

7. Genetics

This is what you need to know about genetics and its application in breeding our food crops and animals

Niels P. Louwaars

Law Group, Wageningen University, Hollandseweg 1, Wageningen, the Netherlands; and Plantum, Gouda, the Netherlands; niels.louwaars@wur.nl

Abstract

Genetics is the study of heredity and the functioning of hereditary material, the genes. Genetics is relevant to food in two distinct ways: (1) Firstly, the genetic makeup of the organisms producing food (plants, animals and microorganisms) determines to a significant extent the composition of the food in nutritional and anti-nutritional terms. It furthermore relates to other quality components, such as processing qualities, shelf life, and sensitivity to the growth of toxic microorganisms in or on the consumed product. (2) Secondly, on the side of the consumer there may be human-genetic preconditions that determine sensitivities to certain foods. This section focuses on the former and draws examples mainly from food plants. This introduction to genetics is also relevant because debates are arising again about certain genetic techniques that can be used in breeding plants and animals. We therefore introduce the concept of breeding, including its technological developments over time. Breeding is the use and creation of genetic diversity to select plants and animals that respond better to the needs of farmers and consumers.

Key concepts

- ▶ Genetics is the science of heredity and the genes that regulate it.
- ▶ Chromosomes are thread-like structures in the nucleus of a cell, consisting of DNA and proteins.
- ▶ DNA: 'deoxyribonucleic acid'; the very large molecules consisting of a string of four nucleotides, positioned in a double helix structure. DNA is the molecule that harbours genes.

- ▶ Genes are the starting point of all metabolic pathways in the cell; how plants and animals grow and the composition of the food they produce depends on the interplay between the genes and the environment. Genes are a sequence of nucleotides in DNA (or RNA) that encodes a chemical process in a living cell.
- ▶ Allele: a sequence variation of the same gene at the same location on a chromosome, e.g. coding for either blue or brown eye colour.
- ▶ Mutation and segregation are the major sources of genetic diversity, which together with selection shape evolution.
- ▶ All the food we eat is the result of millennia of rearranging the genetics of crops and animals, distancing them from their origins in nature.
- ▶ Breeding is the applied science that uses genetics to shape crops and animals to the needs of humankind: farmers, value chain operators and consumers; all our food originates from bred plants and animals, with the exception of those caught in the wild.
- ▶ Breeding methods are increasingly scrutinised by society, including food specialists.

Case 7.1. The discovery of DNA.

‘Professor, the images are getting sharper’, Raymond Gosling said. Rosalind Franklin looked at the pictures. Photo 51 was intriguing. ‘Can’t we publish this, professor? I truly think this is a key to the structure of DNA.’ ‘I guess, but we need to understand how this structure is biologically functional before we go public.’ X-ray crystallography was a great technology and Franklin’s lab at King’s College London was a forerunner. Individual molecules and their structure could be made visible, that is, when large enough. And DNA is one such large molecule. Her colleague, the physicist Maurice Wilkins, and not exactly her best friend, presented the photo soon after at a conference and sent the picture to James Watson, 100 km north in Cambridge a few months later in 1952.

The young American showed it to his colleague Francis Crick. ‘Something wrong with your camera, James? Is this a flock of geese in a winter sky, using the wrong diaphragm?’ ‘No, no, it’s DNA, I got it from Wilkins and I think it is one of the keys to our research.’ Together they gave it a closer look – and started to use it to build a model of the DNA molecule – a double helix. ‘Wow: this explains a lot – the two strands can connect with weak molecular bonds between the individual bases. In the helix configuration guanine fitted neatly with cytosine and adenine with thymine. The two strands were thus mirrors of each other, which could explain both the solid configuration, and also that it could replicate when the strands separated. How would that work? What makes the strand separate?’ ‘Don’t know, but let’s get this published as quickly as possible before anyone else does.’ Their publication in 1953

on the structure of deoxyribonucleic acid (DNA), which failed to credit Franklin, was possibly not the best example of scientific ethics, but it became the basis of the science of molecular genetics and for their Nobel Prize together with Wilkins nine years later (Franklin had passed away by then). The structure of DNA was thus explained.

The history of genetics is built on many more stories involving both transpiration (Franklin) and inspiration (Crick), from Mendel's gardens in Brno to Charpentier and Doudna's laboratories at Berkeley. All these scientists stand on the shoulders of many others, but there's only space for so many names in the history book of science. Each section of this chapter helps provide an understanding of genetics and its relevance to food. Therefore, here is a brief summary.

