Rhodes, Catherine. "The History of the Biotechnology Revolution." *International Governance of Biotechnology: Needs, Problems and Potential*. London: Bloomsbury Academic, 2010. 8–21. Science Ethics and Society. *Bloomsbury Collections*. Web. 26 Apr. 2023. <<http://dx.doi.org/10.5040/9781849661812.ch-002>>.

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2. The History of the Biotechnology Revolution

The biotechnology revolution is based on massive scientific advances that have been made over the last sixty years. These advances have given scientists an extremely detailed understanding of life processes, have allowed life forms to be deliberately manipulated at the genetic level and enabled the creation of novel organisms containing genes from other species. To understand the history of the biotechnology revolution, it is useful to look at the development of the science that has helped to create it. There was a significant merging of chemistry and biology (still seen by many as two distinct strands of science) in the early 1950s as connections were made between the molecular structure of deoxyribonucleic acid (DNA) and its role in inheritance. The revolutionary techniques of genetic engineering and genome sequencing stem from this convergence.

This chapter studies the history of chemistry and the history of genetics separately until 1953 (but this is not to suggest that there was no earlier interaction between the two), before looking at the development of genetic engineering and of genome sequencing from then until the present day. The scientific advances have rapidly and often quite directly found applications in a variety of products and processes since the mid-1970s. This chapter, therefore, also looks briefly at the history of biotechnology applications. A glossary is provided towards the end of the book for readers unfamiliar with some of the scientific and technical terms used within this chapter.

Chemistry 1770–1953

The links between the development of modern chemistry and modern biotechnology may not be immediately apparent. However, new discoveries and techniques in chemistry have been vitally important to the development of modern biotechnology and the two areas continue to be connected. Of greatest importance was the discovery of the molecular structure (and from this the chemical properties) of DNA. The structure of DNA was discovered by James Watson and Francis Crick in 1953. At this point the fields of chemistry and biology merged in significant ways to produce the tools, techniques and knowledge that drive the biotechnology revolution. A lot of important steps had to be taken in the field of chemistry before scientists were able to define complex molecular structures like DNA, and these will be looked at briefly in this section.

Modern chemistry is usually dated as emerging in the 1770s with the discrediting of the established phlogiston theory. One scientist in particular is considered to have been instrumental in this move to modern chemistry – Lavoisier, who, using the newly refined concept of elements,

came up with the chemical atomic theory that ‘different elements have fundamentally different atoms’ (Hudson, 1992, p. 77). He and others then worked on identifying as many of these elements as possible. Lavoisier listed thirty-one elements in his 1789 book *Elements of Chemistry* (another chemist, Berzelius, listed forty-nine in 1826). However, the chemical atomic theory was not widely taken up or much used until the periodic table was established – Mendeleev first published his periodic table in 1869 – and this was not to be achieved until there had been some agreement between chemists on atomic and molecular weights. An international congress of chemists was called in 1860 seeking to clarify issues on the establishment of atomic and molecular weights. Although no agreement was reached at the congress it did provide the impetus for the resolution of these issues, which occurred during the following decade.

The study of chemistry split between organic and inorganic chemistry around 1860. Organic chemistry concerns compounds containing carbon, whereas inorganic chemistry concerns those that do not. This was a split more in the focus of research than in techniques and the two areas remain connected. The establishment of atomic weights brought progress to both areas, allowing the periodic table to be formed and also enabling molecular formulae to be deduced. The formulae of molecules are important in identifying their structure. Knowledge of the atomic weights of elements allowed their proportions within molecules to be worked out.

The discovery of further elements continued well into the twentieth century. Mendeleev had left gaps in his periodic table at points where he had predicted these elements would fall. Two techniques aided the discovery of new elements. The first, developed in 1860, used a spectroscope that could be used to analyse light produced from burning materials (Hudson, 1992, p. 125). Several elements were discovered in this way that had previously been hard to identify due to them being present only in tiny amounts mixed up with other materials. The second and better known technique was developed in 1898 by Marie and Pierre Curie, who made use of radioactivity to discover new elements including radium and polonium, through their radioactive isotopes.

Increasing knowledge of relatively simple molecular structures enabled increased work to take place on the synthesis of organic compounds from inorganic elements. This had first been shown to be possible in 1828 with the synthesis of urea, but knowledge of molecular structure enabled it to take place more systematically. Soon chemists were also ‘producing compounds that had no natural counterparts’ (Hudson, 1992, p. 144), particularly dyes and drugs.

