

Chapter 24

Evolutionary Aside 24.3—Retroposon DNA

Eukaryotic genomes are filled with DNA that does not code for proteins, and much of it is repetitive DNA. Perhaps the most unexpected finding in comparing the mouse and human genomes lies in the similarities between the repetitive DNA, mostly retrotransposons, in the two species. Retrotransposon DNA in both species shows that it has independently ended up in comparable regions of the genome.

Noncoding DNA (ncDNA) was thought not to affect the phenotype and was thus not visible to natural selection. As a result, changes in noncoding regions could evolve more rapidly, because mutations were not weeded out by selection and thus could change in gene frequency, occasionally become predominant, under the influence of genetic drift.

It is beginning to look like this ncDNA may have more of a function than was previously assumed. If the DNA had no function, differences should begin to accumulate in mouse and human as mutations occur and occasionally become fixed due to genetic drift. The fact that the “junk” regions are so conserved in mouse and human indicates that, in fact, mutations are being selected out to maintain some function, thus keeping them similar. Hence, these regions of DNA must have some function. The point is that the differences in the “junk” DNA between mouse and human are too small to have resulted from genetic drift.

The possibility that this DNA is rich in regulatory RNA sequences is being actively investigated. RNAs that are not translated can play several roles, including silencing other genes. Small RNAs can form double-stranded RNA with complementary mRNA sequences, blocking translation. They can also participate in the targeted degradation of RNAs. For details on other possible functions of ncDNA, refer to chapter 16.

In one study, researchers collected almost all of the RNA transcripts made by mouse cells taken from every tissue. Although most of the transcripts coded for mouse proteins, as many as 4280 could not be matched to any known mouse protein. This finding suggests that a large part of the transcribed genome consists of genes that do not code for proteins—that is, transcripts that function as RNA. Perhaps this function can explain why a single retrotransposon can cause heritable differences in coat color in mice.