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VNTR Lab Questions

2. In a lane where you observe only a primer dimer, the reaction didn’t work.

3. a. There are 15 different alleles represented in our class. 1 in 20 people had “matching” DNA fingerprints. 80 % of people are heterozygotes. The data in the table given is of a large population size, whereas ours only takes into account 20 people.

4. No, I don’t think this protocol alone could be used to link a suspect with a crime or establish a paternity relationship because the uniqueness of the pMCT118 alleles is not very high, therefore you couldn’t single out any particular person. In order to modify the experiment to improve its ability to identify individuals, one would have to look at more chromosomes instead of just one. By looking at these, you should be able to narrow down the number of individuals.

5. a. Individual 2: 37, 24

3: 18

4: 28, 31

5: 18, 25

6: 17, 28

b. 83% of individuals are heterozygous.

c. 18, 28, and 31 appear to be the most common alleles.

6. a. Alleles 18, 29, and 24 appear to be the most common in all populations.

b. Allele 21 and 22 are very commonly found in African Americans but are less commonly found in both Caucasians and Hispanic Americans.

d.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Genotype | U.S. Caucasian | African American | U.S. Hispanic |
| 1 | 18, 31 | .0318 | .0096 | .0348 |
| 2 | 37, 24 | .0096 | 0 | .003 |
| 3 | 18,18 | .0702 | .0062 | .0789 |
| 4 | 28, 31 | .006 | .0211 | .0047 |
| 5 | 18, 25 | .0238 | .0022 | .0214 |
| 6 | 17, 28 | 0 | .0176 | .0003 |

7. Locus A: .075

Locus B: .01

Locus C: .01

Locus D: .02

Locus E: .04

Locus F: .015

Occurrence probability: 9e-11

8.

|  |  |
| --- | --- |
| Distance (mm) | Base Pairs (bp) |
| 79 | 750 |
| 86 | 520 |
| 94 | 500 |
| 79 | 750 |
| 86 | 520 |
| 81 | 725 |
| 86 | 520 |
| 91 | 500 |
| 93 | 475 |
| 85 | 575 |
| 90 | 510 |
| 93 | 475 |

The largest allele in this set of our class data is 750 bp and the smallest is 475 bp. Compared to the largest of the pMCT118 alleles 801 bp and the smallest 369- our data fits this although does not fully include all of these alleles. This could be because of some errors- not everyone’s DNA samples worked- or because our population size was not large enough.