



MINISTRY OF DEFENCE

GENOMICS: SOME IMPLICATIONS FOR DEFENCE

This is the second in a series of Ministry of Defence leaflets on emerging technologies, designed to provide information about topics that are likely to be of growing importance to defence, produced in conjunction with a panel of some of the UK's leading experts. (See box right).

A glossary of terms is to be found at the end of the main text.

MOD'S INTEREST IN GENOMICS

The MOD's interest in genomics as an emerging technology is entirely defensive. We anticipate that scientific developments in this area will have an impact on healthcare applications, including the health of UK Armed Forces, and it is therefore important for us to understand the potential implications. In addition, an understanding of the genomes of pathogens, including certain bacteria and viruses, is likely to improve our ability to defend against such organisms, should they ever be used against us in biological warfare.

WHAT IS GENOMICS?

Genomics is the study of genetic sequence information in living organisms. Genetic sequence information is encoded in the molecule DNA (deoxyribonucleic acid) which is found in the chromosomes of all species. The sequence contains discrete functional units called genes. (See "How DNA Works"). Sequencing of the Human Genome is one of the most significant enterprises in genomics and it will generate results that will affect us all. **The Human Genome Project** is now likely to reach completion by 2003, much faster than expected, due to rapid advances in sequencing technology. Indeed, recently, the journal "Nature" published the first draft of the entire human sequence, based on the work of a publicly funded, international consortium of researchers. (Simultaneously, a draft was also published in the "Science" journal, based on the work of the US company Celera Genomics). But why the need to sequence at all? A driving reason is to understand the human species at the most fundamental level. But this is combined with the possibil-

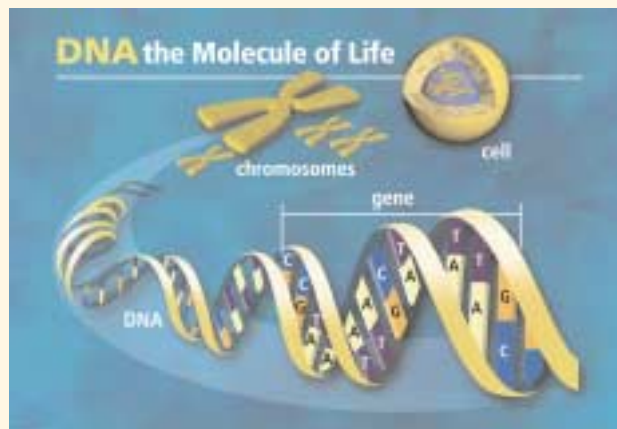


Figure 1: DNA is found in the chromosomes of all cells.

The Expert Panel

Professor Kay Davies: is Dr Lee's Professor of Anatomy, University of Oxford. She is also Honorary Director of the MRC Functional Genetics Unit. Her research programme is dedicated to using genomic and genetic approaches to the analysis of neurological disorders.

Professor Peter G. Blain: is Professor of Environmental Medicine, University of Newcastle and Consultant Physician in Medical Toxicology at Newcastle Hospitals NHS Trust. His research interests include the clinical significance of interactions between an individual's genetic makeup and their environment.

Professor David Moss: is Professor of Biomolecular Structure in the School of Crystallography at Birkbeck College, University of London. He is Chairman of the Research Councils' Collaborative Computational Project in Bioinformatics.

Dr Nigel Spurr: is Head of Discovery Genetics-US at GlaxoSmithKline Pharmaceuticals. From 1985-1996 Dr Spurr was Head of the Human Genetics resources laboratory at the Imperial Cancer Research Fund. In 1996 he moved to SmithKline Beecham and established a human genetics group focusing on the use of genetics in drug discovery.

ities of defining, even down to the individual level, why we succumb to particular diseases - and - most importantly, finding rapid and effective ways to diagnose and treat illness. The completion of the Human Genome Project is therefore a landmark in the scientific literature and, it must be said, in human self-discovery but in many ways it is just the "beginning of the beginning". What scientists must now do is embark on locating all of the genes within the sequence, decipher their functions - and - most importantly, determine the functions of their products, the proteins, which drive all living processes.

