The Human Genome Project

UNIT 14

European Initiative for Biotechnology Education

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MATERIALS

Contents

World Wide Web

Few areas are developing as rapidly as biotechnology. So that they can be revised and kept up-to-date then distributed at minimum cost, the EIBE Units are published electronically.

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December 1998

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About this Unit

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This unit comprises activities, information, texts for discussion, and case studies designed to be used independently or in series as part of a teaching programme. The different parts have been devised by practising teachers and educationalists from several European countries, brought together with support and encouragement from DGXII of the European Commission, under the auspices of EIBE, the *European Initiative for Biotechnology Education.*

All the materials have been tested in workshops involving teachers from many parts of Europe.

This unit consists of several sections:

The Human Genome Project (HGP)

This includes basic information for teachers and students about the Human Genome Project (HGP), i.e. aims, methods and ethical and social implications connected to the HGP. The purpose of this information is to offer insights into the complexity of the HGP and stimulate an awareness of the benefits and problems that may arise from it in the future.

Techniques used in the HGP

This is an activity to enable students to learn about two basic molecular biological methods that are used in the HGP, i.e. the methods of mapping and of sequencing the genome, in order to provide an insight into how such a huge genome as the human genome can be deciphered.

Social and ethical implications of the HGP

Two activities are described involving ethical, social and legal implications of the HGP which are as equally important to the teaching of this topic as the biological and technological aspects. One of the problems related to the HGP is the how insurance companies will use the information which becomes available from the project. Students are provided with information to guide them in recognising possible consequences of the availability of results from the HGP, a problem that they may have to face personally in the future. They are also given guidance in finding their own standpoint on the topic.

This part of the Unit includes a case study that deals with the problem of how the patenting of DNA sequences can be handled. On the basis of the case study, students use an ethical analysis as a model of the decision-making process. First, guidance is given on ways of reasoning out an ethical problem related to the HGP. Secondly, support is provided for coming to a personal substantiated judgement about one problem connected with the HGP.

Comments on these materials are very welcome, especially from teachers, at whom they are principally aimed. Comments and queries about this Unit should in the first instance be sent to:

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TEACHER'S NOTES

Introduction

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The Human Genome Project

The Human Genome Project (HGP) is an international programme aiming to improve understanding of the basis of human heredity. It focuses on the complete characterisation of the human genome, all the human genetic material, including the estimated 50,000 to 100,000 genes contained in human DNA. The HGP is one of several genome projects designed to describe the genomes of bacteria, yeast, crop plants, farm animals, and organisms used in medical research. One central aim of all these projects is to promote the understanding of the basic biochemical processes of living organisms. It is hoped that outcomes of the HGP will be to make possible early detection of human diseases, effective preventative medicine, efficient drug development, and personalised therapies.

Techniques of the HGP

The HGP, which is expected to last for 15 years, has two major components: first, the creation of maps of the 23 pairs of human chromosomes and secondly, the sequencing of the DNA making up these chromosomes.

Geneticists use two types of maps to characterise the human genome: genetic linkage maps and physical maps (see Fig.1). The maps depict the relative positions of DNA markers; both known genes and DNA sequences with no known coding function.

