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Popular Article

Concept of Epigenetics in Livestock and Breeding

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Introduction

C.H. Waddington in 1942 described epigenetics as the study of the mechanisms by which genotype leads to phenotype (Satheesha *et al.*, 2020). The field of epigenetics investigates how cells regulate gene function without altering the DNA sequence. In Greek, "epi-" means on or above, and "epigenetic" refers to elements other than the genetic code. Gene activation is controlled by epigenetic changes to DNA. These alterations are connected to DNA and do not alter the order in which the DNA building blocks are arranged. The epigenome, which is all of the changes that control how genes are expressed inside a cell's whole set of DNA, is referred to as the genome. By affecting the choice of which genes are turned on or off, epigenetic changes have an impact on the production of proteins in cells. This control ensures that each cell generates just the proteins required for its activity. For instance, muscle cells do not create the proteins that support bone formation. The patterns of epigenetic modification vary among individuals, between tissues within an individual, and even between individual cells within a tissue. Different epigenetic modifications have an impact on gene expression. The following are examples of epigenetic modifications: DNA methylation, histone modification and non-coding RNA.

Applications of epigenetics

1. Growth and development: Epigenetics plays a critical role in genome reprogramming and the expression of genes that affect animal growth and development. Several biological processes, including fetal growth and development, metabolism and behaviour are regulated by gene or genome imprinting.
2. Callipyge mutation in sheep: Callipyge, which means "beautiful buttocks," is a father-inherited genetic mutation that causes lambs to develop huge and muscular rumps.
3. Feeding system:

- a) Animals fed concentrate or unified diets are predicted to be methylated differently than animals fed a less intense system based on pasture feeding.
 - b) Significant changes in the expression of two histone acetyl transferases (HAT1 and HAT2), which influence milk fat synthesis, have been seen in dairy cows whose diets were supplemented with unsaturated fatty acids.
4. Nutriepigenomics
- a) The mother's nutritional state during pregnancy can cause drastic changes to the foetus through the programming of development raising the likelihood of obesity and type 2 diabetes.
 - b) In pigs, it was discovered that excessive and restricted protein intake during pregnancy affected the epigenetic marks and the expression of vital metabolic genes in the progeny.
5. Epigenetics and milk production: miRNA expression in farm animal mammary glands, adipose tissues, and liver contributes to the establishment and maintenance of subcut fat tissue, mammary lipid synthesis, and lipid metabolism.

Limitations

1. In comparison to human epigenetics, there has been very little study done in the cattle industry.
2. Inadequate acknowledgment of the role of epigenomic contributions to the establishment of economically important cattle phenotypic and disease characteristics.
3. The tools and financing for epigenetics research in the cattle industry are limited.
4. The creation of epigenome maps in the cattle industry is limited due to the limited engagement of academics on a worldwide basis.

Bibliography

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