But it is not only the human genome that is being sequenced. The

entire sequence and list of genes is already available for many different viruses and bacteria; and many more are in progress including those of significance for biological defence such as the bacterium *Bacillus anthracis*, which causes anthrax. Other genetic sequences already available include those for yeast (*Saccharomyces cerevisiae*), for a worm (a nematode worm called *Caenorhabditis elegans*), for the fruit fly, *Drosophila melanogaster*, and for the plant *Arabidopsis thaliana* (Thale cress). Soon others will join the list, including the mouse. These initiatives represent a huge burgeoning of information which will be collated, assessed and analysed in many different ways. **Why are these genomes of interest ?** One answer is the information that can be gleaned by comparing genomes (comparative genomics). This process can be highly instructive because even distantly related species share many similar genes, often organised in much the same way. And it is often possible to understand gene function by studying parallels in other organisms. For example, between humans and the great apes there is only a 1-2% difference in their DNA. Even humans and plants share over 50% of their DNA sequence. To give but one very specific example -; a gene called sonic hedgehog plays a key role in the growth and orientation of a fly's wings during its development. In human embryos, an equivalent gene is directly involved in the growth and orientation of limbs.

In this leaflet, we will select some aspects of this vast subject to look in more detail at the **human genome** and **microbial genomes** since these may have the most direct impact on defence interests, particularly for **healthcare applications** and for **chemical/biological defence**.

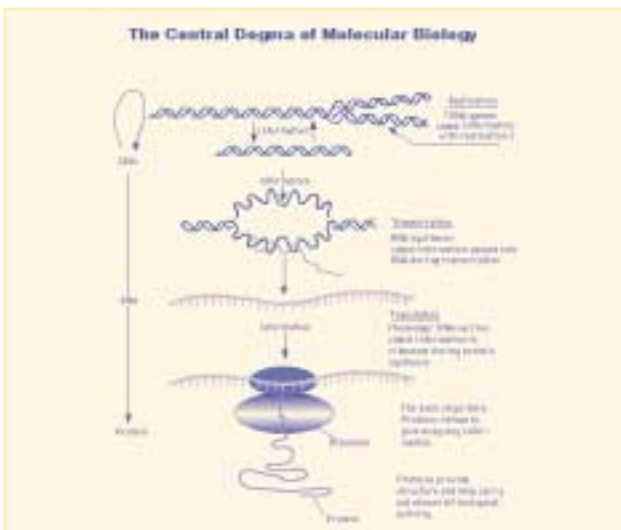


Figure 2: diagram illustrating the transcription of RNA from DNA, and translation of RNA into protein - the so called central dogma of molecular biology.

HOW DNA WORKS

DNA (deoxyribonucleic acid) is found in the chromosomes of all living organisms and it is the molecule that stores the information about all proteins. It is a double-stranded molecule in the form of a helix and the important parts of its structure as far as the code is concerned are the components called bases. These can be abbreviated from their chemical names to A,T,C and G (which is how they appear in a published sequence) and an important phenomenon is that they always pair in a specific way- : thus A in one strand always bonds or pairs with T on the opposite strand ; and similarly C with G. Hence the term "base pair(s)".

The order of A,T,C,G is critical. It forms the genetic sequence, which contains discrete functional units called genes and it underlies the genetic code. Genes direct the making of proteins. A sequence of three bases (a triplet such as ATG or TGA for example) specifies the information for a single constituent (an amino acid) in a protein. To achieve a string of amino acids from the original code in the DNA, it is first transcribed into messenger RNA (ribonucleic acid, a very similar molecule but single stranded). Then, with the help of other RNA molecules, the transcribed code is used to line up amino acids to form a protein molecule.

STRUCTURAL GENOMICS AND PROTEOMICS

Knowledge of genetic sequences and genes is the beginning of a much more complex enterprise - to establish what products (proteins) the genes encode- ; to unravel the complexities of protein structures ; and to define which proteins are used for particular functions at different times in different cell types. Fulfilling this objective is the next key landmark. These activities have been called structural genomics and proteomics and the information will constitute the "proteome" - a compilation of all of the protein structures and their functions/activities in an organism throughout its life.

