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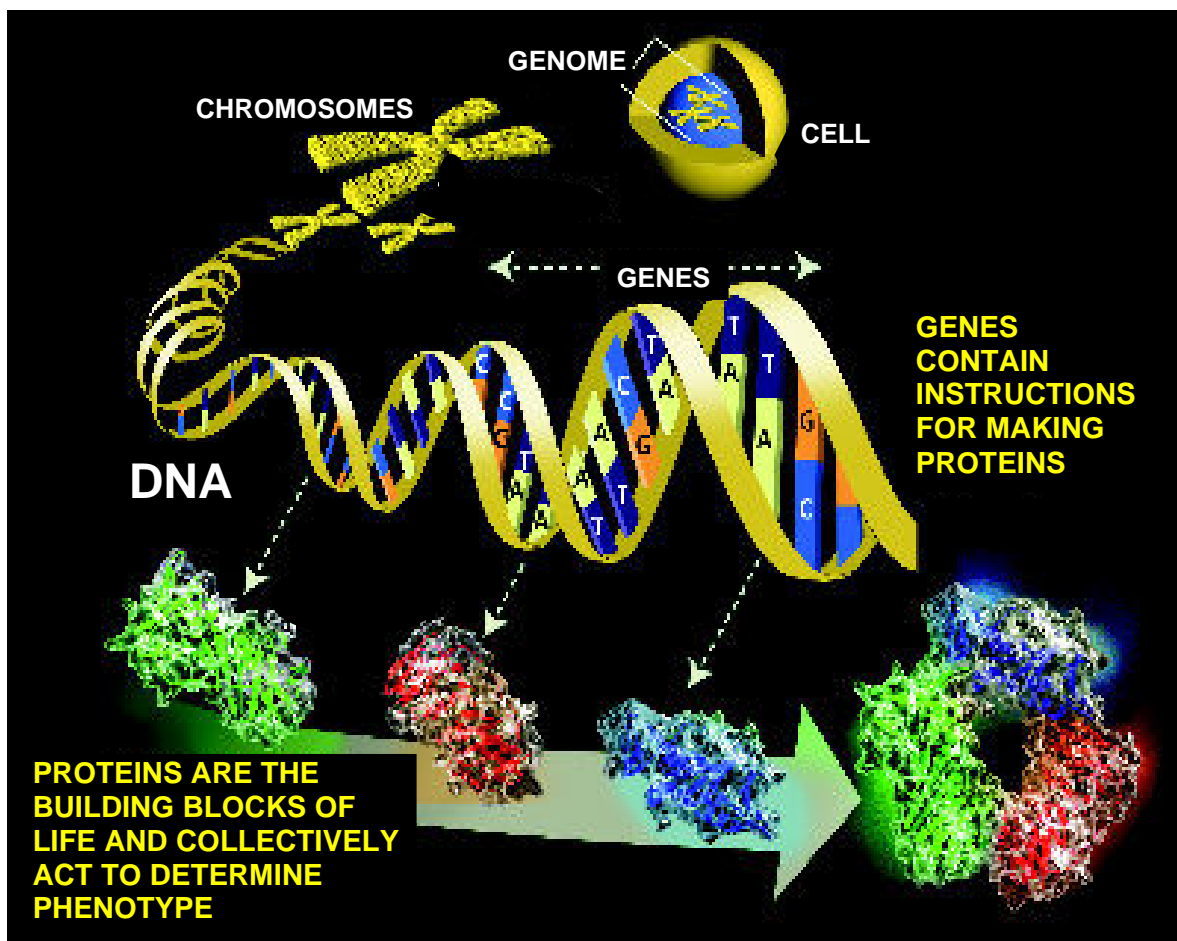
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MARKER-ASSISTED SELECTION BACKGROUND

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DNA (deoxyribonucleic acid) is a molecule that is shaped like a double helix and made up of pairs of **nucleotides**. DNA transmits genetic information. DNA is packaged into chromosomes which are located within the nucleus of all cells. Every cell in the body contains all of the chromosomes that collectively make up the **genome** of that organism. DNA codes for **amino acids** which are linked together to make **proteins**. A **gene** is a stretch of DNA that specifies all of the amino acids that make up a single protein. Proteins are the building blocks of life. There are thousands of proteins in the body (encoded by thousands of genes). The interaction and structure of proteins determines the visible characteristics or **phenotype** of an organism, while the **genotype** refers to the genetic makeup.