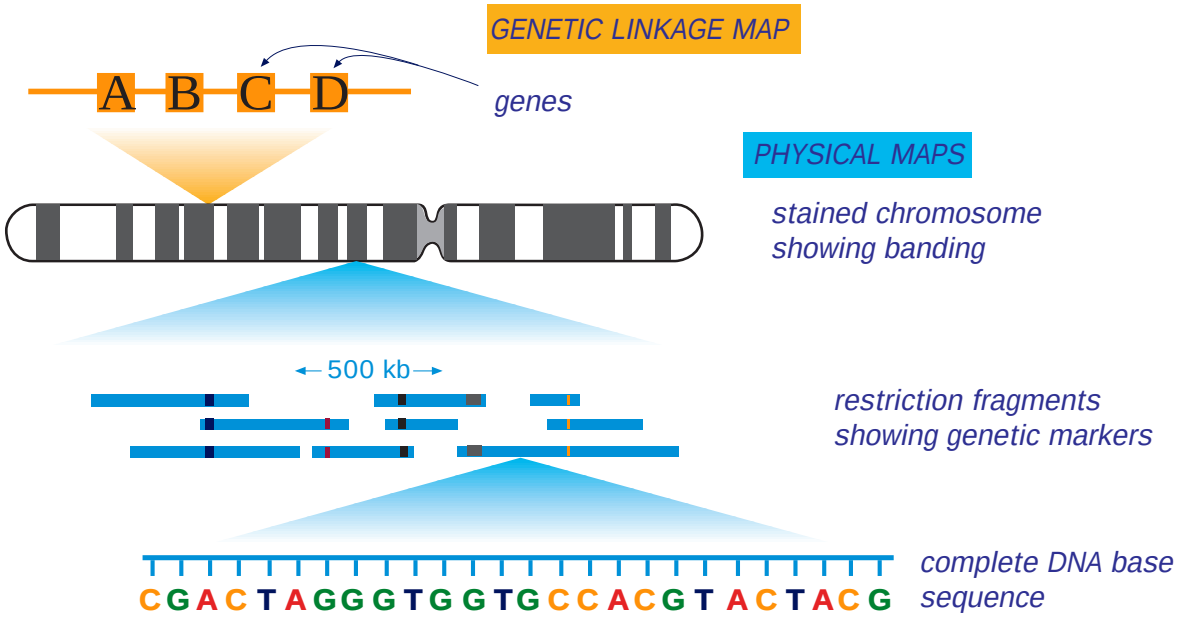
Genetic Linkage Maps

At the lowest resolution genetic linkage maps depict relative chromosomal locations of DNA markers and are created by following the pattern in which they are passed through family pedigrees in relation to other known markers.

Physical Maps

Physical maps describe the characteristics of the chromosomal DNA molecule and can be at several levels of resolution. At the lowest resolution is the cytogenetic map, showing the chromosomal banding visible in stained chromosomes. Higher level physical maps are achieved by dividing the chromosomal DNA into shorter fragments (which may include the markers of the genetic linkage map) with restriction enzymes. The fragments are then

Figure 1. Mapping a chromosome



duplicated and characterised. The correct location and order of the fragments on the chromosome is then deduced using overlapping common sequences as guides.

Sequencing

Ultimately the characterisation involves determining the complete base sequence of the fragments (the highest resolution physical map). One of the most frequently used sequencing methods is that of Sanger (*see page 8*).

An important technique used to propagate DNA fragments in the mapping and sequencing activities of the HGP is the *polymerase chain reaction* (PCR). A detailed description of this can be found in EIBE Unit 2 *DNA-profiling*.

Social and ethical implications of the HGP

The HGP is planned to be completed by the year 2005. It is expected to enable progress in medical and pharmaceutical research, and in medical diagnosis and treatment to be made on a scale that was not dared to be hope for some years ago. However, as well as these hoped for outcomes of the HGP, several objections have been raised concerning ethical, social and legal questions.

A major criticism of the HGP is that the high costs of this project cannot be justified. The whole project will cost at least 3 million dollars. Funding such a huge project reduces the financial resources left for smaller research programmes that perhaps would be more effective than the HGP. In addition, it is questionable whether the expected advances in the treatment of so-called illnesses of civilisation, such as cancer, heart disease, Parkinson's and Alzheimer's disease, can a priori legitimise such a large expenditure of money at the cost of provision of services in primary health care.

The results of the HGP will increase knowledge about single gene disorders without necessarily any immediate possibility of therapeutic treatment. Additionally, the publicity about research connected to the HGP is possibly raising expectations among the people concerned that the project cannot fulfil. As most diseases are polygenic and multifactorial, the question of handling more precise knowledge about susceptibility, without possibilities of treatment, will become a problem.

The amount of information coming out of the HGP is unbelievably huge. It has been estimated that the whole DNA base sequence printed in small letters on thin paper would need 220 000 pages or eight metres of a shelf space. In parallel with the advances in biology and methodology that are necessary for deciphering the human genome, developments in computing will continue to be needed to store, process and analyse all the data. Furthermore, questions still remain about who will own the data, who may use them and how their use will be supervised, as well as the ethical and legal aspects whether or not DNA sequences can be patented.

Another ethical problem is the questions of the 'right of not being willing to know' and the obligation to be informed. This will occur if, for example, genetic screening of employees or in pregnancy were to become a legal requirement

