



# Latest Progress in Research on lncRNAs in Bovine Transcriptomes: A Review

Zhiqiang Han<sup>1</sup>, Hongliang Zhang<sup>1</sup>, Haiyan Zhang<sup>1</sup>,  
Meimei Zhu<sup>1</sup>, Wenjie Chen<sup>2</sup>, Qun Wei<sup>3</sup>, Hongxi Xu<sup>1,2</sup>

10.18805/IJAR.BF-1831

## ABSTRACT

With the increasing development of deep sequencing techniques and bioinformatics tools, a large number of functional lncRNAs have been discovered. In this paper, a search of the NCBI PubMed and NCKI databases was conducted to select the functional genes that regulate muscle, fat, reproduction and immunity from the research literature of the past 5 years. The paper provides a comprehensive review of the latest research progress on the regulatory effects of lncRNAs in the transcriptomes of muscle, fat, reproduction and disease resistance, which are the key traits for improving the economic performance of the dairy and beef cattle industries.

**Key words:** Bovine, Genome, lncRNA, Transcriptome.

Long non-coding RNA (lncRNA) is a class of non-coding RNAs longer than 200 nucleotides that are produced in large quantities during the transcription of protein-coding genes. Although lncRNAs do not have protein-coding capacity, they can influence gene expression through transcriptional regulation, post-transcriptional regulation and epigenetic modifications, thereby affecting trait phenotype (Yang *et al.*, 2021). With the development of RNA-Seq technology for transcriptome sequencing, researchers can analyse and study the structure and function of RNA at a deeper level, revealing the relationship between differentially expressed genes and organisms (Wang *et al.*, 2017). In modern livestock production, research into the quality and yield of meat, milk and other by-products and into enhancing the regulatory role of immune factors, cytokines and other disease-fighting factors is particularly important for improving animal health, reproductive efficiency, economic benefits, animal welfare and public health (Chang *et al.*, 2021).

## lncRNAs in bovine muscle and fat transcriptome

Beef is mainly composed of muscle and fat and it is important to explore the key genes that regulate muscle and fat production in cattle to improve beef quality traits. lncRNAs regulate muscle and adipocyte differentiation in bovine their genesis, growth and development.

## lncRNAs in the bovine muscle transcriptome

Beef muscle quality was assessed by the marbling of the longest dorsal muscle cross-section at the 12<sup>th</sup> to 13<sup>th</sup> sternal ribs in the same part of the carcass after cooling and acid removal and the physiological maturity of the cattle as the main assessment index. The transcriptome expression profiles of the longest dorsal muscle of yak crossbred cattle and yak showed 791 lncRNAs were differentially expressed and the lncRNA-targeted genes were significantly enriched in the HIF-1 pathway and the PI3K-Akt pathway, pathways related to myoblast differentiation and development (Huang *et al.*, 2021). A novel

<sup>1</sup>Heilongjiang Academy of Agricultural Sciences, Harbin 150038, Heilongjiang, China.

<sup>2</sup>Wenzhou Vocational College of Science and Technology, Wenzhou 325006, Zhejiang, China.

<sup>3</sup>Keqiao District Animal Husbandry and Veterinary Medicine Institute, Shaoxing 312030, Zhejiang, China.

**Corresponding Author:** Hongxi Xu, Heilongjiang Academy of Agricultural Sciences, Harbin 150038, Heilongjiang, China.

Email: hongxixu@yeah.net

**How to cite this article:** Han, Z., Zhang, H., Zhang, H., Zhu, M., Chen, W., Wei, Q. and Xu, H. (2026). Latest Progress in Research on lncRNAs in Bovine Transcriptomes: A Review. *Indian Journal of Animal Research*. **60(5)**: 759-765. doi: 10.18805/IJAR.BF-1831

**Submitted:** 17-06-2024 **Accepted:** 08-11-2024 **Online:** 17-12-2024

lncRNA in the nucleus is highly expressed in myoblasts lnc23 is differentially expressed at different stages of embryonic development and myoblast differentiation. lnc23 is involved in key processes of myoblast differentiation, such as cell fusion and lnc23 may inhibit myoblast differentiation by decreasing cell-to-cell and cell fusion. lnc23 is a binding protein of PFN1, which is a binding protein of lnc23. lnc23 promotes myoblast differentiation by binding to PFN1 to reduce the inhibitory effect of PFN1 on RhoA and Rac1 and promoting the expression of RhoA and Rac1 proteins (Chen *et al.*, 2021). In the genome-wide identification and analysis of lncRNAs in the dorsal longest muscle tissues of Kazakh and Xinjiang brown cattle, 182 lncRNA transcripts were found to be differentially expressed between Kazakh and Xinjiang brown cattle, of which 102 were up-regulated and 80 were down-regulated and the differentially expressed lncRNAs were associated with mitogen-activated protein kinase, Ras and phosphatidylinositol 3-kinase (PI3K)/ Akt signalling pathway (Yan *et al.*, 2021). (Yan *et al.*, 2021) identified a novel lncPRRX1 highly expressed in muscle tissues. lncPRRX1 promotes the

