Int.J.Curr.Microbiol.App.Sci (2020) *9*(6): 1582-1590

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 6 (2020)**
Journal homepage: http://www.ijcmas.com

Review Article https://doi.org/10.20546/ijcmas.2020.906.195

A Review on Epigenetics: Importance in Livestock Breeding and Production

G. M. Satheesha[1]*, R. Nagaraja[2], H. M. Yathish[1], R. Jayashree[3], A. M. Kotresh[4], A. Sahadev[5] and S. Naveen Kumar[1]

[1]Department of AGB, Veterinary College, Bangalore, India
[2]Veterinary College, Gadag, Karnataka, India
[3]Department of AGB, Veterinary College, Shivamogga, India
[4]Department of VPB, Veterinary College, Shivamogga, India
[5]Department VGO, Veterinary College, Bangalore, India

**Corresponding author*

Keywords

DNA, Epigenetics, Methylation, Imprinting

Article Info

Accepted:
18 May 2020
Available Online:
10 June 2020

A B S T R A C T

Epigenetics is the study of heritable changes in gene expression and other genomic functions without altering the underlying DNA sequence. It is associated with gene expression and the expression of different phenotypes mainly by a level of genetic regulation which is independent of the DNA sequence and transmitted somatically or inherited through modification of DNA regions and allows organisms on a multi-generational scale to switch between phenotypes. Gene expression due to epigenetics is mainly due to internal and external environmental effects present around an organism and these changes play a role in short-term adaptation of individuals and include reversibility. DNA methylation, chromatin remodelling and modifications through non coding RNA (ncRNA) are the main mechanisms involved in epigenetics. It plays a role in animal breeding as it helps in finding part of the missing causality and missing heritability of complex traits and diseases. Epigenetic factors respond answers to external or internal environmental cues like nutrition, pathogens, and climate, and have the power to vary gene expression resulting in emergence of specific phenotypes and it has a potential benefits in overall animal growth, production and reproduction.

Introduction

Until the middle of 19th century, it is believed that all the activities a organism carry out are controlled by the genetic information which is present in 25,000 to 35,000 genes in the entire genome. However, in reality these genes amounts to only 5% and remaining 95% is controlled by the additional instruction which are present in the 'epigenome' in the form of epigenetic information which instruct how, when and where the information present in the genome should be used in the form of series of switches called has Epigenetic marks. The rate of phenotypic variations and genetic mutations are considerably different,

which can't be explained merely based on genetics as the primary molecular mechanism. Additional mechanisms such as epigenetics can help explaining this phenomenon. Many traits do not follow normal Mendelian inheritance and are difficult to be explained by the classical genetics.

Epigenetics is the study of heritable changes in gene expression and other genomic functions without altering the underlying DNA sequence, "epi" means "over, above, outer" on top of genetics' (Richards, 2006). Here changes in gene expression are mitotically and/or meiotically heritable and do not involve a change in the DNA sequence. It can be transmitted somatically or inherited through modification of DNA regions and allows organisms to switch between phenotypes and are influenced by environmental factors and can be transferred to the progeny in cell lines and complex organisms, including livestock. It plays a role in short term adaptation of individuals and includes reversibility.

History

Lot of advances happened in the mid of 19th century with respect to epigenteics, but although the conceptual origins date back to Aristotle (384-322 BC), where in his theory of Epigenesis he proposes that the development of individual is from organic form from the unformed, later Jean-Baptist Lamark (1744-1829) proposes soft inheritance or inheritance of acquired characters describing that an organism can pass on the characters to its offspring. Charles Darwin in 1859 in his 'theory of evolution by natural selection' he rejected the Lamark's theory, later Gregor Johann Mendel proposes Laws of inheritance. In 1942 C.H. Waddington is the one who defined epigenetics as the study of the processes by which genotype gives rise to phenotype. First evidence for transgenerational effects of epigenetic modifications were reported in pregnant Dutch women suffering from big local famine in 1944 and gave birth to low-weight babies. These women again gave birth to low weight babies, even though not suffering from famine. This shows that epigenetic imprint during pregnancy can be inherited and there is a transgenerational relationship between food and genes (Bastiaan *et al.,* 2008, Heijman *et al.,* 2008).

