

Arabidopsis when the synergid promoter was used; egg and central cell promoters failed. Synergids appear to have a specialized secretory system that has evolved to pump out pollen tube attractants [12].

Arabidopsis ovules expressing ZmEA1-GFP were placed next to wild-type *Arabidopsis* ovules in an *in vitro* system where maize pollen tubes could be grown (Figure 1C). In control experiments, one of the two *Arabidopsis* ovules expressed GFP, and only about 15% of maize pollen tubes headed toward it, and these kept growing past the ovule. In contrast, >50% of maize pollen tubes were attracted to an *Arabidopsis* ovule expressing ZmEA1-GFP; of these, ~30% stopped very near the micropyle.

This result shows that expression of a single molecule is sufficient to re-orient the direction of an extending maize pollen tube so that it would grow toward an *Arabidopsis* ovule. As representatives of the two classes of flowering plants, maize (monocot) and *Arabidopsis* (dicot) shared a common ancestor ~150 million years ago [13], suggesting that pollen tube guidance in all flowering plants may be governed by a system of attractants that can be transferred from one species to another.

Can pollen tube attraction be engineered for extreme plant breeding? Plant breeders introduce useful traits (e.g. disease resistance, drought tolerance, nutrition) to crop plants by cross-pollination followed by selection of recombinants with desired traits. Prospects for continued improvement of crops are diminished when the group of plants that can be crossed with each other is limited or lacks genetic diversity [14]. The experiments published by Márton *et al.* begin to test the concept that reproductive systems could be engineered so that genomes from two plants of different species, genera, perhaps even family, order, or class, could be combined.

Márton *et al.* have shown that pollen tubes of maize can be brought to an *Arabidopsis* ovule. This result suggests that barriers to extremely wide crosses can be overcome, but many significant challenges remain. Maize pollen tubes stopped at the *Arabidopsis* micropyle, but did not enter it, and did not burst to release sperm, so it was not possible to evaluate whether a zygote containing

a maize/*Arabidopsis* genome could be produced. The signals that instruct the pollen tube to burst and release sperm are also specific [15], and there is evidence that molecules required for sperm to fuse with the egg and central cell are not compatible between divergent species [16]. Additional challenges will be to overcome embryo lethality caused by aberrant chromosome segregation and imbalance of gene dosage in hybrids. While these obstacles are significant, this is an exciting time for plant reproduction research, and our understanding of the critical mechanisms is increasing rapidly. With continued progress, the goal of engineering reproductive systems to produce novel plant genomes could be achievable.

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Genome Evolution: Where Do New Introns Come From?

A new study reports creation of spliceosomal introns in multiple related fungal species by proliferation of cryptic elements. Resonances to a case in unrelated algae suggest such elements hold general answers to long-standing mysteries of intron evolution.

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The discovery 35 years ago that the DNA encoding an mRNA can be interrupted by introns — intervening sequences that are removed from

transcripts — was one of the most unexpected discoveries in the history of molecular genetics [1]. This discovery immediately raised a host of questions that remain debated to this day. Do introns have a general function? What are the fitness

implications of introns? Are introns recent or ancient or somewhere in between? A report by van der Burgt and coauthors [2] in this issue of *Current Biology* forges significant progress on perhaps the most elusive question: how are new introns created?

The majority of intron sequences appear to be largely unconstrained, and consequently intron sequences change rapidly over evolutionary time. These changes quickly erase sequence clues to the mechanisms by which new introns are created; thus, identifying recently created introns is vital. Nearly ten years ago, we performed the first large-scale search for intron gains, in some 1,500 pairs of mouse–human orthologs [3]. The results were deeply surprising: no evidence for intron creation was found in either species in 80 million years, a conclusion that was later extended to the entire genome [4]. Subsequent studies found a similar dearth of intron creation among related species in many biologically and phylogenetically diverse eukaryotic lineages. At the same time, comparisons of more distantly related eukaryotes revealed significant differences, indicating dramatic episodes of intron creation during some periods of eukaryotic history (indeed, the qualitative interspecies differences in intron–exon structures, from only a handful of introns in some unicellular species to some 200,000 per vertebrate genome, require massive recurrent remodeling of gene structures through evolution [5]). In total, the data suggested a highly punctate history: many or most lineages experience little intron creation, with occasional bursts. What was needed was the discovery of ongoing modern bursts.

Worden *et al.* [6] reported the first well-characterized case a few years ago. In sequencing the green alga *Micromonas pusilla*, they found thousands of otherwise typical introns with highly similar sequences. This pattern suggests widespread creation of introns by a family of proliferating elements (termed Introner) within the last few millions years, implying a rate of intron insertion many orders of magnitude higher than that in mammals. However, given the sheer dissimilarity to all other studies of intron evolution, it was unclear whether this case represented the long-sought grail, both revealing the

mechanism of intron gain and explaining the punctate phylogenetic distribution of intron gains, or a mere exceptional curiosity, or something in between.

Van der Burgt *et al.* [2] report families of highly similar intron sequences in several different closely related species, suggesting evolutionarily sustained proliferation of introns over millions of years. As with the *Micromonas* Introner, these Introner-Like Elements (ILEs) are efficiently removed from transcripts, harbor canonical spliceosomal splicing motifs, and are found in unrelated genes across the genome. The finding that proliferation is ongoing and limited to a group of closely related species suggests a single origin of a proliferating element capable of creating introns. ILE sequences appear to diverge quickly: elements from the most distant species do not have recognizable sequence similarity to each other. They also provide evidence that ILEs have preserved RNA secondary structures, suggesting that an RNA intermediate is involved in the mechanism of ILE spread.