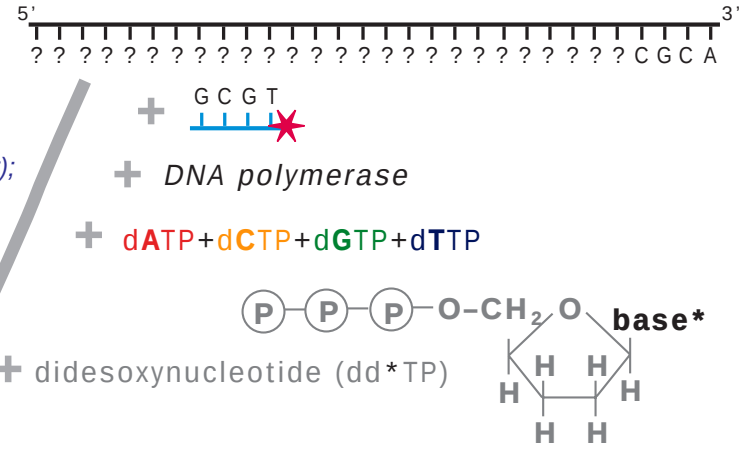
Some of the implications referred to above require a legal answer, e.g. data security, commercialisation and patenting. Others, however, have relevance to the ethical values of individuals and society as a whole. They touch on fundamental ethical questions and even the problem of moral pluralism. This unit, therefore, gives students an opportunity to become aware of aspects of the HGP that are inherent to the project by confronting them with case studies which involve some of these key questions. It is also the intention to help them to make their own personal, rational decisions on at least some of the questions by using a model of ethical analysis.

Figure 2.

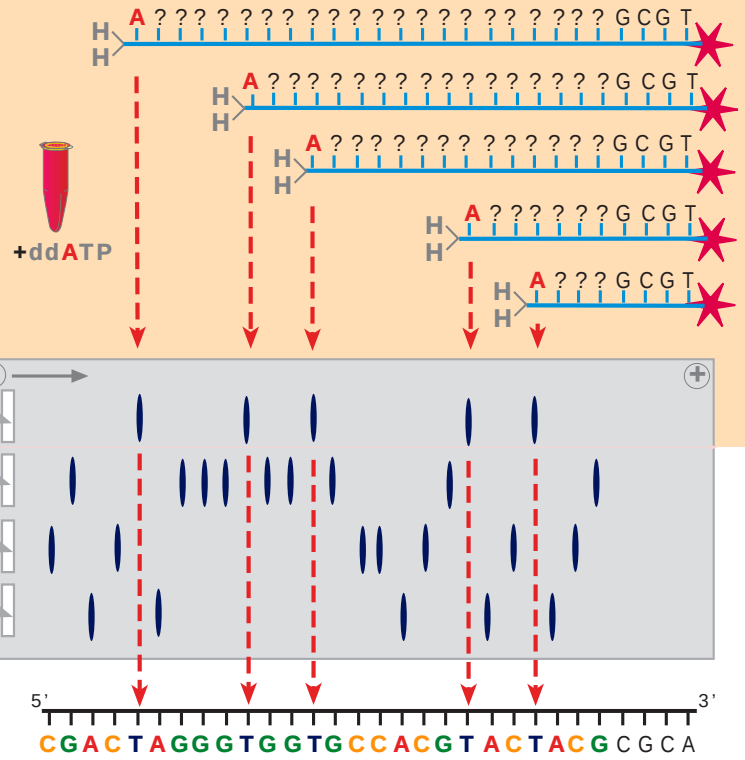
DNA sequencing using the Sanger method

The Sanger method involves the synthesis of radioactively labelled DNA strands that are complementary to the single-stranded DNA fragment under investigation.

The complementary DNA is synthesised using:
a short radioactively labelled starter (the primer);
the enzyme DNA polymerase;
four nucleotides;
one didesoxynucleotide.



When a didesoxynucleotide, e.g. ddATP in the red tube, is incorporated into the DNA molecule (in place of dATP) the chain terminates at that point so that fragments of different lengths are formed that have grown until the ddATP stopped the chain at a point of incorporation of an adenine base.



Four parallel reaction mixes are used, each containing one of the four didesoxynucleotides.

Gel electrophoresis is then used to separate the fragments by size.

The radioactive label reveals the positions of the fragments and from the size of the fragments in each mix the base sequence of the complementary, and hence the original DNA fragment can be deduced.