proliferation of bovine myoblasts by regulating the miRNA-137/CDC42 axis (Zhang *et al.*, 2022); (Ma *et al.*, 2023) screened for expression of enriched lncRNAs in bovine muscle tissues. Real-time fluorescence quantitative PCR identified 33 differentially expressed lncRNAs in different bovine tissues and screened one lncRNA13 that had an impact on bovine muscle development, named it lncRNA 5.8S rRNA-OT1 and cloned and constructed its overexpression vector pcDNA3.1-lncRNA 5.8S rRNA-OT1 (Ma *et al.*, 2023). A novel lncRNA insulin-like growth factor 2 antisense transcript promotes proliferation and differentiation of bovine myoblasts (Song *et al.*, 2020). The mRNA and lncRNA expression profiling at the stage of cell proliferation and differentiation in buffalo myoblasts revealed a total of 4820 differentially expressed genes, 12,227 mRNAs and 1352 lncRNAs, which were enriched in important biological processes such as the cell cycle, the p53 pathway, RNA transporter and calcium signalling pathway (Zhang *et al.*, 2021).

### lncRNAs in the bovine fat transcriptome

Bovine intramuscular fat deposition is a key indicator of the grade of marbling in the cross-section of the longest dorsal muscle. Intramuscular preadipocyte differentiation plays a key role in intramuscular fat deposition. The whole transcriptome of Qinchuan cattle intramuscular adipocytes was sequenced and analysed for mRNAs, circRNAs, lncRNAs and miRNAs at different different stages of differentiation and 31 potential key genes were identified during intramuscular preadipocyte differentiation, which included genes as shown in Table 1 and provided novel molecular breeding of beef cattle with new These genes are included in Table 1, providing new candidate marker genes for molecular breeding of beef cattle (Yang *et al.*, 2022). Among the lncRNAs associated with intramuscular preadipocyte differentiation and lipid deposition in yak, the lncFAM200B gene exists, which regulates the process of preadipocyte differentiation in lncFAM200B yaks (Ran *et al.*, 2022). A 12 bp insertion/deletion (indel) variant (rs72034 3880) site was detected in the promoter region of the adipose tissue-specific lncRNA gene associated with carcass traits in cattle (Zhang *et al.*, 2022). High-end marbled beef from Nellore cattle lncRNA 3191.1 partially overlaps with exons of the ITGAL gene and lncRNA 512.1, lncRNA 3721.1 and lncRNA 41.4 partially overlap with introns of the KRAS and MASP1 genes. KRAS and ITGAL genes are enriched in the integrin-signalling pathway associated with the pathway, marbling trait-related lncRNAs associated with calcium binding, muscle hypertrophy,

skeletal muscle, adiponectin and oxidative stress response pathway associated with several related genes, lncRNA region annotated QTLs identified beef tenderness genes located on chromosome tender distributed on chromosomes 14 and 25, marbling genes distributed on chromosomes 5, 8, 25 and X (Muniz *et al.*, 2022). Subcutaneous fat deposition in dairy cows has a variety of important immune and protective effects *in vivo*. By integrating genomic and transcriptomic datasets, it is possible to identify key candidate genes for subcutaneous fat deposition in high-yielding dairy cows. 46 protein-coding genes were analysed as candidate genes for regulating subcutaneous fat deposition in Holstein cows in a genome-wide association analysis study, of which 6 genes, such as NID2, STARD3, UFC1, *etc.*, are the most critical as shown in Table 1 (Zhang *et al.*, 2023).

### lncRNA in the transcriptome of bovine reproduction system

Cattle reproductive performance directly affects the economic benefits of cattle breeding and herds with excellent production performance and high breeding value often suffer from abnormal oestrus and ovulation, low pregnancy rates, long calving intervals, lactation difficulties, low calf survival rates and male sterility. The high genetic heterogeneity and feeding environment of cattle make the study of genetic mechanisms associated with fertility very difficult (Shome *et al.*, 2021) and the development of high-throughput sequencing technology and bioinformatics has accelerated the pace of research in genetic breeding (Jia *et al.*, 2023).

