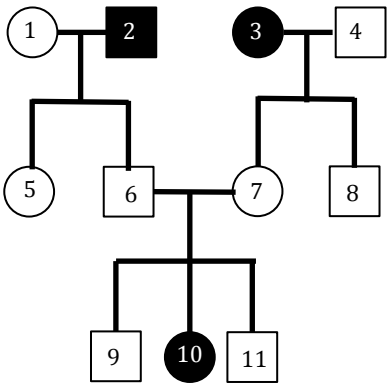
ANSWER KEY Lab EXAM 1, Spring 2015 *Mean = 64.1*, Stdev = 13.4, Median score = 65. Range 24-98. A+ = 100-98, A = 97-80, A- = 79-74, B+ = 73-71, B = 70- 67, B- = 66-63, C+ = 62-58, C = 57-51, C- = 50-40, D+ = 39, D= 38-36 D- =35-34, F = 33 or less. Please see the answer key posted on bCourses for explanations of answer.*

1	D	6	D	11	E	16	C	21	C	26	B	31	B	36	E	41	D	46	A
2	B	7	E	12	A	17	C	22	B	27	C	32	C	37	C	42	A	47	D
3	D	8	A	13	B	18	B	23	D	28	A	33	B	38	C	43	C	48	C
4	E	9	A	14	E	19	D	24	C	29	A	34	B	39	D	44	C	49	C
5	D	10	A	15	D	20	B	25	D	30	B	35	B	40	B	45	D	50	

1) There are 300 A alleles and 90 B alleles and thus there are 27,000 possible mating types. (Note I rounded numbers a bit from the actual scientific data to make the math easier).
2) The electron transport chain pumps protons from the stroma into the thylakoid space/lumen. Oxidation of water occurs in the thylakoid space/lumen which also increases the proton gradient.
3) From the 100X total magnification you know that each ruler is 10 μm long (200 μm /20). At 200X total magnification each ruler mark represents ½ of the value at 100X and is 5 μm . Thus 15 X μm = 75 μm.
4) Image is of *Trichonympha* from the lab manual and from the pre-lab.
5) 1 cell gives rise to 2 cells via mitosis and cytokinesis. Those 2 cells then give rise to 4 cells via mitosis and cytokinesis. The 4 cells then each give rise to 4 cells via meiosis and cytokinesis. Total = 16 cells, 1N.
6) Homozygous is the condition when both alleles are the same, heterozygous when different and hemizygous when only one is present.
7) The consensus sequence is looking at the sequence from both the 5' end and the 3' end. The primers must be matched- forward and reverse. This eliminates A and D. BLAST is the local alignment tool. For this software, you enter a query sequence, submit it and then it is compared to the database of submitted questions. In this case your data consisted of your sequence data from Forward and Reverse.
8) With a hollow tube you will be able to see the outside edges and inside edges. If you are raising the stage the item on top will come into focus first.
9) You are collecting light from a smaller area and thus must have less light emerging (this is the reason you typically need to increase light intensity or open the aperture diaphragm with increasing magnification).
10) Depth of focus decreases with increased magnification. The optical section is thinner.
11) X^{min} is the notation for the miniature allele, X^{min+} is the notation for the wild type allele, Y is the notation for the Y chromosome. Female genotype is $X^{min}// X^{min}$ and the male genotype is $X^{min+}//Y$.

	X^{min+}	Y
X^{min}	Female, wild type	Male, miniature

12) Analyze each statement. A) Adding additional substrate when the enzyme is already saturated will not affect activity. B) Adding addition enzyme will increase the rate when the enzyme molecules are already saturated (excess substrate). C) Non-competitive inhibitor will decrease the activity of each enzyme molecule. D) Changing the pH 4 fold is a significant change in the pH and will most likely affect activity. E) Changing the temperature 45 degrees C is a significant change and will most likely affect activity.
13) If the allele for a trait is dominant then it should be present in every generation. Thus it must be recessive (use d for notation). Individuals are numbered in the key. If the trait was X linked recessive then individual 2 must be $X^d//X^d$ and son 5 should have the disease. If Y linked then individual 2 can't have the disease. Only B works.



14) C = Abs/lZ. A transmittance of 1% = 1/100 = absorbance of 2. Thus concentration is 2 = 2/ 4/M cm X 1 cm = 0.5 M. The dilution was 5 fold (1 part Y and 4 ml water). Thus the original is 2.5 M.

15) In our negative control we want to test for potential contamination with a template. Thus we need all ingredients so the reaction could work if provided with a template. Thus the only thing absent should be D.

