



## INTISARI

Corpus luteum persisten (CLP) merupakan salah satu gangguan reproduksi yang menyebabkan penurunan tingkat produktivitas sapi betina. Secara fisiologis, regresi corpus luteum dipicu oleh sinyal hormonal berupa prostaglandin dari uterus, yang memicu penurunan progesteron dan memulai kembali siklus estrus. Proses ini diatur oleh ekspresi gen-gen tertentu pada jaringan luteal seperti gen STAR, PTGFR, NR5A2, dan PSSR53. Ekspresi gen diketahui memiliki peran dalam regulasi hormon prostaglandin yang berperan penting untuk regresi corpus luteum (CL). Tujuan penelitian adalah menganalisis ekspresi gen-gen luteal pada sapi yang mengalami CLP. Penelitian ini diharapkan dapat memberikan informasi tentang ekspresi gen sapi normal dan CLP sehingga dapat digunakan sebagai marker seleksi sapi betina produktif atau unggul.

Penelitian ini dilakukan di Laboratorium Biokimia PAU UGM pada Agustus 2024-Juli 2025. Penelitian terdiri dari desain primer gen luteal, pengumpulan sampel darah, isolasi RNA dan RT-qPCR. Sampel yang digunakan pada penelitian ini adalah darah dari sepuluh ekor sapi betina dengan 5 kondisi normal dan 5 dengan kondisi CLP. Desain primer menggunakan Primer 3 Plus. RT-qPCR dilakukan menggunakan Bio-Rad CFX96. Ekspresi gen dinormalisasi menggunakan gen *housekeeping* actin- $\beta$ . Analisis ekspresi gen dilakukan berdasarkan metode Livak

Hasil ekspresi mRNA menunjukkan gen Gen NR5A2, STAR, HSD3 $\beta$ 1, ISG15 terekspresi lebih tinggi pada sapi yang mengalami corpus luteum persisten dibandingkan sapi normal. Gen PRSS35, PTGFR, dan LHCGR terekspresikan rendah pada sapi yang mengalami CLP dibandingkan sapi dengan kondisi fisiologis. Perbedaan ekspresi dari gen-gen ini diharapkan bisa dasar pengetahuan dalam menemukan biomarker gen untuk sapi yang mengalami gangguan reproduksi CLP.

**Kata Kunci:** Corpus luteum Persisten, Luteal, Luteolisis, PGF2 $\alpha$ , Steroidogenesis



## **ABSTRACT**

*Persistent corpus luteum is one of the reproductive disorders that leads to decreased productivity in female cattle. Physiologically, the regression of the corpus luteum is triggered by hormonal signals in the form of prostaglandins from the uterus, which induce a drop in progesterone levels and initiate a new estrous cycle. This process is regulated by the expression of specific genes in luteal tissue, such as STAR, PTGFR, NR5A2, and PRSS35. Gene expression is known to play a role in regulating prostaglandin hormones, which are crucial for corpus luteum (CL) regression. The aim of this study is to analyze the expression of luteal genes in cattle with CLP. This research is expected to provide insights into gene expression profiles in normal and CLP-affected cattle, which may serve as genetic markers for the selection of high-performing or productive females.*

*This study was conducted at the Biochemistry Laboratory, PAU UGM, from August 2024 to July 2025. The research steps included luteal gene primer design, blood sample collection, RNA isolation, and RT-qPCR analysis. Blood samples were collected from female cattle: five with normal reproductive function and five diagnosed with CLP. Primer design was conducted using Primer3Plus software, and RT-qPCR was performed using the Bio-Rad CFX96 system. Gene expression levels were normalized using the  $\beta$ -actin housekeeping gene, and analyzed using the Livak method ( $2^{-\Delta\Delta Ct}$ ).*

*The mRNA expression results showed that NR5A2, STAR, HSD3 $\beta$ 1, and ISG15 genes were more highly expressed in cattle with persistent corpus luteum compared to normal cattle. In contrast, PRSS35, PTGFR, and LHCGR genes were expressed at lower levels in CLP-affected cows than in physiologically normal cows. These differences in gene expression may serve as a foundation for identifying potential biomarker genes related to CLP in cattle with reproductive disorders.*

**Keyword:** *Persistent Corpus Luteum, Luteal, Luteolysis, PGF2 $\alpha$ , Steroidogenesis*