### lncRNA in the transcriptome of the bull reproductive system

Under the large-scale breeding mode, the production performance of bulls is directly related to the economic benefits of the whole cattle farm and is a key factor affecting the genetic quality of the herd. There are more and more research reports on lncRNAs related to male reproduction. Studies have shown that 10 lncRNA genes are associated with sexual maturation and spermatogenesis in bulls (Liu *et al.*, 2021). The function of lncRNA regulation in the transcriptome of bulls can provide insight into the genetic mechanism of male sterility in Pian cattle. RNA-seq and bioinformatics analyses were used to determine the expression profiles of lncRNAs in bovine and yak testes. Testicular lncRNAs NONBTAT012170 and NONBTAT010258 from different yak individuals showed high similarity and the down-regulation of the target genes of these genes during

**Table 1:** Transcriptome lncRNA-related functional genes identified in beef tissues.

Items	Transcriptome lncRNA-related functional genes have been identified
Bovine organelle (Chen <i>et al.</i> , 2021; Yan <i>et al.</i> , 2021; Zhang <i>et al.</i> , 2022; Ma <i>et al.</i> , 2023; Song <i>et al.</i> , 2020; Zhang <i>et al.</i> , 2021)	PFN1, RhoA, Rac1, lnc23, MCMC4, SERDINE1, ISLR, LOC100847835, LOC102394806, LOC102403551, MYLPF
Bovine adipose cells (Yang <i>et al.</i> , 2022; Ran <i>et al.</i> , 2022; Zhang <i>et al.</i> , 2022; Muniz <i>et al.</i> , 2022; Zhang <i>et al.</i> , 2023)	FOXO1, miR-330, circRNA2018, MSTRG.20301, GPAM, miR-27b, ciRNA489, SESN3, miR-433, circRNA2627, MSTRG.20342., NID2, STARD3, UFC1, DEDD, PPP1R1B, USP21

the S phase of the mitotic cell cycle resulted in abnormal DNA replication and spermatogenic blockage (Cai *et al.*, 2021). The lncRNA and mRNA differential gene assays in PY and Yak, DEFB124, DEFB126, DEFB125 and 10 other genes are shown in Table 2, which are downregulated and involved in immune response and spermatogonial maturation (Zhao *et al.*, 2021). Up-regulation of target genes of genes such as IGF1 and VGLL3 in lncRNAs may be related to disorders of spermatogonial maturation and cellular proliferation (Zhao *et al.*, 2021). lncRNAs are involved in the regulation of testicular development and spermatogenesis in Holstein cows. 8-week-old calves and 80-week-old adult bulls were subjected to testicular developmental whole-transcriptome analysis and further Hub analyses yielded six lncRNAs, which regulated 71 mRNAs enriched in the testes of adult bulls, forming lncRNA-mRNA functional pairs. Adult bulls were subjected to testicular cell cycle regulation, spindle assembly and sister chromatid segregation and had higher spermatogenesis than 8-week-old young bulls (Zhao *et al.*, 2022). From the presence of lncRNA and mRNA differential expression in high and low sperm motility in the semen of Holstein bulls, the lncRNA target node gene EFNA1 is a functional gene for reproduction in bulls (Wang *et al.*, 2019).

### lncRNAs in the transcriptome of the bovine reproductive system and early embryo

Bovine oocyte growth is supported by the mutual exchange of growth signals and growth factors between granulosa cells and oocytes around its cell membrane, which support oocyte growth and regulate meiotic progression and the overall transcriptional activity of the oocyte to gain maturation capacity. mature oocyte combines with sperm to fertilise the early embryo and lncRNAs in the transcriptome of the oocyte are involved in cell adhesion, cellular differentiation, development, cell proliferation, embryonic development, signal transduction, apoptosis and aromatic compound biosynthesis (Zhao *et al.*, 2022). lncRNAs are involved in the regulation of many key signalling pathways during oocyte maturation from the germinal vesicle stage to the mid-meiotic stage and the particularly abundant lncRNA MSTRG.19140 gene mediates oocyte meiotic resumption, progesterone-mediated oocyte maturation and cell cycle regulation

(Li *et al.*, 2021). Apoptosis and autophagy in granulosa cells surrounding oocytes are highly correlated with follicular development and atresia and lncRNA MEG3, miR-23a and apoptosis signal-regulated kinase 1 (ASK-1) are associated with it. Up-regulation of lncRNA MEG3 expression inhibited granulosa cell autophagy and promoted apoptosis and the presence of FSH or LH in yak granulosa cells reversed the effect of lncRNA MEG3 on the level of miR-23a. miR-23a levels as well as ASK1/JNK axis-mediated apoptosis and autophagy (Han *et al.*, 2023). The X-inactivation specific transcript (XIST) of lncRNA mediates the inflammatory response in bovine mammary epithelial cells through the NF- $\kappa$ B/NLRP3 inflammasome pathway (Ma *et al.*, 2019) and the XIST gene is also a major regulator of X-chromosome inactivation in the early stages of bovine embryonic development (Jali *et al.*, 2023). During the bovine embryo transfer process embryos hatch and implant into the maternal endometrium around the time of implantation stage, blastocysts hatch and implant into the endometrial cells of the mother and endometrial extracellular vesicles (EVs) contain miRNAs and lncRNAs, which regulate physiological events, such as the epithelial-mesenchymal transition (EMT) and trophoblastic cell fusion and play a key role in the establishment of the physiological environment of the uterus (Imakawa *et al.*, 2022). Bovine oocytes were vitrified and frozen at the germinal vesicle (GV) stage and freezing temperature and cryoprotectant concentration affected oocyte transcriptome lncRNA activity and expression and deep sequencing yielded 14 differentially expressed target genes corresponding to 17 differentially expressed lncRNAs (Cai *et al.*, 2022).

