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Most of our genes code for several different proteins. This should not be surprising since we have only about a third as many genes as we do proteins. Some genes act in consort with other genes to produce the same protein. Some genes do not code for proteins at all. Recent research has shown that at least 200-255 of our genes code for **micro RNA** (miRNA) molecules instead. These are not messenger RNA's that transport the recipe for protein synthesis. Rather, they are small RNA molecules consisting of around 20-25 base units. They perform important functions similar to enzymes in regulating chemical reactions in our cells, especially in the embryonic stage at the beginning of life. It is thought that at least 1/3 of human genes are controlled in some way by micro-RNA molecules.

About half of the sequences of base units in human DNA are "**mobile elements**." They move around inserting new copies of themselves. When these insertions go into a gene, the result is a changed protein recipe. This is a major source of new genetic variation and potentially a cause of genetic diseases such as hemophilia and muscular dystrophy in families that did not previously have these defective genes.

Whether a gene is copied for protein synthesis and what the product of that copy becomes is largely determined by signals from proteins acting as markers and switches along the DNA double helix structure. This chemical signaling system, referred to as the **epigenome**, is very likely as important as the DNA itself in determining the phenotype of individuals. It is becoming increasingly clear that epigenetic signals can be altered by the environment and that these changes can then be passed on to future generations because the epigenome proteins are inherited along with DNA in chromosomes from parents. Unlike mutations in DNA sequences, however, epigenetic changes potentially can be reversible. For example, if an alteration in an epigenetic protein causes a disease, it could be possible to alter that protein and bring about a cure. As a consequence, learning more about the human epigenome is likely to be an important area for future research.

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