JUMPING GENES AND THE
SPECTACULAR EVOLUTION
OF FLOWERING PLANTS

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The emergence and rapid rise of flowering plants is one of the most extraordinary and yet still not fully explained phenomena in evolutionary history. Could what Darwin himself called an “abominable mystery” be caused by jumping genes?

Flowering plants are amazingly diverse organisms. At one extreme are species of duckweed that comprise single floating leaves just 1 mm in length. At the other extreme are giant banyan trees that may cover an area of more than a hectare and species of eucalypts standing more than 80 metres tall.

All told, there are at least 350,000 species of flowering plants distributed globally from the tropics to even the continent of Antarctica, where two species of grasses exist.

Flowering plants are second only to insects in terms of species diversity on Earth, and include all annuals as well as all plants with a carnivorous or parasitic lifestyle. This sharply contrasts with their non-flowering relatives, such as conifers and cycads, which comprise barely 1000 species and seem to be evolving slowly.

The apparent abrupt origin of flowering plants in the Cretaceous period 90–135 million years ago and their extraordinarily rapid diversification did not go unnoticed by Charles Darwin. He famously referred to this phenomenon as an “abominable mystery” as it appeared to conflict with his notion of evolutionary gradualism in which “nature does not make a leap”.

Modern explanations for the spectacular success of flowering plants include their propensity to undergo duplications of their entire genome as well as interspecies hybridisation, while much diversity is associated with modifications for pollination by birds and insects and seed dispersal.

While valid and persuasive, these and other factors still do not fully account for the amazing diversity of flowering plants. For a more complete and satisfactory explanation we must additionally consider the crucial role played in plants by DNA sequences called transposable elements (TE) – more simply known as “jumping genes”.
Jumping genes have created a huge amount of phenotypic variation that plant breeders have harnessed to develop foods like blood pranges, purple broccoli, sticky rice and Roma tomatoes.

The TE Thrust Hypothesis

Jumping genes are mobile segments of DNA that can actively insert themselves, or a copy of themselves, into new positions within the genome. They can arise either spontaneously from DNA sequences within a genome, or can be introduced into a genome by transferring across from other species.

Although jumping genes were once thought to be nothing more than “junk” or “parasitic” DNA, the past two decades of research have revealed numerous instances where these mobile DNA elements have been responsible for the generation of beneficial traits in a wide variety of multicellular organisms. This led us to propose jumping genes as powerful facilitators of evolution and formalise this into the “TE thrust” hypothesis (AS, Jan/Feb 2012, pp.18–21).

TE thrust, or a lack of it, explains:
- why some biological lineages have a great number of species and others have few;
- different rates of evolution; and
- the existence of seemingly unchanged species known as living fossils.

Since jumping genes vary in activity over time, TE thrust also supports a “punctuated equilibrium” model of evolution – periods of rapid evolution interspersed by slower periods – consistent with the fossil record.

The ability of jumping genes to cause genetic change can be either active or passive in nature. In the active mode of TE thrust, evolution is facilitated by the movement or “jumping” of these mobile DNA sequences into and around genes, often in intermittent bursts. The passive mode of TE thrust can subsequently occur once these DNA elements have copied and pasted themselves extensively throughout a genome.

Huge numbers of similar jumping genes promote a form of “genetic confusion” that increases the chances of DNA rearranging inappropriately or of chromosomes pairing and crossing over incorrectly, resulting in a gain or loss of intact genes. Sometimes jumping genes can themselves be transformed into novel genes with a useful function, a phenomenon known as “molecular domestication”.

Jumping Genes and the Origin and Diversification of Flowering Plants

Flowering plants generally have high numbers of fairly active jumping genes, with many species having the majority of their genome comprised of them. For example, an incredible 84% of the large maize genome has originated from jumping genes.

