Imagine that you are studying snakes in Southern California. Your study populations are all completely isolated from one another (no gene flow) and are derived from a single ancestral stock population that was broken up by development in the last 100 years. Before urbanization the entire range of this species extended within 10 miles of the Pacific coast from present-day San Clemente, California to Tijuana, Mexico. The entire species was comprised of N diploid individuals in the generation before urbanization happened. You are studying selection on a behavioral trait that is controlled by a single genetic locus with two alleles (A and a) that were in Hardy-Weinberg equilibrium in the generation before urbanization.

1 Imagine that in the ancestral population, selection on this behavior imposed directional selection for the A allele. What would be the frequencies of A and a before and after one generation of selection in the ancestral population? In addition, discuss the assumptions you must make about the ancestral population for this calculation to be applicable?

2 Sewall Wright explored the evolutionary implications of population structure on selection. Specifically, he developed methods to quantify the degree of population differentiation, and the evolutionary consequences of such population subdivision and structure. Today, we would call such population structure a metapopulation. In this portion of the question, you should do the following:
   a Describe the statistics he developed to quantify genetic population differentiation, and explain what each level of these statistics actually quantifies.
   b Explain in conceptual terms how Wright's views of selection in subdivided populations would predict how the impact of urbanization would change the evolutionary dynamics due to selection and selection's interaction with other evolutionary forces would of this behavioral trait in the newly formed metapopulation?

3 Now imagine that the a allele is deleterious to individuals within
each subpopulation in the urbanized metapopulation, but is globally favored in the entire metapopulation.

First, explain what possible modes of selection must be operating to generate such fitness differences at different spatial scales.

Then, show how such selection within and between subpopulations affects change in the frequency of the a allele after one generation of selection in the entire metapopulation.