STUDENT NOTES

The Human Genome Project

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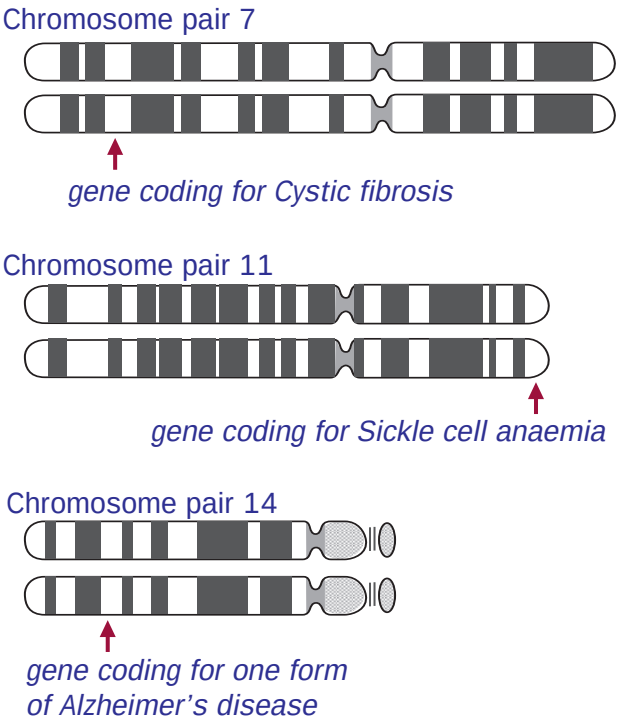
The eminent British molecular biologist Sydney Brenner brought a hearty laugh from his audience by suggesting that some future graduate student might define a mouse as 'ATC, GCC, AAG, GGT, GTA, ATA ....'. Every year, however, the idea of defining an organism by the sequence of its DNA bases seems a little less far fetched (see http://www.gene.com/ae/AB/IE/Future_Of_Genetic_Research.html). This is also true for Man because in the middle of the 1980s a huge project, named the Human Genome Project (HGP) was begun with the aim of deciphering the complete human DNA.

When, about forty years ago, it was proved that the DNA molecule is responsible for heredity, it brought together two groups of researchers; some were interested in the determination of the loci and the function of genes, while others wanted to know the structure of those molecules that include the information for control of biochemical processes. As a result of this great interest, during the following years more and more improved techniques for the isolation, multiplication, manipulation and analysis of DNA fragments were developed. A key outcome was the so-called recombinant DNA technology which revolutionised medical/biological research. It made possible the identification of genes for several hereditary diseases. The knowledge gained by this technique showed that research on the decoding of the whole human genome and the locating of all genes could be taken a long way further. The achievement of this became the declared aim of the HGP.

Figure 3. Three human chromosomes with known loci for hereditary diseases



The two sets of 23 chromosomes in human cells contain about 50 000 to 100 000 genes that make up probably not more than 5% of the whole DNA. The first aim of the HGP is to determine the location of all genes on the 23 chromosome pairs, i.e. on the 44 autosomes and the 2 sex chromosomes. This is followed by determination of the base sequence, very important information for the identification of the particular gene function. Finding the localisation of the genes is known as **mapping**; the determination of the base sequence is **sequencing**. The final aim of the HGP is the sequencing of the whole human DNA including the non-coding parts.

The information from these investigations will lead to new knowledge about human diseases and to new ways of diagnosis and treatment of disease. In addition, the findings will give information about the origin of the various population groups and the evolution of Man.

The dimensions of the project are difficult to imagine. For example, if you magnify the size of a human cell to the circumference

Table 1. Chronology of research on the human genome

1953	*James D. Watson and Francis F. Crick find out the double helix structure of the DNA.*
1966	*The genetic code is deciphered: three base pairs build one triplet and determine one amino acid in a protein.*
1973	*Herbert Boyer and Stanley Cohen prove that DNA that has been cut and recombined is active in a living cell.*
1977	*The first human gene is isolated; the gene for insulin.*
1985	*Renato Dulbeco proposes the sequencing of the whole human genome.*
1987	*The Italian Human Genome Project (HGP) is started.*
1988	*The Human Genome Organisation (HUGO) is founded at Cold Spring Harbor (USA) involving more than hundred members in many countries worldwide.*
1990	*The Human Genome Project is started officially in the USA with funding of 3 billion US dollars and a timespan of 15 years .*
	The French HGP is started.
1995	*The German HGP is started with annual funding of 50 million DM*
1996	*85% to 90% of all human genes are identified.*

of the earth, one chromosome would have the dimension of a country, a gene the dimension of a city and the bases would be the equivalent of the inhabitants. In this 'world of a cell', researchers working on the HGP are looking for at least 50 000 genes (cities). Ultimately, it is the intention to find out the sequence of a line of three billion bases (inhabitants).

Questions and activities

1. What is the HGP?
2. Why is the HGP being carried out?

Sit together in groups of three to four. Try to find and formulate as many ideas as possible on the following questions and write down your ideas.

3. The HGP is expected to cost about 4 billion pounds sterling, about a tenth of what it cost to put a man on the moon. Do you think that this will be money well spent?
4. Can you think of any benefits from the information that will become available?
5. How do you think that this knowledge could best be used for the benefit of all mankind?
6. All of the data is being put on a database by HUGO (the Human Genome Organisation) which was set up in 1989 to co-ordinate the various activities in the contributing countries. Who do you think should own the data and who should be allowed access to them?
7. Should the information generated by this project be exploited for commercial reasons?
8. Would you like to know the details of your own genome? Who else should know about this information? Who should not have this information?