7.1 History of genetics as a field of science

heredity

That there is something like heredity has been known for millennia. Children take after their parents, and some features, such as eye colour, are even predictable to a certain level without any knowledge about how this may work. Plants and animals have been selected since the dawn of agriculture, attempting to bring about certain traits in the offspring. Darwin (1859) based a significant part of his theory of evolution on the observation of domestic dog breeds. He could explain that breeds could be kept 'pure' when mating was restricted to animals of the same breed; he was, however, quite puzzled by the enormous diversity of dogs when it was assumed that all dogs stem from domesticated wolves. He further sharpened his ideas when he came across the diverse finches on different islands of the Galapagos.

Jean-Baptiste Lamarck had postulated in 1809 that traits could be acquired during the lifetime of an organism, and transferred to the next generation, a theory that remained popular under Stalin's regime. It fitted in very well with his idea to create the perfect socialist society. It led to a 'war' between his chief geneticist Trofim Lysenko, and the already established ideas about heredity by the director of the Lenin All-Union Academy of Agricultural Sciences at Leningrad, Nikolaj I. Vavilov. The latter lost and succumbed in the Gulag. The balance between 'nature' (genetics) and 'nurture' (environment) is, however, still the subject of many debates.

segregation

The search for understanding heredity was on in the 19th century. It was Gregor Mendel who identified in 1866, in his experiments crossing peas with other crops, that a segregation ration of 1:3 was very common, or 1:3:3:9 when two independent dominant characteristics are studied. This led to the conclusion that whatever causes heredity, it behaves in duplicate form, and a character (allele) is either the same in both (homozygous) or different (heterozygous).

population genetics

The observed ratios are found when one allele is dominant over the other; otherwise a 1:2:1 ratio is expected (for example in white, red and pink flowering individuals). Mendel's publication from 1866 remained unnoticed until three scientists independently (or not) rediscovered it in 1900. It created a revolution in biological sciences, notably in plants and after its extension to population genetics by Hardy and Weinberg in 1908 also in animal breeding. Plant and animal breeding became (applied) sciences using prediction through calculation rather than trial and error only.

genes

In the meantime, Hugo de Vries, one of the discoverers of Mendel's publication in 1900, had already identified in 1889 that heredity has a material origin, which he called 'pangenes'. This was later shortened to 'genes' by Wilhelm Johannsen in 1909, who also made the important distinction between genotype (the genetic identity) and phenotype (the visible expression thereof). This means that the environment in which an organism lives influences the expression of the genotype and that the traits that Mendel looked at, which were not affected by the environment, were either lucky shots or an example of serendipity. The genetic basis of many traits can thus not be identified by simply looking at them. On that basis, Ronald Fisher developed the science of quantitative genetics through his analysis of variance (ANOVA) methods of statistical analysis in the 1920s. He thus bridged the divide between Mendel's and Darwin's theories.

chromosomes

Nobody knew what this material origin was. Chromosomes, threads in cells that became visible after dyeing dividing cells under a microscope had already been observed in 1879 by Walther Flemming, but the pieces still had to be put together. Following the material origin of heredity, however, De Vries also hypothesised that genetic diversity arises through heritable changes that occur naturally, which he called 'mutation'. We now know that the large changes that de Vries observed were likely the result of large chromosomal abnormalities, such as chromosome duplications, but the concept and the term 'mutation' is still very important. It is currently mainly used to indicate small changes in the DNA. Nobel prize winner Hermann J. Muller identified chromosome changes in fruit flies when these were subjected to irradiation as recently as 1927. This knowledge was quickly put to use in plant breeding. The technique of mutagenesis was born. Large-scale mutagenesis trials in barley resulted in improved brewing quality and disease resistance. Probably all the beer that we drink nowadays is brewed from barleys that have these mutants in their pedigree. However, the trouble with such randomly induced mutations is that often tens of thousands of individuals need to be screened to identify such a 'lucky shot', which is only possible for easily selectable traits such as a flower colour. Almost all chrysanthemums are mutants; a breeder creates a new flower type or better vase life through crossing and selection, and then mutates the new plant to create all colour sorts.

mutation

These hypotheses proved very useful in practice, but they kept us in the dark about the material structures responsible for heredity, and how these actually create the observed expression of traits.

