X107A Test #1, Fall 2000, Answer Key

Tests were good.

15 = A, 14 = B+, 12 = B, 11 = B-, 8 = C.

Mean = 14.3, median = 15. High scores: 2 at 18, 3 at 17.5.

This is a time to evaluate how you are doing. People take the course with different backgrounds and needs -- and time commitments -- so you are the judge. But if you are disappointed at this point, there are two general likely reasons: inadequate background or inadequate effort. I encourage those who are behind to turn in regular homework, for written feedback. (In terms of final course grade, Test 1 is least important. Although I start by averaging the three tests equally, it is easiest to overlook a low Test 1.)

I would be happy to talk with you individually about your situation.

Note sheet. The same note sheet procedure will be used for each test. Think about how it helped you -- and how it might have helped more. That is, think about what you might like to do differently with your note sheet next time. Students indicate that the usefulness of the note sheet is in the following areas: useful in preparing, whether used on test or not; useful as outline to organize key ideas; useful for some facts. (Test #2 is a take home, but is exactly the same test style as #1.)

Here is a brief answer key for the test. If there are questions, we can discuss them in class or privately.

1. a.

Phenotype	Genotype
24 hr	$\tau^+\tau^+$
22 hr	$\tau^+\tau^-$
20 hr	$\tau^-\tau^-$

I have used τ^+ for the wild type allele, two of which are found in the "normal" 24 hr hamsters, and τ^- for the defective allele. You might reasonably use other symbols, including τ^{24} and τ^{20}.

It is "good" to explicitly write definitions of your symbols. However, with a good clear table, the meanings are so obvious that separate definitions are not essential.

Insights… You should know that hamsters are diploid -- like most higher organisms (basic biology). (If you do not know what a hamster is, you should ask!) The original mutant (22 hr) carries one mutation, thus is heterozygous. That further breeding gives the more extreme

phenotype (20 hr) tells you that there is no dominance here; rather, each copy of the mutant allele reduces the clock by 2 hr. (Recall the snapdragon flowers for an example of non-dominance, Ch 1 hw.)

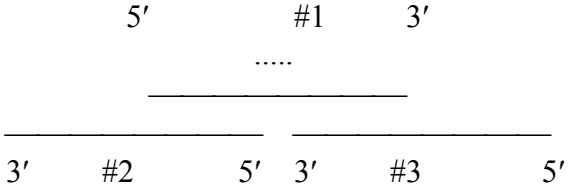
b. Think about (insight and general plan)… You get this <u>first</u> "22 hr" hamster (heterozygous) "by accident"; all you have to mate it with is "24 hr" hamsters (homozygous wild type). That mating will yield more heterozygotes, and then mating two of those will yield some of the "20 hr" hamsters (homozygous mutant). The following gamete matrix is for cross 1, as requested:

wild type parent → the mutant ↓	τ^+	τ^+
τ^+	$\tau^+\tau^+$	$\tau^+\tau^+$
τ^-	$\tau^+\tau^-$	$\tau^+\tau^-$

Each progeny box represents 25% of the total. Thus this first cross will yield 50% each 24 hr (wild type, $\tau^+\tau^+$) and 22 hr ($\tau^+\tau^-$) hamsters.

> This question was originally inspired by an item in BioScience 39:75, 2/89. Since then, much progress in understanding circadian rhythms has been made in several organisms. A recent paper on τ: P L Lowrey et al, Positional syntenic cloning and functional characterization of the mammalian circadian mutation tau. Science 288:483, 4/21/00. + News article, Young, p 451. They show that the τ mutation is in the gene for an enzyme casein kinase; the homologous gene in Drosophila, double-time, is a known gene for circadian rhythm. They discuss how the enzyme, and the mutant, may act.

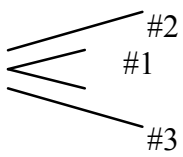
2. a,b,c.



For part b: It is ok if ALL strand ends are just the opposite of what is shown here. (However, it is common that the upper strand of a structure is shown 5′→3′.)

For part c: The part of #1 marked with a dotted line just above it is relatively flexible, because it is single-stranded. The rest of #1 -- those parts that are in DS regions with either #2 or #3. are relatively rigid. The point then, is that the SS region (dotted) is a "hinge". (To be more precise, a nick is all that is needed to produce the hinge. There does not need to be an actual gap.)

d.



Note that d is the original structure, folded back along the hinge region of #1. Emphasize that drawing it folded like this is for convenience, in seeing what to do next. Fundamentally, this is a flexible structure.

e.  #4 (hopefully easier to draw by hand. Idea is that it brings the ends of 2 and 3 closer together.

f. 

g. As you add strand 4 and then strand 5, alternating, you will go back and forth between the situations drawn in parts e and f. Remember that strand 1 of the original structure (part a) has a hinge in the middle, and two ends. Strand 4 brings those two ends of strand 1 close together; adding strand 5 removes strand 4, thus allows the two ends of strand 1 to flop around freely. In effect, strand 4 closes strand 1, or (better) closes the strand 1-2-3 structure. And strand 5 opens it. One might think of the 1-2-3 structure as a pair of tweezers. Strands 4 and 5 operate the tweezers, opening and closing them.

> Parts a-e are all based on fairly standard DNA issues; however visualizing all this can be a problem. Parts f-g are more complex.
>
> Based on B Yurke et al, A DNA-fuelled molecular machine made of DNA. Nature 406:605, 8/10/00. Their Fig 2 is roughly equivalent to the parts of this question.

3. a. hydrogen bonds (polar interaction, between <u>backbone</u> $H^{\delta+}$ and $O^{\delta-}$ in peptide bonds along the chain)

b. hydrophobic interactions (repulsive interaction of nonpolar hydrocarbon chains and water)

c. covalent. Also accepted amide bond or peptide bond; people who use those terms hopefully understand that they are examples of covalent bonds.

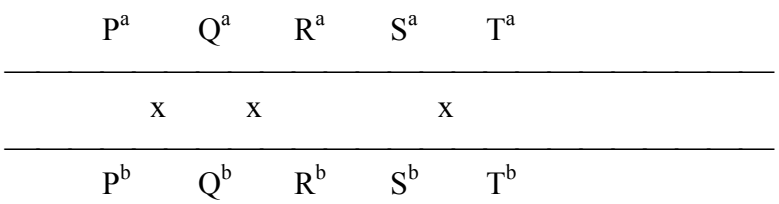
4. No; DNA and RNA are informationally equivalent. Both processes entirely involve transfer of information from one nucleic acid strand to another nucleic acid strand, by base pairing. The form of the information, in base pairs determined by the pairing rules, is the same in both.

> This was emphasized in both the Ch 2 handout (DNA vs RNA) and Ch 3 handout (Central Dogma).

5. a. LH b. Z c. anti-parallel

> Figure on test is from J Chemical Education 69:A113, 4/92.

6. 3 crossovers:



This produces: (starting at bottom left, and following the x events) $P^bQ^aR^bS^bT^a$, which was requested. It also produces the reciprocal $P^aQ^bR^aS^aT^b$.

It's ok to make three separate drawings, each showing one crossover. But it really is simpler (easier to see) to show all in one drawing.

Be sure to distinguish "cross" (an organismal event) and "crossover" (chromosome or DNA event).

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