BIODIVERSITY STUDIES

Biodiversty Studies (BiSt)
2025, 4(1): 1-5
https://doi.org/10.56494/dnbgt.2025.22

REVIEW

Contributions of *JY-1, an* Oocyte-Specific Gene, to Reproductive Biology and Biodiversity

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How to cite: Beyler, B. and Öner, Y. (2025). Contributions of *JY-1*, an Oocyte-Specific Gene, to Reproductive Biology and Biodiversity. *Biodiversity Studies (BiSt)*, *4*(1), 1-5.

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Article History:
Received: 05.05.2025
Accepted: 10.06.2025
First online: 30.06.2025

Keywords
Bovine, genetic polymorphism, reproductive performance, *JY-1 gene*

Abstract

Fertility problems are among the leading causes of significant economic losses in livestock production. Understanding the genetic substructure of fertility and identifying the genes that may be effective on fertility and the mutations in these genes, and examining their possible effects are very important in terms of sustainable livestock production and in terms of contributions to studies on reproductive problems in mammals.

Oocyte-specific genes play a crucial role in orchestrating early developmental events, and regulating ovarian follicle function; among these, *JY-1*, a recent identified oocyte-specific gene, stands out as a bovine oocyte-derived secreted protein that critically influences granulosa cell activity and is indispensable for proper embryonic progression, underscoring its unique and species-specific contribution to reproductive success.

In this context, several polymorphisms in the *JY-1* gene have been identified, some of which are associated with reproductive performance traits and in vitro embryo production. As a bovine-specific, maternally derived oocyte-secreted protein, *JY-1*, provides critical insights into the genetic basis of female fertility and offers new opportunities for improving reproductive traits and maintaining biodiversity in cattle. Despite its potential contributions to animal breeding and the conservation of genetic resources, studies on this gene remain limited. In this study beside general information on the gene, genetic polymorphisms and their importance intended to summarized.

INTRODUCTION

In animal production, all economically important traits are closely linked to reproduction. Hence reproductive performance has strong impact on profitability. Due to the low heritability of most reproductive traits, it is difficult to accurately estimate their breeding values (Darwash et al., 1999). Reproductive efficiency constitutes the foundation of all productive traits and is critical for ensuring both sustainability and profitability in livestock production. Notably, Brumatti et al. (2011) demonstrated that selection for early puberty yields a 4- to 13-fold greater increase in profitability for the production system compared to selection based on growth traits.

Unlike other mucosal tissues in the body, the female reproductive tract is characterized by extraordinary genetic and immunological diversity, which varies markedly among individuals and fluctuates throughout each reproductive cycle. This diversity spans the entire tract, from the vagina to the ovarian follicles, making it a uniquely adaptable and dynamic system (Namlı Kalem et al., 2016). Recent genetic research has revealed the crucial influence of numerous genes across different reproductive organs and stages, with some genes displaying highly localized, organ-specific expression, while others are broadly active throughout the reproductive tract. Such findings underscore the intricate regulation and specialization required for successful female reproduction (Kalem et al., 2019).

The ovary is a fundamental component of the female reproductive system, responsible for gamete production and the secretion of steroid hormones. As the cornerstone of this system, the ovaries undertake both endocrine and exocrine functions through a complex process extending from the development of primary follicles to ovulation. During folliculogenesis, primordial follicles undergo growth and differentiation phases, transforming into preantral, antral, and ovulatory follicles. Throughout this developmental process, bidirectional signalling occurs between the oocyte and surrounding granulosa and theca cells. This signalling is regulated via paracrine and autocrine pathways and encompasses numerous biological processes such as gene expression, cell proliferation, differentiation, and survival (Lee et al., 2014; Occhio et al., 2020).

Within this context, oocyte-specific genes such as NOBOX, FIGLA, BMP15, GDF9, and JY-1 have been reported to regulate follicular reserve, oocyte quality, and embryo development in both humans (Suzumori et al., 2002; Heath et al., 2017; França and Mendonca, 2022; Wu et al., 2002) and bovines (Zhang et al., 2009; Tripurani et al., 2011, 2013). Mutation and polymorphism analyses demonstrate that these genes are directly associated with clinical conditions such as human infertility and reproductive traits such as embryo viability and twinning rates in animals. These findings highlight the importance of molecular characterization of oocyte-specific genes, not only for advancing fundamental scientific knowledge but also for developing genetic counselling strategies, early diagnostics, and targeted therapeutic approaches. Furthermore, these genes are strategically significant for animal breeding, conservation of endangered species, and improving livestock reproductive efficiency.

