

# Overview of long non coding RNA and its application in animal breeding

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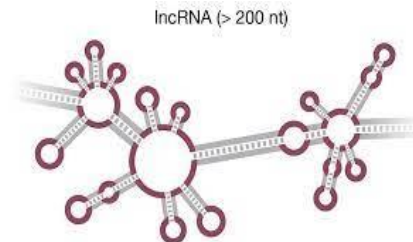
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## Introduction

Non-coding RNAs (ncRNAs) are RNA molecules that do not code for proteins. Among the most characterised ncRNAs are long non-coding RNAs (lncRNAs) and microRNAs (miRNAs). lncRNAs are defined as non-coding transcripts longer than 200 nucleotides (**Hu et al., 2022**). The first ncRNAs were mouse H19 and human X chromosome-specific transcripts identified by Brennan *et al.* in 1990 and Brockdorff and Brown in 1992. lncRNA-encoding genes consist of own promoters and transcription factors (TFs), can be spliced, capped and polyadenylated as mRNA molecules (except cirRNA), lncRNAs do not undergo the standard mRNA processing, can regulate the expression of nearby and distant coding genes. lncRNAs have limited coding potential as they lack Open reading frames (or short-ORF) and 3'-untranslated regions (**Mattick et al., 2023**). Based on their genomic position, lncRNAs are classified as intergenic: localized between two protein coding genes and transcribed from intergenic regions, intronic: processed from introns of protein coding genes, antisense: transcribed from the complementary strand of a protein coding gene (may overlap with any region of mRNA), bidirectional: transcribed from both strands, enhancer: transcribed from enhancer regions (**Yousefi et al., 2020**). lncRNAs have wider application. Some of the applications are discussed below:

## Application

1. **Genome imprinting:** lncRNAs are involved in some imprinting processes. Example: Insulin-like growth factor-2 (Igf2)



and insulin-like growth factor-2 receptor (Igf2r) are maternally and paternally imprinted genes, respectively, which regulate fetal growth (**Dhanoo et al., 2018**).

2. **Milk synthesis:** lncRNAs plays an important role in the regulation of the lactation cycle and development of the mammary gland in cows. Example: lncRNA XLOC\_002110 is found correlated with SLC2A8 gene which is involved in active transport of glucose (**Mumtaz et al., 2022**).
3. **Feed efficiency:** lncRNAs regulates feed efficiency in cattle. Example: TCONS\_00119451 (lncRNA) in muscle) overlapped 07 Quantitative Trait Loci (QTL) for RFI and 11 QTL for fat deposition related traits (**Alexandre et al., 2020**).
4. **Litter size:** lncRNAs affect ovarian functions by regulating their target mRNAs. Example:

SRD5A2, LOC102191297 and LOC102171967 are differentially expressed (DE) mRNAs that are known to be involved in steroid hormone biosynthesis (**Lian et al., 2020**).

5. **Disease:** lncRNAs play an important role in regulating the immune response. Example: CCL8, PIK3R5 are DE-lncRNAs involved in the Chemokine signalling pathway (**Gupta et al., 2019**).

### Conclusion

Numerous biological processes, including cell differentiation, cell signaling, transcriptional control, and epigenetics, are significantly influenced by long noncoding RNAs (lncRNAs). lncRNA expression is critical for more precise utilization of genetic diversity in phenotypic traits in livestock. Significant relationships between lncRNAs and several quantitative trait loci, including feed efficiency, egg laying, litter size, estrus detection, and spermatogenesis, have been found. The identification of lncRNAs related with various diseases in livestock species can help to choose disease-resistant animals.

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