16) 0.01 X 10^{-6} M OH is the same as 1.0 X 10^{-8} M. Thus pH is 6.

17) Since you see a difference between males and females the trait is sex linked and since the F1 females have six legs the mutant allele is recessive (F1 females are heterozygous). Use X^f to indicate mutant allele. Females are thus X^{f}/X^{f}.

18) Affinity is inversely related to Km. The smaller the Km value the higher the affinity.

19) Cyanobacteria lack chloroplasts and thus lack thylakoid membranes. The DNA of bacteria is typically circular (E is not an answer).

20) Mary is 50% related to her mother (her mother gave her ½ of her DNA). Mary's mother is 50% related to her mother. Thus Mary is 25% related. (1/2 X ½).

21) Again I somewhat simplified the approach used in the study. Any form of microscopy is fairly ineffective at identify species diversity. Your DNA sequence from 16s rRNA allowed you to compare it to all of the other 16s rRNA sequences entered into the DNA database.

22) Ortholog refers to homologous genes that are present in different species. Note that D is more like a definition of analogous genes.

23) Emission must be of less energy (longer wavelength) accompanied by heat.

24) Please draw out PCR. With only the reverse primer you will make the complement of the template strand. In the next round you can only bind to the template – that after 30 rounds you will have 30 copies of the template. With both types of primer present the first round will allow only the Reverse primer to bind. At the start of round 2 you have the original template plus the complementary strand. This you essentially have double strand. From now on it is the typical process for PCR. For 30 rounds it is essentially identical to 29 rounds starting with one double stranded template.

25) At Km you have a velocity of ½ Vmax. Thus Vmax is 0.8 O.D units. Remember the Km curve is determined by varying substrate concentration. At saturation (excess substrate) you reach Vmax.

26) Each start molecule has 1 reducing unit at the end (thus 200 X 1 initially). When each starch molecule of 40 linked glucose units is cleaved into maltose (disaccharide) then there are 20 maltose and 20 reducing units. Thus at the end = 200 X 200 = 4,000. Net change is 3,800.

27) The band shows that the PCR product is 500 bp long and that there is 480 ng present in the band. If we had 1 MOLE of 500 bp long DNA it would weigh (500 X 600) = 3 X 10^5 grams. Thus there are 480 X 10^{-9} g/3 X 10^5 g/mole = 1.6 X 10^{-12} MOLES. Multiply by 6.0 X 10^{23} = 9.6 X 10^{11} molecules.

28) Since there is sucrose present in the chloroplasts the outer membranes will remain intact. Thus the DCPIP would not be adjacent to the thylakoid and you would not expect reduction of DCPIP.

29) For an animal the cell must be 2N =4. Four chromosomes composed of 2 sister chromatids should be aligned. Haploid cells in animals do not undergo mitosis.

30) M1, M2 and M3 represent one complementation group (those that fail to complement). M 4 and M6 another group. M5, M7, M9 another group. M8 and M10 another group. Thus there are at least 4.

31) Within a complementation group you lose the function—in this case assayed by the conversion of a compound to another compound. Since there are 2 different loci there must be two different alleles and the easiest explanation is the enzyme responsible for the conversion must have two polypeptides. Alternative splicing occurs at one locus – it would not involve two completely different chromosomes as it is from one pre-mRNA.

32) In lab you looked at acetone extracts of chloroplasts. These extracts fluoresce greatly because the excited pigments cannot transfer an electron, instead they release the energy as fluorescence and heat.

33) The DNS solution was very basic – pH 14. This is how it denatures amylase and another reason for the safety glasses. The base would drive the reaction such that aspartic acid would donate the proton.

34) Endergonic reactions require a net input of energy but all reactions have to overcome the energy of activation.

35) T6Q means the normal amino acid T, at position 6 (numbered from the N terminus) is replaced by Q.

36) Bacillus means "rod shaped" and Gram-negative bacteria would be stained red.

37) There are 5 X 10^6 chloroplasts. 20 ml represents a total of 2 mg chlorophyll. Thus there is 2 mg/5 X 10^6 = 0.4 X 10^{-6} mg/chlorophyll = 4.0 X 10^{-7} mg/chlorophyll.

38) Sperm = 1N = 14 chromosomes. Kidney cells are 2N and there should be 28 chromosomes. 1 mole bp = 600 grams. Thus 600 grams/6.0 X 10^{23} molecules means one base pair weighs 1 X 10^{-21} grams. 4.8 X 10^{-12} grams/ = 4.8 X 10^9 base pairs.