Among these, *JY-1* stands out as a recently identified bovine oocyte-derived secreted protein, uniquely influencing granulosa cell activity and embryonic development. The characterization of *JY-1* across species not only expands our understanding of reproductive biology but also supports the development of new molecular markers for improving cattle breeding programs and conserving genetic resources (Camargo et al., 2013, 2014; Silveira et al., 2021). The purpose of this review is to summarize current knowledge regarding the *JY-1* gene and its polymorphic variants, offering a reference for researchers focused on reproduction and genetics.

Molecular Structure and Evolution of *JY-1*

The *JY-1* protein is oocyte-specific and plays crucial regulatory roles in folliculogenesis, oocyte maturation, and early embryonic development. During follicle development and oocyte maturation, the storage and processing of proteins and messenger RNAs are critical for all stages up to embryonic genome activation. The maternally derived *JY-1* protein, expressed exclusively in oocytes, has been identified among these proteins.

The first comprehensive study on molecular characterisation and function of *JY-1* was carried out in the first decade of the 2000's by Bettegowda et al. (2007). The gene also symbolized as LOC100126230 in database located on 29th chromosome of bovine genome (NCBI Gene, 2025). It consists of three exons (25 bp, 92 bp, and approximately 1,400 bp) and two relatively long introns (~12.8 kb and 1.5 kb). It encodes an 11 kDa protein.

As an oocyte-specific gene, *JY-1* is uniquely characterized in cattle. Genomic analyses have revealed limited conservation of its complete coding sequence in other vertebrates. Although related sequences appear in syntenic regions of species such as humans, mice, and dogs, these lack critical exons necessary for producing a functional protein analogous to bovine *JY-1*. This suggests that *JY-1* has evolved primarily within the bovine lineage, highlighting the importance of investigating species-specific regulatory mechanisms in oocyte biology and fertility (Bettegowda et al., 2007). Moreover, the presence of *JY-1*-like genetic elements in other species, particularly the conserved 3' untranslated region (3' UTR), suggests that *JY-1* homologs in these species may serve distinct regulatory functions. While the complete protein-coding sequence is not preserved, the conservation of the 3' UTR region implies potential roles in post-transcriptional regulation or noncoding RNA-mediated mechanisms, indicating that *JY-1*-related sequences might contribute to species-specific regulatory pathways beyond their established function in cattle.

Functional Roles of *JY-1* in Reproduction

Studies have shown that recombinant *JY-1* protein, when added to cultures of bovine granulosa cells stimulated with FSH (to mimic the preovulatory stage), significantly inhibits cell proliferation, reduces estrogen production, and increases progesterone secretion. In the context of early embryonic development, it has been shown that *JY-1* mRNA is of maternal origin and is essential for progression to the blastocyst stage. Functional knockdown experiments revealed that *JY-1* plays a particularly crucial role prior to embryonic genome activation, specifically at the 8- to 16-cell stage of embryogenesis. Notably, inhibition of *JY-1* expression in both parthenogenetic and in vitro fertilized embryos led to a substantial decrease in blastocyst formation. Taken together, these results highlight the indispensable function of *JY-1* in early embryonic development, particularly for the transition from the 8- to 16-cell stage to the blastocyst stage (Bettegowda et al., 2007; Lee et al., 2014).

Genetic Polymorphisms of *JY-1* and Their Relevance to Breeding

Among the exons, the third exon (~1,400 bp) contains the majority of molecular variation sites (Camargo et al., 2013; Silveira et al., 2021). The first polymorphism study conducted in Bos indicus subspecies focused on the third exon of the *JY-1* gene and identified seven SNPs. Of these, one SNP was located within the protein-coding region which lead to proline-to-leucine substitution in 77th position of the protein, while the remaining six were found in the 3' untranslated region (3' UTR). However, the authors reported no significant association between these SNPs and either early puberty or growth traits in *Nellore heifers* (Camargo et al., 2012). In a follow-up study that included the first and second exons and part of the third exon, 18 polymorphisms were identified. Some SNPs which were found at third exon lead to amino acid substations on various positions of the protein (Camargo et al., 2013). When the same group expanded the sample size in the Nellore population, they found 17 SNPs, including previously reported ones. (Camargo et al., 2013; 2014). The authors examined associations with the SNPs and reproductive traits. According to finding there were several associations between age at first calving, days to calving, early pregnancy and the SNPs. The previously described SNPs located on second exon at position 12 999 which lead to methionine to lysine substitution and may inhibit protein translation by affecting the initial methionine codon exhibited strong effect on early pregnancy (Camargo et al., 2013; 2014). After a long time, the first study carried out to investigate *JY-1* polymorphisms and their effect on reproduction in *Bos taurus* subspecies by using Holstein cattle objected the first and second exons and the first intron of the gene, as well (Silveira et al., 2021). The study revealed three novel SNPs, in addition to eight previously reported SNPs (Camargo et al., 2013; 2014). Two SNPs were identified in both the second intron and the second exon, while the remaining SNPs were located in the third exon. Among these, a missense variant located in the second exon, which causes a leucine-to-isoleucine substitution, was found to be strongly associated with in vitro embryo production, similar to several other SNPs identified in the study. However, the association was detected only in embryos produced through in vitro methods, whereas no such association was found in embryos generated in vivo.

