

The evolution revolution

One hundred and fifty years ago Charles Darwin published his theory of evolution by natural selection in 'On the Origin of Species'.

Darwin had observed that there were differences among the individuals in many of the animal and plant populations he had studied. He recognised that these variations meant some individuals would be less well adapted to a particular environment than others and, therefore, less likely to survive, less likely to reproduce and less likely to pass on their characteristics to future generations. If variations that affected reproductive success were inherited, then over time the environment would eliminate (select out) the individuals who were least successful in reproducing. A changing environment could select for (and against) individuals with particular characteristics - 'natural selection'. He realised that, given enough time, this could result in dramatic changes and that populations could evolve into distinct new species.

An explanation of how variations are inherited followed shortly (in 1865), when Gregor Mendel published his studies on inheritance of parental characteristics by their offspring.

In the middle years of the 20th century, DNA and genes were identified as the physical basis of inheritance, the carriers of the information from one generation to the next, and that DNA mutations, and other genetic changes, caused the variation on which evolution depended.

Questioning evolution - Plant origins?

The earliest flowering plants appear in the fossil record about 180 million years ago and 144 million years ago the direct ancestors of modern flowering plants emerged. Their primitive, flower-based reproductive systems were the first steps towards the flowering species' 100 million year dominance of land plants. Today, 90%



Gerbera daisy

of the plant kingdom are flowering species, while algae, conifers, ferns, horsetails, mosses, liverworts, and their relatives, make up the remaining 10%.

The humble origin of flowering plants is recorded in their DNA. For example, researchers have identified two genes in flowering plants that control the growth of root hairs on roots. These genes are also found in mosses, where they control growth of specialised cells that increase the surface area for water and nutrient absorption (caulonema) and provide anchorage (rhizoids). Flowering plants inherited these genes from the ancient ancestor they share with mosses, but have recruited them to perform a new, although related, role in their lifecycle.

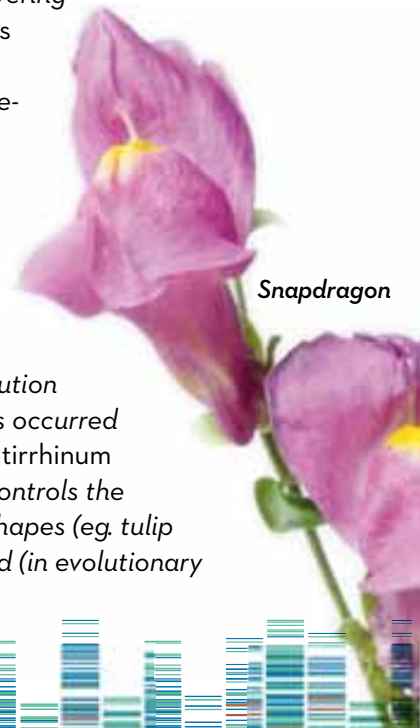
Questioning evolution - Plant diversity?

Remarkably, the enormous diversity of flowering plants appears to result from natural selection acting on simple genetic control systems. Leaf, flower and inflorescence (flower spike) structures all seem to be explained by simple rules controlled by a few genes.

There are many leaf shapes, but there are only two leaf types - single-veined and net-veined leaves. Studies on two web-veined flowering plants (*Thale cress*, *Arabidopsis thaliana* and *Snapdragon*, *Antirrhinum majus*) and a single-veined club moss (*Selaginella*) suggest that an interaction between the same two genes controls leaf development in all three of these species. This shared genetic control system seems to contradict traditional thinking, which is that leaf evolution in club mosses and other plants occurred independently. Research on *Antirrhinum* has shown that a single gene controls the switch from symmetric flower shapes (eg. tulip and rose) to the more advanced (in evolutionary



Wood fern



Snapdragon



Rose

terms) asymmetric flower shapes associated with insect pollination (eg. orchids and legumes). The gene establishes a single axis of symmetry in the flower meristem. The flower parts are then able to develop and differentiate according to their position in relation to this axis.

Production of the three types of inflorescence structure found in plants is controlled by the same few genes that determine shoot tip branching and the switching of meristems (growing tips) from vegetative growth to flower production. Differences in the timing, and levels, of activity among these few genes generate the wide range of inflorescence shapes that exist.

Evolution tends to retain and recycle genes so, by looking at changes in DNA, scientists are able to create detailed maps of the relationships within and between species, families and more widely. This also provides insights into how new gene functions and new developmental pathways have evolved. Of particular interest are the conflicts and contradictions that arise between DNA-based analysis and existing ideas about how species are related.

Evolving answers - Putting evolution to work!

Agriculture began about 10,000 years ago when humans first began to create crops by cultivating and domesticating wild plants. Initially through crude selection, and more recently through directed plant breeding, this process dramatically altered the characteristics of the crop plants that we grow. Changes include; creating new species (cereals), reducing the levels of natural toxins (tomato fruits and rapeseed oil), eliminating the shedding of ripe seed (cereals), altering flowering times and inflorescence (flower



Tomatoes

spike) structure (cauliflower and broccoli) and modifying nutritional and processing quality (broccoli and cereals).

Crucial to any breeding programme is the ability to find useful genetic variation for important characteristics (e.g. disease and drought resistance, improved nutrient uptake, higher yield) and introduce it into the crop. Potentially useful variation can be found in related species and either selectively bred into the crop, introduced by genetic modification or generated by inducing mutations in the crop's genetic code.

Scientists have developed many DNA-based technologies to analyse and modify plant genomes that supplement these established methods.

'Comparative genomics' compares the relationships between plants at the level of their DNA. This technique allows us to create genetic maps from 'model species', which then help in understanding the genetics of other species in the same family.

'Tilling' is a technique that enables scientists to make targeted changes in a plant's DNA, allowing specific changes to the DNA sequence to be 'designed' into the genome.

'Marker-assisted breeding' uses the tight association between specific genes and unique DNA sequences to 'track' the presence of a particular gene by looking for its DNA 'marker' sequence.

Genetic modification, controversially, gives researchers the ability to exchange genetic information among a wide range of organisms. More importantly, it allows genes to be modified at the level of the DNA code, providing a tool for plant improvement and, most significantly, for understanding plant biology.



Broccoli