### lncRNAs in bovine disease resistance transcriptome

Bovine nutrition, breeding environment and autoimmunity are key factors affecting bovine health, which is influenced by lncRNAs and corresponding regulatory target genes in the bovine transcriptome. Extracellular vesicles in colostrum consumed by newborn calves contain regulatory target sites of lncRNA genes that are relevant to their immune and healthy developmental functions (Shome *et al.*, 2021). lncRNA-LRTN4RL1-AS regulates milk fat synthesis in mammary epithelial cells of dairy cows by competitively binding to miR-27a-3p to regulate PPAR $\alpha$  expression (Jia *et al.*, 2023).

**Table 2:** Transcriptome lncRNA-related functional genes identified in the bovine reproductive system.

Items	Transcriptome lncRNA-related functional genes have been identified
Bull reproductive system (Fonseca <i>et al.</i> , 2022)	COX7A2, COX6B2, TRIM37, PRM2, INHBA, ERBB4, SDHA, ATP6VOA20FGF9, TCF21, DEFB124, DEFB126, DEFB125, DEFB127, DEFB129, CES5A, TKDP1, CST3, RNASE9, CD52, IGF1, VGLL3
Reproductive system of the cow and early embryo (Li <i>et al.</i> , 2021; Han <i>et al.</i> , 2023; Ma <i>et al.</i> , 2019; Jali <i>et al.</i> , 2023; Imakawa <i>et al.</i> , 2022; Cai <i>et al.</i> , 2022)	MSTRG.19140, MEG3, XISTMSTRG.12295.5, MSTRG.37123.1, MSTRG.37930.2, MSTRG.40464.9, MSTRG.8869.3, MSTRG.26680.6, MSTRG.3578.3, MSTRG.40576.3, MSTRG.6723.5, MSTRG.32862.4, MSTRG.1184.4, MSTRG.33110.3, MSTRG.40454.2, MSTRG.41073.2, MSTRG.44732.4, MSTRG.6729.3, MSTRG.12295.5, MSTRG.37930.2, MSTRG.40454.2, MSTRG.8869.3, MSTRG.6723.5, MSTRG.35129.6

### lncRNAs in the transcriptome of bovine nutritional diseases

Nutritional levels in cattle are related to feed formulation and feeding procedures and there are many differences in metabolic efficiency and meat quality between grass- and grain-fed beef cattle, mainly caused by changes in gene expression of metabolic pathways and changes in hepatic metabolite content mediated by lncRNAs, miRNAs and ceRNAs (Jia *et al.*, 2021). Subacute rumen acidosis (SARA) due to high concentrate ration excess is a common metabolic disease in dairy farming and differentially expressed lncRNA target genes were associated with proteasome, peroxisome and hypoxia-inducible factor-1 signalling pathways by KEGG pathway analysis (Chen *et al.*, 2021). lncRNAs have a role in energy and lipid metabolism, the urea and tricarboxylic acid cycles and gluconeogenesis regulatory roles, especially in the regulation of lipid metabolism by fibroblast growth factor 21 (FGF21) secreted by the liver there are a large number of differentially expressed related lncRNA genes (Nolte *et al.*, 2022).

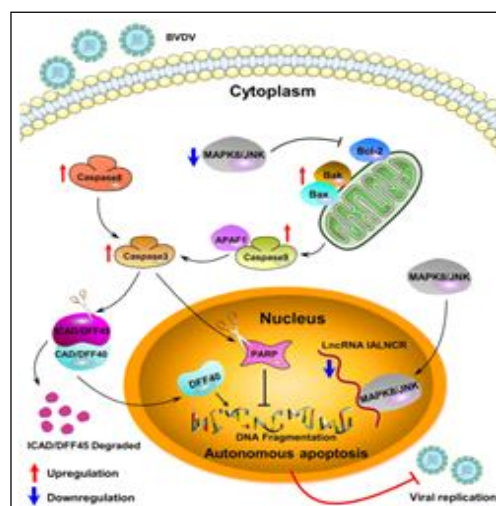
### lncRNAs in the transcriptome of bovine environmental adaptation

Organisms' adaptation to the environment is the result of their long-term survival and development and yaks, which have been settled for a long time and widely distributed in high altitude environments, can be used as an ideal natural animal research model for the adaptation of other high altitude species, including human beings. Lungs and heart are two key organs that exhibit adaptive transcriptome changes in high altitude environments and a large number of differentially expressed genes non-linear regulation in lung tissues at different altitude environments (Ge *et al.*, 2021). In a comparison of the transcriptomes of yaks and common cattle, 4975 mRNAs, 3326 lncRNAs and 75 miRNAs were differentially expressed; a total of 756 mRNAs, 346 lncRNAs and 83 miRNAs were differentially expressed in yaks at three different altitudes (Wang *et al.*, 2021). Brain tissues such as cerebrum and cerebellum, which are the most oxygen-consuming tissues of the organism in the Class Wuqi yak, Tibetan yak and Sanjiang cattle yak,

were studied and 91 candidate genes related to hypoxia were screened (Huang *et al.*, 2019).

