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Calculating Probable Theoretical Offspring Genotype in Fruit Flies

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Calculating Probable Theoretical Offspring Genotype in Fruit Flies

Abstract

Being able to calculate an offspring's theoretical genotype is critical in genetic sciences. We calculate the theoretical genotype and phenotype of fruit fly offspring. Using the product rule, we determine the probability for each trait and then for each genotype. In conclusion, we calculate 64 different genotypes that are supposed to be possible, but only 8 phenotypes are possible.

Keywords

fruit fly, offspring, genotype, phenotype, product rule, Punnett square

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PROBLEM STATEMENT

Determine the expected phenotypes of the offspring of fruit flies grown in the lab. Compare theoretical and observed phenotypes.

MOTIVATION

Humans have been selectively breeding different organisms for thousands of years. From plants to dogs, we can select and try to encourage beneficial traits in these organisms by breeding selected individuals together. Genes are units of heredity that determine the characteristics of an organism, and are passed down from parent to offspring. During conception, gametes from both parents, containing only half of the parents' genes known as a haploid, fuse together to create a full set of genetic material and produce a diploid zygote. Because of this, the offspring will contain a combination of both parents' genes; the blending of genes can result in traits that are different from either parent. By understanding how offspring inherit traits from their parents, we can determine how genes are recombined and interact.

MATHEMATICAL DESCRIPTION AND SOLUTION APPROACH

In the lab, we are provided 20 fruit flies (*Drosophila melanogaster*), 15 females of which exhibit wild type phenotypes and 5 males which exhibit mutant allele types. The wild type alleles are dominant to the mutant; this dominance will affect phenotype expression. The parental generation's genomes can be simplified as:

$$A^+AB^+BC^+C \times A^+AB^+BC^+C$$

To determine the probability of each trait, we construct a Punnett square; this helps to visualize genetic recombination of the offspring.

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Figure 1: Punnett Squares for F1 generate cross breeding

The first equation used is the product rule, which is used to determine the probability of an offspring's phenotype based on the sum of each trait's individual probability.

The expression can be written as:

$$P_p = P_1 * P_2 * \dots * P_n$$

All genes with at least one wild type allele will express the wild type phenotype, because offspring with the same traits may have different genomes (Table 1).

DISCUSSION

Once we establish the probability for each genome independently we then can calculate the probability for each genome combination.

$$A^+AB^+BC^+C = (1/2) * (1/2) * (1/2) = 1/8 = 12.5\%$$

$$AAB^+B^+C^+C^+ = (1/4) * (1/4) * (1/4) = 1/64 = 1.56\%$$

In total there are 64 different genomes possible for an offspring from cross breeding $A^+AB^+BC^+C$ flies. But only 8 different phenotypes are possible due to the dominance of the wild type allele. Based on these calculations we can predict that the most common phenotype for the offspring will be gray bodies, red eyes and long wings. Once the offspring have matured and their traits observed and recorded, those observations can be compared to the theoretical data, this can be useful in determining if an allele is dominant or recessive or codominant (Table 2).

CONCLUSION

Being able to predict the probable genome of offspring is a useful tool in genomic sciences. Although a three trait cross is relatively basic, these methods are used in genetic counseling for family planning and for breeding desirable traits in livestock.

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APPENDIX

Table 1:

Genotype	Probability	Trait
A^+A^+, A^+A	$\frac{3}{4}$	Gray body
AA	$\frac{1}{4}$	Black body
B^+B^+, B^+B	$\frac{3}{4}$	Red eyes
BB	$\frac{1}{4}$	Sepia eyes
C^+C^+, C^+C	$\frac{3}{4}$	Long wings
CC	$\frac{1}{4}$	Miniature wings

Table 2:

	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
ABC	AABBCC	AABBcC	AAbBCC	AAbBcC	aABBCC	aABBcC	aAbBCC	aAbBcC
ABc	AABBCCc	AABBcc	AAbBCCc	AAbBcc	aABBCCc	aABBcc	aAbBCCc	aAbBcc
AbC	AABbCC	AABbCc	AAbbCC	AAbbcc	aABbCC	aABbCc	aAbbCC	aAbbcc
Abc	AABbCc	AABbcc	AAbbCc	AAbbcc	aABbCc	aABbcc	aAbbCc	aAbbcc
aBC	AaBBCC	AaBBcC	AabBCC	AabBcC	aaBBCC	aaBBcC	aabBCC	aabBcC
aBc	AaBBCCc	AaBBcc	AabBCCc	AabBcc	aaBBCCc	aaBBcc	aabBCCc	aabBcc
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
abc	AaBbCc	AaBbcc	AabbCc	Aabbcc	aaBbCc	aaBbcc	aabbCc	aabbcc

Phenotype	Count	Percent
[aA aB cC]	27	42.2
[aA aB cc]	9	14.1
[aA ab cC]	9	14.1
[aA ab cc]	9	14.1
[aa aB cC]	3	4.7
[aa aB cc]	3	4.7
[aa ab cC]	3	4.7
[aa ab cc]	1	1.6