As more was discovered about the structure of simple molecules, chemists were able to progress to working out the more complicated structures of some of the larger, complex molecules that existed in nature. It was work in this area that was to lead to the discovery of the structure of DNA.

A new technique of X-ray crystallography, developed in 1913, was to enable the identification of the structures of much larger molecules. This technique essentially allowed a photograph of a molecule to be produced from its crystalline form, by making use of X-ray diffraction, i.e. the way X-rays are deflected from their original course when they hit the molecule. This technique was refined over the following decades, allowing sharper images to be produced. Such a picture of DNA, produced by Rosalind Franklin in 1952, gave Watson and Crick significant clues about its structure.

There was also an obstacle of how to deal with the large amounts of information that would be produced when dealing with more complex molecules containing thousands of atoms. The invention of electronic computers helped to overcome this obstacle (Hudson, 1992, p. 224).

Other discoveries about the chemistry of DNA had also assisted Watson and Crick, particularly the discovery by Erwin Chargraff that the number of adenine bases was equal to the number of thymine bases and the number of guanine bases was equal to the number of cytosine bases. Franklin also suggested (based on her photograph) that the sugar-phosphate 'backbone' of DNA ran along its outside. Further discoveries about the chemical properties of DNA and how it functions followed. Those are dealt with later in this chapter.

Developments in modern chemistry from the late eighteenth century onward enabled the structure of DNA to be worked out in 1953. Knowledge of the structure, properties and functions of DNA, combined with the realisation in the field of genetics that DNA carried hereditary information, allowed new techniques of genetic engineering to be rapidly developed, and these techniques underpin the biotechnology revolution.

Genetics 1900–53

Many of the modern developments in biotechnology are based on a detailed knowledge of genes and genetics. This knowledge has been built up over the past century.

Modern genetics study is said to have begun in 1900 with the rediscovery of Mendel's work on the inheritance of factors in pea plants (factors later to be termed genes). Mendel had published his work in 1866, but it attracted little attention until the same principles were independently discovered by three scientists (Carl Correns, Hugo de Vries and Erich Von Tschermak) in 1900. Study of cells (cytology), aided by improvements in the clarity and magnification of microscopes, had led to the observation of chromosomes in 1879, and by 1900 it had also been shown that protein and nucleic acid were present within cells. Through experimentation in the early twentieth century it was established that genes were located on the chromosomes. However, it was not until 1952 that it was widely accepted amongst geneticists that DNA carried genetic information; the proteins in cells had seemed better candidates for this role.

Acceptance of the role of DNA combined with the new knowledge of its molecular structure (announced by Watson and Crick in 1953) was to bring about the rapid development of new tools and techniques in genetic engineering, which in turn brought huge advances in biotechnology.

Following Darwin's work on evolution (*Origin of Species* was published in 1859) many people sought to discover how characteristics could be passed on from parents to offspring. These were suggested to be 'material factors' and were recognised by Hugo de Vries (writing in 1910) to be 'the units which the science of heredity has to investigate. Just as physics and chemistry go back to molecules and atoms, the biological sciences have to penetrate these units in order to explain, by means of their combinations, the phenomena of the living world' (Fruton, 1972, p. 225). (The units in fact turned out to be molecules of DNA.)

By the end of the nineteenth century cytologists studying the behaviour of chromosomes had observed the processes of mitosis and meiosis, different types of cell division, providing good evidence that these parts of the cell could carry genetic information. There was a mechanism for duplication which occurred during routine cell division (mitosis) and there was also a mechanism which allowed for the inheritance of both parents' genes in the reduction in the number of chromosomes by half in meiosis (cell division in the germ cells), which then combined with the other parent's half set during reproduction.

Studies of genetic changes (mutations) in the early twentieth century provided further evidence about the role and functions of chromosomes, and also of the location of genes upon them. Significant work was done with the fruit fly *Drosophila melanogaster*. This fly breeds quickly and that meant that mutations could be studied through many generations. Experiments with mutations reinforced Mendel's theory that some characteristics were inherited separately from one another, but also showed that some were linked in inheritance. The phenomenon of 'crossing-over' was also observed (and named) by Thomas Hunt Morgan. This is where sections of a pair of chromosomes swap with each other during meiosis causing mutations to occur. Morgan realised that this might allow the locations of genes to be established and A. H. Sturtevant used statistical study of mutations and the frequency of crossing-over to establish the relative positions of six genes on one of *Drosophila's* chromosomes in 1913. He then produced the first chromosome or linkage map based on this. By 1925 Morgan's team had located 100 genes on *Drosophila's* four chromosomes.