TEACHER'S NOTES

Techniques used in the HGP

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Mapping and sequencing

The HGP is possibly the most important, interesting and challenging scientific project at the present time. We are inundated with information about it in the media which often stimulates students to ask questions. Thus the HGP provides many opportunities for placing the educational process in a relevant context.

When discussing the mapping and sequencing of the human genome, students invariably ask how is it actually achieved. It is relatively easy to talk about such matters in general terms but the principles are difficult to explain. However, providing students with an active learning situation offers more fruitful approach to learning . Although the practical techniques that researchers use are not applicable to schools, a situation has now been reached where equipment is available for students to have an opportunity to cleave DNA with restriction enzymes and separate the resulting DNA fragments in a gel tank. For example, the National Centre for Biotechnology Education (NCBE) at The University of Reading has produced such a kit containing gel tanks, microsyringes, DNA and restriction enzymes at an affordable price of around £125.

An alternative, and very cost effective, method is to mimic the practical situation which not only demonstrates the principles involved but also provides opportunities for students to think and to solve problems.

The size of the problem

The human genome has been estimated to consist of 4 Gb (one gigabase = 10^9 bases). It has, however, been estimated that around 95-98% of the genome is "junk". Note that it is described as junk and not garbage - garbage we throw away, whereas we keep junk in the hope that someday it might be useful! Researchers are divided into two camps - those who think that we should concentrate on mapping and sequencing the 2-5% that codes for polypeptide sequences (about 100,000 genes), and those who think that we should look at the complete genome since much of the junk could be found to have important functions such as regulating the genes. Interestingly, it has been found that those organisms with rapid life cycles, e.g. unicellular microbes and some multicellular organisms such as nematodes, do not possess junk DNA. They appear to keep their genomes streamlined so that the process of cell division is speeded up.

Unfortunately, at present there are no easy and inexpensive methods for sequencing DNA. Even if there was a machine that could produce a million nucleotide pairs of sequence each day, it would still take about 20 years to sequence the entire human genome - and this is about 100 times greater than the present production of sequences by research centres in the whole world. It is likely, therefore, that the most important genes will be sequenced first, and then, as the technology improves, the remainder of the genome will gradually be completed. Although a date of 2005 has been set for completion of the HGP, this could be an optimistic aim although the increases in the use of automated methods could help in attempts to achieve this target.

Base sequencing - the activity

In this paper exercise, DNA is broken up or cleaved using a variety of restriction enzymes (restriction endonucleases). How can the sequence of bases then be assembled in the correct order? The resulting short strands of cleaved DNA are examined for any overlapping sequences and these are then matched.

This exercise mimics the following restriction enzymes which cut DNA at the

specific base sequences indicated (only single stranded DNA is shown):

Enzyme	Site	Colour
Hae III	GG ▮CC	pink
*Eco*R I	G ▮AATTC	green
*Eco*R II	▮CCTGG	yellow
Hpa II	C ▮CGG	blue

The base sequence in the Appendix is photocopied onto the four different colours of paper indicated above. These are then cut along the dotted lines so that there are plenty of DNA strands of each colour. Make sure to trim the ends close to the printed bases so that the ends cannot be identified.

Each student is given a copy of Worksheet 1, a pair of scissors, two single strands of DNA of different colours - one student might have a green and a yellow strand, another green and blue, etc. (there are six possible combinations). Do not give out Worksheet 2 at this stage.

Notes on Student Worksheet 1

Make sure that students DO NOT write down the sequence of bases in the strands at the start. Also, make sure that they understand how to cut the strands at the particular restriction sites - the colour of the strand determines which restriction enzyme to use. For example, the restriction sites for *Hae* III are :

C C T G G ▮C C G G ▮C C T G G ▮C C T G
G A A T T C C G G ▮C C T G G A A T T C
C G G A A T T C C G G A T T C C T G G

Make sure that each student mixes the strands so that the original order is lost.

After this they should have two coloured sets of different lengths of fragments. When this has been correctly done, give out Worksheet 2.

Notes on Student Worksheet 2

Students must think about this on their own, using overlapping sequences to help them. Do not give any help; let them work it out for themselves. Remember, however, that they are not making base-pairs; the bases of each strand must match as follows:

G G A A T T C C T G G
C C T G G A A T T
matching sequence

The DNA base sequence has been designed to provide different levels of difficulty, depending on the restriction enzymes used:

- Blue + green — Quite easy
- Yellow + blue / Yellow + green — More difficult
- Pink + blue / Pink + green — Even more difficult
- Yellow + pink — Impossible

If the exercise is repeated with different colour combinations, the students learn how to do the exercise and usually complete their second attempt more quickly. You might prefer them to use the easier combinations first. As there is more than one possible sequence for yellow + pink, you can provide an extra, different, strand if requested.

