Group Number from Canvas Max Group Members = 6

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Name	Student Number
1)	
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Question 1

a) The phylogeny in Figure 1 shows the relationship among genera of orchids. Add taxon labels to Figure 2 so that both trees show the same relationships among the orchid genera. (3 marks)



b) What genus/genera is/are most closely related to *Maxillaria*? (2 marks)

Erycina, Otoglossum, Oncidium and Telipogon are equally related to Maxillaria

c) Did the ancestor of *Coryanthes* and *Gongora* look like *Zygopetalum*? Briefly explain your reasoning. (3 marks)

No, Zygopetalum is not ancestral to Coryanthes and Gongora. These species shared a common *Coryanthes, Gongora* and *Zygopetalum* shared a common ancestor but all of these lineages have continued to evolve since the time that they shared a common ancestor.

Question 2

a) You are studying a population of four o'clock flowers in a field in 2017. White flowers are F^WF^W , pink flowers are F^WF^P and purple flowers are F^PF^P . The table below summarizes the numbers of each flower morph in the field. Fill in the blank cells in the tables. Give answers to two decimal places (4 marks)

	Number of Individuals Observed in 2017	Observed Frequency in 2017	Expected Frequency in 2017
White	78	= 78/228= 0.34	 = p^2 = 0.39 Note that the value of p is not rounded before making this calculation to avoid propagation of rounding error – if you used 0.62 as the frequency for p that would be fine.
Pink	128	= 128/228= 0.56	2pq=0.47
Purple	22	=22/228=0.10	q^2= 0.14

F ^W Frequency (p)	=0.62
F ^P Frequency (q)	=0.38

Space for rough work – will not be graded.

b) Is the population in Hardy-Weinberg equilibrium? Explain how you arrived at this conclusion. (3 marks)

No, the population is not in HW equilibrium. In this population the frequency of heterozygotes is much higher than expected. The observed frequency of heterozygotes is 0.56 however, if the population was in equilibrium we would only expect the frequency of heterozygotes to be 0.47. The observed frequencies of both of the homozygotes are lower than expected. The observed frequency of white individual is 0.34 but we would expect a frequency of 0.39. For the purple individuals we observe a frequency of 0.10 but would expect a higher frequency of 0.14

c) Over the course of monitoring the field you collect data on the frequencies of the alleles for flower color. These are summarized in the table below. Your lab mate is very excited about your results and states that you are seeing natural selection for the F^P allele. Is natural selection responsible for the change in allele frequency? Explain your reasoning with specific reference to the criteria for natural selection. (6 marks)

Year	2018	2019	2020	2021
Frequency of the F ^P	0.39	0.44	0.45	0.57
allele				

No, it can't be concluded that natural selection is responsible for the increase in the frequency of the F^P allele in this population since only two of the three criteria for selection are met.

Variation in the population – this criterion is met, there are white pink and purple flowers in the population.

Variation has a genetic basis – this criterion is met – there is a single gene with two alleles that determines flower color in this population.

Individuals differ in fitness – this criterion is not met, we don't know if differences in flower color result in differences in fitness – although the frequency of the F^P allele has increased from 2018 to 2021 this could be the result of evolutionary mechanisms other than selection. Genetic drift or gene flow could also be responsible for changes in allele frequency.

Ouestion 3

Tuberculosis in humans is caused by the bacterium, *Mycobacterium tuberculosis* (*M. tuberculosis*). A vaccine for tuberculosis has been developed. This is a live vaccine where living *M. tuberculosis* cells are injected just under the skin. The bacteria used in the vaccine is an attenuated (non-virulent) genotype. This attenuated genotype doesn't cause disease but elicits an immune response. The attenuated strain was produced by isolating a single cell from a human host and then growing it in the laboratory in broth containing glycerin, bile and potato. The culture was maintained by periodically transferring a sample to new broth. The transferred sample contained several thousand cells. Regular transfer of cells to new media and subsequent growth, resulted in a large number of generations being grown in the lab outside of host animal (humans). In addition to losing virulence in humans after many transfers to new media, the bacteria were observed to grow more rapidly in culture than the original isolate. Given your knowledge of evolution, explain how both virulence is lost and growth rate increased after prolonged growth in the lab. Your answer should be clear, legible, logically organized and refer to specific evolutionary mechanisms acting on the bacterial population. (8 marks)

Attenuation of virulence in *M. tuberculosis* and increase in growth rate in the lab culture medium) are due to adaptation of the bacteria to growth in culture in the lab.

The initial culture derived from a single cell from a human host would have no genetic variation. As the bacteria grow in lab culture, mutations will occur generating genetic variation within the population. Any mutation that increased the fitness (i.e. growth rater) of the bacteria in the laboratory media would experience strong selection and would increase in frequency. Individuals that carried a mutation that increased growth would produce more offspring than other genotypes, eventually the new mutation would become fixed in the population. Over time, the expectation is that multiple mutations would occur that increased growth would occur and experience selection.

Since the bacterium is growing outside of the host, mutations could occur in genes responsible for virulence (the ability to cause infection) in humans. These mutations could result in the loss of function of the gene for virulence but mutations that resulted in a loss of virulence would not be selected against in the lab and could increase in frequency due to drift or selection if the loss of virulence resulted in an increase in fitness in the lab.

In this scenario, repeated bottlenecks associated with transfer to new culture media would increase the effect of genetic drift on changing allele frequencies in the population. As a result, mutations that negatively affected virulence but had no effect on growth in culture could become fixed due to drift.