These findings underscore that studying the *JY-1* gene is essential for advancing knowledge in reproductive biology and critical for sustaining genetic diversity, improving fertility efficiency, and developing conservation strategies not only in bovine (Lee et al., 2014) but potentially in other uniparous species as well.

CONCLUSION

Reproduction is a key trait for animal production, shaped by multiple genetic and environmental factors. Female reproductive health and performance are highly complex phenomena, and a deeper understanding of genes associated with reproductive traits will significantly contribute to both livestock productivity and animal health. Although most previous studies on reproduction in cattle have focused on genomic regions related to the nervous system and lipid metabolism, recent attention has shifted to oocyte-specific genes such as *BMP15, GDF9, FIGLA, NOBOX*, and particularly *JY-1*. These genes play central roles in female reproductive biology and represent valuable targets for enhancing reproductive efficiency, maintaining genetic diversity, and ensuring the long-term sustainability of livestock populations.

JY-1, in particular, is a recently identified, bovine-specific oocyte gene whose functional and genetic diversity is just beginning to be explored. Although dramatic findings have been reported regarding its effects on fertility, studies are still limited—primarily to Nellore and Holstein breeds. To gain a more comprehensive understanding of *JY-1*'s role in bovine reproduction, future research should investigate the polymorphisms and functional effects of *JY-1* in a wider range of cattle breeds raised under diverse breeding conditions. Expanding such research will deepen our understanding of reproductive biology and open new avenues for genetic improvement and conservation in cattle.

REFERENCES

Bettegowda, A., Yao, J., Sen, A., Li, Q., Lee, K., Kobayashi, Y., Patel, O.V., Paul, M., Coussens, P.M., Ireland, J.J. & Smith, G.W. (2007). JY-1 an oocyte-specific gene regulates granulosa cell function and early embryonic development in cattle. *PNAS*, *104*, 17602–17607.

Brumatti, R.C., Ferraz, J.B.S., Eler, J.P. & Formigonni, I.B. (2011). Development of selection index in beef cattle under the focus of a bio-economic model. *Archivos de Zootecnia*, *60*, 205–213.

Camargo, G.M.F., Cardoso, D.F., Gil, F.M.M., Fonseca, P.D.S., Zetouni, L., Braz, C.U., deFreitas, A.C., Souza, F.R.P, Aspilcueta-Bor-quis, R.R., Baldi. F., Albuquerque, L.G., Regitano, L.C.A. & Tonhati, H. (2012). Firstpolymorphisms in JY-1 gene in cattle (Bostaurus indicus) and their association withsexual precocity and growth traits. *Molecular Biology Reports*, *39*, 10105–10109

Camargo, G.M.F., Baldi, F., Regitano, L.C.A. & Tonhati, H. (2013). Characterization of the exonic regions of the JY-1 gene in Zebu cattle and buffaloes. *Reproduction in Domestic Animals*, *48*, 918–922.

Camargo, G.M.F., Costa, R.B., Albuquerque, L.G., Regitano, L.C.A., Baldi, F. & Tonhati, H. (2014). Association between JY-1 gene polymorphisms and reproductive traits in beef cattle. *Gene, 533*, 477–480.

Darwash, A.O., Lamming, G.E. & Woolliams, J.A. (1999). The potential for identifying heritable endocrine parameters associated with fertility inpost-partum dairy cows. *Animal Science*, *68*, 333–347.

França, M. M. & Mendonca, B. B. (2022). Genetics of ovarian insufficiency and defects of folliculogenesis. Best practice & research. *Clinical endocrinology & metabolism*, *36*(1), 101594. https://doi.org/10.1016/j.beem.2021.101594

Galloway, S.M., McNatty, K.P., Cambridge, L.M., Laitinen, M.P., Juengel, J.L., Jokiranta, T.S., McLaren, R.J., Luiro, K., Dodds, K.G., Montgomery, G.W., Beattie, A.E., Davis, G.H. & Ritvos, O. (2000). Mutations in an oocyte-derived growth factor gene (BMP15) cause increased ovulation rate and infertility in a dosage-sensitive manner. *Nature Genetics*, *25*, 279–283.

Galloway, S.M., Gregan, S.M. & Wilson, T. (2002). Bmp15 mutations and ovarian function. *Molecular and Cellular Endocrinology*, *191*, 15–18.

Hanrahan, J.P., Gregan, S.M., Mulsant, P., Mullen, M., Davis, G.H., Powell, R. & Galloway, S.M. (2004). Mutations in the genes for oocyte-derived growth factors GDF9 and BMP15 are associated with both increased ovulation rate and sterility in Cambridge and Belclare Sheep (Ovis aries). *Biology of Reproduction*, *70*, 900–909.