Phenotypic expression of any character is the combination of genome and epigenome. Epigentic variation contributes to phenotypic variation knowing it could improve the prediction of the phenotype. Epigenetic mechanism links environment and with genome i.e. it is an interaction between environment and genotype. Epigenome is the collection of epigenetic marks, mainly DNA methylation, histone tail modifications, chromatin remodeling and non-coding RNA species that exist in a cell (Rakyan *et al.,* 2011). The genome of a cell is fairly stable, the epigenome is highly dynamic throughout life and is governed by a complex interplay of genetic and environmental factor. The epigenome refers to the complete description of these potentially heritable changes across the genome. (Bernstein *et al.,* 2007). Epigenetics is ubiquitous found in bacteria, fungi, plants, animals and it is a key to our differences and control cell specialisation and differentiation (Rakyan *et al.,* 2011). It is mechanistic link between nature and nurture because epigenetic changes occur in response to environmental signals, including nutrients, stress and hormones. Each individual has only one genome but multiple epigenomes, which differ by cell and tissue types. They explain why people are different in temperament, interests, behaviour and taste. Activation/deactivation of different genes and combinations of genes make each person unique.

Food, climate and lifestyle reprogram human/animal health at the epigenetic level, causing chemical modifications that turn genes on or off. Even though the epigenetic profile in highly conserved and maintained from the evolution, our livestock management has a major influence on it. Most of the epigenetic alterations are non-programmed. It can produce polymorphism depending upon the requirement, whereas, mutations are programmed where a new mutation is helpful than it will be activated otherwise it will be eliminated.

In epigenetic mechanisms the regulation of gene expression happens at the transcriptional and post transcriptional levels and therefore contributes to different phenotypes. There are lot of studies conducted on the regulatory role of epigenetic factors in livestock phenotypes like diseases (Karrow *et al.,* 2011; Luo *et al.*, 2011), reproduction (Urrego *et al.,* 2014) and milk production (Singh *et al.,* 2010).

Major mechanisms of epigenetic expression

Multiple level of packing consists of histones, linker DNA present in the cell to fit the DNA in to the cell nucleus. In epigenetic processes chromatin and the nucleosome are the key players. Change in the expression pattern of a particular gene under the influence of epigenetic forces is called as an epigenetic alteration which is induced by epigenetic markers like DNA methylation, histone modification and RNA interference are very important.

Methylation of DNA

It is the covalent addition of the methyl group to a cytosine nucleotide in palindromic DNA sequence. Methyl group is added to the C or G base of the non-coding DNA sequences; hence it is not recognized by an enzyme. Methylation causes transcriptionally inactive DNA which in turn altered phenotype. The function of the gene or gene expression is altered by the addition of methyl group (CH_3) by enzyme DNA methyltransferase (DNMTs) (James, 2011). DNA methylation in the promoter region of genes is associated with transcriptional repression, while their hypomethylation is linked with transcriptional activation leading to increased expression of genes. Different tissue/cell types have a unique DNA methylation profile and it is susceptible to nutritional and environmental influences which in turn changes the gene expression profiles, diverse phenotypes in the form of increased or decreased productivity and disease risk (Choi and Friso, 2010; Jang and Serra, 2014).

DNA methylation is essential for normal growth and development of organisms (Pathogen invading) and its patterns are specific to each cell and tissue type and can be used as a means of identification. Altered DNA methylation patterns during childhood may lead to multifactorial disorders such as cancer, diabetes, heart disease and respiratory illness and differential expression of the genes in various organs or different environments. The epigenetic components could help to explain the differences in level of production between members of same breed across the different environmental conditions.

Histone modification

Modification in histone arrangement hinders DNA packaging, where amino terminal tails of histones are subjected to chemical modifications where in it alters gene expression by altering chromatin structure. Modification of histone-DNA packaging activates or inactivates transcription process. Processes of apoptosis, DNA replication, DNA repair, cell cycle and transcription are highly regulated by acetylation of histone, (Bernstein *et al., 2007*).

Chromatid remodelling

It is the dynamic modification of chromatin architecture to allow access of condensed genomic DNA to the regulatory transcription machinery proteins, and thereby control gene expression. This is mainly carried out by covalent histone modifications by specific enzymes like histone acetyltransferases (HATs), deacetylases, methyltransferases, kinases, and by ATP-dependent chromatin remodeling complexes which move, eject or restructure nucleosomes (Teif *et al.,* 2009). Chromatin modeling and remodeling process are highly conserved and tightly regulated, error in chromatin modeling results in alteration of gene expression. Besides actively regulating gene expression, dynamic remodeling of chromatin imparts an epigenetic regulatory role in several key biological processes, egg cell's DNA replication and repair; apoptosis; chromosome segregation as well as development and pluripotency.

