

In 1953, scientists working in Cambridge discovered the structure of DNA, the material that makes up the genes of all plants, animals and microbes – everything from the tiniest bacteria, to the smallest weed to humans and the blue whale.

They found that DNA is shaped like a spiral staircase, so they called it 'The Double Helix.'

It was one of the most important discoveries of the twentieth century. The helical structure immediately suggested precisely how genes could hold information, copy themselves and pass on the information to future generations. The discovery of the Double Helix revolutionised our understanding of evolution and how heredity works. No wonder the scientists shared a Nobel Prize for their discovery!

Here we show how the DNA double helix has altered what we know about plants, how we use them and develop new varieties, and how we can preserve biodiversity and aid conservation.

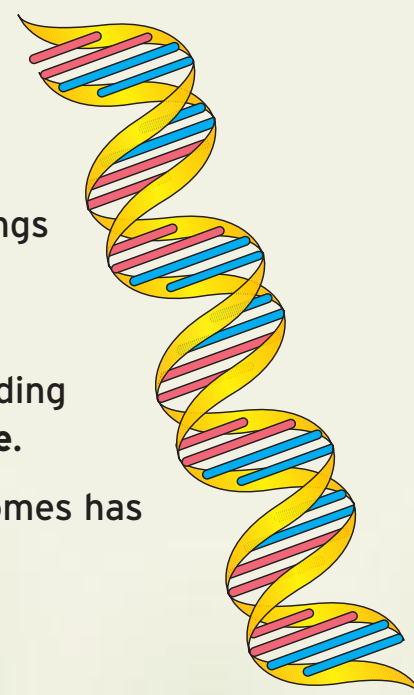


DNA: a matter of size...

All plants and animals use the thread-like molecule DNA as their genetic material. DNA stores instructions for making the components of living things and enables this information to be passed to future generations. It acts like a blueprint for the organism.

One complete copy of the DNA of an organism, including bits that don't code for anything, is called its **genome**.

Measuring the total amount of DNA in different genomes has revealed some big surprises!



Quantity can have major consequences

The amount of DNA (or C-value) in plants differs dramatically between species. Some fritillaries and lilies have hundreds of times as much DNA in their genomes as *Arabidopsis* or the horse chestnut tree (*Aesculus hippocastanum*).

Unwinding the DNA from the genome of the largest fritillary would stretch a staggering 42 metres, compared with just over 1 metre in our genome, and 53mm in the *Arabidopsis* genome. Does this matter? Yes!

The tiny amount of DNA in *Arabidopsis* was one reason why it was chosen as the first flowering plant species to have its complete genome sequenced; it was relatively quick, inexpensive and straightforward.

Large amounts of DNA carry high inherent biological costs.

Fast or slow?

The more DNA, the longer it takes to copy it (just as it takes longer to photocopy 1000 pages

than one page) and the longer it takes for cells to divide and the plant to develop. Plants with large genomes thus grow slower than their slim-genomed relatives. This can restrict the type of life strategy that a plant adopts. For example, *Arabidopsis* can grow fast from seed to seed in just 4 weeks. Yet it takes the fritillary the same time to complete just one round of genome 'copying' and cell division. At this rate, the slow growing, large-genomed fritillary is restricted to being a perennial whereas *Arabidopsis* can be a speedy annual.

Survive or die?

Plants with large genomes are more sensitive to radiation damage than those with smaller genomes. In radiation field trials, plant species died in order of decreasing genome size - so bread wheat and pine trees which have large genomes were early casualties compared with the small-genomed species such as rice and oak trees.

So, information about genome size helps predict plant behaviour.

