

A lot has been said and countless articles about genomics have been written over the last few years. There is a greater understanding of the topic in the industry and the advantages and process of genomic selection have been highlighted, but what about the basics? How did we get to this stage? What exactly is genomics and does it only apply to animals?



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Genomics is the study of genomes, the molecular genetic component of an organism, and is therefore a specialised field of genetics, in the same way paediatrics, orthopaedics and gynaecology are specialised fields of biology. Genomic selection is only one practical use of genomics in the livestock industry. This article will provide a rough timeline of major discoveries that led to the development of genomics and consequently genomic selection.

### Mendelian inheritance

The biological relationship between parents and offspring has intrigued humans for centuries, raising questions such as:

- Why are there similar features within a family?
- Do both parents contribute equally?
- How are traits carried over from parent to offspring?

Gregor Mendel, an Austrian priest, also known as the father of modern genetics, made the first major breakthrough in how traits are inherited. He discovered what is now known as Mendelian inheritance through experiments using pea plants in the 1850s. He observed various traits such as texture of the peas, length of the plants and colour of the flowers. His work was initially largely ignored and only accepted after his death.

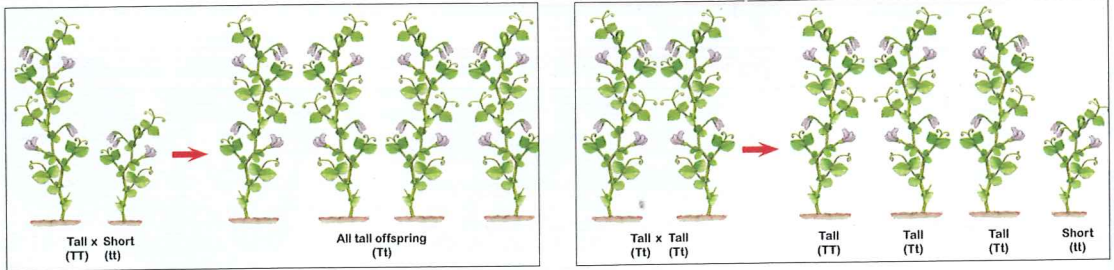
Before Mendel, it was believed that an individual receives the average effect of their parents' characteristics. For example, if you have a tall father and short mother, your height should, according to that principle, be intermediate. One of Mendel's experiments involved the height of pea plants and the results disproved this theory of an average effect. He determined that we get one copy of a gene (what he then referred to as "factors", which are located on what we now refer to as an allele) from each parent and the expression of this trait relies on these copies, which may or may not be the same.

As an example, we can say that the copy of one gene codes for tall (T) and another for short (t). Each plant has two copies, one from the mother and one from the father. He discovered that the combination TT and Tt will deliver tall plants, but only tt will deliver short plants. It is therefore said that T is dominant, and even if the copy for short is present in a plant, the presence of the T copy will lead to tall plants. The t copy is therefore said to be recessive. Pairing of two short



A stamp printed in Austria in 1984 honouring the priest and scientist Gregor Mendel, also known as the father of genetics.

**Figure 1: Mendel's experiment with height of plants.**



plants will only deliver short offspring, but two tall plants can deliver short plants if the offspring received the recessive t copy from both parents.

It is very important to note that some traits do show an "average" effect and this is because of no dominance, where both alleles are expressed equally.

### Chromosome

DNA strings are very long and must be compacted into units, which form the chromosome (which literally means coloured bodies because they became clearly visible after exposure to specific dyes). The chromosome was discovered by a German called Walther Flemming and, along with other important aspects of cell division, his discovery was published in 1878. This was before the discovery of the DNA structure and experts therefore didn't know more detail about chromosomes. Chromosomes in the cell nucleus (core) of mammals have an X shape, with the exception of the Y chromosome in males, and are found in pairs inside cells. Different species don't have the same number of chromosomes in their cells, as shown in Table 1.