Mutations are very significant to the study of genetics and methods were later developed to increase mutation rates through radiation and chemical means. The early work on chromosome mapping helped to lay the basis for later, more complex, mapping of the genomes, including the Human Genome Project (HGP).

By the 1920s the concept of the gene as the unit of heredity had been established, the study of genetics was well underway and it was understood that gene expression and inheritance relied on processes occurring within the chromosomes. There had also been some suggestion that mutations might occur due to interference in the production of enzymes.

The puzzles remained of how the cell used the genetic information, where the genetic instructions came from and why the information was expressed differently in different cells despite the same chromosomes being present. The theory was that proteins were responsible. Proteins are present in the cell, and enzymes (which are a form of protein) are used in many cytological processes.

There had been a suggestion as early as 1884 by the scientist Oskar Hartwig that 'Nuclein is the substance that is responsible ... for the transmission of hereditary characteristics' (Aldridge, 1996, p. 7). But this view was largely ignored until the early 1950s, partly because of a theory called the 'tetranucleotide hypothesis' put forward by Phoebus Levene in the 1930s. This held that the four nucleotides of DNA (adenine, thymine, guanine and cytosine) made up a string of repetitive code and were therefore incapable of carrying the complex code that would be needed for holding the genetic instructions. Proteins did not have this problem. Proteins are a type of complex molecule known because of its structure as a 'polypeptide chain'. They are made up of amino acids and 'there are 20 amino acids commonly found in proteins' (Aldridge, 1996, p. 13), allowing the variation necessary to hold a long and complicated code.

It was also decided in the 1920s that genes (and therefore what they were made of) had to be autocatalytic, that is able to make themselves replicate. Geneticists tried, but failed, to come up with a satisfactory theory as to how proteins achieved this. Once the molecular structure of DNA was established its autocatalytic properties were self-evident as Watson and Crick noted: 'It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material' (Hudson, 1992, p. 225).

Further evidence of mutations being linked to a lack of a particular enzyme led to another theory (by Beadle and Tatum) that also hindered the recognition of the significance of DNA. The 'one-gene, one-enzyme' hypothesis, while not essentially wrong, did lead some to the erroneous conclusion that enzymes were genes. The theory has since been revised to the 'one-gene, one-polypeptide' hypothesis, but it was along the right lines, genes do code for enzymes.

It was not until the tetranucleotide hypothesis was disproved by Erwin Chargraff in 1948 that the possibility of DNA carrying genetic information was taken seriously. He showed through paper chromatography that the nucleotides did not form a repetitive sequence, and so it was possible for DNA to be carrying a code. Experiments on pneumococci bacteria by

Oswald Avery in 1944 had shown that DNA was likely to be the 'transforming principle' exchanged between bacteria and led to the statement that: 'nucleic acids of this type must be regarded not merely as structurally important but as functionally active in determining the biochemical activities and specific characteristics of pneumococcal cells' (Fruton, 1972, p. 248, quoting Avery, McLeod and McCarty in 1944).

Yet it seems to have been experiments on bacteriophages by Hershey and Chase (who published their findings in Hershey and Chase, 1952) that finally convinced geneticists that DNA was the molecule of heredity. Using radioactive tags (one that attached only to DNA and one that attached only to protein) they showed that it was through the transference of DNA that bacteriophages attack bacteria.

Cytology combined with genetics to lead in just over half a century to the crucial discovery of the role of DNA in inheritance and its importance in the functioning of cells. Coupled with new knowledge about the molecular structure of DNA, this led to rapid development of new genetic engineering tools and techniques which underpin the biotechnology revolution.

Genetic Engineering from 1953 Onwards

By 1953 there was widespread acceptance among geneticists that DNA carried genetic information and its molecular structure had been discovered. This opened up the possibility that genes could be manipulated at the molecular level, their function understood and possibly corrected or controlled. First scientists had to work out how genes are expressed, that is how DNA codes for proteins.

