PART A. VISUAL SEARCH ONLINE with NCBI REV 9 2015

Uses the NCBI website, with its great visual maps showing locations from which the many cloned segments were taken, along with detailed DNA sequences arranged in rows (as used in this lesson):

1. Go to http://www.ncbi.nlm.nih.gov/mapview/. Here you will see many species under Primates. Find Homo sapiens...........human...........Annotation Release 107 (or higher number if there) Click on that AR number, which takes you to Homo sapiens (human) genome view (of all human chromosomes).

2. Click on the 2 for chromosome 2 (long wait for data to download). This displays chromosome #2 details.

3. Find the centromere (constriction almost 1/3 down from top end). See detail of the region in Fig. 3.

4. Note: the dark and light bands in the upper portion (above the centromere constriction) are labeled with a “p” (e.g. in 2p16.3); the bands in the lower portion are labeled with a “q” (e.g. in 2q24.1).

5. Find the white band called 2q13. Look just to the right to see the vertical blue lines. The blue lines are called “contigs”. Look carefully (in Fig. 3) for the ID number of the contig that includes 2q13.

   What is that number?  NT-__________

6. Click on that NT number, then click on the enlarged pop-up "Symbol" of that number, which looks like:

   Symbol  NT 005403.18

7. This brings up the detail page for that contiguous sequence (“CONTIG”).

8. On the “LOCUS” line, notice that the NT_005403.18 contig has 147.7 bp. That means there are over 147 million basepairs in that region of chromosome #2 (the lower "q arm" of chromosome 2!)

9. Scroll down to where all the CONTIGs are listed. These are the many short “sub-contigs” contained within the larger one. Most have blue “AC...” numbers, but search down the left column until you come to AL078621_19 (about 1.5 screens down). About the only AL number listed.

10. Clicking on this number brings up the detail page for that short sub-contig “AL078621.”

11. On the LOCUS line, notice that there are 176,734 basepairs in this sub-contig.

12. Scroll quickly down through other information and a long list of “FEATURES” (with various titles as links), until you see the ORIGIN of this nucleotide (bp) sequence. Here’s a sample of the first few lines:

   ORIGIN
   1  gaattcttctt tctgttatatta gaaaccacact cacgttacctt gatatttgigg tattttaagtc
   61  atgaaaggta tttcttctag gaagcagtga ttctaaagtg tatgctttaac cagtcagttg
   121  agtgtctact cttgtgttgtt cacaagtgtg cacaaa
gtt ttggtaaatt aagaatatta
   1

13. Each number represents the first base (bp) on that line, and on each line there are 6 sets of bases (bp), with 10 bp in each set (total of 60 bp per line): bp#1 is g; bp#71 is t; what is bp#121?___; bp#150?___

14. What number would you expect to find for the last bp in the entire sequence? _______(see #11 above). Scroll down to the very bottom of the page to see if that number is correct. What is that letter?___

15. Start searching for the fusion-transition sequence expected where the telomeres had to meet and overlap. Start with a quick scroll down from the top line, looking for any repeat pattern that stands out, and getting a feel for the massive amount of DNA represented here. (Part of the fusion region is shown below; it’s about 1/2 way through the entire contig). Notice the many multiples of g, followed suddenly by many multiples of c. Don’t spend too much time here, maybe 5 minutes, max (it could take hours!) If you find this region, record the bp number where that change occurs:___________. (Don’t tell anyone). Now go on to Part B to see if you are right.

   aggggggggg ttggggttag gtttagggggt ttgggttggt ggtgggttgg ttggggtggg
tgggggtgg ggtaggggtta gctaaaccta gcaacaacca ccaaccaaccc aacaacacca
taacccctct ctaaccctctt ccaacacccc aacaaccaaccc aacccccccc ctaaccctctt
tacccctctt ccacccctt ccacccctt ccacccctt ccacccctt ccacccctt ccacccctt

   16. Don’t feel bad if you can’t find it! Very few people do. Instead, do what scientists do: a “BLAST2” search, in which you ask the online computer to search the entire sequence using a probe (short DNA sequence desired). It then shows you the areas that match, and how closely they match. Let’s try it. [Go on to Part B: BLAST2 search; or, if assigned, go to Part D for the paper search].