### DNA structure

The structure and detail of DNA were only discovered in 1953 by James Watson and Francis Crick, who received a Nobel Prize in 1962, along with another scientist named Maurice Wilkins. However, the work that formed the basis of their study was actually done by Rosalind Franklin, who died of cancer at the age of 37, because of the radiation she was exposed to during

**Table 1: Animals and their number of chromosomes.**

ANIMAL	NUMBER OF CHROMOSOMES
Field horsetail	216
Carp	104
Red viscacha rat	102 (highest known in mammal)
Hedgehog	88
Pigeon	80
Chicken	78
Dog	78
Horse	64
Cow	60
Sheep	54
Chimpanzee	48
Human	46
Rat	42
Cat	38
Pig	38

Chromosome literally means "coloured body" because it became clearly visible after exposure to specific dyes. Chromosomes of mammals have an X shape, with the exception of the Y chromosome in males.

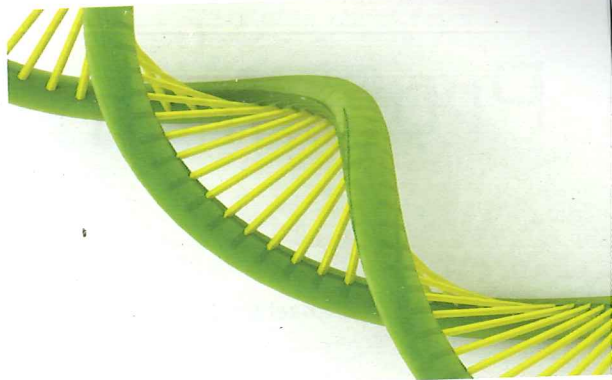


her experiments. Unfortunately, she was never nominated for a Nobel Prize as the rules forbid posthumous nominations. The famous structure of DNA is in a helix-form and DNA itself consists of a phosphate group and sugar molecule to keep the structure, and four nucleotides. The sequence of these nucleotides is responsible for all expression and variation. Subsequent discoveries were made in exactly how DNA is copied and the formation of new cells, how their expression is controlled, and other factors controlling or affecting its expression. Further research and experiments have led to breakthroughs such as genetically modified organisms and genetic testing for disorders and diseases.

### BLUP

While much progress was being made in the molecular aspect of genetics, population and quantitative genetics were also examined. Population studies examine different groups by using observational data (phenotypic – the animal's actual appearance and measurements) to determine some genetic factors and frequencies of specific genes. Quantitative genetics focuses on quantitative traits (traits that cannot be grouped into specific classes and has continuous variation, such as weight) and is used in animal breeding.

Jay Lawrence Lush was a pioneer in the development and application of population genetics to the improvement of animal breeding and wrote a very influential textbook on his work in 1937. He used statistical methods to find more accurate ways to measure quantitative traits. Charles Roy Henderson was a post-graduate student of Lush and was the one who composed the mixed animal model using BLUP to take environmental effects into account and estimate breeding values. His work has been used since 1953, but its application to big populations and complicated traits was limited by the lack of computational



power and memory available at the time. Estimated breeding values (EBVs) became a valuable and most accurate tool for genetic improvement in animals and opened the door for research and development.

### Genomic selection

Genomic selection comes down to using a combination of EBVs (as traditionally calculated) and molecular/genomic information to increase the accuracy. It has been researched intensively and successfully applied in various countries. It will surely become a standard practice in future once the costs involved decrease.

Genetics is a field of endless discoveries and mysteries yet to be solved. Great progress has been made in molecular and quantitative/population genetics. Combining various specialised fields to improve the accuracy of selection in animal breeding is essential. There are great expectations of using the approach of genomic selection and future research should be able to make this method even more effective and affordable. Regardless of all the progress made, measurements of animals and accurate pedigree records are now even more important and cannot be neglected since they are needed for interpretation of the genetic code.

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