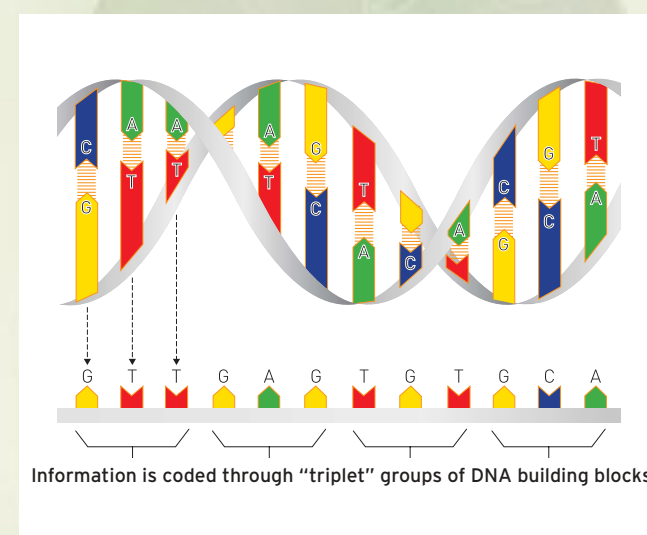
or sequence?

Science...

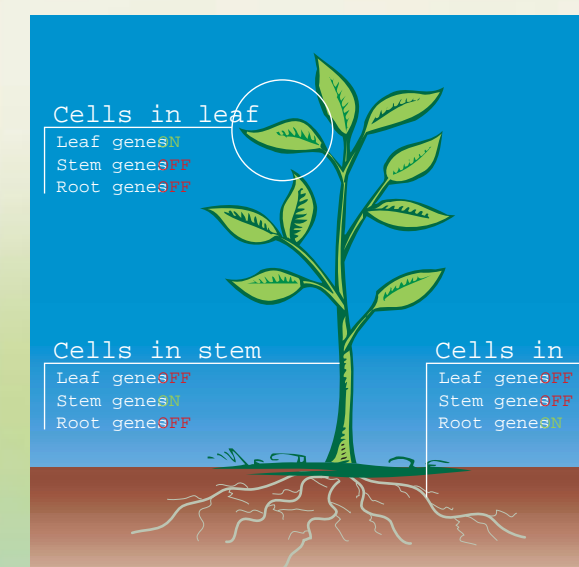
DNA is so important that it is the only molecule in cells that is repaired.

Genes are stretches of DNA. Like all DNA they are made up of four building blocks, and it is the sequence of these that acts as a code. Just as the meaning of a sentence changes if you change the letters in it, so disruptions (**mutations**) to the DNA code can alter the product made from it.

THE CAT SAT ON THE MATTRESS (normal text)
THE CAT SAT ON THE MAT (a new meaning)
THE SAT ON THE MATTRESS (nonsense)



Mutations occur naturally. They cause natural variation between individuals. Mutations can also be introduced deliberately, for example, by scientists and plant breeders, using traditional means or newer genetic modification techniques.



Different parts of a plant, such as the leaves, roots and petals all contain identical DNA. But in the leaf, the leaf genes are working; and in the root, the root genes are working and so on.

When you take a leaf cutting, genes other than the leaf genes get switched on and help the leaf to make a new stem and roots for the new plantlet. This is cloning.

families and friends

Many genes are very similar in all plants, and in plant families even the way they are arranged on chromosomes is alike. Wheat and rice evolved separately from a common ancestor about 60 million years ago. Today, although wheat has 40 times as much DNA as rice, the genes and the way they are ordered are very similar in the two crops. Such basic similarities between different species

mean that scientists can use DNA data to:

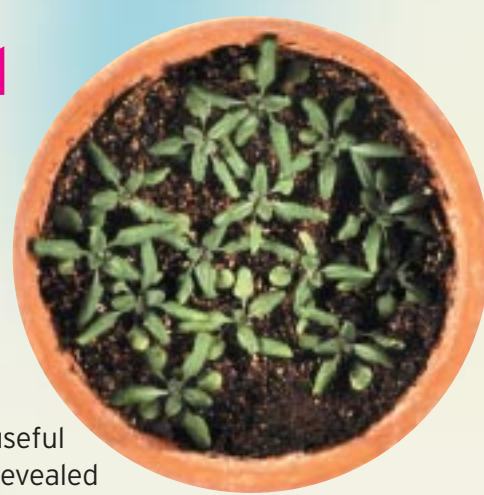
- Understand evolution and plant relationships
- Develop classification techniques and protect biodiversity
- Improve plant breeding
- Find useful genes in plants

