

Schools' Day Projects for 2011

Glow-in-the-dark gene expression

Peter Fraser

In many ways, the cell nucleus is the centre of the cell: it's here where our genetic information is stored, in the DNA. Some of this genetic information holds specific lengths of code (genes) telling the cell how to make proteins. However, much more of the DNA holds information telling the cell where, when and how many of the genes should be used. All of these are extremely important decisions, as when things go wrong, diseases like cancer can be one of the consequences. The nucleus holds more than 30,000 genes and all their associated regulatory regions, so to ensure the correct genes are active in the correct time and place, the DNA must be highly organised within the nucleus – for example, different regions of the nucleus may hold active genes and inactive regions of DNA. The role that this organisation plays in regulating gene expression is the area of research that our lab is interested in. In this project, you will get a glimpse of the highly complex nuclear architecture of the cell. We will specifically light up a particular gene in the nucleus, so that it glows in the dark, and use this to see where the gene is located.

More information: <http://www.babraham.ac.uk/chromatin/fraser.html>

What is the difference between a muscle stem cell and a muscle fibre?

Sarah Elderkin

Muscles are the most abundant tissue of the human body. Muscle stem cells enable the growth and regeneration of muscles through a complex process known as differentiation. During growth or regeneration, after injury or disease, muscle stem cells differentiate into multinucleated myofibers. Muscle stem cell differentiation is a highly orchestrated process in which many different proteins are involved. In this project you will analyze the morphology of muscle stem cells and differentiated myofibers by microscopy. Additionally you will compare the protein content of muscle stem cells to differentiated myofibers by SDS polyacrylamide gel electrophoresis and subsequent protein staining.

How many proteins in a cell? How much protein in a cell?

Geoff Butcher

Proteins perform many different cellular functions. They are made from long chains of amino acids and there is enormous variation between proteins, both in the number of amino acids in the chain and the order in which they are linked together. This sequence variation allows different proteins to adopt distinct molecular 'shapes' due to complex folding and turning of the amino acid chain. This variety of structure is the key to the versatility of proteins.

The purpose of this project is to discover how much protein is present in a single cell, and to learn how differences in amino acid chain length can be used to separate cellular proteins.

More information: <http://www.babraham.ac.uk/lymphocyte/butcher.html>

Molecular biology - the cut and paste of biology

Simon Cook

With the completion of the genome mapping project we now know all the genes it takes to make a human and the proteins that these genes code for. However, while we know the precise function of some of these proteins, for example amylase which hydrolyses starch, there are still many proteins whose function is unknown to us. One way to study protein function is to introduce many copies of a gene into a cell thereby increasing the amount of the protein that the gene codes for. We can then monitor cells for changes in their behaviour which correlate with the increased protein level and this can provide important clues about protein function. For example, one gene that we are interested in a gene called BIM which is a suicide gene that instructs cell to die – death is quite an easy phenotype to monitor! To increase the amount of BIM in a cell we need to transfer the BIM gene from one cell to another. We do this using circular pieces of DNA called vectors which allow us to shuttle genes around cell to cell. We insert genes into these vectors by cutting the DNA with special enzymes called restriction enzymes and pasting the BIM gene in using another enzyme called DNA ligase. At the end

of this procedure we need to know if the gene has been successfully pasted in or not. You are going to help us find this out by cutting DNA with restriction enzymes and looking at the products of this reaction. At the end you should be able to tell which vectors have the BIM gene and which don't and we can then go ahead and use these in our research

More information: <http://www.babraham.ac.uk/signalling/cook.html>

FISHing in the dark: visualizing gene activity by fluorescence microscopy

Cameron Osborne

How the genome is organized in the nucleus of the cell has a large impact on the activity of genes. For a gene to be active, it must move to specialized areas in the nucleus called 'transcription factories'. Studying the location of genes in relation to transcription factories, in addition to other genes helps us to understand how genes are regulated normally, and gives us important insight into what goes wrong in diseases, such as cancers. In this project we will use a handy method that shows us when and where genes are active. RNA fluorescence in situ hybridization (RNA FISH) detects newly-synthesized RNA from active genes by tagging it with fluorescent molecules that we will then visualize using a fluorescence microscope.

More information: <http://www.babraham.ac.uk/chromatin/osborne.html>

Genomics, Proteomics and Beyond

John Coadwell

Bioinformatics is a newly emerging interdisciplinary research area that may be defined as the interface between biological and computational sciences. However this is not the only definition and there are probably as many definitions as there are bioinformaticians. The project provides collections of DNA sequence fragments and takes the student through the diverse arts of assembly, transcription, translation and visualisation using the Internet and various local algorithms. Database mining, comparative genomics, alternative transcripts and three dimensional protein structural display will be included - time permitting! **Please note this project is not laboratory based.**

More information: <http://www.babraham.ac.uk/facilities/bioinformatics.html>

Assessments of experiments involving animals

Colin Gilbert, Veterinary Services

This project is aimed to stimulate discussion around the ethical issues confronting scientists doing biomedical research. Most biologists agree that experiments involving living animals or fresh animal tissues are undesirable but in some cases unavoidable if advances in medicine and biology are to be made. In Britain, decisions on how and when animals are used in experiments are not made by the scientists directly concerned, but by independent panels and government officials. The objective of this project is to find out how this process works. The project will begin with an introductory talk about animal use in research. Working in groups, students will then look at some hypothetical research proposals and discuss them according to the law and ethics of animal use (expert guidance will be available)! Students will then report back to the whole group. There will also be case studies highlighting breakthroughs in medicine and healthcare treatments that have only been possible through doing research with animals. **Please note this project is not laboratory based.**