Within twenty years the possibility of working with DNA at the molecular level had been realised. One of the most important steps was the development of recombinant-DNA (rDNA) techniques. rDNA involves the insertion of one piece of DNA into another, including between unrelated organisms. rDNA was immediately recognised to be an extremely powerful technology, and fears about its use soon emerged, leading to a temporary halt in rDNA experiments. The experiments restarted a couple of years later. The technology was soon applied to a range of new biotechnological products including pharmaceuticals and transgenic organisms.

Erwin Chargraff had shown that the four bases of DNA, adenine (A), thymine (T), guanine (G) and cytosine (C), did not form a repetitive sequence and could therefore be capable of carrying the genetic code. It remained to be shown how this code functioned and how the information from the code could be transferred to enable the building of proteins.

In 1957 it was suggested by Frances Crick and George Gamow that the genetic code referred to the sequence of the amino acids that make up proteins. There are twenty amino acids to code for and four bases to code for them. This meant that it was most likely for the bases to code for amino acids in groups of three, because this would produce sufficient variations in

the code. The bases separately could code for only four amino acids, in pairs for sixteen, while triplets gave sixty-four possibilities. The triplets of bases are referred to as codons.

Marshall Nirenberg made the first link between a codon and the amino acid it specified in 1961. This corresponded to an AAA codon on a strand of DNA and specified the amino acid lysine. Nirenberg's team had worked out the rest of the codon 'dictionary' by 1966. In some cases two or more codons specify the same amino acid and three codons do not specify an amino acid, but instead a point in the code at which translation (the reading and converting of the code) should stop – they are therefore referred to as stop codons.

It was known that DNA would have a replication mechanism and the process of replication was observed in 1957. It was later discovered how ribonucleic acid (RNA) carried sections of the genetic code out of the nucleus to build proteins. RNA is similar to DNA although it is normally single stranded and the base thymine of DNA is replaced by the base uracil (U) in RNA, so it has the bases A, U, G and C. In studies of the cell, RNA had been shown to be present both in the nucleus and in the cytoplasm (the part of the cell surrounding the nucleus).

There are three types of RNA in cells and each has a different function. The only one present in the nucleus of cells is messenger ribonucleic acid (mRNA) and it is this that carries the genetic code from the DNA out into the cytoplasm where the proteins are built. It was observed that certain sections of DNA will unravel temporarily and the mRNA will match up to one side of the strand and by matching the nucleotide bases A to T, U to A, C to G and G to C can then carry the code away while the DNA rewinds. Back in the cytoplasm the mRNA is then translated into amino acids which the transfer ribonucleic acid (tRNA) collects and the ribosomal ribonucleic acid (rRNA) builds into proteins.

The discovery of how genes code for proteins was an important step towards the development of rDNA techniques. Also important were the discovery of restriction enzymes and DNA ligase. Restriction enzymes can 'cut' DNA at specific points in the base sequence and were discovered by Hamilton Smith and David Nathans in 1971. Such enzymes are used by viruses to insert their RNA into a host's DNA. DNA ligase is an enzyme that can 'stick' two strands of DNA together. In 1972 the biochemist Paul Berg used a restriction enzyme to cut strands of DNA and used ligase to stick two strands together in a novel way. This created the first rDNA molecule.

With this new technique it became possible to transfer genetic information across species boundaries and to manipulate DNA in a controlled manner 'to modify genes or to design new ones, to insert them into bacterial cells ... and thus to form cells with new biochemical properties' (Asimov, 1987, p. 591). Concerns were soon raised within the scientific community about the safety of rDNA experiments, with particular fears about accidental release

of genetically altered bacteria or viruses. This led to a halt in experiments following discussion at the 1975 Asilomar Conference, until guidelines had been introduced. The United States National Institutes of Health (NIH) issued guidelines the following year and research continued.

rDNA gave scientists ‘methods of participating directly in gene activity’ (Asimov, 1987, p. 591), and the ability to create entirely new products from biological processes brought about many biotechnological applications. Early examples include the production of human insulin (1978) and human growth hormone (first cloned in 1979), transgenic mice (1981) and later genetically modified crops (first field trials in 1985) and gene therapies (1990).