### lncRNAs in the transcriptome of bovine immunity to pathogenic microorganisms

Studies have shown that bovine paratuberculosis, bovine viral diarrhoea, ticks, mastitis and endometritis in dairy cows are prevalent and cause huge economic losses to the global cattle industry. lncRNAs can regulate the immune response in humans and animals at three levels, namely, transcriptional, epigenetic modification and post-transcriptional and are widely involved in the pathological regulatory processes of inflammatory diseases (Jia *et al.*, 2022). The complete gene regulatory network lncRNA-mRNA-TF genes associated with bovine paratuberculosis infection was constructed by deep sequencing of lncRNAs, TFs and mRNAs and functional genes associated with the pathogenesis of bovine paratuberculosis (Heidari *et al.*, 2021). A comprehensive analysis of lncRNAs and mRNA expression profiles in the study of bovine viral diarrhoea virus infection of bovine kidney cells, lncRNAs play an important role in host-virus interactions (Gao *et al.*, 2021).



**Fig 1:** Schematic diagram of MAPK8-targeted lncRNA lALNCR binding to antagonise bovine viral diarrhoea virus proliferation while regulating cell-autonomous apoptosis.

**Table 3:** Potential transcriptome lncRNA-related functional genes identified in bovine disease resistance systems.

Items	Transcriptome lncRNA-related functional genes have been identified
Yak hypoxic environment (Huang <i>et al.</i> , 2019)	ADRA1A, MYLK, TNNC1, PRKCH, ACOX1, COX7C, INPP4, TPM3
Anti bovine paratuberculosis (Heidari <i>et al.</i> , 2021)	SLC11A1, MAPK8IP1, HMGCR, IFNGR1, CMPK2, CORO1A, IRF1, LDLR, BOLA-DMB, BOLA-DMA
Bovine viral diarrhea (Gao <i>et al.</i> , 2021)	IL1R1, PPP3CC, BIRC2, LPIN1, TIAM1, MAPK8, IGF1R, JAK1, CYLD, ACLY, HMGCR, ACSS2, MAP3K1
Cow mastitis (Jia <i>et al.</i> , 2022)	lncRNA H19, lncRNA TUB, lncRNA XIST, LRRC75A-AS1
Endometritis (Negin <i>et al.</i> , 2021)	IRAK1, CASP3, CCDC40, CCDC39, ZMYND10, FOXJ1, TLR4, IL10, STAT3, FN1, AKT1, CD68, ENSBTAG00000049936, ENSBTAG00000050527, ENSBTAG00000051242, ENSBTAG00000049287, bta-miR-449, bta-miR-484, bta-miR-149, bta-miR-30b, bta-miR-423



In the early stage of bovine viral diarrhoea virus infection, the level of lncRNA lALNCR in the host cells was reduced, inhibiting the expression of MAPK8 protein and promoting the expression of caspase-3 and Bcl-2 proteins and the targeting of MAPK8 to lncRNA lALNCR antagonized viral proliferation and regulated cell-autonomous apoptosis as shown in Fig 1 (Gao *et al.*, 2022).

Extracellular vesicles in bovine plasma are tick identification and prophylactic biomarkers containing various types of RNAs, including miRNAs and lncRNAs exerting regulatory functions at the post-transcriptional level and are differentially expressed between different tick-resistant groups of cattle (Abeyasinghe *et al.*, 2021). Dairy cow mastitis is an inflammatory disease caused by infection by pathogenic microorganisms, trauma or other factors. Its incidence is high and difficult to cure, causing great harm to cow health and dairy product safety. The susceptibility or resistance of individual dairy cows to mastitis is mainly determined by genetic factors and the lncRNAs that play a role in mastitis in dairy cows are shown in Table 3 (Jia *et al.*, 2022). Endometritis is a serious infectious disease in dairy cows after parturition. mRNA, lncRNAs and miRNAs genetic genes are involved in the pathogenesis of endometritis and their functional genes are shown in Table 3 (Sheybani *et al.*, 2021).