James Watson and Francis Crick published the structure of DNA as a double helix in 1953, based on X-ray crystallography work done by Rosalind Franklin. The Cambridge team won the Nobel Prize for their chemical and structural clarification of the material basis of heredity. The double helix explains how DNA is able to replicate: when the double strands separate, individual bases connect into a new strand completing the double helix again as a true copy. It also laid the foundation for the next question: that is, how such a molecule could be the basis of all life functions in an organism. DNA itself had already been chemically identified in 1929 by Phoebus Levene. Based on his work on RNA in 1909, he identified the deoxyribose sugar and suggested that DNA consists of a string of four nucleotide units linked together through the phosphate groups. Nikolai Koltsov had already proposed in 1927 that there should be a 'giant hereditary molecule' made up of 'two mirror strands'. These two suggestions were thus confirmed in 1953 by Watson and Crick.

molecular genetics

The science of molecular genetics developed soon after, and became an applied science when Marc van Montagu in Ghent identified the bacterial Ti-plasmid and the way it can by nature transport DNA fragments and include them in plant DNA. And so, genetic modification was born. Transgenic crops are grown in many countries, but in Europe on a limited scale only. Research on transgenic animals (Herman the bull producing offspring that could produce human lactoferrin) is limited due to ethical concerns (see also Chapter 3; Wernaart, 2022), but a wide range of animals have been created for research purposes, e.g. mice for cancer research, and also GM salmon, malaria mosquitos and others. GM technology is widely used with little public concern in medicine, including vaccine development. Molecular genetics also led to the development of various gene-editing systems like TALEN (Zhang *et al.*, 2014) and ODM (Dalbadie-McFarland *et al.*, 1982), and the easiest and therefore most widely used technologies based on CRISPR (clustered regularly interspaced short palindromic repeats) identified in bacteria by the group led by Van der Oost in Wageningen (Brouns *et al.*, 2008), and put to practical use by Emmanuelle Charpentier and Jennifer Doudna in Berkeley for which they were recognised with the Nobel Prize in Chemistry in 2020.

There is much more to say about the discoveries in the field of genetics and the inventions based on them. For example, genetic linkages and chromosomal crossovers may confuse expected outcomes of a cross based on Mendel's laws. All kinds of 'mistakes' occur in cell division (mitosis) and even more so in the development of haploid sex cells (the meiosis). There is also DNA outside the

**messenger RNA
(mRNA)**

cell nucleus, i.e. in cell organelles such as chloroplasts and mitochondria, which are commonly inherited only through the maternal line, similar to the genes in the X-chromosome in mammals. There is also much more to say about ploidy levels, where Mendel's peas (and humans) have pairs of chromosomes (diploid), potato has four and strawberry has eight sets. In vegetatively propagated species also aneuploidy occurs, when sets are incomplete and still the plants look healthy and thrive both in nature and in our greenhouses. And, some species don't have DNA at all, but live on the basis of RNA (ribonucleic acid).

7.2 How do genes regulate biological processes?

Deoxyribonucleic acid (DNA) is a long molecule that consists of four nucleotides: adenine (A), cytosine (C), guanine (G), and thymine (T). These form a string of quite indefinite combinations of letters that replicate when cells divide. So, in principle, every cell in an organism has the same genetic code. Particular combinations of letters can form a functional gene, that includes 'start and stop' codes. Such genes can be 'read' by a similarly constructed molecule, RNA (in which uracil replaces thymine), in a process known as transcription. Such 'messenger RNA (mRNA)' can carry the information out of the cell nucleus towards other organelles in the cell, called ribosomes, where the mRNA code is 'read' to form proteins, in a process known as translation. Each triplet of RNA bases binds with one of 20 possible amino acids, and when connected in an RNA-defined sequence forms a very specific protein, each creating a special 3-dimensional structure. These are responsible for biological functions, as starters of metabolic pathways, for example by acting as enzymes, facilitating chemical reactions in the cell. It is these pathways that determine the biological functions and chemical composition of a cell, and thus – among many other things – the nutritional characteristics of a plant or animal product, and indeed also the occurrence of toxins and allergens. These pathways also determine the biological activity of microbes used in food processing, as well as the functions of pathogens and the response of cells to invading pathogens.

However, it is important to realise that even though every cell has the same DNA, cells in an organism have very different functions and require very different parts of the DNA to be activated – and others not. Similar to gene × environment interactions, which made the simple Mendelian genetics much more complex, neither knowledge of the chemical structure nor the exact sequence of the roughly three billion base pairs of the human genome, help us 'understand the language in which God created life' as Bill Clinton expressed it when celebrating the finalisation of the Human Genome Project in 2000. It was indeed a milestone in the history of genetics, but there is much more to learn.

