

8. ter Beek, J., Guskov, A., & Slotboom, D. J. *J. Gen. Physiol.* **143**, 419–435 (2014).
9. Ward, A., Reyes, C. L., Yu, J., Roth, C. B. & Chang, G. *Proc. Natl Acad. Sci. USA* **104**, 19005–19010 (2007).
10. Doerrler, W. T., Gibbons, H. S. & Raetz, C. R.

- J. Biol. Chem.* **279**, 45102–45109 (2004).
11. Zhou, G.-P. & Troy, F. A. 2nd. *Glycobiology* **13**, 51–71 (2003).

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PARTICLE PHYSICS

Positrons ride the wave

Experiments reveal that positrons — the antimatter equivalents of electrons — can be rapidly accelerated using a plasma wave. The findings pave the way to high-energy electron–positron particle colliders. [SEE LETTER P.442](#)

PHILIPPE PIOT

Particle accelerators and colliders have been the backbone of research into elementary particle physics for almost a century. The next generation of colliders must be able to generate collision energies for lepton particles, such as electrons and positrons, in the teraelectronvolt range (1 TeV is 10^{12} electronvolts). This will complement discoveries being made by the Large Hadron Collider at CERN, Europe's particle-physics laboratory near Geneva, Switzerland. On page 442 of this issue, Corde *et al.*¹ report a system for accelerating positrons — the antimatter counterparts of electrons — that might enable such instruments to be realized.

An experimental configuration of choice for colliders consists of smashing electrons (e^-) into positrons (e^+). The two particle beams are accelerated in two linear accelerators pointing towards each other, to collide head-on. The designs of e^+e^- linear colliders have mostly been based on conventional accelerator technologies that use devices known as radio-frequency resonators. But these have allowed accelerating gradients of no more than about 100 MeV per metre. The TeV-energy colliders are therefore expected to be large and costly — for example, the proposed 0.5-TeV International Linear Collider is expected to be about 30 km long².

Alternative acceleration methods have been sought since the early 1980s (ref. 3). One class of such methods is plasma wakefield beam-driven acceleration (PWFA), in which the accelerating medium is an electrically neutral plasma composed of positively charged ions and highly mobile free electrons. As a group of electrons called the drive bunch travels through the plasma, it repels the plasma electrons. This leads to spatial modulation of the plasma's electronic density, which in turn induces a strong electric field commonly called a wakefield. When another group of electrons — the witness bunch — travels at an appropriate distance behind the drive bunch, it interacts with the wakefield. This interaction causes the witness bunch to accelerate rapidly.

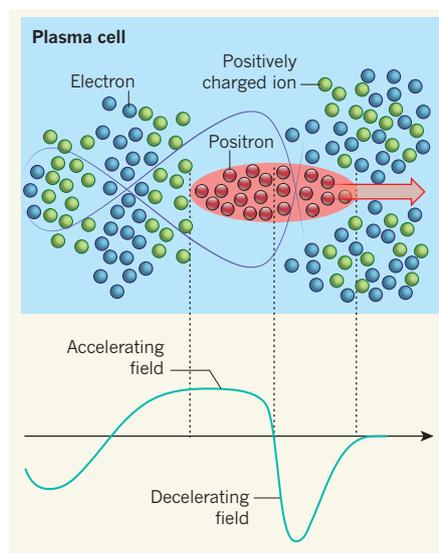


Figure 1 | Mechanism for positron acceleration.

Corde *et al.*¹ report that positrons can be accelerated in a lithium plasma composed of positive ions and free electrons; only some of the ions and electrons are shown. As the positron bunch moves from left to right, the electrons move towards it because of charge attraction; the blue line indicates a sample electron trajectory. This movement organizes electrons and ions into 'layers' behind the bunch, generating an electric field called a wakefield (depicted as a cyan trace on the lower plot). The positrons at the head of the bunch decelerate in response to the negative region of the wakefield, but positrons in the bunch's tail accelerate in an approximately uniform, positive region of the field.

The PWFA method proposed⁴ in the mid-1980s for electron acceleration was initially developed in the linear regime, in which the electron beam has a lower particle density than the plasma. It was subsequently realized that this approach could also operate in a nonlinear regime (in which the electron beam has a higher particle density than the plasma), giving rise to sharp transitions in the plasma-density modulations that could support higher accelerating fields⁵. Using the latter mechanism, often referred to as a blowout regime, accelerating gradients of about 52 GeV m⁻¹

have been attained for electron bunches⁶.