The high percentage of mobile DNA sequences in flowering plant genomes means that they will strongly exhibit the extra evolutionary boost that TE thrust can provide, both in its active and passive modes. Indeed, jumping genes have helped drive the origin and diversification of flowering plants by facilitating a multitude of genetic changes.

Most spectacular are instances where crucial genes that underpin key characteristics of flowering plants were directly derived from jumping gene sequences. This includes the Mustang and Sleeper genes that are found only in flowering plants and play important roles in growth, reproduction and flower development. Other prime examples where jumping genes have provided the raw material to create entirely new genes are Fhy3 and Far1, which are responsible for key light-sensing mechanisms that are critical for processes such as shade tolerance, seed germination and flowering.

Thus jumping genes appear to be directly implicated in the earliest origins of flowering plants while conferring upon this lineage adaptive advantages that have aided their extraordinary diversification.

Plants cannot move, so they must adapt to many environmental stresses such as drought, disease, soil conditions and temperature. This is another area of flowering plant biology
where jumping genes have proved beneficial. For example, tolerance of sorghum to aluminium in soil is due to a tiny mobile DNA element called a MITE that inserted itself in front of a resistance gene called AltSB. The MITE acts as a control switch to turn the gene on in cells of the root tip, and thus lead to aluminium removal.

Even more remarkable was the creation of the stress response gene, *ILP*, in certain wheat species. Not only did a mobile element actively create this gene using its copy-and-paste mechanism to duplicate a pre-existing gene, but a separate jumping gene acted as a control switch to enable this new gene to work. Such an instance nicely illustrates the unparalleled ability of jumping genes to generate genetic novelties and thus potentially underpin all manner of evolutionary innovations.

**Jumping Genes in the Domestication and Diversification of Crops and Ornamentals**

Besides promoting evolutionary advancements naturally in the wild, jumping genes have also made significant contributions to the domestication of flowering plants for use by humans as food crops and ornamental flowers. This should hardly be a surprise: while human selection in generating cultivated plants has foresight and strategy, it must nevertheless rely on the same generators of genetic change as natural selection in the wild (unless employing modern genetic modification technology).

A prominent example of this comes from maize. During domestication, the corn plant went from a highly branched wild progenitor called teosinte to its modern, single upright main stem. This transformation can be explained in large part by the insertion of a jumping gene in front of a gene called *tb1*. This created a new control switch that led to increased production of the *tb1* gene product, whose biological function is to repress the development of branches.

This genetic event predated maize domestication by at least 10,000 years, which illustrates how ongoing TE thrust can generate adaptive potential that can be realised later due to natural selection or, as in this case, human selection.

Further to plant domestication, jumping genes have created a huge amount of phenotypic variation in cultivated plants that humans have gradually selected to breed various cultivars of crops. Purple broccoli, blood oranges, sticky rice and Roma tomatoes are just some of the foods for which we have jumping genes to thank.

By hopping into a gene responsible for plant pigmentation, a jumping gene also led to the emergence of white grapes, thus facilitating the ability to make white wine. In a fitting connection back to the birth of genetics as a science, jumping genes are even responsible for producing the wrinkled pea seeds made famous by Gregor Mendel.

Together, these findings reveal that jumping genes are likely to be a major source of new genetic variations in flowering plants. They also reveal that jumping genes can destroy genes, as well as create them. This means that they are likely to be a significant factor in a phenomenon known as regressive evolution, where certain species lose features that are no longer necessary, such as floating aquatic plants that have no roots.

**Conclusion**

Jumping genes are a dominant and inescapable feature of most flowering plant genomes. Accepted factors underlying the spectacular success of flowering plants include hybridisation, genome duplication and co-evolution with animals for pollination and seed distribution. Together with these factors, jumping genes can explain much about the rapid advancement, extraordinary worldwide diversification and eventual dominance of flowering plants that has occurred within the past 200 million years.

Darwin’s “abominable mystery”, the inexplicable rapid rise and evolution of the flowering plants, may now not be quite so mysterious after all.