

Knotted threads of darkness

Dark lines within a laser beam can be manipulated to form stable vortex knots.

Destructive interference may lead to complete cancellation when light waves travelling in different directions cross, and in three-dimensional space this occurs along lines that are vortices of electromagnetic energy flow¹. Here we confirm theoretical predictions^{2,3} by experimentally creating combinations of optical laser beams in which these dark threads form stable loops that are linked and knotted.

Since Kelvin proposed his vortex atom hypothesis⁴, temporally persistent vortex knots have been sought in fluid mechanics^{5,6}, superfluid flow⁷, field theory⁸ and nonlinear excitable media⁹. The optical vortices that we synthesize here are embedded in light beams created by a single-frequency laser (Fig. 1a; for methods, see supplementary information). A direct consequence of the linearity of Maxwell's equations for the electromagnetic field is that the intensity pattern in free space is static, so our optical vortices are stable in both space and time.

The optical phase cannot be defined on these dark threads: it is singular there (like the angle of longitude at the North Pole, for example). Consequently, there is a circulation of electromagnetic energy around the optical vortex. Around such a singularity, the phase changes by an integer multiple of 2π ; this integer, m , is the strength of the singularity.

We combine Laguerre–gaussian beams¹⁰, which have an optical vortex of integer strength m along the beam axis and two further variable parameters: p , the discrete radial number (the number of nodal rings about the beam axis), and w , the continuous waist width (which sets the transverse scale of the beam). These additional degrees of freedom allow us to create the same basic structures as those proposed in refs 2 and 3, but with the vortices more clearly defined by the surrounding intensity.

The loops, links and knot structures arise from the coaxial superposition of four beams. Three of these beams have an on-axis vortex with the same strength m , but different values of p and w . The amplitudes are chosen so that both the field and its radial derivative are zero at a specific radius in the focal plane. The resulting destructive interference forms a dark loop around the axial strength singularity. Adding a simple gaussian beam with small amplitude distorts this loop into an $(m, 2)$ torus knot¹¹, threaded by an m -stranded helix of strength-one vortices. If $m=2$, the vortices form two linked loops (Fig. 1b); if $m=3$, they form a trefoil knot (Fig. 1c).

Our optical beams are produced by using a single-frequency helium–neon laser beam illuminating a hologram. This forms the

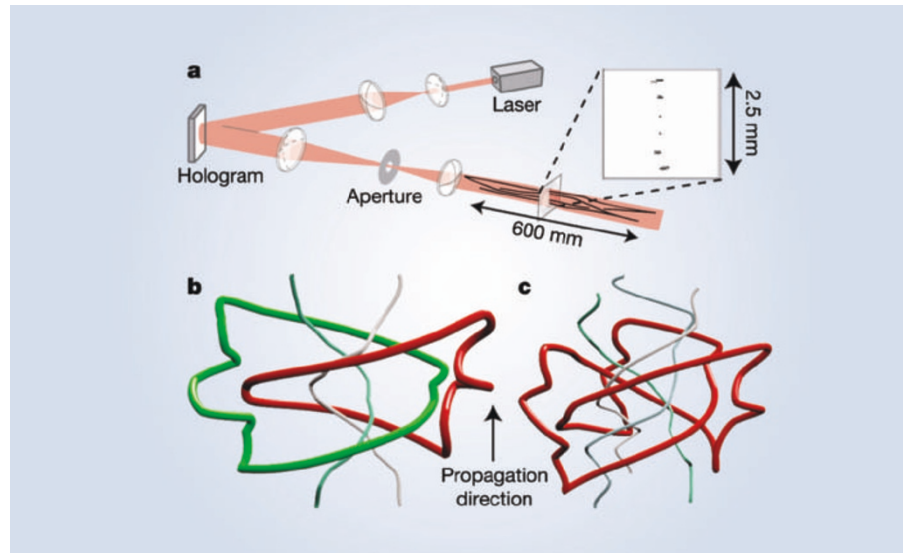


Figure 1 Knotted lines of darkness. **a**, Light from a hologram is passed through a spatial filter and a camera images the beam cross-section in various planes. Thin black lines represent the threads of darkness that form the link or knot. Inset shows the observed oversaturated beam cross-sections at the beam waist of the link; dark points indicate positions where the optical vortex threads cross the observation plane. **b,c**, Three-dimensional representations of measured link (**b**) and trefoil knot (**c**) configurations. The link and knot are threaded by further vortices (represented by the thinner tubes) that follow the axis of the light beam.

intensity and phase structure of the desired superposition of Laguerre–gaussian beams. As the fine structure of the singularities lies in regions of near darkness, it is necessary to oversaturate the camera to determine their positions in the beam cross-section accurately. The resulting image contains points of darkness corresponding to the positions of the dark threads as they intersect the plane of the camera.