You may wish to make your own base sequences, even longer ones, and use other restriction enzymes. Looking at the problems of mapping human genes raises many interesting and stimulating issues. Some questions are given on page 10.

Of course, this exercise is a great oversimplification of the real-life situation but it does give students an idea of the principles involved and the complexity of the problems. Recently, methods have been developed which use computers to search

for overlapping sequences. Other new techniques are continually being developed to improve and speed up the process of gene sequencing, including the use of fluorescent-labelled gene probes and the scanning tunnelling electron microscope.

Further reading

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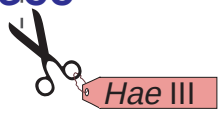
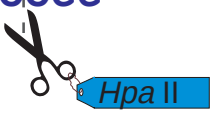
WORKSHEET 1

DNA Sequencing 1

1. Examine one of the two strands of single-stranded DNA that you have been given. Starting from the left, identify the restriction sites at which the restriction enzyme would cut. Use the appropriate restriction enzyme for the coloured strand according to the colour code:

Enzyme	Restriction Site	Colour
Hae III	GG CC 	pink
*Eco*R I	G AATTC 	green
*Eco*R II	CCTGG 	yellow
Hpa II	C CGG 	blue

Cut the strand of DNA carefully and as neatly as possible at the restriction sites with scissors.

You should now have a number of segments of DNA of different lengths.

2. Repeat procedure 1 with the second strand of DNA.

3. When you have completed this, mix all the segments and go to Worksheet 2.

WORKSHEET 2

DNA Sequencing 2

4. Your next task is to reconstruct the original sequence (order) of the bases (A, T, G and C). Look for overlapping sequences; these will help you. Remember that you are not making base-pairs. The bases of each differently coloured strand must match as follows:

G G A A T T C C T G G

C C T G G A A T T

By moving the pieces around and trying various combinations you should be able to reconstruct the original sequence. Once you have finished, check the sequence with the teacher.

Methods have now been developed that use computers to search for overlapping sequences. In this way the complete sequence of bases of all the genes in the human genome will be worked out.

APPENDIX


CCTGGCCGGCCTGGCCTGGAATTCCGGCCTGGAATTCCGGAATTCCGGATTCCTGG

TEACHER'S NOTES

Life insurance - an ethical dilemma?

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Aims

The aims of this activity are to:

- develop students' skills for resolving moral problems;
- demonstrate that some problems do not have clear, objective solutions but, that in an ethical decision making process, feelings and emotions often predominate;
- show that scientific discoveries have consequences for the whole of society.

Organisation

A possible way to proceed with this activity would be, after a balanced introduction of the concept and scientific content of the human genome project , to use the activity text (*page 17*) as an introduction to some moral problems related to genetic disorders and life insurance.

The two cases and some related issues could be discussed, further information obtained if required (e.g. from insurance companies), and possible solutions considered, initially working in small groups. Conclusions could then be presented to the whole group in a plenary session.

Background information and questions for discussion

Insurance

An insurance company calculates premiums by considering the actual situation and relating it to the risk that has to be insured. The premiums for group insurance and private insurance are different. Group insurance premiums are calculated on the basis of an average population with a predictable risk factor where the insurer has an obligation to insure every member of that particular population. There are many more options in private life insurance, when every potential policyholder can choose when to be insured, how much premium to pay and the length of the period of insurance. The insurer also has choices and, before accepting a policy holder, may demand some medical guarantees. With this procedure, insurers are able to develop homogeneous risk groups within which everyone pays the same amount for the same risk.

Genetic diagnosis

With the present techniques of genetic diagnosis, an individual with a possibility of Huntington's disease is examined for that disease only, and not for cystic fibrosis or other known genes. However, with knowledge gained from the HGP and automated DNA screening techniques it may be possible in the future to provide a complete 'genome checkup'.

Is this the purpose of the HGP?
What about the right of privacy?
Could this right of privacy be used to prevent an insurance company from rejecting an application for life cover?
Why would anyone want to look into a crystal ball when there is a substantial risk of learning some distressing news about expectations for the future?

One of the concerns about genetic diagnosis is its ability to identify a multitude of possible inherited diseases. Such knowledge can, however, be of great value in helping people take important decisions. For example, a couple with a history of an inherited problem might want more information before deciding to have children, a sportsperson with a family history of inherited muscular problems might want further information before undergoing rigorous training. It might be valuable to screen individuals for an inherited condition which could lead, without surveillance, to a serious disease. Uncertainties about risks are often harder to bear than the certain knowledge of being a gene carrier.