39) Each of the 10 liver cells would have 46 chromosomes, each composed of sister chromatids. Each chromatid is double stranded DNA. Thus there are 4 single strands after denaturation. There would be 184 per cell x 10 cells – 1,840. For each chromosome the sister chromatids are identical. Thus each chromosome would yield 2 strands which are complementary – not identical. Thus there are 92 unique strands.

40) [(4 ml x 6 M) + (6 ml X 10 M)]/10 ml = 8.4 M. [(10 ml X 8.4 M) + (90 ml X 0.0 M)]/100 ml = 0.84 M.

41) Acetone will extract hydrophobic molecules which were present in the membrane. Pigment 1 is more hydrophobic than pigment 2 as it migrated further.

42 & 43) The double recombinants are ABC and A+B+C+. The parental chromosomes are A+BC and AB+C+. The one allele that appears different is A. Thus A is in the middle. The correct parental genotype for the two chromosomes are BA+C and B+AC+. Thus recombination between A and B would yield B+A+C and BAC+ (and also the double recombinants). Total = 90 + 90 + 10 +10 = 200.

44) Total = 0.17 (0.16 + 0.01)

	P .4 b+E+	P .4 bE	r .1 b+E	r .1 bE+
P 0.4 b+E		YES (0.16)		
P 0.4 be+				
r 0.1 b+E+				
r 0.1 bE			Yes (0.01)	

45) Crossing over occurs between homologous chromosomes during prophase I of meiosis.

46 & 47) Examine each locus independently. Trait 1 r = 1600, D = 1,600 = hetero with homo recessive. Trait 2 r = 800, D = 2,400 hetero with hetero. Trait 3 r = 800, D = 2,400 hetero with hetero. Thus if Trait 1 and T2 assort independently expect ½ T1 r X ¼ T2 r = 1/8 (400). You find 640 which is more than expected. Thus this must be due to a parental type of chromosome. ½ T1 r X ¾ T2 D = 3/8 (1,200). You find 960 which is less than expected and this must be due to a recombinant type of chromosome. ½ T1 D X ¼ T2 r = 1/8 (400). You find 160 which is less than expected and this must be due to a recombinant type of chromosome. ½ T1 DX ¾ T2 D = 3/8 (1,200). You find 1,440 which is more than expected. Thus this must be due to a parental type of chromosome. The parental genotype for these two loci are r r/ D D. This individual is heterozygous for both loci with the recessive alleles on the same chromosome.

Lets examine T1 and T3. Thus if Trait 1 and T3 assort independently expect ½ T1 r X ¼ T3 r = 1/8 (400). You find 400 which is expected if the traits are unlinked. You can do the additional analysis (1/2 T1 r X ¾ T3 D, ½ T1 D X ¼ T3 r, 1/2 T1 D X ¾ T3 D) but this is enough to stop the analysis .

Lets examine T2 and T3. Thus if Trait 2 and T3 assort independently expect 1/ 4 T2 r X ¼ T3 r = 1/16 (200). You find 200 which is expected if the traits are unlinked. You can do the additional analysis ((1/4 T2 r X ¾ T3 D, 3/4 T2 D X ¼ T3 r, ¾ T2 D X ¾ T3 D)

48) In the ddG tube (lane) you only find molecules that primer + 2 long. Thus there must have been dATP in the tube (and no ddATP) and at the 2nd position there must have been either ddTTP only or something that allowed the incorporation of dTTP but no further addition – no dGTP or ddGTP). Choice B does NOT work. If dATP were present we would add dATP to the primer and then opposite the A in the template we would dTTP and thus we are primer + 2. At the next position opposite the C we would incorporated ddGTP which would mean the molecule is primer + 3 long. There is NO band at that position.

49) Within the question we know there are 2 genetically unlinked loci and the mutations are recessive and they map to the Z chromosome. Thus the males in the wide beak population 1 have the genotype. Z $^{wb1;\ wb2^+}$// Z $^{wb1;\ wb2^+}$. Thus the females in the wide beak population 2 have the genotype. Z $^{wb1^+;\ wb2}$// W. The F1 males are Z $^{wb1;\ wb2^+}$// Z $^{wb1^+;\ wb2}$ and the F1 females are Z $^{wb1;\ wb2^+}$//W. See the Punnett square for the predictions for the F2 3/8 have normal narrow beak.

	Z $^{wb1;\ wb2^+}$	Z $^{wb1^+;\ wb2}$	Z $^{wb1;\ wb2}$	Z $^{wb1^+;\ wb2^+}$
Z $^{wb1;\ wb2^+}$	Wide beak	Narrow beak	Wide beak	Narrow beak
W	Wide beak	Wide beak	Wide beak	Narrow beak