Name; Nicemode Charles

Professor: Elizabeth Jeffress

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MUTATION AND NATURAL SELECTION LAB REPORT

Introduction

Gene Expression is the process by which DNA directs the synthesis of proteins which includes two stages and these are transcription and translation. Gene expression involves the flow of information from gene to protein. Mutations are changes made to the genetic information and these affect the proteins and leads to a wide range of genes formed due to mutations (Urry et al. 201). Point mutations are the type of mutations that cause a single change in the nucleotide pair of a gene and can be passed on to offsprings which leads to hereditary disease.

Mutations can occur naturally such as when the DNA fails to replicate well or can be due to environmental factors such as chemicals that are called mutants or exposure to radiation. Since mutation is normally rare, the effect it shows in the allele frequency in each generation is normally small. Natural selection can be a cause of most evolutionary change which is based on differential success in survival and reproduction. Organisms have variable traits and those variable traits help them survive in the environment tend to produce more offsprings than others. Molecular Evolution is a change in the chemical composition of molecules such as DNA, RNA, and proteins overtime as a result of DNA and selective pressures. Scientists have developed techniques to study molecular evolution and these are DNA sequencing and comparative

genomics that allow us to determine and compare organisms' DNA sequences. In the lab we used two experimental techniques, PCR and gel electrophoresis, to examine specific regions of the human, owl monkey and squirrel monkey genome. We also used comparative genomics to examine and compare the DNA sequences from these genomic regions. From the lab, we saw how mutations and natural selection can play a role in the evolutionary process.

In our first experiment we were investigating the effect of natural selection in non functional genes and on the gene for chorionic gonadotropin. Our hypothesis stated that the effects of natural selection will be seen on the gene for chorionic gonadotropin, a hormone important for fetal development and no effects of natural selection will be seen on non functional genomic regions. In our second experiment we examined and compared the similarity of the CG and variable regions between different species of organisms using the BLAST website. Our hypothesis stated that there will be a similarity between the CG regions and no similarity between the Var regions of the species.

Methods

In the first week, we used PCR reactions to amplify the chorionic gonadotropin (CG) gene from the human, owl monkey and squirrel monkey genome. In the second week we analyzed what we got after the PCR reaction by using gel electrophoresis. That same week we set up another PCR reaction to amplify the non functional region from the human, owl monkey and squirrel monkey genome. In the third week we analyzed the result of the PCR reaction on non functional regions of the species using gel electrophoresis. We used comparative genomics to compare the non functional regions of the human, owl monkey and the squirrel monkey from the DNA sequence

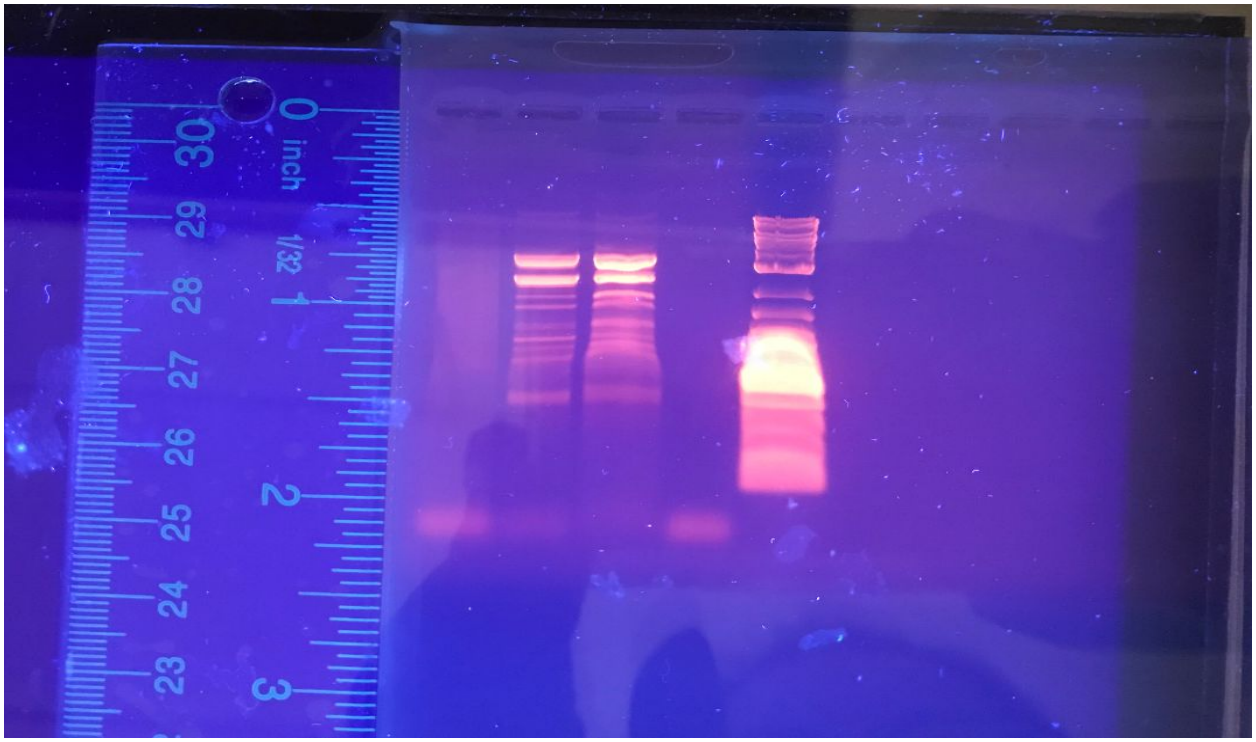
for the cg gene. We used BLAST which is an alignment tool to examine and compare the DNA sequences of the gene for CG from the non functional regions of the human, owl monkey and the squirrel monkey.