So, both pressures outside (neighbouring cells or physical stresses) but also inside the cell may switch transcription off or on and thus affect gene expression. A cell's DNA harbours thousands of genes that need to be active at any given moment. A liver cell needs to express different genes from a brain cell. In an organism, cells affect each other so much that cell functions are commonly fixed depending on the functions they have to perform in a certain organ. Much medical research is currently being done to 'unlearn' cells, i.e. to make them function as totipotent stem cells that can still differentiate in new directions and replace damaged tissue.

The cell has several methods to control the expression of genes. Transcription factors are regulatory proteins that 'cover' DNA or make it available for transcription into mRNA, so they determine which parts of DNA are activated at any point in time. Knowledge of the ways such transcription factors work allows us to greatly influence the cell processes without changing the genetics. There are also structural features where DNA is more permanently inhibited from transcription, e.g. by binding (methylation) to the DNA molecule. Such bonds may even continue to exist after cell division and even into a next generation. Such 'epigenetic' (Weinhold, 2006) effects change expression while leaving the DNA sequence intact. This, for example, is used to explain why the prevalence of obesity is high in people whose parents have suffered from undernutrition.

7.3 How can genetic changes occur?

The material nature of DNA also explains the changes that are required to illustrate evolution (Darwin) and mutations (de Vries). Changes may occur either through natural (physical or biological) means or human intervention.

natural genetic changes

Mutation: small or larger changes in the DNA, often through external influences like (cosmic) radiation, and through biological means, i.e. 'mistakes' in the duplication of DNA when cells split (mitosis) and particularly in the meiosis, when sex cells are created with half the amount of DNA. Mutations can also be the effect of transposons (or jumping genes), a DNA sequence that can move in a genome, identified by Barbara McClintock (1950). Mutations occur every day in plants and animals. Most mismatches and breaks are resolved by the natural repair mechanisms of the cell. They are only inherited when they occur in gametes (sex cells) or their precursors. Natural changes can also occur when cells are attacked by microorganisms; bacterial genes can enter plant cells and stay there. Sweet potato is the best-known example of a crop harbouring bacterial genes that apparently have evolutionary advantages.

Recombination: when plants or animals cross sexually, the genes of the parents mix, creating diversity among individuals in a next population. In regions where wild relatives of the species occur, occasional interspecific crosses may also occur, bringing new diversity into the species (introgression). This diversity through recombination (and introgression) and mutation, combined with Darwin's concept of survival of the fittest individuals in such diverse populations, feeds evolution.

human intervention Human intervention to obtain diversity to select from in plant and animal breeding builds on these same principles:

Targeted cross breeding, which has been done since the domestication of animals, was increasingly pursued in (ornamental and fruit) plants after Rudolf Jacob Camerarius published in 1694 that plants also have male and female organs. The breeding of major food crops starting in the 19th century; interest in crop improvement flourished and greatly intensified in the 20th century when genetics became a science after Mendel and others. Targeted crossing aims at combining 'positive' traits in the progeny.

Random mutagenesis is the wilful stimulation of mutations throughout the DNA using irradiation (known in the 1920s, but popular from the 1950s onwards) and treatments with chemical mutagens, notably colchicine and ethyl methane sulfonate (EMS) (Talebi *et al.*, 2012). These may cause breaks or other changes in the DNA that may, when they occur in a functional gene, appear as visual or physiological changes. For example, 'variegated' ornamental plants with dark and light green parts of leaves, are the effect of mutations in certain cell layers.

Transgenesis is the transfer of functional genes between species, based on molecular genetics experiments in the 1970. And cisgenesis is the transfer of genes within the species, initiated in the early 21st century to improve difficult-to-breed crops, such as polyploids (potato) and tree species (apples), where the generation time makes repeated (back)crossing impractical. Initially, such genes were randomly inserted into the host DNA; more recently these genes can be placed in particular locations. Transgenesis evolved from the observation that bacteria like *Bacillus thuringiensis* (Bt) naturally exchange bits of their DNA with their hosts. Such random transgenesis can also be done by connecting DNA to particles that are 'shot' into the cell. Such techniques make it possible to channel specific genes from basically any origin into crop plants.

Targeted mutagenesis is the creation of changes (mutations) in a particular location in the DNA, either a deletion or a specific change of one or a few base pairs. This has been done since the early 21st century, but is greatly facilitated by the developments of CRISPR technologies developed from 2014 onwards.

