TABLE 1: Genotype results for all four lab groups tested.

Genotypes (gel results)	Monday (Zoghby)	Tuesday (RJ)	Weds. 1:30 (Warrick)	Weds. 5:00 O'Dor nell
TT	3	2	3	4
Tt	7	7	4	9
tt	6	7	4	4
Undetermined Gel results	0	1	3	0
Phenotypes				
T_ (taster)	10	11	12	13
tt (non-taster)	6	6	2	4

Discussion: Begin by restating your hypothesis.

Before beginning any other relevant experimentation, I would first retest my DNA to provide conclusive data that confirms my genotype as a PTC taster. An experiment that essentially models this could be conducted on other genes within the human genome. Other experiments could include mutations to this gene through use of mutagenesis process that would examine the importance of other nucleotides on the gene and the specific proteins created by this gene. The experiment conducted on the PTC taster gene (or other more easily determined genes in the human genome) are simplications of gene tests geneticists would run on patients to determine an individual's genotype.

From this experiment, I was able to identify the genotype of a small portion of my get ome. This demonstrates the advancement of genetics in recent decades. With this progression in genetics, mutations in an individual's genome and the likelihood of an individual to pass on this mutation to offspring or for other family members to possess this mutation can be determined. It is important for doctors and scientists to understand the mechanisms of DNA, its mutations, and repair processes; these mutations have led to the evolution of species over time. By making further advancements in the study of genetics, scientists would be able to gain a more detailed grasp of the evolutionary process in the past, present, and in the future. The genotype data collection from my lab group and all lab groups demonstrates the consistency of genotypic ratios within a population: the percentages calculated from the values on the table are very close to normal percentages of taster vs. non-taster in a large population.

The evolutionary process is also modeled in the comparisons of sequences from the bioinformatics. All three of the primate sequences appear to be tasters because their genes n ore closely resemble the human PTC taster sequence. This suggests that the bitter taste receptor is more important in primates but, through evolution, humans no longer necessitated this trait to survive (so the SNPs continued on into offspring). The bonobo and the chimpanzee seem to be more closely related in the taste receptor gene, though the chimpanzee and the gorilla also seem to possess similarities. The gorilla most closely resembles the human being, which makes sense from an evolutionary star dpoint.

Children.