RNA Interference (RNAi)

It's also called has post transcription gene silencing (PTGS) because RNA molecules inhibit gene expression or translation, by neutralizing targeted mRNA molecules.MicroRNA (miRNA) and small interfering RNA (siRNA) are the two types of small ribonucleic acid (RNA) molecules which are important in RNA interference.

These are the valuable biomarkers or tool for diagnosis of a number of disease conditions including CVD, cancer, neurodegenerative disorders, and infectious diseases (Li *et al.,* 2009; Tüfekci *et al.,* 2014). miRNAs are involved in many processes in farm animals (Wang *et al.,* 2013a) including roles in disease (Karrow *et al.,* 2011; Luo *et al.,* 2011), adipogenesis (Romao *et al.,* 2014), and milk production (Singh *et al.,* 2010).

Livestock breeding and epigenetics

Role of epigenetic in growth and development

Epigenetics plays a very important role in genome reprogramming and in the expression of genes that control growth and development in livestock. Among them gene or genome imprinting, regulate a wide range of biological processes including fetal growth and development, metabolism, and behavior (Jiang *et al.,* 2007). Imprinting plays physiological roles in metabolism and body composition throughout life and as such contributes to the typical variation and architecture of complex traits (Smith *et al.,* 2006). The genome contains two copies of every gene and for a small number of genes, only the copy from the mother gets switched on; for others, only the copy from the father is turned on, this pattern is called as imprinting. The epigenome distinguishes between the two copies of an imprinted gene and determines which should be switched on. Mechanism where one allele's expression differs depending on which parent it was inherited from. This implies that imprinted genes are dissimilarly altered in the egg or sperm, or perhaps seen as different in the early zygote (Monk, 1995).Typical gene pair is silenced by an epigenetic process such as methylation or acetylation. Imprinting is established during development of germ cells into sperm or egg (Reik and Walter, 2001). An imprinted gene functions as a haploid which makes it more vulnerable to negative mutational effects (Jirtle and Weidman, 2007) consequently, a single mutation can change the epigenome.

Economically important traits such as milk yield and milk quality, back fat thickness, body weight and growth seem to be associated with imprinted and X-linked quantitative trait loci (QTL). Maternally derived genes are growth-limiting and

paternally derived genes are growth enhancing. The mark only lasts for one generation because each generation it is set by whether it is transmitted through a sperm or an egg. (Jirtle and Weidman, 2007). In beef cattle, ten carcass quality traits were found to be influenced by imprinting, contributing between 8 and 25% of the total additive genetic variance. The maternal contribution to the imprinting variance was larger than the paternal. It affects traits such as milk yield, growth and carcass traits, fat and meat deposition and fetal development. The implementation of breeding programs will require changes in the current standard breeding programs as imprinting should be taken into account (Neugebauer, *et al., 2010).*

Callipyge mutation in sheep

Genetic mutation that causes lambs to develop large and muscular rumps and trait is known as callipyge means 'beautiful buttocks'. The trait first appeared in a sheep born in Oklahoma in 1983 in solid gold sheep, where in they have enlarged muscles resulting from hypertrophy of fast-twitch muscle fibers, accompanied by a substantial decrease in total body fat and meat is not tender. The trait *only* occurs in lambs that inherit the callipyge mutation from the father, the gene from the mother is normal. Lambs born with two copies of the mutation appear normal where mutation occurs in *CLPG1 gene* and the effect is known as 'polar over dominance which shows that imprinted genes are turned on during specific periods of development (Edward, 2002).

Epigenetics and breeding programs

If the Epigenetic variance due to imprinted genes was sufficiently large, selection on male and female lines could be done separately. Mating programs could be designed considering the imprinting status of the progenitors to accommodate the most favourable epigenetic status to complement the breeding value. Animals with concentrate and unifeed diet systems are expected to be differently methylated than animals in a less intensive system based on a pasture feeding systems. It will be important to detect what practices are associated to favourable methylation patterns that affect disease resistance and other economically important traits (Goddard and Whitelaw, 2014).

Nutriepigenomics

Maternal nutritional imbalance during pregnancy predisposes to disease susceptibility later in life (DelCurto *et al.,* 2013). Nutritional status of mothers during gestation can induce radical changes to the fetus through the developmental programming and increasing the risk of obesity and type 2 diabetes (Barker *et al.,* 2002).

