debated.

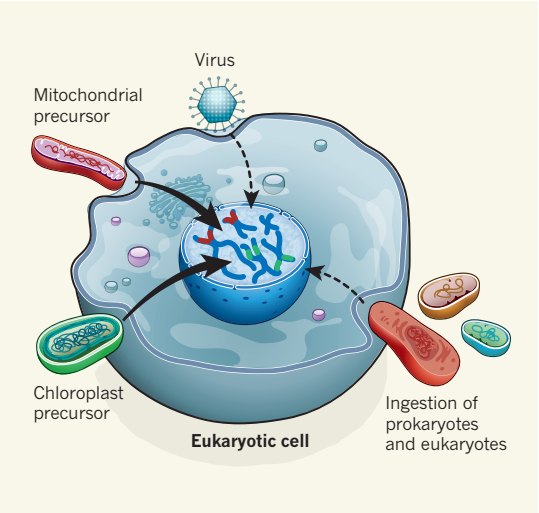

Figure 1 | Acquiring foreign DNA. The nuclear genome of eukaryotic (nucleus-containing) cells is a mosaic of genes from various sources, including prokaryotes (bacteria and archaea). Foreign DNA may enter eukaryotes when they ingest other cells, or through viruses, which can act as gene-transfer vectors. Ku *et al.*[2] report that such lateral gene transfer has had a minimal impact on the nuclear genome (indicated by dashed arrows), but that the origin of organelles called mitochondria and chloroplasts from bacterial endosymbionts provided a rich source of foreign DNA.

Ku *et al.* studied thousands of genomes from across the breadth of cellular life. Their analytical framework is based on the following premise: if prokaryote-to-eukaryote LGT has played a meaningful part in eukaryotic evolution, then its long-term impact should be detectable and cumulative. Nuclear genomes should accumulate prokaryotic genes and become increasingly different from one another over time. By contrast, the accumulation of prokaryotic genes due to EGT will be episodic.

The authors compared just over 950,000 protein sequences inferred from the genomes of 55 different eukaryotes to one another and to more than 6 million prokaryotic sequences. The analysis identified 2,585 sequence families, each comprising related (homologous) proteins encoded by two or more eukaryotic genomes and five or more prokaryotic genomes: these families were designated as eukaryote–prokaryote clusters. The remaining 26,117 families were labelled eukaryote-specific clusters.

An overview of the distribution of eukaryote–prokaryote clusters reveals an expectedly large evolutionary footprint associated with the endosymbiotic origin of chloroplasts. Hundreds of nuclear genes are absent in species lacking chloroplasts but are shared by various groups of photosynthetic eukaryotes (and are abundant in cyanobacteria, from which chloroplasts evolved[4]). The endosymbiotic footprint of mitochondrial evolution is also apparent, albeit less distinct.

Phylogenetic trees inferred from each eukaryote–prokaryote cluster paint a remarkable picture of the history of prokaryotic genes in eukaryotes. For 74.8% of these clusters, the proteins from different eukaryotes are on adjacent branches (they are monophyletic), and eukaryote monophyly cannot be ruled out for an additional 12.7% of protein families. This pattern would not be expected if eukaryotes were steadily acquiring genes from different prokaryotic groups.

Instances of eukaryote monophyly could, nevertheless, be the result of a single prokaryote-to-eukaryote LGT

followed by multiple LGT events between eukaryotes. Indeed, eukaryotic homologues in the eukaryote–prokaryote clusters are often patchily distributed: some are present in only two of the six recognized high-level groups of eukaryotes, and many more are limited to three or four such groups. Although patchy gene distributions are often interpreted as evidence for LGT[1,5,10], Ku *et al.* conclude that the trees in which eukaryotic sequences are monophyletic are not the product of eukaryote-to-eukaryote LGT. Why? Statistical tests showed that the trees for eukaryote–prokaryote clusters are generally compatible with those inferred from the eukaryote-specific clusters, which are considered to be the product of vertical evolution.

The remaining 12.5% of trees for eukaryote–prokaryote clusters show the eukaryotic homologues branching apart from one another, consistent with prokaryote-to-eukaryote LGT. Ku *et al.* provide alternative explanations for such patterns, including sequencing contaminations and errors inherent in phylogenetic reconstructions. However, the authors identified several blocks of genes whose lineage-specific distributions are so striking that LGT is the only reasonable explanation. It will be interesting to see how these LGTs stack up against those identified by others[11].