Results

The results we got after analyzing the amplified the CG gene from the human, owl monkey and squirrel monkey through gel electrophoresis are displayed in the first Image in Figure 1. The calculated base pair from our calculations for the Owl monkey and Squirrel monkey cg gene were both 200 base pairs. The human CG and the control had the least prominent band. In the second week we amplified the non functional functional gene from the human, owl monkey and squirrel monkey and analyzed it in the gel electrophoresis. From the second gel electrophoresis image we calculated the base pair size of the squirrel monkey variable region to be 3000 base pairs. The control, human and the owl monkey had the least prominent bands in the gel.

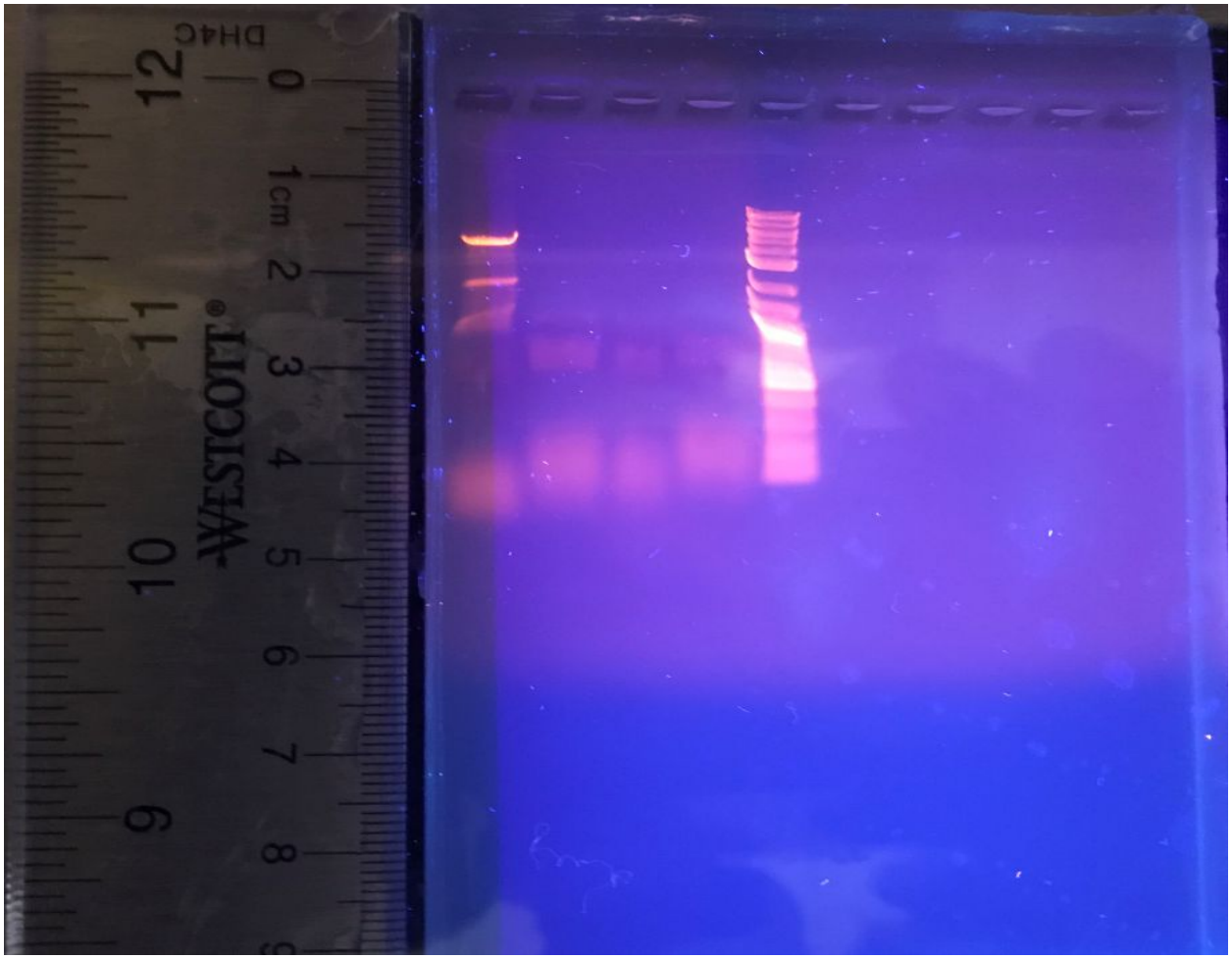
Figure 1

Image 1: Showing result of gel electrophoresis where the gene for CG in owl monkey and the squirrel monkey have the most prominent band in the gel. The arrangement of the lanes from the left near the ruler moving towards the right is as follows Control, Hcg -200bp, OMcg-200bp, SMcg, Marker.