Arabidopsis, the amazing weed

Arabidopsis is distantly related to the brassica family, including cabbages, cauliflower, broccoli, Brussels sprout, kohlrabi, kale, turnip, Chinese cabbage and oilseed rape.

It has a very small genome, which was sequenced in 2000. Scientists use the *Arabidopsis* genome as a map to locate useful genes in crops and other plants. This has revealed genes that make plants resistant to disease, as well as others that control flowering, plant shape, and the way plants respond to temperature. These genes are valuable for farmers and gardeners.

The National *Arabidopsis* Stock Centre in Nottingham has over 250,000 types that can be used by researchers.



Plants with more than meets the eye

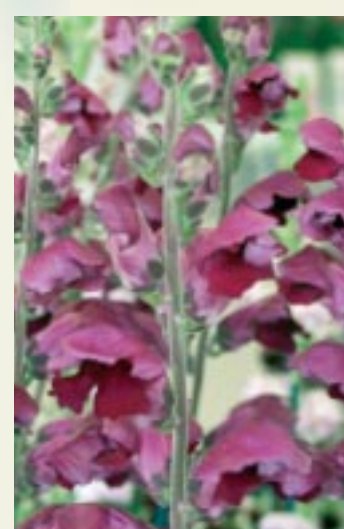
We are beginning to understand how the shape of flowers and leaves, and even their colours, spots and stripes, reflect their DNA.

Scientists at the John Innes Centre have found a single 'master' gene in snapdragon (*Antirrhinum*) that controls whether a flower or a shoot is produced. Similar genes are thought to control flowering in many other plants. Other snapdragon genes also have an effect, including one that controls whether the flowers are tall and spiky or short and bushy.

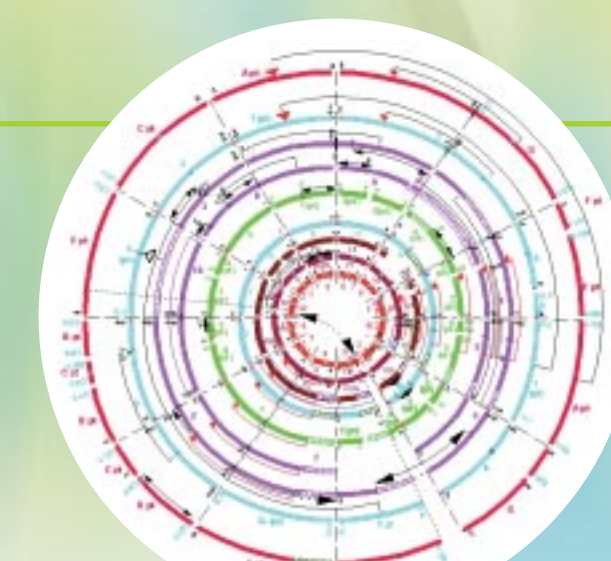
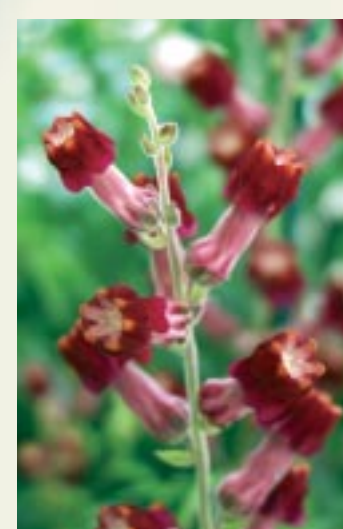
Patterning (variegation) in leaves and flowers can be caused by virus infection disrupting the normal functioning of the plant's own DNA. An example is variegated honeysuckle. Similar effects can arise when a mutation occurs in some layers of cells and not others; for example, the pale margins in the leaves of the weeping fig.