Structural genomics and proteomics are still in their infancy and although new technology now allows the identification of perhaps hundreds of proteins a week, it is still not as automated as genomics. But realising the goal – a global picture of cell function - will be vitally important for realising improvements in healthcare such as finding new drug targets, and investment is beginning to increase. Currently, relatively few protein structures are completely understood, with the three-dimensional folding of these molecules posing the most difficult problems. Without such detailed knowledge, understanding of protein function will be very difficult to achieve. Proteins which form cell membrane structures are particularly difficult structures to solve although they will offer promising future targets for novel drugs. However, once this problem is solved, it is likely that, as with genome



Figure 3: a 3-dimensional protein structure.

sequencing, the technology will move very fast. Much faster (at the moment) than proteomics is transcriptomics, a complementary technique which captures the intermediate stage of protein synthesis. It enables all of the messenger RNA in a cell at a given time to be identified and provides a snapshot of the cell's

plans for proteins. Microarrays (See “Microarrays or DNA Chips”) can be used to identify the messenger RNAs rapidly and comprehensively. On a smaller scale, these approaches can be used to identify all of the proteins involved in a particular disease and how genetic variations affect both the proteins and therefore may influence the course of the disease itself. Which genes are switched on, and in what order, will almost certainly be crucial to our understanding of some diseases.

THE HUMAN GENOME

Each cell in the human body contains 23 pairs of structures called chromosomes. These contain the genetic material or DNA, which is extracted for sequencing. The sequence is usually described in terms of its order of bases (see “How DNA Works”) and similarly, quantities of DNA are usually described as total “base pairs”. The human genome consists of some 3 billion base pairs. However, not all of this sequence consists of genes. In the human genome there are probably about 32,000 genes (far fewer than was expected at the start of the project). In between the genes is non-coding DNA and in fact this makes up about 95 % of the total. Genes are the most important part since their sequences code for the production of proteins and it is the genes which are the units of inheritance. The number of genes in the human genome turns out to be not so very different from that in much humbler organisms – equivalent in fact to about 3 fruit flies (worth of genes) or 2 nematode worms. And yet they are responsible for the entire complexity of the human body. Some of this complexity is achieved by the way in which

genes are used in the human genome. Unlike some simpler organisms, where one gene tends to correspond to one protein, many genes appear to be fragmented and can be combined together in different ways to provide the information for several different proteins. Modifications may also be made to proteins after they have been produced, and these may be important for variations in function between different cells and at different times.

Non-coding DNA is also important because some of it at least controls when genes are turned on or off, in time and in space – for example, during development of the foetus and to allow different functions in the body (for example, so that a liver cell functions differently from, for example, a brain cell). We also know that the total amount of DNA in an organism's genome is not related to its complexity. Some very simple organisms have more DNA in total than man.

Differences between individuals, and the extent to which these differences have a genetic basis, will also be illuminated by the Human Genome Project. Part of its output will be a database of the most common sequence variations that could distinguish one person from another. In almost all humans, all genes are identical but some individual bases and some short sequences can vary. Some of these may have no effect; others can lead to differences in features such as eye colour, height and so on; yet others may affect individual susceptibility to disease. Variations in a single DNA base called single nucleotide polymorphisms (SNPs) can be used as landmarks, to understand gene variants in a population and to assess their role in disease. Some 1.4 million SNPs have already been mapped.

Despite these differences what is emerging from the human genome studies is the remarkable similarity in the genetic code between individuals. In fact, every person is likely to share some 99.9 (9)% of the same genetic code with other people. The degree of diversity is very low. Thus it is likely that people within “ethnic groups” are more different genetically from each other than their group is from other groups. This has important implications for defence in terms of our assessment of the future threat where we have been concerned about the potential mis-use of human genome information. Based on what we now know of genetic variation, the prospect of mis-using human sequence information, for targeting specific groups - so-called genetic weapons – would appear to be greatly diminished.

INVESTMENT AND DRIVERS

Total investment either nationally or internationally is difficult to define because “genomics” strays into many complementary fields. However, data compiled by the Stanford-in-Washington Program¹ indicates that in 2000, Government and non-profit funded bodies alone invested some £550M in genomics worldwide. The main players tend to be in the US and Europe including the UK. A survey of investment by the private sector (including those specialising in genomics but also established biotechnology and pharmaceutical companies) adds a further £1billion.