Genome editing is a term used for both targeted mutagenesis and targeted gene transfer. For example, CRISPR Cas9 was developed from the observation that bacteria had a cluster of similar genetic sequences (repeats) that appeared to be a library to help the bacteria identify invading viruses, which then could be cut and destroyed. This natural phenomenon is now used to identify and cut DNA in a specific location. It can be used simply to cut the DNA allowing the natural repair mechanisms to do their job, which may lead to minor mistakes, or mutations, for example making the whole gene dysfunctional (silencing, Zhang *et al.*, 2020). This is particularly useful for the study of gene functions. Alternatively, CRISPR can ‘cut and replace’, creating a specific predefined mutation in the gene. When ‘cut and replace’ involves a whole functional gene, then we can speak of targeted trans (or cis-) genesis.

next step – selection The plants and animals that provide the food we eat are quite different from those found in nature. A wild tomato is a tiny little berry in a family (Nightshade) known to harbour quite toxic species. Almost all cabbages, from Brussels sprouts to broccoli and kohlrabi, originate from one wild species selected for different growth habits and edible plant organs. This illustrates that selection, which follows the creation (or collection) of genetic diversity, is a major force shaping our food. Also, selection has undergone quite some changes with the inclusion of molecular biology in plant and animal breeding. Originally, mass selection was the only tool farmer-breeders had in order to select in their crops and breeds: removing poor-looking individuals (negative mass selection) or allowing only the best to multiply (positive mass selection). Line selection and family selection looked at the progeny of a certain cross to significantly speed up selection and to establish the breeding value of certain individuals (notably male animals). Genetics came in as a science after Mendel and even more so after Ronald Fisher brought mathematical statistics (analysis of variance) into breeding.

The applied science of plant breeding subsequently ‘absorbed’ new sciences. Molecular biology greatly improved not only the creation of diversity, but also the selection methods that breeders use. Marker-assisted selection uses genetic markers to predict important traits in segregating populations (after a cross). A tiny leaf can tell the breeder whether the individual plant carries the desired trait(s) – all other plants can be removed and will not take part in further multiplication. This significantly speeds up the selection processes. When sequencing (actual ‘reading’) of DNA became cheaper and quicker,

genomic selection was introduced (Lin *et al.*, 2014), identifying the ‘perfect’ set of parents for a cross in order to reach the desired outcome, and selecting at the DNA level. This development requires the analysis of big data, and artificial intelligence is becoming part of the breeder’s toolbox.

Obviously, breeders need a lot of knowledge about the species they breed; their physiology, pathology and organic chemistry are important for the users (processors, consumers) of the crops and animals they breed. This makes breeding an applied science building on quite different basic sciences.

However, we are not just interested in the genetics, but in the expression of the genetics into useful characteristics of plants and animals, useful for the farmers (productivity, resilience to diseases and environmental factors), the processors (brewing and baking qualities) and consumers (taste, looks, nutrition, reduced decay during storage). Production systems, obviously, also influence the final outcome – genotype-by-environment interactions remain important. When particular soils do not contain sufficient chemical compounds, the levels in plants (e.g. the anti-carcinogenic glucosinolates in broccoli requiring sulphur) are also bound to be reduced irrespective of the genes. When grain is harvested and stored in moist conditions, fungi are likely to render it unsafe for consumption.

7.4 Plant breeding and food quality and safety

Plants can be seen as complex biochemical factories producing large numbers of compounds. We need several such compounds as food in order to live. We need carbohydrates (cereals), proteins (legumes), oils (oilseed rape), fibres (potato) and various micro-nutrients and vitamins (vegetables).

toxins

Mankind has selected plant species that produce nutritious food, and bypassed most of the obviously poisonous ones. However, several food plants still produce such toxic compounds, such as cassava and almonds (cyanides), potatoes (glycoalkaloids), beans and especially castor beans (lectins), soybeans and quinoa (saponins) (Centre for Food Safety, 2007). We have learned to deal with these in our food processing; e.g. boiling dry beans to disable the action of lectins. All these compounds are the result of the genetic makeup of the plant and the environment in which it grows.