Despite the apparent complexity of flower shapes, all flowers come in two basic types: those like roses and tulips, which have radial (or multiple planes of) symmetry, and those like peas and snapdragons which have bilateral (or a single plane of) symmetry.

In flowers with bilateral symmetry, such as *Antirrhinums*, a particular gene is switched on in one region of the developing flower bud. This region provides a reference point that allows the developing flower organs to develop different shapes based on their positions (right).



If the key gene is inactivated by mutation, then no reference point is established and the flower organs develop equally, resulting in flowers with radial symmetry (right).



Cereal Relations

Wheat, maize, rice, sugar cane and millet plants look very different from each other, but their gene maps are so similar that they can easily be aligned, showing the plants' close relationship.



Hereward, a short modern variety of wheat with upright leaves, growing in front of the old and taller variety Squarehead's Master, which has a more relaxed leaf posture. Experiments at Rothamsted suggest that weeds cannot grow as well with Squarehead's Master, because its leaf canopy limits the amount of light getting down to them. But crop yield is less with the old variety because it puts relatively more of its energy into growing stem than ears, and because only its upper leaves benefit from sunlight.



Selaginella

All leaves, however different they look, belong to one of only two types. They are either single-veined or web-veined. Recent research at Oxford suggests that all plants might use the same mechanism to control leaf formation. An interaction between two genes appears to govern leaf formation in the web-veined *Arabidopsis* and *Antirrhinum*, and a very similar

interaction may influence leaf formation in the single-veined club moss *Selaginella*.

Yet the fossil evidence and traditional plant classification suggest separate evolution of leaves for the club mosses and other plants. What's going on here? Could exactly the same genetic mechanism have evolved twice?

...and surprises

Some stretches of DNA don't seem to code for anything. They look like "junk" - but almost certainly aren't; no one knows for certain what they do. But the amount of DNA is not always related to the number of genes.

Arabidopsis
26,000 genes
Human
~35,000 genes

It has been known for many years that in plants and animals (but not in bacteria) the DNA sequences of genes typically contain stretches that have to be "cut out" from the gene message molecule before the product (a protein) is made. This makes the editing process used to make a film or video. Scientists are exploring the evolutionary significance of this process, which could be one way in which organisms can use the same stretch of DNA to make more than one protein. This might explain why some genomes (e.g. the human one) contain fewer genes than expected.

Some tobacco plants contain stretches of DNA from viruses, incorporated millions of years ago during evolution - a sort of natural genetic modification.

Relatively recently, researchers have found that tiny differences in the three-dimensional structure of DNA are important. For instance, they enable the cell machinery to find and interact with particular stretches of DNA to switch genes on and off.



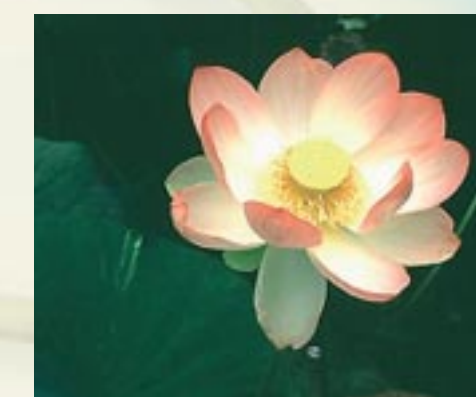
Some plants, like wheat, have multiple sets of genes. Some varieties of conventionally bred wheat contain stretches of rye DNA.

The Tree of life

DNA reveals who's related to who in plants

People have classified plants since prehistoric times. In the past, relationships were assigned largely on how they looked. Today, studies on plant relationships can employ DNA information - and this has revealed just how deceptive appearances can be.