The main driver is healthcare and the search for new and more easily producible drugs. But other drivers include agriculture and industries’ search for new compounds to support food and chemicals (for example). Work on genome diversity and proteomics which follows on from genomics, will largely be funded by the pharmaceutical industry, with academia continuing to provide basic research and emerging technologies. Government will play a role as well. Not only will it need to develop the regulatory and ethical frameworks which future work will demand, it must also foster a climate in which research can thrive, including support to major Bioinformatics (See “Technologies to Support Genomics”) initiatives such as the European Bioinformatics Repository.

Education will also be a key issue for the future. The developments described will have a major impact on society and these need to be understood as widely as possible. Public acceptability will need to be taken into account at all stages.

APPLYING THE INFORMATION

How will genomics information be used ? One of the most significant impacts will be on **human health and disease**. Most, if not all, diseases, have a genetic component and genetic sequences, combined with a study of the proteins they produce, will enhance our understanding of how genes influence our susceptibility to disease, and may ultimately lead to improvements in diagnosis and treatments. In the most straightforward cases a single gene is known to be involved such that its malfunction almost always results in the disease. We have known for some time, prior to the advent of genomics, that some diseases have a genetic basis, because they run in families e.g. cystic fibrosis, Huntingdon’s disease. Genomic information will allow rapid and more reliable **tests of susceptibility** for people who are at risk of inheriting these conditions. It also offers, within about 10 years or so, the prospect of early treatment (for example, by gene therapy, where a defective gene is

replaced or supplemented), for those who have the disease.

Within the next 10 years or so, it is likely that we will also understand the contribution that genes make to most other human diseases and conditions, such as heart disease, stroke, Alzheimer’s, where many different genes and their variants may be involved. In these cases, factors other than genetics are also very important, particularly environmental components such as diet, pollution and lifestyle generally (e.g. smoking). But genomics combined with population studies will help us pin down the relative contribution of genetics, and an individual’s predisposition to a complex disease. This means that doctors will eventually be able to advise on the risk to an individual and also advise on the effectiveness of different interventions such as a change in lifestyle. Earlier prediction of some conditions such as coronary heart disease and diabetes will almost certainly be achievable within 10 years although researchers and physicians are sensitive to the fact that treatments must be available alongside improved diagnosis to avoid anxiety. Ethical debate will need to underpin all of the anticipated medical developments.

Understanding the genetic basis of disease will certainly offer opportunities for **new treatments including new drugs**. By understanding the genes – and their variants- responsible for or associated with disease – and the functions of the proteins they code for, it will be possible to design new drugs or to optimise use of existing drugs. Even now, it is possible to tailor chemotherapy in the treatment of breast cancer, based on which particular genes are activated in an individual patient.

It has been estimated that all the new drugs ever developed interact with just 500 or so molecules (targets) in the body. It is also estimated that the number of potential drug targets could rise to several thousand. Drugs which interact with these targets could be designed in a rational way, based on knowledge of structure and function (as was the anti-flu drug, Zanamivir) ; or large numbers of candidate drugs, produced more conventionally by synthetic chemistry, could be screened against this larger number of targets. It will also be possible to improve the use of existing drugs. Some individuals experience side effects from drug treatment, and this may have a genetic basis. **In the next 5-10 years it will become possible, in combination with genetic tests, to tailor drugs on an individual basis, to minimise such side effects. This could lead to the concept of personalised medicines tailored to an individual’s genetic**

¹ World Survey of Funding for Genomics Research, September 2000, www.stanford.edu

profile. For example, it may become possible to test individual genetic profiles against panels of drugs for a specific condition and select the drug offering greatest benefit. However, realising these goals depends on investment in, and success of, proteomics (See “**Structural Genomics and Proteomics**”) and thus some delays are to be expected between the development of new genetic tests and provision of the most appropriate treatments.

What might 20 years bring us? In this time frame, possibilities are more speculative, and as with the difficulties acknowledged above of diagnosis in the absence of treatment, ethical considerations will need to be debated alongside advances in science. However, in 20 years, it may be possible to use our understanding of genetic mechanisms to alter human behaviour- e.g. to reduce aggression or reduce depression. Life enhancement may be feasible through routine organ replacement, and it may become possible to preserve memory. Developments in proteomics may lead us into a new biology whereby it is possible to produce computer models and simulations of living cells and living systems as a whole. Understanding the genetics and functions of lowly animals such as nematode worms may enable us, at an even earlier stage, to reduce our reliance on mammals to test vaccines and drugs. In general, the prospects are for a much higher quality of life.

