

INTISARI

Penelitian ini bertujuan untuk mengevaluasi ekspresi gen Insulin-like Growth Factor 1 (*IGF1*) dan karakteristik elemen regulator genetiknya sebagai kandidat marker molekuler dalam seleksi sapi potong betina unggul untuk mengurangi kejadian ovulasi tertunda. Analisis karakteristik reproduksi dan fisiologis menunjukkan perbedaan signifikan antara kelompok sapi normal dan sapi dengan ovulasi tertunda yang meliputi kegagalan inseminasi buatan, durasi estrus, panjang siklus estrus dan kadar progesteron di fase estrus ($p < 0,05$), yang dikonfirmasi melalui penurunan ekspresi gen *IGF1* pada kelompok ovulasi tertunda. Identifikasi *Single Nucleotide Polymorphism* (SNP) pada promotor gen *IGF1* tidak ditemukan varian fungsional, dan prediksi CpG island juga menunjukkan tidak adanya wilayah metilasi potensial yang relevan. Sebaliknya, prediksi *Transcription Factor Binding Sites* (TFBS) mengungkapkan 17 situs pengikatan dari lima jenis faktor transkripsi, dengan dominasi tiga TF yang bersifat represif termasuk JDP2, FOXO1 dan BCL6 yang berpotensi menekan transkripsi gen *IGF1* dan berkontribusi terhadap ovulasi tertunda. Meskipun terdapat indikasi hubungan antara ekspresi gen *IGF1* dan kondisi reproduksi, bukti yang diperoleh belum cukup untuk menetapkan gen *IGF1* sebagai biomarker molekuler yang valid. Diperlukan studi lanjutan dengan pendekatan fungsional dan populasi yang lebih luas untuk mengonfirmasi potensi gen *IGF1* dalam program seleksi genetika sapi potong betina.

Kata kunci: *promoter region IGF1*, ovulasi tertunda, *Transcription Factor Binding Sites*, sapi

ABSTRACT

This study aims to evaluate the expression of the Insulin-like Growth Factor 1 (IGF1) gene and the characteristics of its genetic regulatory elements as candidate molecular markers in the selection of high-quality female beef cattle to reduce the incidence of delayed ovulation. Analysis of reproductive and physiological characteristics revealed significant differences between the normal cattle group and the delayed ovulation group, including failed artificial insemination, estrus duration, estrus cycle length, and progesterone levels during the estrus phase ($p < 0.05$), which was confirmed by reduced IGF1 gene expression in the delayed ovulation group. Identification of IGF1 in the delayed ovulation group. Identification of Single Nucleotide Polymorphisms (SNPs) in the IGF1 gene promoter did not reveal functional variants, and CpG island predictions also indicated the absence of relevant potential methylation regions. Conversely, Transcription Factor Binding Sites (TFBS) revealed 17 binding sites from five types of transcription factors, with a dominance of three repressive TFs including JDP2, FOXO1, and BCL6, which have the potential to suppress IGF1 gene transcription and contribute to delayed ovulation. Although there are indications of a relationship between IGF1 gene expression and reproductive conditions, the evidence obtained is not sufficient to establish IGF1 gene as a valid molecular biomarker. Further studies with functional approaches and a broader population are needed to confirm the potential of IGF1 gene in genetic selection programs for female beef cattle.

Keywords: *IGF1 promoter region, delayed ovulation, transcription factor binding sites, cattle*