In food animal species, suboptimal condition in utero during gestation leads to compromised health, slower growth rate, increased fat deposition, reduced muscle mass, and reduced meat quality in progeny (Wu *et al.,* 2006). Severe under nutrition or heavy feeding in early pregnancy can lead to a decline in embryo survival (Bellows *et al.,* 1963) and it has been reported that late gestation, maternal nutrition can impact postnatal body composition, insulin sensitivity, and growth rate in ruminants (Radunz,2012). Some nutrients, bioactive food components and dietary interventions including high/low fat diets, protein/caloric restrictions, bioactive micronutrients, and plant derivatives have the ability to modify epigenetic marks and alter cellular signalling in the offspring and during growth and development (García-Segura *et al.,* 2013). Feeding a high- concentrate corn straw diet to dairy cows led to alteration of the

methylation state of specific genes involved in fat and protein synthesis in the mammary tissues of dairy cows (Guozhong *et al.,* 2014). Supplementing the diets of dairy cows with rich in unsaturated fatty acids showed significant alterations in the expression of two histone acetyl transferases (HAT1 and KAT2) which effects milk fat synthesis. In pigs, the effect of dietary protein restriction and excess during pregnancy was shown to alter epigenetic marks and the expression of key metabolic genes in offspring (Cong *et al.,* 2012).

Epigenetics and milk production

Producing milk of desired nutritional composition is the need of the hour. Some of the strategies employed to tackle this include alteration in the nutrition and genetics of the animal. Along with genetic markers for these traits, regulatory roles of epigenetic marks on lipid metabolism and adipogenesis, and milk production have been demonstrated (Eveline *et al., 2017,* Singh *et al.,* 2010,). miRNA expression in the mammary gland, adipose tissues, and liver of farm animals leads to development and maintenance of subcutaneous fat tissue, mammary lipid synthesis, and lipid metabolism. miRNA expression differences have been reported between lactating and nonlactating mammary glands , between lactation stages, between peak lactation and dry period, and between early and late lactation in cattle and goats. (Eveline *et al.,* 2017). 59 distinct miRNAs are identified in cattle and initial involvement of these molecules in mammary gland functions (Zhiliang *et al.,* 2007).

Epigenetics and milking interval

Available data suggest that heifers fed more milk develop more mammary epithelial cells that become milk-secreting cells with when first lactation begins. It has been proved that cows milked four times daily during the first 3 weeks of lactation and then two times daily thereafter produces considerably more milk than cows milked two times from freshening. The four times milking early in lactation apparently stimulates development of more milk-secreting cells and these then remain throughout lactation, even when milking frequency drops to two times daily(Eveline *et al., 2017).*

Epigenetics and fertility

Negative epigenetic effects occur when eggs (oocytes) are developing within the ovary when a cow is under stressful conditions (Sartori *et al.,* 2010). microRNAs cab be helpful as noninvasive biomarkers in the diagnosis of fertility where miRNAs have been found to be secreted into the extracellular environment and in serum, urine, and saliva during stress full conditions (Chen *et al., 2*008).

Epigenetics and health

Experimental challenge of the bovine mammary gland with pathogenic *Escherichia coli* bacteria resulted in remethylation of a hypomethylated region of the upper promoter of alpha S1 casein gene and consequently shutdown of alpha S1 casein synthesis (Vanselow *et al.,* 2006).In the peripheral blood cells of clinical mastitic Chinese Holstein dairy cows, aberrant promoter methylation of CD4 gene has been demonstrated, suggesting that the presence of bacteria changed the DNA methylation status of CD4 promoter in cows with clinical mastitis (Wang *et al.,* 2013). Examining DNA methylation patterns in chicken Marek's disease (MD) resistant line 63 and MD-susceptible line 72 at 21 days after Marek's disease virus type 1 infection. A number of studies have revealed that miRNAs are differentially expressed in a wide range of

tissues and immune-related cells when pathogenic agents are present (Eveline *et al.*, 2017).

Epigenetics and gene editing in livestock

Some of genome editing technologies like ZFN, TALEN and CRISPR/Cas9 have been used to achieve efficient genome editing. Epigenetic editing at loci of interest represents an innovative method that might selectively and heritably alter gene expression. For animal breeding purpose, these technologies can be used to introduce or fix favorable alleles and epigenetic marks for increased productivity. The promotion of alleles for polygenic traits by genome editing could double genetic gains when compared to conventional genomic selection (Vojta *et al.*, 2016).

