Part 2

Mutation and the Conservative Nature of Natural Selection

Chapter IV

Mutation as a Change in the Base Sequence of a DNA Cistron

Due to an inherent complementality which exists between the two base pairs, adenine-thymine and guanine-cytosine, DNA is endowed with the unique property of being able to make an exact replica of itself before each cell division. Yet, if the mechanism of DNA replication were perfect and there was no room for mistakes, the creation of divergent living creatures from a common ancestor could not have happened.

Changes in the base sequence of individual cistrons do occur and such changes are the cause of individual variability within a population. Natural selection exploits these individual differences and evolution occurs. A heritable change in the base sequence of a cistron is defined as a mutation. The observation that one mutation usually affects only a single base pair within a cistron attests to the fact that the mechanism of DNA replication is nearly perfect and that mistakes do not occur very often. Because of this stable replication mechanism, however, a new mutation which is favored by natural selection can perpetuate itself as a new inherited trait.

Different types of mutations shall be defined in this chapter. Mutations that affect structural cistrons which specify polypeptide chains shall be contrasted with those which affect cistrons for *transfer* RNA.

1. Mutations Affecting Structural Cistrons

a) *Frame-shift* Mutations

A rare type of mutation which most profoundly affects the assigned function of a structural cistron is a *frame shift* mutation. This type of mutation is due to either the deletion or the insertion of a single or two consecutive base pairs. When a *messenger* RNA transcribed from an affected cistron is translated, a growing peptide chain would receive the proper amino acid sequence until the point of deletion or insertion. However, because of the coding mechanism based on base triplets, from then on to the carboxyl end, the amino acid sequence would be completely altered, so that very little homology would remain between the original wild-type peptide chain and a mutant polypeptide.

A *frame-shift* mutation due to the deletion of a single base pair has actually been found at the gene locus for lysozyme of a bacteriophage. A portion of a *messenger* RNA