## CONCLUSION

At present, the research of lncRNA in the production performance, reproduction, cell differentiation, disease, breeding and other aspects of ruminants such as beef cattle and dairy cattle is still in its infancy. lncRNA as a major transcriptional regulator binds to the targeted target genes and affects their expression. The use of deep sequencing technology can be studied to prevent diseases affecting major economic traits, such as the antioxidant function of the trace element selenium has a role in preventing mastitis in dairy cows and RNA sequencing technology yields lncRNA profiles, identifies Se-associated specific lncRNAs and their associated target genes, performs functional annotations and explores selenium molecular markers for the prevention of mastitis in dairy cows to provide a new way of thinking (Jing *et al.*, 2022). However, the research on data related to milk and beef cattle breeding is still insufficient. With the increasing demand for high-end milk and meat, strengthening the breeding of high-quality milk and beef cattle and improving the economic benefits of farming, the research on the mechanism of lncRNA regulation of gene expression in high-end milk and beef cattle will surely become a hot topic.

## Authors' contributions

Hongxi Xu: Writing-Original draft preparation; Hongliang Zhang, Qun Wei, Haiyan Zhang and Meimei Zhu: Conceptualization; Wenjie Chen: Supervision.

## Funding

This work was supported by Natural Science Foundation of Heilongjiang Province-Co-guided (grant no.LH2022C092)

and Special Project for Wenzhou Science and Technology Specialists (grant no. X2023070).

## Conflict of interest

The authors declare that there is no conflict of in this research.

## REFERENCES

- Abeyasinghe, P., Turner, N., Peiris, H., Vaswani, K., Cameron, N., McGhee, N. and Mitchell, M.D. (2021). Differentially expressed extracellular vesicle, exosome and non-exosome miRNA profile in high and low tick-resistant beef cattle. *Frontiers in Cellular and Infection Microbiology*. **11**: 780-424.
- Cai, M.D., Xu, Z.Q., Liu, Y.H., Liu, J.Q., Zhao, S.Y., Wang, X.J. and Li, X.X. (2022). LncRNA-mediated effects of vitrification temperatures and cryoprotectant concentrations on bovine oocyte development following vitrification at the GV stage. *Theriogenology*. **186**: 135-145.
- Cai, X., Wu, S., Mipam, T., Luo, H., Yi, C., Xu, C. and Zhong, J. (2021). Testis transcriptome profiling identified lncRNAs involved in spermatogenic arrest of cattleyak. *Functional and Integrative Genomics*. **21**: 665-678.
- Chang, W., Cui, Z. and Wang, J. (2021). Identification of potential disease biomarkers in the ovaries of Dolang Sheep from Xinjiang using transcriptomics and bioinformatics approaches. *Indian Journal of Animal Research*. **55(4)**: 412-419. doi: 10.18805/ijar.B-1265.
- Chen, M., Zhang, L., Guo, Y., Liu, X., Song, Y., Li, X. and Guo, H. (2021). A novel lncRNA promotes myogenesis of bovine skeletal muscle satellite cells via PFN1 RhoA/Rac1. *Journal of Cellular and Molecular Medicine*. **25(13)**: 5988-6005.
- Chen, Q., Wu, C., Yao, Z., Cai, L., Ni, Y., Mao, S. and Zhao, R. (2021). Whole transcriptome analysis of RNA expression profiles reveals the potential regulating action of long noncoding RNA in lactating cows fed a high concentrate diet. *Animal Nutrition*. **7(4)**: 1315-1328.
- Fonseca, P.A.D.S., Suarez-Vega, A. and Canovas, A. (2022). Unrevealing functional candidate genes for bovine fertility through RNA sequencing meta-analysis and regulatory elements networks of co-expressed genes and lncRNAs. *Functional and Integrative Genomics*. **22(6)**: 1361-1376.
- Gao, X., Niu, C., Wang, Z., Jia, S., Han, M., Ma, Y. and Xu, Y. (2021). Comprehensive analysis of lncRNA expression profiles in cytopathic biotype BVDV-infected MDBK cells provides an insight into biological contexts of host-BVDV interactions. *Virulence*. **12**: 20-34.
- Gao, X., Sun, X., Yao, X., Wang, Y., Li, Y., Jiang, X. and Xu, Y. (2022). Downregulation of the long noncoding RNA lALNCR targeting MAPK8/JNK1 promotes apoptosis and antagonizes bovine viral diarrhoea virus replication in host cells. *Journal of Virology*. **96(17)**: e01113-22.
- Ge, Q., Guo, Y., Zheng, W., Zhao, S., Cai, Y. and Qi, X. (2021). Molecular mechanisms detected in yak lung tissue via transcriptome-wide analysis provide insights into adaptation to high altitudes. *Scientific Reports*. **11(1)**: 77-86.
- Han, X., Pan, Y., Fan, J., Wang, M., Wang, L., Wang, J. and Yu, S. (2023). LncRNA MEG3 regulates ASK1/JNK axis-mediated apoptosis and autophagy via sponging miR-23a in granulosa cells of yak tertiary follicles. *Cellular Signalling*. **107**: 110-680.