Genome Sequencing

Another important development in genetic engineering has been the sequencing of genomes. This developed from the early work of geneticists on locating and mapping genes on chromosomes. Current techniques and knowledge now allow much more sophisticated mapping to be done and sequencing is a first step in the mapping process. Advances in sequencing tools, and particularly the increased speed at which the information produced can be processed, meant that it was possible to begin sequencing the human genome in 1990 and a full draft of the human genome was published in April 2003. Sequencing of genomes has greatly increased the amount of genetic information available to scientists, and this will, among other things, enable them to gain increased knowledge of human diseases – ‘When we have a detailed genetic map we will be able to identify whole sets of genes that influence general aspects of how the body grows or how the body fails to function’ (Kevles and Hood, 1992, p. 94).

Mapping of genes is the ‘Determination of the relative positions of genes on a DNA molecule (chromosome or plasmid) and of the distance, in linkage units or physical units, between them’ (Kevles and Hood, 1992, p. 379). The first linkage or chromosome map was created by A. H. Sturtevant in 1913 and mapped the relative locations of six genes on one chromosome of the fruit fly *Drosophila melanogaster*. Early mapping used mutations (genetic changes) to establish the location of genes on particular chromosomes. Mutations can be studied relatively easily in fruit flies as they breed rapidly, allowing genetic changes to be followed through many generations, but it was difficult to do this work on humans because their life cycle is far longer. A new technique, developed in 1967, changed this. Somatic cell hybridisation enabled work to be done on mapping human genes. Somatic cell hybridisation mixes chromosomes from human cells and mice cells, creating single cells containing both sets of chromosomes. These cells are not very stable and as they divide human chromosomes are lost. When only one human chromosome is left in the cell, any human proteins produced by the cell must be the expression of genes on that chromosome.

Genetic sequencing determines the sequence of nucleotides (the individual nucleic acids adenine, thymine, guanine and cytosine) present in a gene. Sequencing of genes did not become possible until the structure and role of DNA were understood. The development of the codon dictionary was particularly important to this.

Frederick Sanger began work on DNA sequencing in 1977, building on his previous work on establishing the sequence of amino acids in proteins. He completed the first genome sequence (of a bacteriophage named phiX174) in 1978. Another method of sequencing was developed at the same time which used chemicals instead of dideoxynucleotides to split up the DNA. 'Since then, the two methods have been standardized, speeded up and in a large part automated' (Kevles and Hood, 1992, p. 66).

The development of the polymerase chain reaction (PCR) in 1980 by the Cetus Corporation helped to speed up the process of sequencing. PCR is a method of replicating fragments of DNA many times over, rapidly providing large amounts for analysis and sequencing. Computers helped both to automate the process and to store the vast data produced.

These developments made conceivable the sequencing of larger genomes, such as the human genome, the idea of which began to be discussed in the mid-1980s. The Human Genome Project, a massive, international, public project to sequence and map the human genome, was approved by the US Congress in 1988 and work began in 1990. The human genome is far larger than any genome previously sequenced (to compare phiX174 has 5,375 nucleotide bases, the human genome has approximately 3,000,000,000). An ambitious target for completion of the sequence in 15 years was set. The work on sequencing the human genome (only one part of the overall project) progressed slowly until a privately funded initiative was set up in competition, in May 1998. This made use of a different sequencing method and promised far quicker results for less money. This move was and still is hugely controversial, but did spur on efforts within the public project. Both projects published rough drafts of the human genome in February 2001, and the public project released a full draft in April 2003.

The human genome sequence will provide the basis for detailed mapping of genes and their functions. One of the most direct benefits to come from sequencing of the human genome will be enhanced understanding and therefore improved treatment of many human diseases, but the information resulting from the HGP will have many other applications as well.

It is not only the human genome that has been sequenced, but also key reference genomes such as the fruit fly, nematode worm and common house mouse; over 1,200 other genomes have been completely sequenced (Genomes Online Database, 2009), most of them microbial. The fruit fly was sequenced by the private team prior to their work on the human genome, to show that their sequencing method worked, and the nematode worm was sequenced by the public project to serve as a reference genome.

The mouse genome will also serve as an important reference for the HGP as it 'will allow researchers to gain insights into the function of many human genes because the mouse carries virtually the same set of genes as the human but can be used in laboratory research' (National Institutes of Health, 6 May 2002).