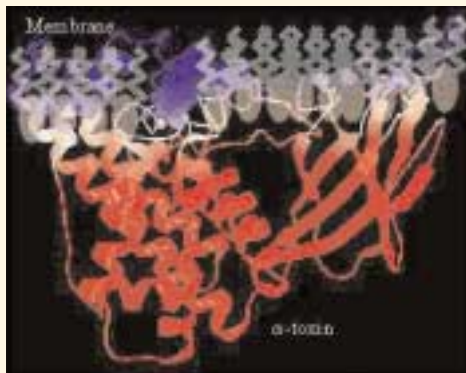


Figure 4: 3-D structure of the protein alpha-toxin (the gas gangrene toxin) from the bacterium *Clostridium perfringens*, showing it interacting with a cell membrane. This interaction eventually leads to cell death. Knowledge of the protein's structure will allow the design and testing of possible inhibitors, which may prevent its toxic effects.

MICROBIAL GENOMES

Over 40 microbial (bacteria and viruses) genomes have been completely sequenced, more than for any other group of organisms, and many more are currently in progress. This is partly because their genomes are relatively small but also because of their importance, particularly in infectious disease, which may affect people, livestock and crops.

In MOD, we continue to be concerned about the potential use of pathogenic microbial organisms as a means of warfare. The UK abandoned its offensive biological warfare capability in the 1950s and in the 1972 was a co-signatory of the Biological and Toxins Weapons Convention, which prohibits the production and acquisition of such weapons. And the UK is currently playing a leading role in the negotiation of a protocol to strengthen the Convention. Provision of robust protective measures against the effects of biological agents also remains a pillar in our strategy to counter their potential use in warfare. We assess that they would be used mainly in the form of an aerosol (small particles designed to travel on the wind), which would infect via the lung. We are therefore interested in all means possible to counteract the effects of microbes used by an aggressor in this way, which could include bacteria such as *Bacillus anthracis* (which causes anthrax) and *Yersinia pestis* (which causes plague), and viruses such as *Variola major* (which causes smallpox). The genomes of some biological warfare agents (e.g. *Variola*) have already been sequenced. Others (e.g. *Bacillus anthracis*, *Yersinia pestis*) are underway and/or will soon be published.

In the next 5-10 years, genomics will assist biological defence efforts in a number of ways. It will help us understand more precisely how biological agents cause disease, based on an understanding of gene sequences and their functions. This will enable more accurate threat assessment and so help us to tailor our defence response. It will enable us to identify in a systematic way DNA sequences which can be exploited as gene probes for the rapid identification of agents in the field, perhaps using Microarrays (See “**Technologies to Support Genomics**”) to screen for many agents at once. These sequences could also be used to diagnose disease in individuals. Eventually, it may become feasible to sequence a microbe in the field, which would be particularly beneficial if we faced a new or unexpected agent for which our probes were not designed.

Sequencing and characterisation of genes will reveal new ways of defeating microbial infection and how some of them may resist existing treatments. It will reveal new antibiotics and other therapeutics. Many of these will come from civil research designed to counter naturally occurring diseases. But these new therapies may also counter infections from agents used for biological warfare. Genome sequencing is already leading to the development of new antibiotics and antiviral drugs by industry. These might also be valuable for treating or preventing the diseases caused by infectious biological warfare agents. It will also suggest ways of minimising the evolution of drug resistance (including how this might be enhanced artificially by opponents).

Finally, we will be able to identify new genes which could form the basis of novel vaccines, including vaccines that might protect against more than one pathogen in a single shot.

IMPACT ON DEFENCE AND THE MOD

Genomics and proteomics will impact on defence in three main ways. Firstly, the medical or health-care benefits which will accrue over the next 20 years will affect us all, including UK Forces and MOD civilians. MOD will benefit from all civil developments in diagnosis and treatment, with medicine becoming more tailored to the individual, maximising health, well being and performance. This may bring particular benefits for the performance of our Forces in a number of ways – for example, any side effects of drugs or other countermeasures could be eliminated by tailoring drugs to the individual. We may also better understand the risks of exposure to toxic materials, from whatever source, based on genetic variation in susceptibility. And we may anticipate other benefits such as improved treatments for traumatic injury.