At present genetic screening is performed

on single gene mutations such as Huntington's disease, myotonic dystrophy, cystic fibrosis, Duchenne muscular dystrophy, etc. Multifactorial diseases such as heart aberrations, diabetes, asthma, etc. are more common in the population but it is harder to identify which genes and which exogenous factors are responsible. Knowledge of the human genome, together with improved DNA-screening techniques would make it easier to detect the genes involved. This information when correlated with lifestyle could be used to predict quality of life and life expectancy.

What would be the implications for life insurance?

As the amount of knowledge continues to grow, it is not just the rare genetic disorders that have the attention of insurers (as a high risk category) . The increased knowledge about the hereditary aspects of cancer of the breast and colon, and the development of heart and vascular problems leads to many more individuals experiencing exclusion - the refusal of life insurance or enormous increases in insurance premiums.

What could be the result of this situation?

With the growth of public awareness about hereditary disorders and their relation to other risk factors (hypertension, smoking, overweight, etc.) in the development of certain diseases, insurance companies also fear that individuals and families with a high risk status will be eager to obtain a high level of insurance, known in the trade as the phenomenon of anti-selection.

To what could this lead?
What would you do if you were an insurance inspector?

It could be argued that this makes a good case for insurance companies to transfer these risks to those taking out life insurance policies. Selection as a weapon against anti-selection - a lucrative business for insurance companies?

Medical ethics

The process of selecting applicants for life insurance depends on examination by a medical doctor who is employed by the insurance company. Does this conflict with the medical and ethical principles of the Hippocratic oath?

Would such an examination conflict with the principle of a doctor acting in the best interests of the patient?

There is less of a problem with the principle of not doing the patient harm, although a certain amount of harm is unavoidable, e.g. violation of the rights of privacy.

The principle of justice is more complicated. An increase in life insurance premiums may be seen as unjust, but the insurance company considers that it is correct to treat all members of a homogeneous risk group in the same way.

The principle of respect for autonomy, or letting a patient make decisions in a well-considered way, requires that the patient is fully informed about a proposed course of treatment. The decision lies with the patient, a problematic situation in a medical examination for a life insurance contract!

What would be the consequences if, for instance, insurance companies were to put Down syndrome or other genetic problems on the list of uninsurable diseases? How would this influence our feelings towards handicapped people?

What exactly are the basic insurance needs of a person or a family, and how can a fair system be organised to meet the needs of the whole of society?

STUDENT TEXT 1

Life insurance - *an ethical dilemma*

Rapidly increasing knowledge about the human genome together with new testing techniques will make it easier to diagnose certain genetic conditions. What if the prognosis is early death or a lifelong mental handicap? Does testing in this case makes sense? Consider the following examples.

Example 1

You have applied for life insurance. You completed the forms sent to you by the insurance company asking questions about your medical history and any diseases in your family, and you have passed a medical examination.

Last week you received a letter from the insurance company stating that personal life insurance was only possible if a DNA test confirmed that no hereditary disease was likely to reduce your life expectancy.

This came as a complete surprise and you consulted a geneticist at the local university before deciding whether to have the test. On hearing that your son had cataract, the geneticist wanted to know more about the rest of the family and drew up a family tree. This showed three family members suffering from cataract. You then told him about your son's motor problems and that he had been given a programme of special physical exercises. According to the geneticist, the combination of cataract and motor problems could indicate myotonic dystrophy, or Steinerts' disease. This is characterised by progressive muscular weakness and spasms.

It is possible for this illness to be present in a family without it being recognised as such. If this diagnosis is correct, there are also likely to be complications such as disturbances of heart rhythm, glucose intolerance, and accompanying educational and career problems. It is also likely that the problem will become more and more serious in future generations, a phenomenon known as anticipation.

The geneticist points out that if the DNA test shows the presence of this autosomal dominant condition, you are facing a huge dilemma! Myotonic dystrophy is on the list of diseases that would exclude you from life insurance. A confirmed diagnosis would mean that you and some members of your family will no longer be eligible for life insurance!

Your dilemmas:

What if you refuse the DNA-test?

What about the possibility of passing on the disease to future generations?

What about treatments?

What if an insurance company puts pressure on other members of your family to have a DNA-test for carrier status (and therefore to no longer be eligible for life insurance). Is this acceptable?

What about freedom of choice?

Example 2

Many firms and organisations offer their personnel the opportunity of taking out life insurance. Frequently these schemes do not require detailed information about the health of the family, or even about the person insured! The insurance company accepts everyone, without medical screening, on condition that a certain proportion of employees take up the insurance.