Sequencing of the genomes of other organisms has established that sequencing tools and techniques work, and has provided important reference information, as well as giving an understanding of the particular organism involved. An offshoot of the HGP is a Microbial Genome Program, which will increase understanding of various microorganisms in order that they might be better utilised by humans in waste treatment and environmental management and so that disease-causing microbes can be more effectively targeted by drugs. Information on many other genome sequencing projects can be found through websites such as the Genomes Online Database (<http://www.genomesonline.org>).

The sequencing and mapping of genomes have contributed to increased knowledge of the biological processes of various organisms and to understanding of genetic functions. They provide vast amounts of data to which the tools of genetic engineering can be applied, in turn increasing the scope of biotechnology applications.

Biotechnology Applications

Humans have been making use of living organisms and biological processes for thousands of years; the earliest applications were probably in the production of food and drink products such as beer, bread and cheese. Early applications made use of entirely natural processes and did not require any understanding of what these processes were. Some applications of modern biotechnology still use naturally occurring processes, which are now far better understood. Genetic engineering has been used to improve understanding of biological processes and to improve them, and it has also been used to create new sources of particular products and completely novel products that have never before occurred in nature. Biotechnology is now applied across a huge range of industries and there has been great expansion in the scope of its applications since the development of rDNA techniques.

The present range of industrial sectors using biotechnology includes health care, food, mining, plastics, chemical, textiles and waste treatment. It is also widely used in agriculture and animal husbandry. There are far too many applications for them all to be discussed here, but some of their uses within these sectors are briefly outlined.

Health Care

The earliest applications of rDNA were to address problems of human health, and the pharmaceutical industry is the area where modern biotechnology has had its biggest impacts so far. The first applications of rDNA were to

produce bacteria to ‘manufacture’ human proteins. An early example of this was the adaptation of *E. coli* bacteria to produce human insulin. Insulin for the treatment of diabetes had previously been sourced from animals. The human version is better suited to fulfil this function and the huge quantities necessary to treat the 220 million people worldwide that have the disease (WHO, November 2009) and can be produced more reliably. The license to market human insulin produced in bacteria was granted in 1982 (Biotechnology Industry Organisation, 2002).

There are currently products approved for the treatment of many diseases and disorders including haemophilia, hepatitis, certain cancers, heart disease, anaemia, cystic fibrosis and epilepsy. Recombinant vaccines and new diagnostic tests have also been developed.

Agriculture

Biotechnology has been applied to agriculture in a number of ways, to both plants and animals. In food crops genetic engineering has been used to transfer or create a number of desirable traits. These include increased yields, reduced need for inputs like pesticides and herbicides and the production of plants with improved nutritional value for both human consumption and use in animal feed. Currently there are genetically modified crops being developed to produce other useful products such as pharmaceutical drugs, vaccines, blood-clotting factors and chemicals for use in industrial processes (Union of Concerned Scientists, 15 December 2004).

Animals have also been genetically engineered to enhance desirable traits and to act as ‘factories’ for producing other useful products. For example cows have been genetically engineered to produce some human proteins in their milk. Similar developments have occurred in aquaculture or fish farming, particularly with the aim of speeding up growth rates.

Food and Beverage Industry

This is the area with the longest history of applications of biotechnology. Natural biological processes have traditionally been exploited in processes such as the fermentation of alcohol, bread-making and cheese-making. Modern biotechnology is being used to increase understanding of and improve these processes. Rennet, for example, used to be sourced from calves’ stomachs, but can now be produced in genetically engineered bacteria, which produces a cheese suitable for consumption by vegetarians. New uses and processes have also been developed, particularly as the properties of more yeasts and fungi have been discovered and exploited. Further examples of uses are in preservatives and flavourings.

Mining

Modern biotechnology has enabled the replacement of chemical methods for extracting some mineral ores by biological ones, which are often more

effective and create fewer unwanted by-products. Sometimes the bacteria used are entirely natural, although genetic analysis may have been used to work out the most suitable bacteria and the optimum conditions for them to work under. Other bacteria may be specifically designed to do this work.

Environmental Management

Biotechnology is extremely useful in the treatment of waste products since biological processes are involved in the degrading of all wastes. Biological processes are used by many industries to treat their waste products in order to reduce the amount of pollution they create. Biotechnology is also used in the general treatment of public waste water and sewage. Scientists have also begun work on optimising the action of bacteria in landfill sites to speed up processes of degradation. Bacteria can also be used as a method of cleaning up oil spills. Similar to the use of bacteria in mineral extraction, many of the current applications make use of naturally occurring processes which are now better understood and can therefore be more effectively applied. There can also be genetic modification of the bacteria involved, for example to enable them to work under specific conditions and cloning can be used to create large amounts of either naturally occurring bacteria with specific traits or the custom-made versions.