Heath, D. A., Pitman, J. L. & McNatty, K. P. (2017). Molecular forms of ruminant BMP15 and GDF9 and putative interactions with receptors. *Reproduction (Cambridge, England)*, *154*(4), 521–534. https://doi.org/10.1530/REP-17-0188

Lee, K.B., Wee, G., Zhang, K., Folger, J.K., Knott, J.G. & Smith, G.W. (2014). Functional role of the bovine oocyte-specific protein JY-1 in meiotic maturation, cumulus expansion, and subsequent embryonic development. *Biology of Reproduction*, *90*(3), 69. doi: 10.1095/biolreprod.113.115071. PMID: 24501174.

Namlı Kalem, M., Demircan, K., Kalem, Z., Demirin, H., Eser, A., Demirel, M. & İltemir Duvan, Z.C. (2016). Versatile Matricellular Proteins and Related Adamts Proteinases in Infertility. *Turkiye Klinikleri Gynecology Obstetrics*. doi: 10.5336/gynobstet. 2015-45243

NCBI Gene. (2025). *National Center for Biotechnology Information (NCBI)*. (2025, January 30). Gene: JY-1 (Bos taurus). NCBI Gene database. Available online: <https://www.ncbi.nlm.nih.gov/gene/ 100126230> (accesed on 27 May 2025)

Kalem, Z., Namlı Kalem, M. & Şimşir, C. (2019). Reproduktif Sistemde ADAMTS Genleri. *Uludağ Üniversitesi Tıp Fakültesi Dergisi, 45*(1), 111-118. DOI: 10.32708/uutfd.504161

Moore, R.K., Erickson, G.F & Shimasaki, S. (2004). Are BMP-15 and GDF-9 primary determinants of ovulation quota in mammals?. *Trends in Endocrinology and Metabolism, 15*, 356–361.

Occhio, M. J., Campanile, G. & Baruselli, P. S. (2020). Transforming growth factor-β superfamily and interferon-τ in ovarian function and embryo development in female cattle: review of biology and application. *Reproduction, fertility, and development, 32*(6), 539–552. https://doi.org/10.1071/RD19123

Silveira, C. R. A., Pierucci, J. C., De Camargo, G. M. F., Barbero, M. M. D., Cardoso, D. F., Dos Santos, D. J. A., Costa, R. B., Tonhati, H., De Albuquerque, L. G., Rodrigues, C. A. & Gimenes, L. U. (2021). Short communication: JY-1 gene variants and embryo production in Holstein cows. *Livestock Science, 244*, 104308. https://doi.org/10.1016/j.livsci. 2020.104308

Suzumori, N., Yan, C., Matzuk, M. M., & Rajkovic, A. (2002). Nobox is a homeobox-encoding gene preferentially expressed in primordial and growing oocytes. *Mechanisms of development, 111*(1-2), 137–141. https://doi.org/10.1016/ s0925-4773(01)00620-7

Tripurani, S.K., Lee, K.B., Wang, L., Wee, G., Smith, G.W., Lee, Y.S., Latham, K.E. & Yao, J. A. (2011) Novel functional role for the oocyte-specific transcription factor newborn ovary homeobox (NOBOX) during early embryonic development in cattle. *Endocrinology, 152*(3),1013-23. doi: 10.1210/en.2010-1134. Epub 2010 Dec 30. PMID: 21193554; PMCID: PMC3040056.

Tripurani, S.K., Wee, G., Lee, K.B., Smith, G.W., Wang, L. & Jianboyao. (2013). MicroRNA-212 post-transcriptionally regulates oocyte-specific basic-helix-loop-helix transcription factor, factor in the germline alpha (FIGLA), during bovine early embryogenesis. *PLoS One, 27;8*(9): e76114. doi: 10.1371/journal.pone.0076114. PMID: 24086699; PMCID: PMC3785419.

Wu, K., Zhai, Y., Qin, M., Zhao, C., Ai, N., He, J. & Ge, W. (2023). Genetic evidence for differential functions of figla and nobox in zebrafish ovarian differentiation and folliculogenesis. *Communications Biology, 6*(1), 1185. https://doi.org/10.1038/s42003-023-05551-1

Zhang, L.P., Gan, Q.F., Zhang, X.H., Li, H.D., Hou, G.Y., Li, J.Y., Gao, X., Ren, H.Y., Chen, J.B. & Xu, S.Z. (2009). Detecting a deletion in the coding region of the bovine bone morphogenetic protein 15 gene (BMP15). *Journal of Applied Genetics, 50*(2),145-8. doi: 10.1007/BF03195665. PMID: 19433911.