Our food plants have changed considerably due to farmer selection and scientific breeding. Almost none of our food crops would survive well in nature. Such changes continue to occur; mutations that may affect the metabolism of the cell occur every day. In view of this, it is quite remarkable that we don’t experience such mutations leading to either the known toxins that protected the

forefathers of our crops like the nightshade family (tomato, peppers, potato and others), or to totally new compounds that may be toxic to us. Mutations occur in the breeding stage, in the multiplication of seeds and in the food production fields, but we apparently don't need to test each lot of wheat, potato or lettuce after harvesting. Plant breeders may screen for the known ('solanine' in potato) toxins when they have crossed their potato with wild ancestors that are known to produce high levels of this toxin (Sinden *et al.*, 1984), and even effectively blocked the pathway of erucic acid production in oilseed rape making the oil edible (Stefansson and Haugen, 1964). However, breeders have never screened their varieties for all possible (unknown) toxins without any negative effects on food safety. We rightfully trust our food that is derived from known crops, even though we know that their DNA is scrambled during mating, mutated due to exposure to UV sunlight both in nature and in breeding. This scrambling could affect metabolic processes in the living cell during plant growth, storage and food processing in the factory or the kitchen. Louwaars (2019) claims that crop plants producing toxins do not have a competitive advantage in the same way that plants in nature have, because we care for the crop and keep animals out. Since mutations leading to such toxic compounds would come at a cost for the plant, they would not be selected by the breeder. The taxonomic knowledge of a professional breeder furthermore prevents 'accidents' with toxins that are known in the species or its relatives.

nutrition

Plant breeding started primarily with the needs of farmers: how to support increasing yields and make crops more resilient to pests and diseases, and environmental stresses like drought. Processing qualities became important for some crops, and in horticulture the looks (flowers) and taste (vegetables) also became relevant. For example, cauliflower size was genetically reduced following the reduction of household size, and the browning of lettuce is avoided now that most lettuce in the supermarket is sold ready-cut. Nutritional content was not a primary breeding objective until recently. Some studies indicate that the level of micronutrients has been reduced, partly as an effect of increased yields (Cursio, 2018). Others, however, conclude that there is no difference when old and new varieties are cultivated side by side under current agronomic conditions, but that there can be significant changes among varieties in general⁴¹, which could be an excellent basis for breeders. It is likely though that fruit-vegetables like tomato and cucumber contain more water and fewer vitamins per kilo, when bred for yield capacity only. And crops like Brussels sprouts in which the bitter taste is bred out have reduced concentrations of the compounds that cause bitterness but potentially have an anti-carcinogenic effect.

⁴¹ See for instance <https://ag.umass.edu/news-events/highlights/growing-nutrient-dense-vegetables>.

On the other hand, breeders working for poor consumers did start to focus on important minerals and vitamins (biofortification, see Bouis, 2002), and those aiming to create health products raised levels of antioxidants (Hanson *et al.*, 2004) and healthy glucosinolates. Breeding for oil composition in crops like soybean and oilseed rape also contributes to healthier products (Abadi and Leckband, 2011).

7.5 Concerns about genetic technologies

Plant breeding has operated away from the public eye for a very long time. Breeders produce varieties and seeds for farmers, and further down the chain very little is known about the genetic origin of food. In the 1970s breeding became known as the solution to the world food situation following the Nobel Prize awarded to Norman Borlaug, a wheat breeder in Mexico, and initiator of what became known as the Green Revolution.

transgenics

Concerns did arise though with the development of transgenics. Natural processes like crossing and selection and even mutagenesis have not caused any food-related concerns, but transferring functional genes from one species to an unrelated one stirred up debates in the 1980s. We wouldn't know how the inserted gene would act in its new genetic environment, notably because we couldn't know where and how many copies of the gene were inserted during the transformation process. The 'precautionary principle' became a leading concept, but with very different interpretations (Hanson *et al.*, 2004; Verkerk *et al.*, 2009). Close to 35 years of experience have not allayed this concern, and genetically modified organisms (GMOs) are legally required to be extensively tested for safety for humans and the environment in most countries before being admitted to cultivation and to the food chain.

genome editing

A similar debate is currently ongoing with regard to genome editing. Should products of targeted mutagenesis be regarded as regulated GMOs and as a result tested and labelled? There are various discussions around this topic. Just as with conventional GMOs, legal specialists, plant scientists, environmentalists, food safety specialists, ethicists and social scientists all debate aspects of the technologies and their socio-economic impact.

