Gene mutations: questions and answers

Archaebacteria and eubacteria are both prokaryotic cells, both are single celled microorganisms, and are relatively tiny compare to that of eukaryotic cells. Both Archaebacteria and eubacteria divide by a process known as binary fission, and move through the use of flagella Archaebacteria and Eukaryotic Cells both possess a plasma membrane. Archaebacteria have genes, and metabolic pathways which are similar to eukaryotes.

Are all mutations dangerous? Explain.

No, all mutations are not dangerous. While there are many mutations which go undetected or neural, without mutations multicellular organisms couldn't exist today. Also some mutations provide beneficial effects such as anabolic resistance in bacteria that allows them to be less susceptible to chemical agents. These types of studies on mutations lead to the advancements in medicine.

What does it mean when a gene is said to be " highly conserved"? What types of genes fall in this category?

A gene which is regarded to be highly conserved is a gene through the history of evolution which is fairly, if not completely similar to a gene sequence in another species. The conserved gene is so highly specialized that it has gone through excessive evolutionary pressure for the gene to remain unchanged.

The protozoan Didinium feeds on other organisms by engulfing them. Why are bacteria unable to feed on other cells in this way?

The protozoan " Didinium" feeds through a process known as endocytosis. Endocytosis is the ability of a cell to absorb molecules and other organisms, by engulfing the object. Bacteria are not able to perform endocytosis, in the way that an animal cell can, because that ability is limited by its cell wall. Only cells which contain a plasma membrane rather than a cell wall can undergo endocytosis.

Your next-door neighbor has donated $100 in support of cancer research and is horrified to learn that his money is being spent on studying brewer's yeast. How could you put his mind at ease?

Brewer's yeast, or " Saccharomyces cerevisiae", is one of the model organisms used in various DNA experiments. It's used as a model organism in many genetics and cell biology labs, because they are easily grown, easily contained in a lab, and produce a high yield of offspring. Model organisms allows for the research on human diseases, i. e. cancer, without the unethical need for human experimentation.

Bonus question: (2 points) Nucleotide sequence comparisons are fundamental to our current conception of the family tree of life, to understand how chloroplasts and mitochondria were acquired and their subsequent evolution, to the importance and magnitude of horizontal gene transfer, and to the notion that by focusing on a few model organisms we can gain valid insights into all of biology. This problem is designed to introduce common methods and assumptions that underlie the art of nucleotide sequence comparison.

A phylogenetic tree represents the history of divergence of species from common ancestors. Construction of such trees from DNA or protein sequences can really only be done with computers; the data sets are enormous and the algorithms are subtle. Nevertheless, some of the fundamental principles of tree construction can be illustrated with this simple example. Consider the first 30 amino acids of the hemoglobin ï ⸸ ¡ chain for the five species listed below:

Human V L S P A D K T N V K A A W G K V G A H A G E Y G A E A L E

Frog L L S A D D K K H I K A I M P A I A A H G D K F G G E A L Y

Chicken V L S A A D K N N V K G I F T K I A G H A E E Y G A E T L E

Whale V L S P T D K S N V K A T W A K I G N H G A E Y G A E A L E

Fish S L S D K D K A A V R A L W S K I G K S A D A I G N D A L S

Which pair of species is most closely related? What is the assumption that underlies your choice?

Based on the chart it seems as though humans and whales are the two species which are the most closely related. The assumption is that, between the whale and humans, there were only 8 differences in the proteins provided in the table, far less than any of the other organisms.

The information in the table can be used to arrange the species on the phylogenetic tree below. The branching order is determined using a simple kind of cluster analysis. The two most similar species are placed on the adjacent branches at the upper left. The species with fewest average

differences relative to this pair are placed on the next branch. In the next step, these species are combined and the average differences from the remaining species are calculated and used to fill in the next branch and so on. Use this method to arrange the species on the tree in the figure below:

Human Whale Chicken Frog Fish

Is the branching order that you determined above the same order that you would get by simply using the number of differences relative to human to place the other species on the tree? Why is the method of cluster analysis superior?

I found the cluster method and the relative differences methods gave provided different orders in arranging the species. I would assume the cluster method would be more accurate result, because it takes the average genetic difference of all species in the chart, rather than just comparing two different species.