The sequence of nucleotides that encode a gene can differ between individuals. These differences are called **genetic variants**. As a result of these nucleotide differences, genetic variants or **alleles** may

differ in the amino acid sequence of the protein they encode, or they may regulate the production of different quantities of the encoded protein. These differences can have an effect on phenotype.

All individuals receive one copy (allele) of each gene from their mother, and one from their father. The DNA sequence of a gene inherited from each parent may be identical in which case the individual is said to be **homozygous** for that gene, or the sequence of a gene inherited from each parent may vary in which case the individual is said to be **heterozygous**. Genetic variants often differ from each other by the sequence of a single base pair. These differences are called single nucleotide polymorphisms **SNPs** (pronounced “snips”). **Genotyping** means using laboratory methods to determine the sequence of nucleotides in the DNA from an individual, usually at one particular gene or piece of a gene. SNPs are commonly the basis of genotyping tests. Genetic tests based on SNPs analyze DNA derived from an individual to determine the genetic variants that are present at one specific location (nucleotide pair) in the midst of the approximately 3 billion nucleotide pairs that make up the genome.

Historically we have not known which genes contribute to performance characteristics (**traits**), and so we have used performance records and **EPDs** (expected progeny differences) to infer the genetic merit of animals. This method has been very successful at improving certain traits. Research has shown that some genetic variants of specific genes are associated in a positive way with a given trait. It is therefore possible to genotype an animal using a DNA-based genotyping test and select individuals carrying the preferred genetic variant. **Marker-assisted selection** is the process of using the results of DNA testing to assist in the selection of individuals to become parents in the next generation. The word “assisted” implies that the selection is also influenced by other sources of information, such as animal’s observed performance and EPDs. The genotypic information provided by DNA testing should help to improve the accuracy of selection and increase the rate of genetic progress by identifying animals carrying desirable genetic variants for a given trait at an earlier age.

It is not known which specific genes contribute to an EPD – the genes are anonymous. **Complex traits**, including most of the economically relevant traits for cattle production (birth weight, weaning weight, growth, reproduction, milk production, carcass quality) are controlled by many genes, and they are also greatly affected by the environment (e.g. feed conditions). Although complex traits are influenced by a number of genes – each one of these genes is still inherited in the same way. An animal inherits one copy of each gene from its sire, and one copy of each gene from its dam. These copies may differ from each other, and these differences may have either a positive or negative effect on the trait that the gene controls or influences. When an animal has a positive EPD for a certain trait, what that is effectively saying is that based on its pedigree and phenotype, it has inherited a greater than average number of “good” genetic variants of each gene affecting that particular trait.

It is important to combine DNA results (which look at single genes) with other criteria, such as EPDs (which look at numerous genes) and the animal’s actual phenotype for the trait (if available), to ensure that selection is distributed over all the genes that contribute towards the trait of interest. Don’t ignore animals that have good EPDs for a given trait and yet are not carrying the favorable form of a gene for that trait. These animals are likely to be a source of good alleles for the many other genes that contribute towards that trait. Ideally the information from genetic tests should be integrated into a genetic evaluation system that weighs all the information about an animal. Combining information from both EPDs and genetic tests into a selection decision will be superior to selection on either EPDs or markers alone. The challenge will be to determine the weight that should be given to the marker information in this decision-making process. The magnitude of the effect of a genetic variant of a gene on the trait may vary among the different breeds, production systems and environments.