We have produced stable link and knot structures formed from vortices in an optical beam. Our observations demonstrate the precision control of light beams that is required to create complex regions of zero light intensity. Such regions could be used, for example, to confine cold atoms and Bose–Einstein condensates in complex topologies¹².

Jonathan Leach*, **Mark R. Dennis†‡**, **Johannes Courtial***, **Miles J. Padgett***

*Department of Physics and Astronomy, University of Glasgow, Glasgow G12 8QQ, UK
e-mail: j.leach@physics.gla.ac.uk

†H. H. Wills Physics Laboratory, Tyndall Avenue, Bristol BS8 1TL, UK

‡School of Mathematics, University of Southampton, Highfield SO17 1BJ, UK

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Plant genetics

Gene transfer from parasitic to host plants

Plant mitochondrial genes are transmitted horizontally across mating barriers with surprising frequency, but the mechanism of transfer is unclear^{1,2}. Here we describe two new cases of horizontal gene transfer, from parasitic flowering plants to their host flowering plants, and present phylogenetic and biogeographic evidence that this occurred as a result of direct physical contact between the two. Our findings complement the discovery that genes can be transferred in the opposite direction, from host to parasite plant³.

Both cases of horizontal gene transfer involve the mitochondrial gene *atp1* and the recipient *Plantago*, a large cosmopolitan genus comprising mostly weeds. We examined 43 *Plantago* species, all containing an intact *atp1* gene. Despite the exceptional divergence of these genes, their relationships

to one another (Fig. 1, top) and their inclusion in Plantaginaceae agree with independent estimates⁴ of the phylogeny for these taxa. This clade of *Plantago atp1* genes is therefore most likely to be the product of standard vertical transmission.

Each of three related *Plantago* species contains a second, full-length *atp1* copy with several frameshift mutations. This clade of pseudogenes is allied with the distantly related genus *Cuscuta*, as indicated by bootstrap (97%) and other analyses (Fig. 1, and see supplementary information), implying that a species of *Cuscuta* transferred a copy of *atp1* to the common ancestor of these three *Plantago* species. *Cuscuta* is a large genus of flowering plants (also known as dodders; Fig. 2) that parasitizes an unusually broad range of hosts⁵, including *Plantago*⁶. The three *Plantago* species are native to Europe and north Africa, as are many dodders, including *C. europaea* (Fig. 1).

Two other species of *Plantago* (*P. rigida* and *P. tubulosa*) also contain a second, full-length copy of *atp1*. These too are pseudogenes and are probably also derived by horizontal gene transfer. *Bartsia*, a genus in the parasitic family Orobanchaceae, is identified as the likely gene donor by phylogenetic analysis (81% bootstrap support; Fig. 1). Biogeography neatly supports this inference, because *P. rigida*, *P. tubulosa* and most species of *Bartsia* are found exclusively at high altitudes in the northern Andes^{7,8}.

Both lineages of *Plantago atp1* pseudogenes were almost certainly acquired by horizontal gene transfer, as indicated by evidence against their inclusion in the *Plantago*-wide clade of vertically transmitted *atp1* genes and in favour of their phylogenetically anomalous inclusion with parasitic plants. (The possibility of DNA contamination can be ruled out; see supplementary information.) Phylogenetic distribution of the transferred genes and molecular clock analysis (see supplementary information) indicate that both transfers were recent (within the past few million years).

Both transfers probably occurred by direct plant-to-plant transmission of DNA from parasitic to host plants. This is indicated by phylogenetic evidence that parasitic plants, which penetrate host plants intracellularly as part of their normal life cycle, served as donors in both transfers. It is also suggested by the striking biogeographic concordance of donors and recipients in the case of the high-altitude, northern Andean *Bartsia*, *P. rigida* and *P. tubulosa*, as well as by the broad host ranges of both groups of parasitic donors. The well documented exchange in both directions of macromolecules, viruses and phytoplasmas between parasitic plants and their hosts^{9–11} is also consistent with plant-to-plant transmission.