For example, close similarities in flower shape and watery habitat once led botanists to think that waterlilies were closely related to the sacred lotus. They are not. Instead Kew scientists have revealed that the closest relatives of the sacred lotus family include the London plane trees!



The sacred lotus (left) and waterlily look similar but are not closely related.

A botanical revolution

By extending these DNA studies to encompass the global diversity of flowering plants (at least 250,000 species) scientists are getting to grips with constructing a tree of life for all flowering plants. Whilst many expected relationships have withstood comparative DNA testing, others have not. Indeed such comparisons have thrown up many surprising and unexpected relationships, leading to what may be considered a botanical revolution.

Who would have guessed that roses are closely related to nettles or suggested that the pawpaw tree is related to cabbage?



A rose by any other name: closely related to stinging nettles.

For the pea and bean family (*Leguminosae*) different experts all used to propose different families as their closest relatives. Surprisingly, DNA comparisons now show that the closest relatives are in fact the milkworts (*Polysalaceae*). Despite superficial similarity in the flower shape between the two families, no taxonomist ever believed that they were related before the new DNA evidence was available.

DNA timeline

1858	Isambard Kingdom Brunel dies
1859	Charles Darwin publishes Origin of Species
1865	Gregor Mendel presents his work on plant hybrids
1871	DNA discovered by Swiss biochemist Friedrich Mieschler
1900	'Rediscovery' of Mendel's work in Britain
1901	Death of Queen Victoria
1905	The term 'gene' is coined to define the elements that control heredity
1914-18	World War I
1928	Fred Griffith proposes that an unknown "principle" alters behaviour of bacteria
1938	Alexander Todd begins work on chemistry of nucleic acids
1939-45	World War II
1944	Oswald Avery identifies genetic material
1951	Rosalind Franklin obtains sharp X-ray diffraction photographs of DNA
1953	Coronation of Queen Elizabeth II
1953	James Watson & Francis Crick propose Double Helix structure of DNA
1961	First man in space
1962	James Watson, Francis Crick and Maurice Wilkins awarded Nobel Prize
1966	DNA code deciphered
1969	Man lands on the moon
1990	Human Genome Project launched
1996	First genetically modified food on sale in the UK (tomato paste) Dolly the cloned sheep is born
2000	First complete DNA sequence of a plant (<i>Arabidopsis</i>)
2001	First draft of Human Genome completed
2003	Results of UK Farm Scale Evaluations and public debate on GM crops

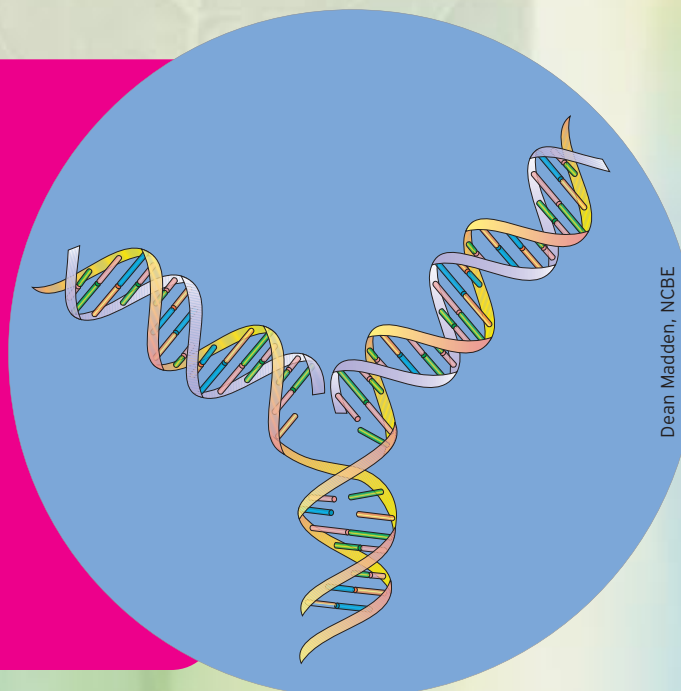
where it all began

There was no general scientific concept of heredity until after the 18th century, although in specialist areas such as plant breeding, transmission of 'traits' was well recognised and used widely to produce new varieties through hybridisation. In fact, humans have been breeding plants for particular characteristics for thousands for years - cultivated emmer wheat (the first cultivated wheat) was grown during the Neolithic period, reaching the British Isles before 4000 BC.

