***The Mating Game* Problem sheet**

**Modeling segregation of alleles at a single locus**

In the following, let’s refer to phenotypes of your progeny generically as being either *wild type* or *mutant*, the latter term to be used in reference to recessive homozygotes (albino phenotype).

1. Please record the number of *wild type* and mutant individuals in the population.

\_\_\_\_\_\_\_\_\_ *wild type* \_\_\_\_\_\_\_\_\_ *mutant*

2. What is the phenotypic ratio (*wt:mutant*)observed in your simulated family of 12 progeny individuals?

3. By inspection of allelic composition in simulated progeny individuals, calculate the *AA:Aa:aa* genotypic ratios.

\_\_\_\_\_\_\_ *AA* homozygotes \_\_\_\_\_\_\_ *Aa* heterozygotes \_\_\_\_\_\_\_ *aa* homozygotes

*AA:Aa:aa* = \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

4. Considering all 24 alleles carried by your 12 progeny individuals, calculate the *A* and *a* allele frequencies, *f*(*A*) and *f*(*a*), respectively, in the population.

# *A* alleles: \_\_\_\_\_\_\_\_\_\_ *f*(*A*) = \_\_\_\_\_\_\_\_\_\_\_\_\_

# *a* alleles: \_\_\_\_\_\_\_\_\_\_ *f*(*a*) = \_\_\_\_\_\_\_\_\_\_\_\_\_

5. Gather the data requested in questions 1-4 above as generated by all student groups in your class session.

Total # *wild type* progeny: \_\_\_\_\_\_\_\_\_

Total # *mutant* progeny: \_\_\_\_\_\_\_\_\_

*wt:mutant* phenotypic ratio (all students): \_\_\_\_\_\_\_\_\_\_\_\_

Total # *AA* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

Total # *Aa heterozygotes*: \_\_\_\_\_\_\_\_\_\_\_

Total # *aa* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

*AA:Aa:aa* genotypic ratios (all students): \_\_\_\_\_\_\_\_\_\_\_

Total # *A* alleles among all progeny families: \_\_\_\_\_\_\_\_\_\_

Total # *a* alleles among all progeny families: \_\_\_\_\_\_\_\_\_\_

*f*(*A*) (all data): \_\_\_\_\_\_\_\_\_\_

*f*(*a*) (all data): \_\_\_\_\_\_\_\_\_\_

**Removal of deleterious genotypes from the population by selection.**

6. Having removed all infertile *albino* progeny segregants from your population and replaced them by copying the genotypes and phenotypes of the nearest flanking *wt* segregants, repeat the calculations of question 5, above. Your teacher will instruct you whether to use just the data from your population or to aggregate data from all student teams.

# *wild type* progeny: \_\_\_\_\_\_\_\_\_

# *mutant* progeny: \_\_\_\_\_\_\_\_\_

*wt:mutant* phenotypic ratio: \_\_\_\_\_\_\_\_\_\_\_\_

# *AA* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

# *Aa heterozygotes*: \_\_\_\_\_\_\_\_\_\_\_

# *aa* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

*AA:Aa:aa* genotypic ratios: \_\_\_\_\_\_\_\_\_\_\_

# *A* alleles among all progeny: \_\_\_\_\_\_\_\_\_\_

# *a* alleles among all progeny: \_\_\_\_\_\_\_\_\_\_

*f*(*A*) (all data): \_\_\_\_\_\_\_\_\_\_

*f*(*a*) (all data): \_\_\_\_\_\_\_\_\_\_

7. Imagine that this scenario was to play-out over many successive generations. Starting from an initial population in which *f*(*A*) and *f*(*a*) were both 0.5, sketch a plot below that indicates the change in values you would expect over the course of many successive generations of growth and reproduction. Please use a solid line to plot *f*(*A*) and a dashed line to indicate *f*(*a*) and be sure to label axes and plots.

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8. Examine the “alleles” remaining in the gene pool container and roughly compare the relative numbers of *A* and *a* alleles. Keeping in mind your response to question 7, please predict how, if ever, the *a* allele frequency *f(a)* would ever reach 0.0—that is, be eliminated from the population.

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\_\_\_\_\_\_\_ *AA* homozygotes \_\_\_\_\_\_\_ *Aa* heterozygotes \_\_\_\_\_\_\_ *aa* homozygotes

*AA:Aa:aa* = \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

4. Considering all 24 alleles carried by your 12 progeny individuals, calculate the *A* and *a* allele frequencies, *f*(*A*) and *f*(*a*), respectively, in the population.

# *A* alleles: \_\_\_\_\_\_\_\_\_\_ *f*(*A*) = \_\_\_\_\_\_\_\_\_\_\_\_\_

# *a* alleles: \_\_\_\_\_\_\_\_\_\_ *f*(*a*) = \_\_\_\_\_\_\_\_\_\_\_\_\_

5. Gather the data requested in questions 1-4 above as generated by all student groups in your class session.

Total # *wild type* progeny: \_\_\_\_\_\_\_\_\_

Total # *mutant* progeny: \_\_\_\_\_\_\_\_\_

*wt:mutant* phenotypic ratio (all students): \_\_\_\_\_\_\_\_\_\_\_\_

Total # *AA* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

Total # *Aa heterozygotes*: \_\_\_\_\_\_\_\_\_\_\_

Total # *aa* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

*AA:Aa:aa* genotypic ratios (all students): \_\_\_\_\_\_\_\_\_\_\_

Total # *A* alleles among all progeny families: \_\_\_\_\_\_\_\_\_\_

Total # *a* alleles among all progeny families: \_\_\_\_\_\_\_\_\_\_

*f*(*A*) (all data): \_\_\_\_\_\_\_\_\_\_

*f*(*a*) (all data): \_\_\_\_\_\_\_\_\_\_

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# *wild type* progeny: \_\_\_\_\_\_\_\_\_

# *mutant* progeny: \_\_\_\_\_\_\_\_\_

*wt:mutant* phenotypic ratio: \_\_\_\_\_\_\_\_\_\_\_\_

# *AA* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

# *Aa heterozygotes*: \_\_\_\_\_\_\_\_\_\_\_

# *aa* homozygotes: \_\_\_\_\_\_\_\_\_\_\_

*AA:Aa:aa* genotypic ratios: \_\_\_\_\_\_\_\_\_\_\_

# *A* alleles among all progeny: \_\_\_\_\_\_\_\_\_\_

# *a* alleles among all progeny: \_\_\_\_\_\_\_\_\_\_

*f*(*A*) (all data): \_\_\_\_\_\_\_\_\_\_

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7. Imagine that this scenario was to play-out over many successive generations. Starting from an initial population in which *f*(*A*) and *f*(*a*) were both 0.5, sketch a plot below that indicates the change in values you would expect over the course of many successive generations of growth and reproduction. Please use a solid line to plot *f*(*A*) and a dashed line to indicate *f*(*a*) and be sure to label axes and plots.

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