A legal debate with different outcomes in different countries: The European Court of Justice ruled in favour of including gene-edited plants as regulated GMO in 2018⁴²; In Argentina, Australia and Japan targeted mutagenesis is not or hardly regulated. A debate among plant scientists seems to have resulted

⁴² See for instance this prejudicial procedure: European Court of Justice, 2018, 18 January. <https://curia.europa.eu/jcms/upload/docs/application/pdf/2018-01/cp180004en.pdf>.

in quite a broad consensus to question the need to extensively test such food plants, since they claim that the mutations could evolve naturally and such natural mutants would not be regulated by the GM laws. The European Food Safety Authority EFSA came to the conclusion in 2012 that risks of cisgenesis are comparable to those after conventional plant breeding (EFSA Panel on Genetically Modified Organisms (GMO) (EFSA, 2012)). Among food safety specialists there is a debate about process-based (where technology has been used) and product-based approaches to risk management (Mampuy 2019); and on the basis of the fact that mutants occur every day and that they might initiate different metabolic processes, there are those who think that, in fact, all products of plant breeding should undergo more extensive risk management. Finally, different ethicists claim that gene editing damages the integrity of the cell and the genome, that species barriers should not be crossed, or that the technology should not lead to greater influence from multinational corporations (Louwaars and Jochemsen, 2021). On the latter argument, opponents say that GM-regulation has actually significantly contributed to the emergence of such multinationals in plant breeding⁴³. As explained in the chapter on legal and regulatory affairs in this book, authorisation procedures are costly, lengthy and their outcome is uncertain. Finally, there are also ethicists who say that in a world with food insecurity and climate change, it is unethical NOT to use such technological tools.

7.6 Looking ahead

Some people thought we knew all there was to know about life when the structure of DNA was unravelled in 1953 and the Human Genome Project was finalised in 2000, publishing the ‘code of life’. However, as with any scientific field, the more we know, the better we know what we don’t know. But also, as with many other areas of science: the more we know, the better we can use that knowledge to solve problems and to make life better. The same is true for genetics. We know how to identify functional genes; we know how to edit them. But there is still a lot to learn about transcription and translation, and the genetic aspects of cell differentiation, and interactions with the environment in both common (natural) biology and man-made uses of our knowledge. We also increasingly know how to identify the chemical and physiological effects of genetics and its interaction with the environment. Technology, such as phenotyping using real-time image analysis (Hartmann *et al.*, 2011) and the application of sensors, connected to big data analysis and artificial intelligence, will continue to teach us how life processes work, and I am sure that they will continue to reveal new unknowns. Many of these developments originate

⁴³ For instance <http://www.genewatch.org/sub-568236>.

from medical research, but such knowledge can help us to produce food more sustainably in the face of climate change, population growth and changing consumer needs. This obviously includes making sure that food optimally contributes – together with processing science, behavioural sciences and many more – to human, animal, and environmental health. The science of genetics will continue to be an important basis for food availability, quality and diversity in order to sustain a good life.

References

- Abbadi, A. and Leckband, G., 2011. Rapeseed breeding for oil content, quality, and sustainability. *European Journal of Lipid Science and Technology* 113: 1198-1206. <https://doi.org/10.1002/ejlt.201100063>
- Bouis, H.E., 2002. Plant breeding: a new tool for fighting micronutrient malnutrition. *Journal of Nutrition* 132:491S-494S. <https://doi.org/10.1093/jn/132.3.491S>
- Brouns, S.J.J., Jore, M.M., Lundgren, M., Westra, E.R., Slijkhuis, R.J.H., Snijders, A.P.L., Dickman, M.J., Makarova, K.S., Koonin, E.V. and Van der Oost, J., 2008. Small CRISPR RNAs guide antiviral defense in prokaryotes. *Science* 15: 960-964.
- Centre for Food Safety, 2007. Natural toxins in food plants. Risk Assessment Studies Report No. 27. Food and Environmental Hygiene Department, Hong Kong. http://www.cfs.gov.hk/english/programme/programme_rafs/files/ras27_natural_toxin_in_food_plant.pdf.
- Cursio, S., 2018, 25 November. What's behind the invisible decline in nutrient density? Medium. Available at: https://medium.com/@stacey_59725/whats-behind-the-invisible-decline-in-nutrient-density-b2227306992f.
- Dalbadie-McFarland, G., Cohen, L.W., Riggs, A.D., Morin, C., Itakura, K. and Richards, J.H., 1982. Oligonucleotide-directed mutagenesis as a general and powerful method for studies of protein function. *Proceedings of the National Academy of Sciences of the USA* 79: 6409-6413. <https://doi.org/10.1073/pnas.79.21.6409>
- Darwin, C., 1859 *On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life*. Murray, London, UK.
- European Food Safety Authority (EFSA), 2012. EFSA Panel on Genetically Modified Organisms (GMO). Scientific opinion addressing the safety assessment of plants developed through cisgenesis and intragenesis. *EFSA Journal* 10: 2561. <https://doi.org/10.2903/j.efsa.2012.2561>
- Hanson, P.M., Yang, R-Y., Wu, J., Chen, J-T., Ledesma, D., Tsou, S.C.S. and Lee, T-C., 2004. Variation in antioxidant activity and antioxidants in tomato. *Journal of the American Society for Horticultural Science* 129: 704-711. <https://doi.org/10.21273/JASHS.129.5.0704>
- Hartmann, A., Czauderna, T., Hoffmann, R. Stein, N and Schreiber, F. 2011. HTPheno: An image analysis pipeline for high-throughput plant phenotyping. *BMC Bioinformatics* 12: 148. <https://doi.org/10.1186/1471-2105-12-148>