20th century insights into the new science of genetics caused some surprises when a chemically simple molecule - a nucleic acid called DeoxyriboNucleic Acid (DNA) rather than a more complicated protein molecule - turned out to be the stuff of genes.

The importance of the Double Helix discovery

The beauty of the Double Helix structure was that it immediately suggested how DNA could replicate - a key property of genes and the driving force behind life itself. Because of the reciprocal relationship of the two strands of the helix, when peeled apart each acts as a unique template to make the missing strand - thus creating two identical 'daughter' molecules.



The very 'modern' approach of Gregor Mendel

One of the most significant features of Mendel's research was his use of mathematical principles to pose questions about inheritance. Today, over a century later, the marriage of high powered computing technology and DNA sequencing is providing new insights into how genes work.

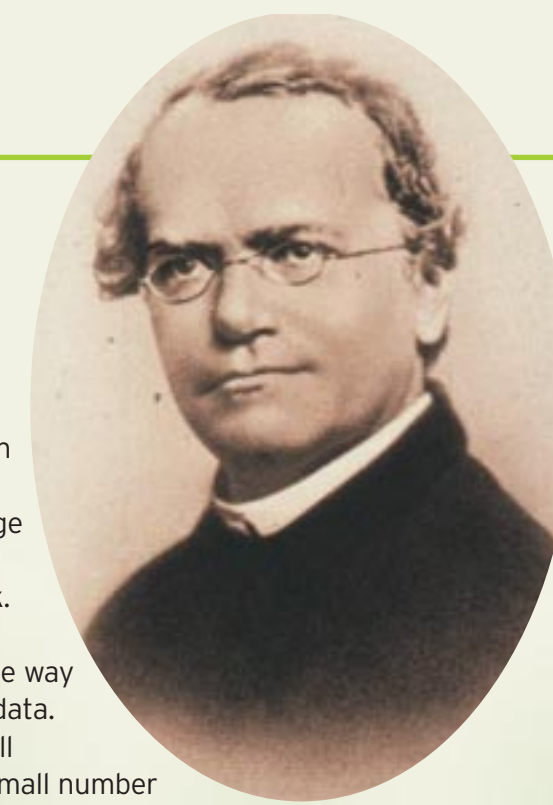
Mendel was fastidious, like a modern day researcher, in the way he planned and replicated experiments and recorded his data. Unlike many of his contemporaries who studied the overall characteristics of plants, Mendel focused on a relatively small number of individual traits having firstly confirmed his parental plants bred true for the traits of interest over two successive years.

Working with the common garden pea *Pisum sativum*, he studied what he called 'pairs of differentiating characters'. Initially he studied fifteen different traits, but later he settled for seven.