- Heidari, M., Pakdel, A., Bakhtiarzadeh, M.R. and Dehghanian, F. (2021). Integrated analysis of lncRNAs, mRNAs and TFs to identify regulatory networks underlying MAP infection in cattle. *Frontiers in Genetics*. **12**: 668-448.
- Huang, C., Ge, F., Ma, X., Dai, R., Dingkao, R., Zhaxi, Z. and Liang, C. (2021). Comprehensive analysis of mRNA, lncRNA, circRNA and miRNA expression profiles and their ceRNA networks in the longissimus dorsi muscle of cattle-yak and yak. *Frontiers in Genetics*. **12**: 772-557.
- Huang, X. (2019). Transcriptomic study of hypoxic adaptation in the brain and cerebellum of yak. Southwest University for Nationalities.
- Imakawa, K., Matsuno, Y. and Fujiwara, H. (2022). New roles for EVs, miRNA and lncRNA in bovine embryo implantation. *Frontiers in Veterinary Science*. **9**: 944-370.
- Jia, C., Bai, Y., Liu, J., Cai, W., Liu, L., He, Y. and Song, J. (2021). Metabolic regulations by lncRNA, miRNA and ceRNA under grass-fed and grain-fed regimens in angus beef cattle. *Frontiers in Genetics*. **12**: 579-393.
- Jia, H.R., Yang, C.Q., Wang, M., Wu, Z.Q., Zan, L.S. and Yang, W.C. (2023). LRTN4RL1-AS mediates milk fat synthesis in bovine mammary epithelial cells through miR-27a-3p targeting PPARY. doi: 10.3168/jds.2016-12264.
- Jia, L., Wang, J., Luoreng, Z., Wang, X., Wei, D., Yang, J. and Ma, Y. (2022). Progress in expression pattern and molecular regulation mechanism of lncRNA in bovine mastitis. *Animals*. **12**(9): 10-59.
- Jali, I., Vanamamalai, V.K., Garg, P., Navarrete, P., Gutiérrez-Adán, A. and Sharma, S. (2023). Identification and differential expression of long non-coding RNAs and their association with XIST gene during early embryonic developmental stages of *Bos taurus*. *International Journal of Biological Macromolecules*. **229**: 896-908.
- Jing, H., Chen, Y., Qiu, C. and Guo, M.Y. (2022). lncRNAs transcriptome analysis revealed potential mechanisms of selenium to mastitis in dairy cows. *Biological Trace Element Research*. **200**(10): 4316-4324.
- Liu, H., Khan, I. M., Yin, H., Zhou, X., Rizwan, M., Zhuang, J. and Zhang, Y. (2021). Integrated analysis of long non-coding RNA and mRNA expression profiles in testes of calves and sexually mature Wandong bulls (*Bos taurus*). *Animals*. **11**(7): 20-06.
- Li, M.H., Niu, M.H., Feng, Y.Q., Zhang, S.E., Tang, S.W., Wang, J.J. and Shen, W. (2021). Establishment of lncRNA-mRNA network in bovine oocyte between germinal vesicle and metaphase II stage. *Gene*. **791**: 145-716.
- Ma, M., Pei, Y., Wang, X., Feng, J., Zhang, Y. and Gao, M.Q. (2019). lncRNA XIST mediates bovine mammary epithelial cell inflammatory response via NF-kB/NLRP3 inflammasome pathway. *Cell Proliferation*. **52**(1): e12-525.
- Ma, Y., Zhao, T., Wu, X., Yang, Z. and Sun, Y. (2023). Expression profile and functional prediction of novel lncRNA 5.8 S rRNA-OT1 in cattle. *Animal Biotechnology*. **34**(7): 2040-2050.
- Muniz, M.M.M., Simielli Fonseca, L.F., Scaletz, D.C.B., Vega, A.S., Silva, D.B.D.S., Ferro, J.A. and deAlbuquerque, L.G. (2022). Characterization of novel lncRNA muscle expression profiles associated with meat quality in beef cattle. *Evolutionary Applications*. **15**(4): 706-718.
- Nolte, W., Weikard, R., Albrecht, E., Hammon, H.M. and Kühn, C. (2022). Metabogenomic analysis to functionally annotate the regulatory role of long non-coding RNAs in the liver of cows with different nutrient partitioning phenotype. *Genomics*. **114**(1): 202-214.
- Ran, H., Yang, Y., Luo, M., Liu, X., Yue, B., Chai, Z. and Wang, H. (2022). Molecular regulation of yak preadipocyte differentiation and proliferation by lncFAM200B and ceRNA regulatory network analysis. *Cells*. **11**(15): 23-66.
- Sheybani, N., Bakhtiarzadeh, M.R. and Salehi, A. (2021). An integrated analysis of mRNAs, lncRNAs and miRNAs based on weighted gene co-expression network analysis involved in bovine endometritis. *Scientific Reports*. **11**(1): 180-50.
- Shome, S., Jernigan, R.L., Beitz, D.C., Clark, S. and Testroet, E.D. (2021). Non-coding RNA in raw and commercially processed milk and putative targets related to growth and immune-response. *BMC Genomics*. **22**: 1-11.
- Song, C., Yang, Z., Jiang, R., Cheng, J., Yue, B., Wang, J. and Chen, H. (2020). lncRNA IGF2 AS regulates bovine myogenesis through different pathways. *Molecular Therapy-Nucleic Acids*. **21**: 874-884.
- Wang, H., Zhong, J., Wang, J., Chai, Z., Zhang, C., et al. (2021). Whole-transcriptome analysis of yak and cattle heart tissues reveals regulatory pathways associated with high-altitude adaptation. *Frontiers in Genetics*. **12**: 579-800.
- Wang, X., Yang, C., Guo, F., Zhang, Y., Ju, Z., Jiang, Q. and Huang, J. (2019). Integrated analysis of mRNAs and long noncoding RNAs in the semen from Holstein bulls with high and low sperm motility. *Scientific Reports*. **9**(1): 20-92.
- Wang, X., Zhang, Y., Zhang, X., Jin, G., Wang, D., Li, B. and Liu, W. (2017). Transcriptome analysis of castrated Bovine reveals the characters of protein accumulation. *Indian Journal of Animal Research*. **51**(6): 1043-1050. doi: 10.18805/ijar.v0i01.8461.
- Yan, X.M., Zhang, Z., Liu, J.B., Li, N., Yang, G.W., Luo, D. and Zhang, J.B. (2021). Genome-wide identification and analysis of long noncoding RNAs in longissimus muscle tissue from Kazakh cattle and xinjiang brown cattle. *Animal Bioscience*. **34**(11): 1739-1748.
- Yang, X., Ma, X., Mei, C. and Zan, L. (2022). A genome-wide landscape of mRNAs, lncRNAs, circRNAs and miRNAs during intramuscular adipogenesis in cattle. *BMC Genomics*. **23**(1): 691.
- Yang, J.Y., Liu, X.Q., Wen, T.Q., Sun, Y.H. and Yu, Y. (2021). Progress on lncRNA regulated disease resistance traits in domesticated animals. *Yi Chuan*. **43**(7): 654-664.
- Yaoyao, M., Tianqi, Z., Xinyi, W., et al. (2023). Expression profile and functional prediction of novel lncRNA 5.8S rRNA-OT1 in cattle [J]. *Animal Biotechnology*. **24**: 1-11.
- Zhang, H., Mi, S., Brito, L. F., Hu, L., Wang, L., Ma, L. and Wang, Y. (2023). Genomic and transcriptomic analyses enable the identification of important genes associated with subcutaneous fat deposition in Holstein cows. *Journal of Genetics and Genomics*. **50**(6): 385-397.
- Zhang, R., Wang, J., Xiao, Z., Zou, C., An, Q., Li, H. and Wei, Y. (2021). The expression profiles of mRNAs and lncRNAs in buffalo muscle stem cells driving myogenic differentiation. *Frontiers in Genetics*. **12**: 643-497.