- Louwaars, N., 2019. Food safety and plant breeding; why are there no problems in practice? Chapter 5. In: Urazbaeva, A., Szajkowska, A., Wernaart, B., Tilkin Franssens, N. and Spirovska Vaskoska, R. (eds) *The functional field of food law*. European Institute of Food Law Series Vo 11. Wageningen Academic Publishers, Wageningen, the Netherlands, pp 89-101.
- Louwaars, N.P. and Jochemsen, H., 2021. An ethical and societal analysis for biotechnological methods in plant breeding. *Agronomy* 11: 1183. <https://doi.org/10.3390/agronomy11061183>
- Lin, Z., Hayes, B.J. and Daetwyler, H.D., 2014. Genomic selection in crops, trees and forages: a review. *Crop and Pasture Science* 65: 1177-1191. <https://doi.org/10.1071/CP13363>
- Mampuy, R., 2019. No rose without thorns; Implications of a product-based regulatory system for GM crops in the European Union. Netherlands Commission on Genetic Modification, COGEM Policy Report CGM/191010-01, 72 p. <https://cogem.net/en/publication/no-rose-without-thorns-2/>.
- McClintock, B., 1950. The origin and behavior of mutable loci in maize. *Proceedings of the National Academy of Sciences of the USA* 36: 344-355. <https://doi.org/10.1073/pnas.36.6.344>
- Sinden, S.L., Sanford, L.L., Webb, R.E., 1984. Genetic and environmental control of potato glycoalkaloids. *American Potato Journal* 61, pages 141-156. <https://doi.org/10.1007/BF02854035>
- Stefansson, B.R. and Haugen, F.W., 1964. Selection of rape plants (*Brassica napus*) with seed oil practically free from erucic acid. *Canadian Journal of Plant Science* 44: 359-364. <https://doi.org/10.4141/cjps64-069>
- Talebi, A., Talebi, A. and Shahrokhifar, B., 2012. Ethyl methane sulphonate (EMS) induced mutagenesis in malaysian rice (cv. mr219) for lethal dose determination. *American Journal of Plant Sciences* 3: 1661-1665. <https://doi.org/10.4236/ajps.2012.312202>
- Verkerk, R., Schreiner, M., Krumbein, A., Ciska, E., Holst, B., Rowland, I., De Schrijver, R., Hansen, M., Gerhäuser, C., Mithen, R. and Dekker M., 2009. Glucosinolates in *Brassica* vegetables: the influence of the food supply chain on intake, bioavailability and human health. *Molecular Nutrition and Food Research* 53: S219-S265. <https://doi.org/10.1002/mnfr.200800065>
- Weinhold, B., 2006. Epigenetics: the science of change. *Environmental Health Perspectives* 114: A160-A167. <https://doi.org/10.1289/ehp.114-a160>
- Wernaart, B.F.W., 2022. Food ethics. In: Wernaart, B.F.W. and Van der Meulen, B.M.J. (eds) *Applied Food Science*. Wageningen Academic Publishers, Wageningen, the Netherlands, pp. 45-64.
- Zhang, D.Q., Zhang, Z.Y., Unver, T. and Zhang, B.H., 2020. CRISPR/Cas: a powerful tool for gene function study and crop improvement. *Journal of Advanced Research* 29: 207-221. <https://doi.org/10.1016/j.jare.2020.10.003>

Zhang, X., Ferreira, I.R.S. and Schnorrer, F., 2014. A simple TALEN-based protocol for efficient genome-editing in *Drosophila*. *Methods* 69: 32-37. <https://doi.org/10.1016/j.jymeth.2014.03.020>

Further reading

While Wikipedia is indeed an excellent source of information on all the technical subjects mentioned, an introduction to the information via the inventors of concepts and technologies is advised.

<https://thebiologynotes.com/microbial-genetics>

There are excellent YouTube films on genetics from National Geographic and others.