Ku *et al.* conclude that gene evolution in eukaryotes is "resoundingly vertical" and that the punctate distribution of prokaryotic genes across eukaryotes is primarily the result of differential gene loss during evolution. Apart from the gene acquisitions associated with mitochondrial and chloroplast EGT, eukaryotes seem to sample prokaryotic gene diversity at a much lower level than do bacteria and archaea. Given evidence for at least some prokaryote-to-eukaryote LGT, the authors suggest that perhaps genes transferred by LGT are retained in the genome for only a short time, or that lineages that engage in LGT tend not to be successful in the long run. This latter idea is at odds with the prevailing view that LGTs are of benefit to the recipient organism[1,10].

At present, there are two types of eukaryotic gene whose histories are uncontroversial: ubiquitous genes that were probably present in the common ancestor of all eukaryotes; and lineage-specific genes with strong signatures of recent LGT. Between these two extremes lies a continuum of genes whose phylogenies and presence–absence patterns are exceedingly complex. The extent to which Ku and colleagues' analyses have fully captured the evolutionary forces that shaped the nuclear genome is unclear. Nonetheless, they have shown that EGT has been the dominant mode of gene acquisition in eukaryotes, that gene patchiness is the norm and that gene loss needs to be taken seriously. We now have the opportunity to compare notes on the strengths and weaknesses of the various approaches currently being used to distinguish lateral from vertical inheritance in eukaryotes. Consider the issue open for discussion. ■

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PHOTONICS

A stable narrow-band X-ray laser

An atomic laser operating at the shortest wavelength yet achieved has been created by bombarding a copper foil with two X-ray pulses tuned to slightly different energies. The results may lead to ultrastable X-ray lasers. SEE LETTER P.446

LINDA YOUNG

X-rays penetrate matter to image a system's internal 3D structure using contrast arising from spatial variations of elemental, chemical or magnetic properties. Lasers that function at X-ray wavelengths go beyond basic structure determination, because they can deliver bright pulses on ultrashort timescales to probe matter at the atomic level. This means that they can be used to characterize dynamic processes, such as chemical-bond formation, charge transfer and light-induced superconductivity, or to determine the macromolecular structure of a system without damaging it. Such lasers have been the subject of extreme fascination since physicist Theodore Maiman demonstrated[1] the first laser that operated at optical wavelengths in 1960. On page 446 of this issue, Yoneda *et al.*[2] demonstrate an atomic X-ray laser that yields a marked improvement in wavelength stability compared with X-ray free-electron lasers (XFELs), taking a major step towards an ångström-wavelength laser that remains in phase over its pulse duration — that is, which possesses longitudinal coherence.

XFELs[3–5], which use a high-energy electron beam as the laser-generating medium, have revolutionized X-ray science by introducing ultra-fast, ultra-intense X-ray pulses suitable for a vast range of applications. These facilities accelerate electron beams close to the speed of light (at energies in excess of 10^9 electron-volts), through 100-metre-long arrays of magnets that are arranged in a periodic pattern of alternating polarity along the beam path. These systems create, in a single passage of the electron beam, intense X-ray pulses lasting only a few femtoseconds (1 fs is 10^{-15} seconds) that contain a trillion X-ray photons and achieve peak brightness a billion times greater than radiation produced by conventional synchrotron light sources. XFELs typically operate on the principle of self-amplified spontaneous emission (SASE), whereby the accelerating electrons' incoherent emission of radiation is further amplified by continuous interaction with the electron beam over the length of the magnetic array.

Although SASE results in intense, short-wavelength laser pulses that are coherent in a plane transverse to the direction of propagation, strong longitudinal fluctuations in the time and spectral domains are observed; these can greatly complicate experiments that use these lasers. Yoneda and colleagues' X-ray laser amplifies light that has a well-defined wavelength of 1.54 Å, generated by transitions of electrons from the 2*p* orbital to the 1*s* orbital of copper atoms. This is the shortest-wavelength atomic laser ever demonstrated, surpassing by a factor of 10 an atomic neon laser that has been shown[6] to operate at 14.6 Å.

The authors' laser uses the photoionization-pumping scheme presciently proposed[7] for copper in 1967. In this scheme, the ejection of an inner-shell electron of a copper atom by a suitable light source (the pump) leaves a deficit of electrons in a lower energy level of the resulting copper ion, achieving what is known as population inversion. Electrons drop into the vacated level, spontaneously emitting photons, which are amplified as they