



# By the Numbers

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## Genetic lingo

*Just in the last week, the words below became used more frequently. In an age of acronyms, some household genetic definitions come in handy.*

### Basic definitions

**Genome** — all the chromosomes that make up an animal, also referred to as all the DNA characteristic of animals in a species.

**Chromosomes** — paired strands of DNA transmitted singly from parent to offspring. Cattle have 30 pairs.

**Gene** — a discrete DNA segment that codes for all the amino acids to create a single protein. Genes occur in pairs in the body cells and are located at a specific site (locus) on a specific chromosome pair.

**Allele** — alternate forms of genes; genetic variants for the nucleotides that make up the DNA. An animal randomly receives one allele of each gene from each parent.

**Nucleotides** — base pairs that make up DNA and are commonly referred to by the letters A, C, G, T (which stand for adenine, cytosine, guanine and thymine). A pairs with T and G pairs with C to develop the structure of DNA. The sequence of these base pairs determines the effect of the gene.

**SNP** — single nucleotide polymorphism. “Snips” denote or describe nucleotide differences, which can be used to characterize animal differences for economically important traits.

**Genotype** — the genetic makeup of an animal. When an animal is genotyped at a lab, the alleles can be identified specific to that animal for a particular location(s) in the genome.

**Phenotype** — visible or measured animal characteristics equal to genotype plus environment. As an example, the marbling that is measured on a set of animals is a function of each of their genotype, or genetic potential to marble, as well as the environment to which they are subjected. The marbling data collected is a phenotypic measure.

**SNP chip** — contains a large number of SNPs (e.g., 50,000, as in the 50k SNP chip) to describe the genotype of an animal, which ultimately will be used in whole genome selection.

**Whole genome selection** — use of DNA markers, such as results from a 50k SNP chip, distributed throughout the entire animal’s genome. Thousands of SNPs from regions of the genome are characterized to account for as much of the genetic variation in a trait as possible with the ultimate goal being to predict breeding values, or molecular breeding values.

**EPD**, or expected progeny difference — one-half the breeding value of an animal. EPDs can incorporate various sources of phenotypic and molecular or genomic values, in addition to pedigree data.

**Heterozygote** — a genotype where the two alleles differ at a locus (Aa).

**Homozygote** — a genotype where the two alleles at a locus are the same (AA or aa).

**FTA card** (Whatman FTA® card) — cards

used to submit a blood sample on an individual animal. Used for genomic tests and parent verification.

**AGI**, or Angus Genetics Inc. — a subsidiary of the American Angus Association that provides genetic evaluation services and conducts collaborative research and implementation of DNA technologies.

**BIF**, or Beef Improvement Federation — A federation of organizations, businesses and individuals interested or involved in performance evaluation of beef cattle. BIF seeks to build beef industry confidence in the principles and potentials of performance testing. The goals of BIF are to achieve utilization of the most efficient and effective performance evaluation methods, uniformity of procedures, development of programs, cooperation among interested entities and education of its members.

### Additional references

The descriptions above are answers to commonly asked questions we’ve received since the implementation of Angus genomic-enhanced EPDs. To read more on these topics, refer to the following references:

Animal Biotechnology. Alison Van Eenennaam. UC-Davis:  
<http://animalscience.ucdavis.edu/animalbiotech/Biotechnology/MAS/index.htm>

Beef Improvement Federation Guidelines:  
<http://beefimprovement.org/>

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**Editor’s Note:** “By the Numbers” is a column by Association performance programs staff to share insights about data collection and interpretation, the NCE, genetic selection, and relevant technology and industry issues.