Dominique Martinez

Professor Rinehart-Kim

Biology 303

Genome Assignment

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Chromosome Maps:

1. I choose chromosome 14.
2. Chromosome 14 has approximately 1200 genes.
3. This chromosome has over 100 million base pairs in which over 80% have been determined.
4. A gene that is located on this chromosome is PS1 (AD3) Alzheimer disease.
5. The physiological function of this gene causes lesions made of fragmented brain cells like Downs syndrome. These lesions are surrounded by an amyloid protein.

Introduction to BLAST:

1. The top sequence description is homo sapiens CFTR promoter region located on chromosome 7.
2. This membrane protein functions as chloride/anion channel in the epithelial cells throughout your body (US), 2018).
3. This CFTR gene in mutated form is cystic fibrosis.
4. It is located on chromosome 7.
5. Other than homo sapiens a 100% match for this sequence is also pan troglodytes.
6. The common name for pan troglodytes is chimpanzee.
7. No this does not surprise me because from an evolutionary stand point, they are what we evolved from.
8. The scientific name is cebus capucinus and the common name is white headed capuchin.
9. There is only one gap.
10. A gap in a sequence can indicate that “one or more amino acid residues have been deleted from the sequence” ("Sequence Alignment: Scores, Gaps and Gap Penalties", 2018).
11. This is associated with pathological functions of cystic fibrosis and the gene is TAR DNA binding protein also known as Tardbq ("BIOL 303 Genetics – Alexandra Cook", 2018).
12. This is ubiquilin 2 (UBQLN2) which is associated with the neurodegenerative disorder ("BIOL 303 Genetics – Alexandra Cook", 2018).
13. This is FUS RNA binding protein (FUS) associated angiomatoid fibrous histiocytoma ("BIOL 303 Genetics – Alexandra Cook", 2018).
14. This is superoxide dismutase I (SODI) which is associated with amyotrophic lateral sclerosis ("BIOL 303 Genetics – Alexandra Cook", 2018).
15. These genes are associated with amyotrophic lateral sclerosis also known as Lou Gehrig’s disease ("Amyotrophic Lateral Sclerosis (ALS) Fact Sheet | National Institute of Neurological Disorders and Stroke", 2018).
16. Genbank is the genetic sequence database consisted an annotated of publicly available sequences ("GenBank Overview", 2018).

Introduction of swiss-prot to study protein sequences:

1. cDNA is short for complementary DNA which is “sourced from mRNA” (H, 2018).
2. This is a match for homo sapiens partial HBB gene for hemoglobin beta chain with 1 isolated exon.
3. There are 3 5’ to 3’ frames.

Amino Acid Sequence Comparisons:

1. Yes, there is a difference between the two people but only in the 3’ to 5’ regions.
2. In frame one the first person had a stop codon and the second one did not. In frame two the first person had no stop codon and the second person had a stop codon with different nucleotide sequences. In frame three neither person had a stop codon but there were differences in the nucleotide sequences.
3. In person 2, it is fibroblast growth factor receptor 3 isoform with 1 precursor in humans.
4. This protein encodes an amino acid sequence on a member of a fibroblast growth factor receptor family.
5. A mutation in this gene may cause craniosynostosis.
6. In doing this assignment I learned to maneuver through the databases more swiftly and I also learned that just a minor change in an amino acid can have such a big impact.

References

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