Techniques to study epigenetic alterations

DNA methylation pattern can be studied by Bisulfite sequencing, Methylation Sensitive Amplification Polymorphism (MSAP), Methylation specific restriction endonucleases, e.g., HspII/MSPI, Global Interrogation of DNA Methylation using Microarrays, Second generation sequencing,FISH. Histone modification can be studied by Chromatin immuno precipitation (CHIP) and RNAi by Deep sequencing.

Limitations of epigenetics in livestock breeding

Very little amount of work has been done in livestock sector when compared to human epigenetics. Insufficient recognition of the importance of epigenomic contributions to the emergence of livestock phenotypes of economic importance and disease traits. Tools and funding for the epigenetics work in livestock sector are very meager. Epigenome maps development in livestock sector is very less, as involvements of researchers on a global scale is very little.

Epigenetic marks determine the transcriptional potential of the cell. They represent an additional level of information to explain the phenotype. They link environment and genome and represent the molecular equivalent of genotype × environmental interactions. Helps in refinement of estimates in selective breeding. Epigenetic studies will provide biomarker for management and/or breeding. So that epigenetics marks can be identified for both production and reproduction traits.

References

Bellows, R.A., Pope, A.L., Chapman, A.B. and Casida, L.E.,1963. Effect of level and sequence of feeding and breed on ovulation rate, embryo survival and fetal growth in the mature Ewe. J Anim Sc., 22(1):101–8.

Bernstein B. E., Meissner A., Lander E. S., 2007. The mammalian epigenome. Cell, 128: 669–681.

Chen, X., Ba, Y., Ma, L., Cai, X., Yin, Y. AND Wang, K., 2008. Characterization of microRNAs in serum: a novel class of biomarkers for diagnosis of cancer and other diseases. Cell Res., 18(10): 997–1006.

Choi S.W., Friso S. 2010. Epigenetic: a new bridge between nutrition and health. Adv. Nutr. 1 8–16.

Cong, R., Jia, Y., Li, R., Ni, Y., Yang, X., Sun, Q., 2012. Maternal low-protein diet causes epigenetic deregulation of HMGCR and CYP7α1 in the liver of weaning piglets. J. Nutr. Biochem. 23, 1647–1654.

Delcurto, H., Wu, G., and Satterfield, M. C., 2013. Nutrition and reproduction: links to epigenetics and metabolic syndrome

in off spring. Curr. Opin. Clin. Nutr. Metab. Care., 16:385–391.

Edward R., 2002. Genetic mutation explains 'beautiful buttocks' in sheep. Winstead Genome News Network.

Eveline M. Ibeagha-Awemu, Hasan Khatib, 2007. Epigenetics of Livestock Breeding, Handbook of Epigenetics.441-463,

García-Segura, L., Pérez-andrade, M., and Miranda-Ríos, J., 2013. The emerging role of MicroRNAs in the regulation of gene expression by nutrients. J. Nutrigenet. Nutrigenomics., 6:16–31.

Goddard M. E., Whitelaw E. 2014. The use of epigenetic phenomena for the improvement of sheep and cattle. *Front. Genet.* 5:247.

Guozhong Dong, Min Qiu, Changjin Ao, Jun Zhou, Khas-Erdene, Xi Wang, Zhu Zhang, and YouYang, 2014. Feeding a High-Concentrate Corn Straw Diet Induced Epigenetic Alterations in the Mammary Tissue of Dairy Cows, PLoS One, 9(9).

Heijmans BT, Tobi EW, Stein AD, Putter H, Blauw GJ, Susser ES, Slagboom PE, Lumey LH 2008. Persistent epigenetic differences associated with prenatal exposure to famine in humans. Proc Natl Acad Sci 105: 17046–17049

Jammes H., Junien C., Chavatte Palmer P. 2010. Epigenetic control of development and expression of quantitative traits. Reprod. Fertil. Dev. 23 64–74.

Jang H., Serra C., 2014. Nutrition, epigenetics and diseases. Clin. Nutr. Res. 3:1–8.

Jiang, L., Jobst, P., Lai, L., Samuel, M., Ayares, D., Prather, R. S., 2007. Expression levels of growth-regulating imprinted genes in cloned piglets. Cloning Stem Cells., 9:97–106.

Jirtle, R. L., and Weidman, J. R., 2007. Imprinted and more equal. American Scientist, 95:143–149.

Karrow N., Sharma B., Fisher R., Mallard B., 2011. Epigenetics and animal health, in Comprehensive Biotechnology,381–394.