Hcg- Human chorionic gonadotropin gene, OMcg- Owl monkey chorionic gonadotropin gene, SMcg-Squirrel monkey chorionic gonadotropin, bp-base pair.

Image 2: Showing result of gel electrophoresis where the gene for var in squirrel monkey has the most prominent band in the gel. The arrangement of the lanes from the left near the ruler moving towards the right is as follows SMvar-3000bp, OMvar, Control, Hvar and Marker



Hvar- Human variable region, OMvar- Owl monkey variable region, SMvar-Squirrel monkey variable region, bp-base pair.

Table 1; Sequence alignment for different species to show the consequences of functional, structural, or evolutionary relationships between the sequences using the CG, Var and growth hormone and oxytocin.

Genes compared **nucleotides**	**E. value**	**% identical**

H CG vs. om CG	0.0	83%
H CG vs. sm CG	0.0	80%
Sm CG vs. om CG	0.0	92%
H Var vs. om Var	1e^-18	75%
H Var vs. sm Var	2e^-94	77%
Sm Var vs. om Var	1e^-111	84%
H CG vs. h growth hormone	No significant similarity	No significant similarity
H CG vs. h oxytocin	No significant similarity	No significant similarity

H-human, h-human, om- Owl monkey, Sm- Squirrel monkey, CG-chorionic gonadotropin

Discussion

In our hypothesis we stated that there will be a similarity between the cg regions and no similarity between the variable regions of the the species. From the results in Table 1 above we see that all the E-values are less than 0.05 showing a meaningful level of similarity but the indent for CG are higher in CG regions in the species than in the variable regions. This result shows that the variable regions differ in a certain amount in their base sequence because the cg regions are the coding or target regions. The variable regions differ from the target region cg as they may have undergone mutation or natural selection. This difference in these regions is hence shown by

the ident value and this also supports our hypothesis which states that the cg regions will have a high percentage of similarity than the variable regions. In addition to this, from Figure 1 in the first image we saw similar results after analyzing the fragment size in the gel electrophoresis we saw the fragment size of the human and owl monkey cg gene which were both 200bp showing consistency with our sequence from BLAST alignment. We could not see the fragment size of the squirrel monkey and this is because squirrel monkey

Alu elements are a family of short interspersed repetitive elements (SINEs) found exclusively in primates (Novick, Herrera,Szmulewicz). These elements are around 300 base pairs long, are found in excess of one million copies per diploid genome, and are dispersed throughout the human genome (Novick, Herrera,Szmulewicz). Although owl monkey and squirrel monkey are closely related species, the results of the PCR in the non functional regions and gel electrophoresis show that even closely related species can be variable. This is shown by the presence of fragment size in the squirrel monkey which was 3000 bp whereby the owl monkey and human did not have any fragment size as no bands were shown. The reason for this variability in the non functional region is because of the Alu insertions. The human and owl monkey have non functional regions in the second PCR reaction which means it has no coding sequences and this is why we do not see any fragment size after running the DNA sequence in the gel electrophoresis. While this is the case, insertion of Alu elements in the squirrel monkey adds more base pairs in its gene sequence and since the Alu elements are able to adopt and reproduce in a new environment, they are amplified and we see the fragment sizes in the gel although we amplified a non functional region.

From our experiment, we saw how mutation and natural selection can affect genes by causing variation and hence makes the offsprings in a generation differ from their parent generation. In this case although owl monkey and squirrel monkey are from the same species, they differ in some of their genetic sequence due to the insertion of the Alu elements. The study of how mutation and natural selection affects organisms is important in the society as it helps scientists understand the relationship between organisms by tracing who their ancestors are. This includes knowing how these variations can benefit or impact an organism. For example if scientists study the role of mutation and natural selection in plants, they will be able to understand what kind of variation leads to drought resistant or pest resistant plants. The study of mutation can also help to find cure for some diseases like cancer. Lastly PCR reactions and gel electrophoresis helps scientists amplify different genes in the laboratory and analyze them to answer and solve different problems. For example scientists can amplify the gene responsible for the production of protein that helps in the formation of a certain antibody and examine and study it so they can create a vaccine that will help the production of antibodies in the human body.

References

Szmulewicz, M. N., Novick, G. E., & Herrera, R. J. (2005, April 14). Effects of Alu insertions on gene function. Retrieved March 26, 2018, from https://onlinelibrary.wiley.com/doi/abs/10.1002/elps.1150190806

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