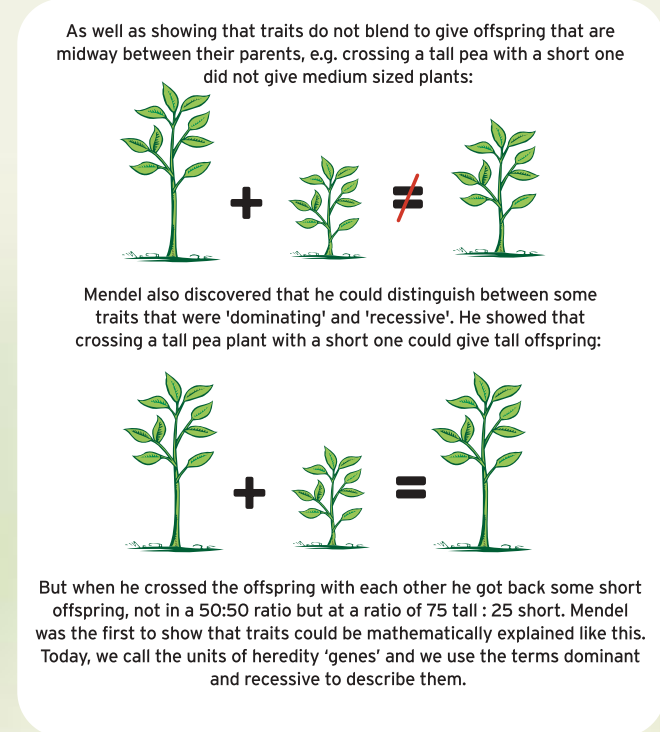
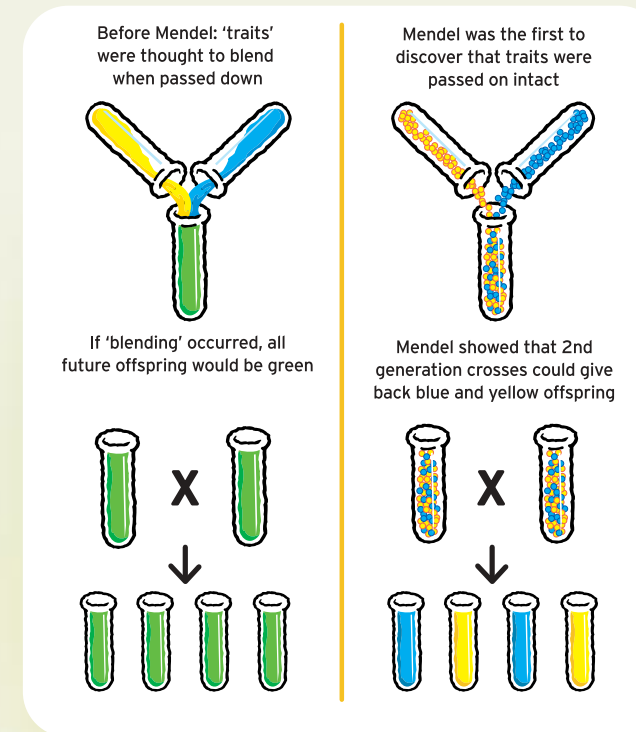


These were:

- Wrinkled or round peas
- Green or yellow peas
- Tint of white or grey in coat of pea
- Smooth or bumpy pod shape
- Green or yellow unripe pods
- Flowers at tip or along stem
- Tall or short plants



Mendel's key finding was that traits are passed on separately and intact, not blended to give offspring that are roughly midway between their parents. This explained how a trait might seem to 'disappear' in one generation, but could 'reappear' in a future one.



It has been estimated that in his studies Mendel counted over a quarter of a million peas!

In the 1980s, over 100 years after Mendel's death, it became clear that five of the seven traits he had studied are each carried on a different pea chromosome, and the other two are on opposite ends of the same chromosome. This meant that the traits were transmitted separately, making it easier for him to interpret his findings.

The population approach of Charles Darwin showed us that:

More organisms are produced than can survive. Organisms struggle for the necessities of life; and compete for resources. Individuals within a population vary in their traits, some of which are passed on to offspring. The presence of some traits in individuals makes them better adapted than other individuals to survive and reproduce. These better-adapted individuals are more likely to pass on their genes to the next generation.



putting DNA to work

Farming, horticulture, gardening and leisure may all be able to benefit from our knowledge of the DNA sequences of plants.

- Crops and other plants can be bred to be particularly suited to their environments, so that chemical and other inputs can be reduced, and environmental damage is minimised.
- Crops and other plants could act as 'factories' to produce a renewable supply of chemicals and medicines.



