

Q1: How many total potential gamete allele combinations are there for genotype pattern #3?

Q2: In a population with a high correlation between traits X and Y, you would expect which of the following sets of phenotypes: 1. Individuals with long deep tunnels and individuals with short shallow tunnels 2. Individuals with long tunnels, individuals with short tunnels, individuals with shallow tunnels, individuals with deep tunnels. 3. Individuals with long deep tunnels, individuals with short shallow tunnels, individuals with long shallow tunnels, and individuals with short deep tunnels

Q3: Based on the data for genotype pattern #4, which gene(s) (A, B, R) would you conclude coded for behaviors X, which genes for Y, and which genes for Z? What is the evidence?

Q4: When behavioral traits are genetically linked, it [DECREASES / INCREASES] the number of different possible behavioral phenotypes in the population? (choose one)

Q5: What two metrics were used to quantify the behavioral phenotypes?

Q6: Based on the data in Figure 63, you would conclude that burrowing behavior is [GENETICALLY INHERITED / CULTURALLY LEARNED] (Select one answer choice). What evidence supports your conclusion?

Q7: What “proportion digging escape tunnel” results would you predict under the alternate hypothesis to Q6)

Q8: Based on the data in Figure 61, the phenotypic variation in burrowing behavior among the BC generation is [GREATER / LESS] the parental generation? (select one choice)

Q9: Based on the data in Figure 61, would you conclude that burrowing behavior has a monogenic or polygenic architecture? Use the model in Figure 57 to explain your reasoning.

Q10: Based on the results in Table 1, would you conclude that tunnel length and the presence of an escape behavior are orchestrated by linked or unlinked genes? Use the model in Figure 57 to explain your reasoning.

Q11: If a chromosomal region is a “QTL” for a behavior, then differences in the _____ at that region, will likely cause differences in _____.

Q12: The results of QTL mapping provides information about whether genes that control a behavior are linked or not. (TRUE or FALSE? Why / why not?)

Q13: LG 5 is not a QTL for entrance tunnel length. What would the results plot look like for entrance tunnel length as a function of LG 5 genotype?