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PTC Lab Questions:

1. My alleles are scored as TT since the bands on the stained gel are seen at 177 bp and 44 bp- although the one at 44 bp is faint.
2. When I tasted the piece of paper, it was very bitter, signifying that I am definitely a taster.
3. The presence of a T allele predicts tasting while the homozygous recessive tt allele predicts non-tasting. However heterozygotes are more likely to taste the PTC weaker than dominant homozygotes. This shows that the “dominant” allele is not completely dominant over the “recessive” allele and that there are probably multiple genes that control the ability for someone to taste the PTC.
4. If the C allele is present at the location of the C-G polymorphism in the TAS2R38 gene, the HaeIII enzyme will cut the DNA sequence at that spot. It recognizes the combination GGCC and cuts the DNA there.
5. This is different because it is required that every product of PCR have both of the primers. So the G in the forward primer is included in the amplification of the PCR but the A is not. This creates a sequence that is not normally seen in the TAS2R38 gene.
6. A synonymous mutation is one that does not affect the amino acid sequence because of the redundancy of the genetic code. A nonsynonymous mutation is one that affects the amino acid sequence. The G-C mutation is a nonsynonymous mutation because the codon CCA (proline) changes to GCA (alanine)
7. There are three common mutations in the TAS2R38 gene that are inherited together and all affect the ability to taste bitterness.
8. In this case, the homozygotes may each be able to taste a specific bitterness, but they may not be able to taste others. Therefore, they both are at a disadvantage, but the heterozygote is at an advantage because they can taste both types of bitterness.
9. Forensic crime labs use CODIS- the Combined DNA Index System which looks at 13 specific STR loci. Each locus is labeled with one of four fluorescent dyes, and each allele is differentiated by DNA sequencing. Forensic crime labs use a chain of custody, as is standard with any type of evidence. This means that there is a specific way to collect the DNA, identification of it, handling, and other procedures. Our procedures do not follow these standards and I would not trust our tests and procedures for any type of lab.
10. DNA typing gives a lot of information about the risk of a patient to certain conditions. Doctors can use this information to prevent conditions in particular patients but this can also cause a great deal of unnecessary stress and concern especially since the results of DNA testing are not set in stone. There are also issues regarding the use of DNA that a person may not be completely aware of, how they are exposed and what kinds of experiments are done on this DNA.

BioInformatics Questions:

Part 1:

2. c. This nucleotide does not match the sequence.

3. a. An E-value of 6e-12 means that there are sequences that are extremely similar in the database.

b. Yes they make sense. This is because they are all examples of the taste receptor in primates and humans.

c. The length of the PCR product amplified by the two primers is 221-bp.

Part 3:

6. I have landed on chromosome 7

8. Most of the genes surrounding this gene have to do with taste and olfactory senses.

Part 4:

6. Looking at all of the organisms compared, they are all relatively similar, with only a few changes. The most important part to note is at bp-145 where all of the organisms are the same except for the non-taster. There is an amino acid change because of that allele change. Therefore we can assume that the other organisms can also taste bitterness.

h/i/j: Apes can taste bitterness. This is because of the allele change which leads to an amino acid change. This leads to a change in the shape of the protein which allows for the ability to taste bitterness or not. This trait is useful because many poisonous plants and things we can consume taste bitter- so the animal should know not to eat them.