Application of the PWFA technique to accelerate positrons over a short distance is a prerequisite for a plasma-based e^+e^- linear collider. Previous work⁷ in this area demonstrated energy modulation of a positron bunch with a peak accelerating gradient of the order of 50 MeV m⁻¹. The possibility of accelerating positrons in the nonlinear regime with high acceleration has long been contemplated, but not achieved. The main hurdles arise because the dynamics of plasma electrons under the influence of a positron drive bunch are different from the dynamics induced by an electron drive bunch, and because electron bunches are not suitable for driving plasma waves that can accelerate positron bunches.

Corde *et al.* now demonstrate positron acceleration with accelerating gradients of about 5 GeV m⁻¹, which is about 100 times higher than the gradients previously reported for positrons⁷. In brief, the authors used a conventional accelerator to produce a positron bunch, and sent it through a metre-long cell of lithium plasma.

The plasma-density wave formed using positrons is different from that produced using electrons because the positron bunch attracts plasma electrons inward. As electrons flow through the bunch, the positrons gain or lose energy depending on their axial locations within the bunch (Fig. 1). At a particular plasma density, the wakefield can be tailored to switch polarity within the positron bunch, thereby decelerating the head of the bunch while accelerating positrons in the tail, effectively transferring energy from the head to the tail.

Corde *et al.* observe that the large positron population (about 1 billion positrons) experiencing the accelerating field effectively 'loads' the wakefield and affects its shape, leading to an approximately uniform energy gain for the accelerated positrons. The experiment therefore demonstrates that, by using appropriate operating parameters, only one positron bunch is needed for acceleration: part of its trailing population is 'trapped' and accelerated quasi-uniformly to higher energies, and so splits from the initial bunch. The authors observe that the newly formed and the accelerated positron bunches are quasi-monoenergetic — the positrons in the accelerated bunch have almost the same energy as each other. This is essential if the bunches are to be further transported and manipulated along an accelerator without substantial degradation of quality, for example before injection into a subsequent stage of a plasma wakefield accelerator.

Several challenges must be addressed to prove the overall suitability of a PWFA-based e^+e^- linear collider. First, several of Corde and colleagues' PWFA modules must be concatenated to reach the desired final energy. The quasi-monoenergetic bunch formed in the first module would have to be used as a witness bunch by subsequent modules, and so the

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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1. Corde, S. *et al. Nature* **524**, 442–445 (2015).
2. ILC Technical Design Report. www.linearcollider.org/ILC/Publications/Technical-Design-Report
3. Joshi, C. & Katsouleas, T. *Physics Today* **56**(6), 47–53 (2003).
4. Chen, P., Dawson, J. M., Huff, R. W. & Katsouleas, T. *Phys. Rev. Lett.* **54**, 693–696 (1985).
5. Rosenzweig, J. B., Breizman, B., Katsouleas, T. & Su, J. J. *Phys. Rev. A* **44**, R6189–R6192 (1991).
6. Blumenfeld, I. *et al. Nature* **445**, 741–744 (2007).
7. Blue, B. E. *et al. Phys. Rev. Lett.* **90**, 214801 (2003).

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 nucleus¹. 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 tree⁴. 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 questioned⁵, and there are compelling examples of recent, lineage-specific LGT in both animals⁶ and plants⁷. Viruses can serve as gene-transfer vectors⁸ and might facilitate LGT in eukaryotes as they do in prokaryotes¹. Single-celled eukaryotes might acquire DNA simply by ingesting and digesting prey⁹. 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

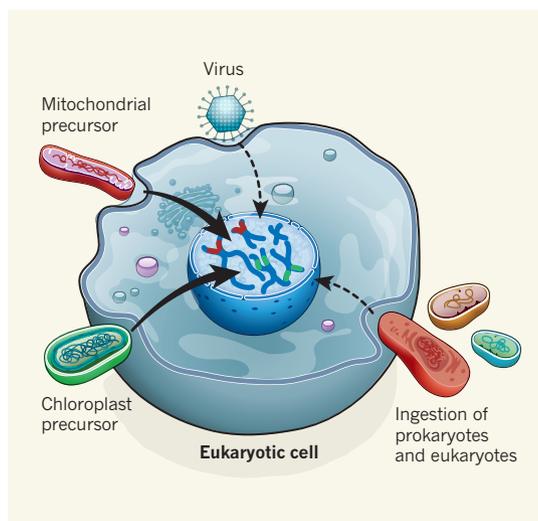


Figure 1 | Acquiring foreign DNA. The nuclear genome of eukaryotic (nucleus-containing) cells is a mosaic of genes from various sources, including prokaryotes (bacteria and archaea). Foreign DNA may enter eukaryotes when they ingest other cells, or through viruses, which can act as gene-transfer vectors. 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.

phylogenetic trees are prone to artefacts and open to interpretation. As such, the true impact of LGT in eukaryotes is debated.

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 evolved⁴). 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