Problem 1

The drawing depicts a 6-nucleotide region of DNA in four strains of *Drosophila simulans* and in one strain of *Drosophila melanogaster*.

At nucleotide site 1 we note that most of the *simulans* strains bear the same nucleotide as the *melanogaster* strain, suggesting that the one strain that does differ is a mutant that recently appeared and is still segregating in the *simulans* population [graph C, expression (a)]

At nucleotide site 2, all the *simulans* strains have a nucleotide different from that which we see in the *melanogaster* genome. Since we observe no polymorphism at this site in either species, our best guess is that there was a substitution (mutation+fixation) event at some point in the combined lineage of the two species [graph A, expression (b)]

Finally, all the *simulans* strains, as well as the *melanogaster* genome show the same nucleotide at site 3. Our best guess, then, is that even if mutations have occurred at this site in the past, they didn’t get an opportunity to fix in the *simulans* or the *melanogaster* population [graph B, expression (c)]

Problem 2

As substitutions accumulate at a given site (thus increasing K with time), some of these substitutions cause the site to revert to its original state. As a result, with time the number of sites that are actually different between the two homologous sequences (*i.e.* P, or D) is increasingly smaller than the number of substitutions that actually happened.

Accordingly, the top curve should be marked as “K,” and the bottom – as “P”.