The resonances between Introner and ILEs, elements from unrelated eukaryotic lineages, is compelling, suggesting a potentially general mechanism for bursts of intron gain. Given the apparently rapid rate of sequence divergence in ILEs, it is hard to test for a direct evolutionary relationship between Introner and ILEs; however, the disparate biology of the two lineages would seem to greatly reduce the opportunities for lateral transfers, suggesting independent evolution. Assuming that Introner and ILEs evolved independently, this suggests a scenario in which rare intron bursts in diverse eukaryotes are due to convergent *de novo* emergence of replicating, intron-creating elements.

However, it is unlikely that ILEs explain the entire story of intron gain. First, a wide variety of other intron creation mechanisms have been demonstrated over the past few years, including recruitment of pre-existing exonic sequence, local tandem duplication, repair of double strand breaks, insertion of organellar sequence, and occasional transposition of individual introns to a single additional site in the genome (reviewed in [7]). In particular, intron gains in a variety of lineages seem to primarily arise from splicing of

stretches of quasi-random sequence inserted during double strand break repair (DSBR) [8]. Thus, even if the bursts of gains caused by ILEs turn out to account for the majority of dramatic intron creation episodes, DSBR and other mechanisms are likely to play a role in background intron gain in a larger number of lineages, and are thus an important part of the story. Second, multiple mechanisms seem to be active in some lineages: most strikingly, widespread intron creation in the dynamic genome of the chordate *Oikopleura dioica* appears to reflect a combination of active mechanisms, including at least transposable element insertion and local transposition of individual introns [9]. In addition, one of the species undergoing ILE proliferation may also have recently experienced intron creation by local transposition of non-ILE introns [10].

These recent studies make significant progress on long-standing questions on the origin of new introns; however, they raise an even larger range of questions. Firstly, how do these newly inserted introns impact organismal function and fitness, and do these effects vary greatly across species? Secondly, do new ILE families arise from existing spliceosomal introns, from more typical transposable elements, or in some other way? Thirdly, how often do new ILE families emerge, and is the origin of ILEs purely serendipitous or dependent on particular organismal features? Fourthly, what is the mechanism(s) of ILE proliferation? Fifthly, can ILEs account for most or all bursts of intron gain during eukaryotic evolution? Discovery of additional cases in other diverged eukaryotic lineages should shed light on the true nature of ILEs and their role in reshaping the intron–exon landscapes of eukaryotic genomes.

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Group Dynamics: Predators and Prey Get a Little Help from Their Friends

Transfer of information about predatory attacks between individuals allows schooling or flocking prey to evade predation without disrupting group integrity. But, predators can mitigate this effect by working together themselves.

Graeme D. Ruxton

You and I will probably not meet a violent end: in the USA, less than four out of a thousand people end up murdered [1]. Things are less cosy in the natural world: for example, some studies suggest that most zebras end their days in the grasp of a lion [2]. Hence, predation is a very potent selective force, and animals show a huge diversity of adaptations that can be understood in terms of managing their predation risk. One widespread and intensively-studied adaptation is group living. There are a number of mechanisms by which grouping can reduce predation risk. If predators can only catch one individual at a time, the risk for group members can be diluted as most will escape when a group is attacked. Moreover, this benefit can increase with group size more steeply than the costs of larger groups, for instance, being more obvious [3]. A group of prey has many eyes to watch out for surprise attacks, and sometimes the facility to mount a collective defence, e.g. when water buffalo form a circle with their horns facing outward and their vulnerable rumps protected in the centre. Furthermore, if the group is moving then predators appear to suffer a confusion effect where they have difficulty tracking a particular moving individual against the distracting background of other

similar moving alternative targets [4]. This last mechanism in particular has often been suggested to explain the extraordinary coordinated displays of schooling fish and some flocking birds.

However, it would be surprising if predators had not co-evolved countermeasures, and in this issue of *Current Biology* Handegard *et al.* [5] provide a fascinating demonstration of such countermeasures in predaceous spotted seatrout (*Cynoscion nebulosus*) attacking schools of juvenile Gulf menhaden (*Brevoortia patronus*). Their observations on naturally occurring attacks in the Gulf of Mexico were made possible by high-frequency imaging sonar giving 2 cm spatial resolution across a 24 m² area and 8 Hz temporal resolution. Handegard *et al.* [5] first of all demonstrated the prey's defensive measures. When a seatrout mounts an attack towards the school, there is a coordinated response of school members to maintain a safe distance from the approaching predator, so a vacuole of empty space in the school opens up in front of the predator and closes behind it (Figure 1). This coordinated movement of individuals requires information transfer over greater distances than those at which fish can detect the predator in the turbid water, and over faster timescales than a fish can swim. Such group-level responses

can be understood as emerging from individuals reacting to the acceleration of their near neighbours only [6].

Seatrout, however, often do not attack alone, but in a coordinated group of individuals attacking in line astern. This tactic prevents the closing off of the vacuole behind the first attacker. Furthermore, different parts of the school respond to the multiple threats such that the coherence of movement across the whole school breaks down, which in extreme cases can lead to a breaking up of the school into smaller parts. The sonar did not allow individual predation events to be recorded, but predators were able to get much nearer to fish when schools were smaller and within-school movements were less coherent. Such close proximity is very likely to lead to predation: the predators are faster than their prey in a straight line and it is only their better manoeuvrability that normally lets prey stay out of close proximity to the predators.

Our understanding the dynamics of coordinated group movement has made great strides over the last decade. This was mainly driven by observation of the emergent patterns from computer models of individuals that react to their neighbours according to rules that the modellers can specify. These models have had conspicuous success in demonstrating that the apparent complexity of coherent group-level movement can be generated by very simple local interactions without centralised control or special sensory or cognitive powers [6–8]. However, in the last few years computational and technological improvements have also allowed empirical work to make dramatic strides [9–14]. These studies suggest