**Genome Architecture**

**Study guide and readings**

***Reading assignments:*** can be downloaded, as pdfs, from Canvas – in the “Files” folder.

* Required: Pennisi\_Dark matter.
* Recommended.
  + Fedoroff\_TE
  + Feschotte et al\_TE

1. When one reads that there are “29,000” gene in Theobroma cacao, what sort of genes are probably being referred to?
2. Review the classic definition of a protein coding gene and be sure to know the names and functions of the essential pieces.
3. Does knowing the chromosome number of a species allow you to predict the number of genes and/or the genome size?
4. What simple calculations lead one to conclude that there must be more DNA in a genome than just protein coding genes?
5. What is the C-value paradox?
6. From the assigned reading - Why is Dark Matter not Junk?
   1. Has genome sequencing revealed more genes than anticipated or more regulatory factors than anticipated?
   2. Protein coding genes account for, on average, 2%, 20%, 100% of a plant genome?
   3. What percentage of the average plant genome would you estimate is transcribed?
      1. 5%,
      2. 20%,
      3. 80%?
   4. Why does conservation of DNA sequence in non-coding DNA imply a functional role for the non-coding DNA?
7. What is the relationship between epigenetics and the C-value paradox?
8. Which of the following allows greater transcription of a gene?
   1. Methylation
   2. Acetylation
9. How does epigenetics related to facultative heterochromatin?
10. What are transposable elements?
11. What is a key difference between the two principal classes of transposable elements?
12. How can transposable elements cause mutations and how could this be “harnessed” to related genes to functions.
13. How do transposons related to the C-value paradox?
14. What does the relatively small genome size of *Fragaria vesca* have to do with transposable elements?
15. Give one example of a famous Mendelian gene where the mutant allele is related to a transposon.