In biological defence we are already reaping some of the benefits of microbial genomics through the design of gene-based probes which can identify and diagnose biological agents and disease. Acquisition of complete sequences and exploitation of Bioinformatics for a range of biological warfare agents will allow us to better understand how they will behave if we encounter them on the battlefield, and how to design vaccines and drugs to counter their effects.

At the same time, we should remain wary through our threat assessment exercises of the potential misuse of genetic information, which will be freely available throughout the world. The human

genome sequence shows us that differences between groups is likely to be very small and this greatly diminishes the prospect of so-called “genetic weapons”, targeted at particular groups. Also, many biological warfare agents are already extremely potent and this brings into question whether aggressors – even those with a sophisticated capability – would invest in the development of “improved” agents through the use of genetics and biotechnology. However, the possibility cannot be discounted completely and new advances may bring new threats, hitherto unknown. MOD must therefore remain aware of these possibilities, and ensure that our defensive systems are as robust as possible against a range of future threats.

TECHNOLOGIES TO SUPPORT GENOMICS

MICROARRAYS OR DNA CHIPS

Microarrays or DNA chips are tiny devices about the size of a postage stamp, which can detect the presence of many genes or gene activity, simultaneously. In a microarray, thousands of different single-stranded DNA sequences – which can be synthesised in the laboratory and can represent single genes – are attached to a glass or silicon surface such as a microscope slide or a computer chip. Chips exploit the property of DNA whereby each of its two strands pairs specifically between complementary sequences. (See “How DNA Works”). Genes which are active in a cell produce copies which bind specifically to their corresponding DNA sequence on the DNA chip where they can then be detected using fluorescence. These arrays therefore allow us to see which genes are active at any given time and circumstance – a snapshot of gene activity in a cell. They



Figure 5: example of a DNA Microarray.

SOME DEFINITIONS

Genome

All the genetic material (DNA) in an organism (contained in its chromosome(s)). Its size is generally given as its total number of base pairs. The human genome contains some 3 billion base pairs.

Base pair (bp)

Two nitrogenous bases (A and T or G and C) held together by weak bonds. Two strands of DNA are held together in the shape of a double helix by the bonds between base pairs.

Nucleotide

A subunit of DNA or RNA consisting of a nitrogenous base (A,G,T,C in DNA ; A,G,U,C in RNA – U replaces T in RNA), a phosphate molecule and a sugar molecule. Thousands of nucleotides are linked to form a DNA or RNA molecule.

Chromosome

The self-replicating genetic structure of cells containing the DNA that bears in its nucleotide sequence the linear array of genes. Genomes of higher organisms consist of a number of chromosomes whose DNA is associated with different kinds of protein.

DNA

Deoxyribonucleic acid, the molecule that contains (or encodes) genetic information. DNA is a double stranded molecule (a double helix) , held together by weak bonds between its constituent subunits called nucleotides. The bonds actually link “bases” in the nucleotides and there are four of these : adenine (A), guanine (G), cytosine (C) and thymine (T). In nature, “base pairs” form only between A and T and between G and C; thus the base sequence of each single strand of DNA can be deduced from that of its partner. It is the particular order of the A,T,C,G that is important and which forms the DNA sequence. The sequence of bases is akin to the ordering of letters in words.

DNA sequence

The relative order of base pairs, in a fragment of DNA, a gene, a chromosome , or an entire genome.

Genetic code

The sequence of nucleotides, coded in triplets (codons) along the messenger RNA, that determines the sequence of amino acids in protein synthesis. The DNA sequence of a gene can be used to predict the messenger RNA sequence, and the genetic code can in turn be used to predict the amino acid sequence (protein constituents).

RNA

Ribonucleic acid is a chemical found in the nucleus and cytoplasm of cells. It plays an important role in protein synthesis. The structure is similar to DNA although uracil (U) replaces thymine (T) in RNA. There are several classes of RNA molecule, each serving a different purpose, including messenger RNA (see below).