We cannot altogether rule out the possibility that the involvement of parasitic plants

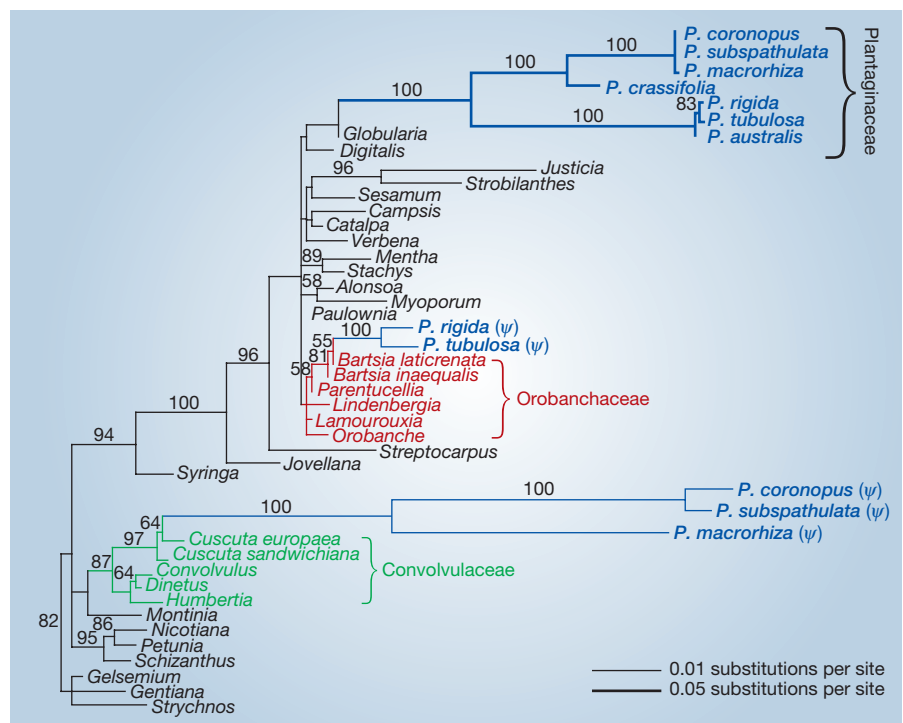


Figure 1 Phylogenetic evidence for two horizontal transfer events of the gene *atp1* into *Plantago* (blue). Seven *Plantago atp1* genes at the top of the maximum-likelihood tree are intact, vertically transmitted, and rapidly evolving (scale reduced by 80%). The other two sets of *Plantago atp1* genes are pseudogenes (ψ) acquired from parasitic plants in the Orobanchaceae (red) and Convolvulaceae (green). Bootstrap values of over 50% are shown. For methods, see supplementary information.



Figure 2 A parasitic dodder (*Cuscuta californica*) in flower, with its haustoria penetrating a host tomato plant.

as donors is fortuitous — for example, some biological vector (such as pollen, fungus, a bacterium or virus, or an insect) may have caused indirect transfer. But our direct-transfer hypothesis is more parsimonious and is supported by the evidence available.

The parasitic lifestyle has evolved roughly a dozen times in flowering plants and there are more than 4,000 species of parasitic plants¹², providing plenty of opportunity for horizontal gene transfer not only from parasite to host, but also from host to parasite³. Parasites with narrow host ranges may exchange genes frequently with their hosts. Those with broad host ranges (dodders, for example) may also act as vectors for gene transfer by directly bridging unrelated host species. In addition to parasitism, other vectors, and non-vectored mechanisms such as grafting, may promote horizontal gene transfer during plant evolution.

Jeffrey P. Mower, Saša Stefanović*, Gregory J. Young, Jeffrey D. Palmer
Department of Biology, Indiana University, Bloomington, Indiana 47405, USA
e-mail: jpalmer@bio.indiana.edu
*Present address: Department of Biology, University of Toronto at Mississauga, Mississauga, Ontario L5L 1C6, Canada

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Evolution: How do characters evolve?

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