Li M., Marin-Muller C., Bharadwaj U., Chow K. H., Yao Q., Chen C., 2009. MicroRNAs: control and loss of control in human physiology and disease. World J. Surg. 33:667–684.

Luo J., Yu Y., Song J., 2011. Epigenetics and animal health, Livestock Epigenetics 131–145.

Monk, M., 1995. Epigenetic Programming of Differential Gene Expression in Development and Evolution Dev Genet., 17(3), 188-97.

Neugebauer N, Räder I, Schild HJ, Zimmer D and Reinsch N. 2010. b. Evidence for parent-of-origin effects on genetic variability of beef traits. Journal of Animal Science 88, 523–532.

Radunz, A.E., Fluharty, F.L., Relling, A.E., Felix, T.L., Shoup, L.M. and Zerby, H.N., 2012. Prepartum dietary energy source fed to beef cows: II. Effects on progeny postnatal growth, glucose tolerance, and carcass composition. J Anim Sci., 90(13): 4962–74.

Rakyan, V. K., Down, T. A., Balding, D. J., & Beck, S., 2011. Epigenome-wide association studies for common human diseases. Nature Reviews Genetics, 12(8), 529–541.

Reik W, Walter J.,2001. Genomic imprinting: parental influence on the genome. Nat Rev Genet 2: 21-32

Richards, E., 2006. Inherited epigenetic variation-revisiting soft inheritance. Nat. Rev. Genet.,7: 395–401

Romao J. M., Jin W., He M., Mcallister T., Guan L. L. 2012. Altered microRNA expression in bovine subcutaneous and visceral adipose tissues from cattle under different diet. *PLoS ONE* 7:e40605 10.1371/journal.pone.0040605

Sartori, R., Bastos, MR. and Wiltbank, MC., 2010. Factors affecting fertilisation and early embryo quality in single- and superovulated dairy cattle. Reprod Fertility Dev., 22(1):151–8.

Singh K., Erdman R. A., Swanson K. M., Molenaar A. J., Maqbool N. J., Wheeler T. T., 2010. Epigenetic regulation of milk production in dairy cows. J. Mammary Gland Biol. Neoplasia 15:101–112.

Smith F. M., Garfield A. S., Ward A., 2006. Regulation of growth and metabolism by imprinted genes, Cytogenet. Genome Res. 113:279–291.

Teif VB, Rippe K., 2009. Predicting nucleosome positions on the DNA: combining intrinsic sequence preferences and remodeler activities". Nucleic Acids Research. 37 (17):5641-55.

Tüfekci K., Meuwissen R., Genç Ş., 2014. The role of microRNAs in biological processes, in miRNomics: MicroRNA Biology and Computational Analysis, 15–31.

Urrego, R., Rodriguez-Osorio, N., and Niemann, H., 2014. Epigenetic disorders and altered gene expression after use of assisted reproductive technologies in domestic cattle. Epigenetics, 9, 803–815.

Vanselow J, Yang W, Herrmann J, Zerbe H, Schuberth HJ, Petzl W,2006. DNA-remethylation around a STAT5-binding enhancer in the αS1-casein promoter is associated with abrupt shutdown of a αS1-casein synthesis during acute mastitis. J Mol Endocrinol 37(3):463–77.

Vojta A, Dobrinic P, Tadic V, Bockor L, Korac P, Julg B,2016. Repurposing the CRISPR-Cas9 system for targeted DNA methylation. Nucleic Acids Res.,44(12):5615–28.

Wang X., Gu Z., Jiang H. 2013. MicroRNAs in farm animals. *Animal* 7 1567–1575.

Wu, G., Bazer, F.W., Wallace, J.M. and Spencer, T.E., 2006. Board-invited review: intrauterine growth retardation: implications for the animal sciences. J Anim Sci., 84(9):2316–37

Zhiliang, G., Satyanaryana, E., and Honglin, J., 2007. Identification and characterization of microRNAs from the bovine adipose tissue and mammary gland. FEBS Lett., 581: 981–988.

How to cite this article:

Satheesha. G. M., R. Nagaraja, H. M. Yathish, R. Jayashree, A. M. Kotresh, A. Sahadev and Naveen Kumar. S. 2020. A Review Article on Epigenetics: Importance in Livestock Breeding and Production. *Int.J.Curr.Microbiol.App.Sci.* 9(06): 1582-1590.
doi: https://doi.org/10.20546/ijcmas.2020.906.195