MedQGo / Filled explanation record

Expected counts are not a quota

An original filled example showing how to use the seven record fields. Not a real learner record, experiment, answer key or official exam material.

1. My conclusion

For the stated Aa x Aa model, the probability of aa is 1/4. In 40 offspring, the expected aa count is 10; it is not a promise of exactly 10 in every batch.

Why this field matters: State the prediction and its limits, not just a ratio.

2. Evidence and source

This is a constructed learning example, not an experiment. Both parents are Aa. The MedQGo Mendelian guide explains the gamete combinations. A fictional observed batch contains 12 AA, 17 Aa and 11 aa. These numbers are invented for comparison with the prediction.

Why this field matters: Separate the given model, the reference and the invented observations.

3. Assumptions

At this autosomal locus, each parent contributes A or a with probability 1/2; fertilisation is random. To compare predicted genotype proportions with surviving offspring, assume equal survival and reliable scoring. Complete dominance is needed for the phenotype grouping, not for the 1:2:1 genotype calculation.

Why this field matters: Name the conditions your calculation uses.

How to use the sample

Read the guide first. Compare this sample with the blank record, then close the sample and write your own explanation. The notes explain what belongs in each field; they do not score your knowledge.

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Continuing the same constructed Aa x Aa example. Read both pages together.

4. Reasoning or calculation

The four ordered pairings are A+A, A+a, a+A and a+a, each with probability 1/4. The two middle pairings give Aa, so genotype probabilities are 1/4 AA, 1/2 Aa and 1/4 aa. Multiplying by 40 gives 10, 20 and 10 expected offspring. Under complete dominance, AA and Aa share the dominant phenotype: expected totals are 30 and 10. The invented observed totals are 12+17=29 dominant and 11 recessive.

Why this field matters: Show the route from gametes to genotypes before grouping phenotypes.

5. Limits and uncertainties

The invented batch does not establish a biological result. An observed 11 aa instead of an expected 10 does not by itself disprove segregation or prove all assumptions. A statistical assessment would require an appropriate analysis. Dominant appearance alone cannot distinguish AA from Aa.

Why this field matters: Do not turn a small discrepancy or an appearance into proof.

6. What I changed

Illustrative correction: I replaced “40 offspring must include 10 aa” with “10 is the expected aa count under this model; an individual batch can differ.” This is a model revision entry, not a report of an actual learner's mistake.

Why this field matters: Explain why the old statement was too strong.

7. Next review

At my next study session, I will hide this sample and rebuild the four pairings. I will explain why Aa has two paths, state the dominance assumption, and separate expected counts from observed counts. I will choose a review date in my own record.

Why this field matters: Specify something you will produce or explain; copying this record is not proof of understanding.

Reviewed parent guide (released November 12)

OpenStax Biology 2e 12.2: conceptual reference

Blank personal record tool