Thus, although anyone with myotonic dystrophy would be excluded from life insurance by personal application, it could be available through the collective insurance scheme of an employer.

Is collectivity, the basic idea of insurance, the way out of the impasse as presented in case 1?

TEACHER'S NOTES

Patenting DNA sequences - an ethical question

★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★

Aims

The student material presents a case study that forms the basis for an ethical analysis. The aim of this analysis is that the students will:

- become aware of the need, in discussions, to differentiate between descriptive and normative statements (for further information see EIBE Unit 10: *Transgenic Plants: Economy, Environment and Ethics*);
- understand the ethical values on which their arguments and decision making are based.

Background information

The model of ethical analysis described here follows Bayrhuber (1994) and Hoessle (Dissertation at the IPN / Kiel, in preparation). It helps outline the different options when tackling a moral problem, so that an assessment can be made of the arguments and their ethical basis (i.e. whether referring to the dignity of mankind or the wellbeing of mankind - fundamental types of ethical argument).

The ethical analysis consists of several steps.

1. Understand the situation.

Students formulate a question to be decided upon, e.g.: *Should the patenting of DNA sequences be legalised or not?*.

2. Enumerate the options for action.

Students outline possible options for action. In the example above, the options would be:

(i) DNA sequences may not be patented;
(ii) only DNA sequences with known functions may be patented;
(iii) all DNA sequences may be patented.

3. Relate the different options to possible ethical concerns which could arise as a consequence of the actions.

Ethical concerns in the example might cover e.g. health, the right of self-determination, economic profit.

5. Make a meaningful decision.

Referring to the values established in step 3, the students make their decision for one of the possible action options named in step 2.

6. Assign the reason(s) for one's own decision to the fundamental types of ethical argument.

See above.

7. Describe the consequences of the decision.

Students consider the consequences of their decision for the individual and for society.

Organisation

Preparatory homework

As an introductory activity the students should collect information about patents; using various sources such as the library, newspaper articles, parents.

Session 1

At the beginning of the next lesson, gather the material collected by the class. Then, by classroom discussion, decide on suitable categories into which the material can be arranged, e.g. definitions, examples, problems connected with patenting. With the students working in groups of about four, allocate the material to appropriate categories. Discuss the findings in a plenary session of the whole class. Assemble and display a summary of the characteristics of a patent.

Session 2

The case study (see *Student Text 2*).

STUDENT TEXT 2

Patenting DNA sequences - *an ethical question*

The Case Study

Read the case study on the right twice.

As a molecular biologist, obviously Ric H. did not see any objections to his idea of patenting human DNA sequences. Do you?

By following the questions below, try to come to your own reasoned opinion about the case.

Questions

1. What is the ethical problem to be considered?
2. What are the possible decisions that could be made?
3. In your opinion, what moral issues are touched on by the various possibilities?
4. Considering the moral concerns, make your own individual decision from those outlined in question 2.
5. Under which of the following two categories of fundamental ethical principles would you put the values that you found to be most important in arriving at your decision:

   a) the dignity of mankind;

   b) the wellbeing of mankind?
6. Describe the consequences of your decision for yourself and for society.

Rick H. is one of the many researchers working on the Human Genome Project, the largest international research programme ever undertaken. He is an excellent molecular biologist and even though he is still a young man, 35 years old, he is already head of an institute which specialises in genome sequencing. In addition to the human genome project, some of his research groups are busy sequencing genomes of different organisms such as bacteria, crop plants and animals that are of interest for pharmaceutical and medical research. They all have to work very hard. However, in order to be a researcher you have to be idealistic because there is no clear relationship between the amount of work you do and the money you earn.

One day Rick read in a scientific journal that particular sequences of a mouse genome had been patented in the USA. This information made him think. Patenting a sequence of DNA would mean that for many years the relevant researchers, or the institution where the sequencing was done, would own the rights of these sequences. That meant that if these sequences were of value for the production of therapeutic agents or for making the diagnosis of a particular disease possible, the patent owners would be the first to use the information commercially and without competition.

Rick sat at his desk late into the night going through all the sequences they had found during the previous year. For some of them they already knew the function or the particular protein coded for. But all of these genes were already used in various ways in the pharmaceutical or medical industry. Suddenly he had an idea: Why not try to patent the human DNA sequences they had found, even though their functions were still unknown?

The next day Rick wrote a patent application for a human DNA sequence that they had discovered two weeks ago. If it is accepted, the institute might earn a lot of money if, in the future, the sequence proved to be of medical importance. When he had posted the letter he was very proud of his idea. He could not wait for the answer to his patent application.