- Zhang, S., Xu, H., Jiang, E., Akhatayeva, Z., Jiang, F., Song, E. and Lan, X. (2022). Screening of bovine tissue-specific expressed genes and identification of genetic variation within an adipose tissue-specific lncRNA gene. *Frontiers in Veterinary Science*. **9**: 887-520.
- Zhang, W., Sun, B., Zhao, Y., Raza, S.H.A., Li, Y., Wang, J. and Zan, L. (2022). Proliferation of bovine myoblast by lncPRRX1 via regulation of the miR-137/CDC42 axis. *International Journal of Biological Macromolecules*. **220**: 33-42.
- Zhao, L., Pan, Y., Wang, M., Wang, J., Wang, Y., Han, X. and Yu, S. (2022). Integrated analysis of the expression profiles of the lncRNA-miRNA-mRNA ceRNA network in granulosa and cumulus cells from yak ovaries. *BMC Genomics*. **23(1)**: 633.
- Zhao, S., Chen, T., Luo, X., Chen, S., Wang, J., Lai, S. and Jia, X. (2021). Identification of novel lncRNA and differentially expressed genes (DEGs) of testicular tissues among cattle, yak and cattle-yak associated with male infertility. *Animals*. **11(8)**: 24-20.
- Zhao, S., Wang, H., Hu, Z., Sahlou, B.W., Heng, N., Gong, J. and Zhu, H. (2022). Identification of spermatogenesis-related lncRNA in Holstein bull testis after sexual maturity based on transcriptome analysis. *Animal Reproduction Science*. **247**: 107-146.
- Zhao, W., Ahmed, S., Ahmed, S., Yangliu, Y., Wang, H. and Cai, X. (2021). Analysis of long non-coding RNAs in epididymis of cattleyak associated with male infertility. *Theriogenology*. **160**: 61-71.