Messenger RNA

RNA that serves as a template for protein synthesis.

Gene

The fundamental physical and functional unit of heredity. It is a sequence of nucleotides located in a particular position on a particular chromosome and which encodes a specific functional product (i.e. a protein or an RNA molecule).

Gene expression

This is the process by which a gene's coded information is converted into the structural and operational molecules (mostly proteins) of the cell and body as a whole. Expressed genes include those that are transcribed into messenger RNA (mRNA) and which are then translated into proteins ; and those which are transcribed into RNA but not translated into protein (e.g. transfer and ribosomal RNAs which have roles in protein production).

are particularly useful in understanding how bacteria behave. Bacteria have only a few thousand genes and DNA from all of them can be accommodated on a microarray to show, for example, which are active during an infection.

DNA arrays are being developed for very rapid and routine diagnosis, by detecting DNA or RNA that sticks specifically to the array, but using lasers or elec-

trical signals to speed up the response to the binding event. For example, it will be possible to assemble perhaps a hundred or more known sequence variations (polymorphisms) on one chip – including those implicated in one or more diseases – and detect which are present in a particular individual. In biological defence, this technology could be used in the future to identify or diagnose biological warfare agents in field laboratories.

RAPID DNA SEQUENCING

Sequencing methods have developed rapidly during the life of the Human Genome Project to become highly automated and miniaturised. This technology is now available to all, and it means that some smaller genomes (such as a bacterial genome) could be sequenced in a matter of days, perhaps as short as one or two days - although in this short time and in the case of a previously un-sequenced genome, it is unlikely that all the functional units, genes, would be identified. However, it does mean that sequencing could be used as a rapid identification tool and could even, in the future, be used in the field to identify biological agents. This might be particularly useful were we to face a surprise or unknown agent, which our prepared probes might not be configured to detect or identify.

BIOINFORMATICS

This is developing as a study in its own right which will allow full exploitation of DNA sequence data. Once genome sequences have been assembled, researchers become engaged in a number of activities including finding genes within the sequence, finding sequence variations between individuals, comparing whole genomes from different species and probably the most demanding task of all, predicting protein structure and function. Bioinformatics applies high-performance computers and statistical techniques to enable these activities and manage, through many different databases, the vast amounts of information that they generate.

Acknowledgements

Figure 1, DNA, The Molecule of Life, courtesy of the US Department of Energy Human Genome Program, www.ornl.gov/hgmis.

Figure 2, The Central Dogma, courtesy of Professor David Ussery, @cbs.dtu.dk.

Figure 3, 3-D Protein Structure, courtesy of the US Department of Energy Human Genome Program.

Figure 4, 3-D structure of alpha-toxin, courtesy of Professor David Moss.

Figure 5, DNA Microarray, courtesy of Dr Nigel Spurr.

THE MOD RESPONSE TO GENOMICS

In terms of the human genome and its future benefits, MOD can largely wait for developments in the civil sector to materialise. However, the scientific and medical community within MOD needs to remain aware of these developments and adapt them for MOD-specific needs wherever they may arise. MOD, along with the civil departments, should also remain sensitive to the ethical debate that will develop alongside the new technologies.

In biological defence, MOD is already exploiting some of the advances in microbial genomics through its applied and corporate research programmes. The Corporate Research Programme through the Defence Science and Technology Laboratory (DSTL) at Porton Down is already working closely with collaborators in the UK and abroad, to sequence the genomes of particular pathogens and to exploit Bioinformatics for new vaccine and antimicrobial targets. All of this work is published in the scientific literature. MOD does not need to establish its own capability but it should invest sufficiently to reap the wider benefits that collaboration can offer. DSTL is also working closely with UK industry to test novel drugs such as antibiotics against biological agents. However, we should also forge links at an earlier stage when new technologies are being evaluated.

Finally, red-team thinking in MOD should be developed so that the potential threat of new technologies such as those described here can be assessed. This should involve a multi-disciplinary team and external advisers, who can assess and calibrate future threats. MOD must contribute to this through maintenance of expertise in threat and hazard assessment, and through its programmes in chemical and biological defence and military medical research.

Contacts

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Produced by MOD DCCS (Media) Graphics 07/01