DNA technology can help:

- In faster and more precise conventional breeding.
- In genetic modification, either within species as in conventional breeding, or for introducing novel genes not possible through conventional breeding.



Grass for all seasons

A risk with conventional breeding is that in selecting for priority traits we may inadvertently lose others that are less important but nonetheless beneficial. The race to develop fast-growing grasses that respond well to the high chemical inputs of intensive livestock production, has meant that other qualities such as efficient use of fertilisers and water have been lost. These are precisely the sort of traits needed for more extensive, lower input farming including organic systems. We can look for genes for these traits in the DNA of wild grasses growing in areas such as natural upland pastures, common land and cliff tops, and breed them back into agricultural grasses to give farmers a choice of varieties for different farming systems.



In the same way, we can provide designer grasses for sports and other amenity uses.

Research at the Institute of Grassland and Environmental Research shows that there are economic as well as environmental benefits in, for example, using high-sugar grasses. An increase of 5% in sugar content is estimated to increase feed efficiency in grazing by 30% and reduce input costs by 5%.



Making rye-grass able to tolerate drought could lead to similar reductions in input costs and water use by increasing grass availability throughout the season without irrigation.



Investigating the function of plant genes

Three major BBSRC research programmes totalling over £8.5M are revealing the role of individual genes in *Arabidopsis*, cereals and brassicas; how they interact with each other and how this information can be used.

The research is co-ordinated by scientists at the University of York, the John Innes Centre (and Scottish Crop Research Institute) and Horticulture Research International, respectively.

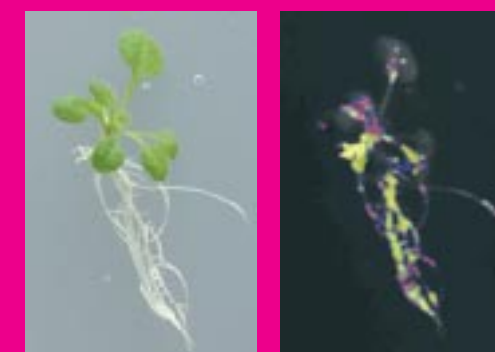
Among the exciting prospects that are emerging are opportunities for:

- improving the quality and taste of foods
- enhancing the nutritional value of produce e.g. anti-cancer agents in broccoli
- reducing chemical inputs in farming
- reducing imports
- improving production of biofuels
- finding plant compounds for tomorrow's new medicines
- developing plants that can thrive in hostile conditions e.g. under drought or high salinity

Some changes may be possible through conventional breeding and genetic modification (GM), others may be possible only through GM.



Plants that glow



A major challenge in plant genetics is knowing where and when genes are switched on in a plant. Researchers have a useful tool in their armoury of laboratory techniques - glowing plants. Attaching a gene that produces a glowing protein to the gene you want to study gives you a visual clue as to where the gene is switched on.

Genes to stay healthy

Plants naturally contain genes that help to protect them against attack by bacteria, fungi and other pests. If plant breeders could introduce new resistance genes (many of which are in wild relatives) into their crops, this could help to reduce the amount of pesticides needed to keep crops healthy.

However, pests and disease-causing organisms can readily evolve to overcome a new resistance gene, so breeding-in a single gene cannot guarantee long-term protection. The answer could be to introduce combinations of different resistance genes, which are likely to be effective for a long time because a pathogen would have to evolve more than one mechanism simultaneously in order to overcome both genes and attack the plant.

Arabidopsis contains over one hundred genes that may be resistance genes, and scientists have located all of them on its five chromosomes. *Arabidopsis* is related to important brassicas such as the cabbage and Brussels sprout, so it can be used as a map to find similar genes in these and other crops. Breeders will then be able to select combinations of resistance genes.



About BBSRC

The Biotechnology and Biological Sciences Research Council (BBSRC) funds academic research and training in the biosciences in universities and research institutes throughout the UK. It is the UK's principal funder of basic and strategic research in plant science.

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