Biotechnology has a major role not only in the treatment of wastes and spillages, but also in preventing environmental damage in the first place by creating more environmentally friendly production processes: 'biotechnology offers us many options for minimizing the environmental impact of manufacturing processes by decreasing energy use and replacing harsh chemicals with biodegradable molecules produced by living things' (Biotechnology Industry Organisation, 2002). Biological processes are already replacing the use of some chemicals in industries such as the paper pulp and textiles industries.

The Industry

Modern biotechnology has been applied across a wide variety of long established industries, and it has also led to the formation of its own industry. The biotechnology industry has developed rapidly since its origins in the mid-1970s. As the applications of modern biotechnology continue to increase based on new scientific developments, so the industry is also likely to continue its expansion.

Over the past thirty years strong links have been developed between academia and industry in the biotechnology area, with commercial applications often coming directly from work in academic laboratories. From the mid-1970s onwards many small biotechnology start-up companies were created, often concentrating on the development of products, which would subsequently be manufactured and marketed by larger, established

companies. The first such company, Genentech, was created in 1976. Genentech's first commercially available product was cloned human insulin (Olson, 1986, p. 85). Over the next few years several other start-up companies were set up by scientists. Genentech did not take its product to market itself but instead licensed production to the pharmaceutical giant Eli Lilly. This made sense because Genentech did not have the capacity to manufacture or resources to market the product, which Eli Lilly as an established pharmaceutical company had.

Following the success of the small companies, the established pharmaceutical companies moved into the area in the early 1980s taking over small biotechnology companies or setting up their own biotechnology sectors. An example of such a company is GlaxoSmithKline, one of the world's largest pharmaceutical companies, which currently has several biotech products approved and on the market. Its first biotech product – a recombinant hepatitis B vaccine – received approval in 1989 (Biotechnology Industry Organisation, 2002). More recently GlaxoSmithKline has moved into genomics to enhance its research and development processes (GlaxoSmithKline, no date).

In the mid- to late 1980s other companies from the chemical and seed industries began to enter the biotechnology area, often consolidating into huge life-science companies. A well-known example of such a company is Monsanto. Monsanto was formed as a chemical company in 1901 and soon expanded its range of products and bought out many other companies. Monsanto has had an agricultural division since 1960 and moved into biotechnology in 1989 (Monsanto, 2002a). Its first biotech product POSILAC bovine somatotropin, designed to improve milk production in dairy herds, was approved in 1993 (Monsanto, 2002b). Since then Monsanto has had over twenty genetically modified crops approved (AGBIOS, 9 March 2010). From 1997 Monsanto became involved through collaborations in genomics research and merged with a large pharmaceutical company in 2000 to form the Pharmacia Corporation. (A new Monsanto company was established as a subsidiary of Pharmacia in 2000 and became a separate company in 2002, which focuses on agricultural biotechnology and genomics.) The industry is predominantly based in major industrialised countries and centres in Europe, Japan and the United States.

Conclusion

Biotechnology, being the use of biological processes to create useful products, has a long history. Rapid scientific developments in the past few decades have produced a knowledge base and set of tools and techniques that enable biological processes to be understood and controlled to an extent never before possible. This has created the biotechnology revolution. During the first half of the twentieth century knowledge from the scientific fields of chemistry and genetics combined to provide the basis for a revolution in the life sciences. Advances in genetic engineering since 1953, which have allowed

the manipulation of life processes at a genetic level, have given modern biotechnology its central tools and techniques. The unprecedented nature of these advances – in particular the ability to transfer genetic material from one organism to another (including across species boundaries) – has given the new biotechnology its revolutionary effects. Modern biotechnology has incorporated genetic engineering to create transgenic plants and animals, novel pharmaceutical products, improved methods of waste treatment and far more.

There has clearly been a revolution in the life sciences based on a new understanding and knowledge of genetics and new tools and techniques to apply this knowledge. The next chapter will examine what the current status of the biotechnology revolution is and how this science-based revolution has extended its impacts into the social and economic spheres.