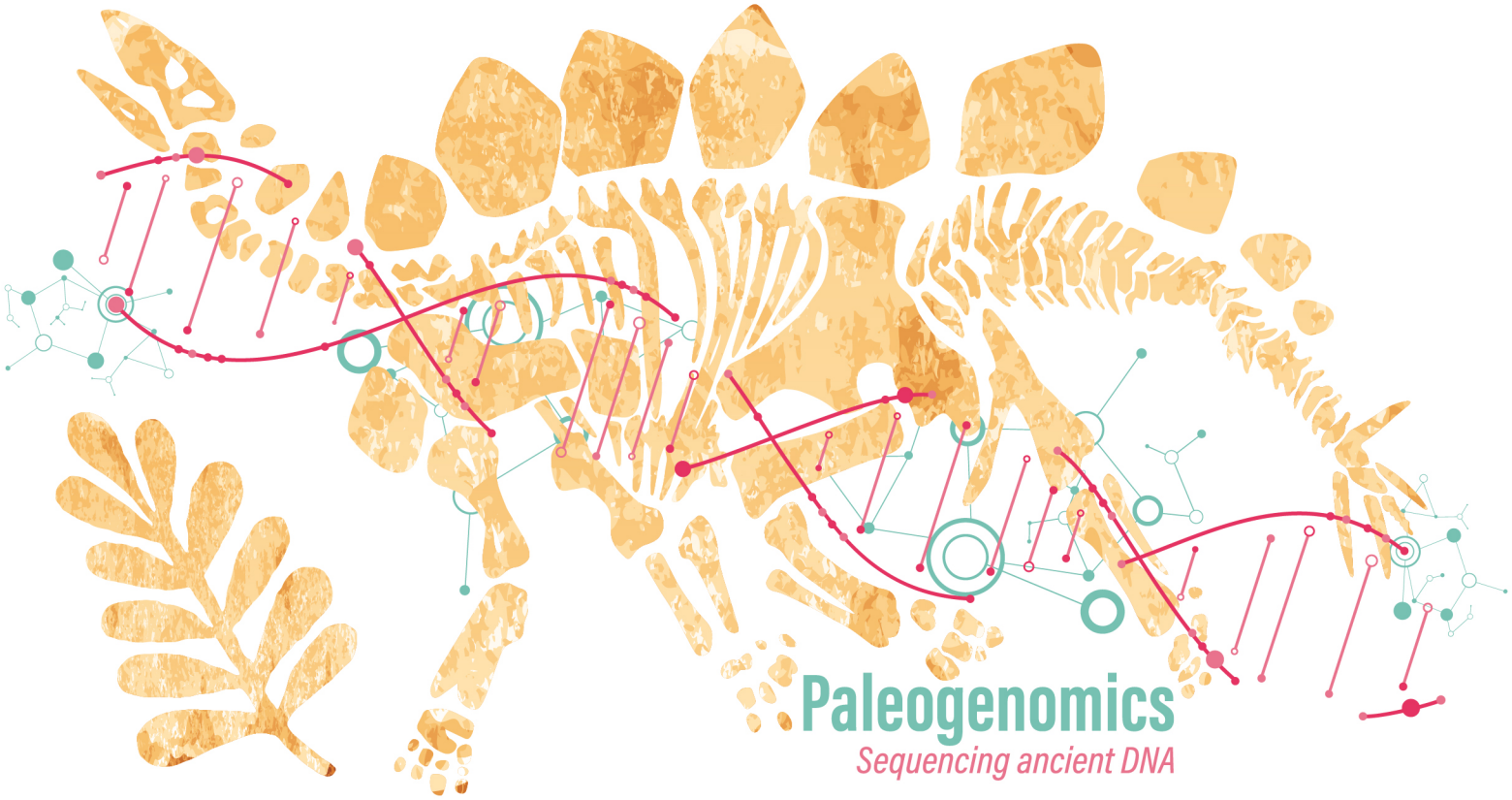

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IDENTIFICATION OF LONG NON-CODING RNAS (LNCRNAS) IN SWINE FETUS

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Abstract:
Long non-coding RNAs (lncRNAs) are non-coding protein RNAs that are involved in several biological processes. However, knowledge regarding lncRNAs action mechanisms and functions are still limited, especially in the early fetal development of swine. Therefore, the aim of this study was to characterize and identify lncRNAs in swine fetuses at 35 days of pregnancy. RNA-Seq libraries of 10 swine fetuses were prepared using the Illumina Stranded Total RNA Prep kit, ligation with Ribo-Zero Plus for ribosomal RNA depletion and then sequenced in Illumina HiSeq2500 platform. After sequencing, data quality control was conducted using Trimmomatic, followed by alignment with HISAT2 against the reference genome (Sus scrofa11.1) and transcript assembly with StringTie. After sequencing, data quality control was conducted using Trimmomatic, followed by alignment with HISAT2 against the reference genome (Sus scrofa11.1) and transcript assembly with StringTie. Before validating potential new lncRNAs, all transcripts with a length <200 nucleotides, located in single exons and a value of Fragments Per Kilobase Million (FPKM) ≤0.5 were removed for further analysis. The Coding Potential Calculator (CPC2), Predictor of Long non-coding RNAs and messenger RNAs based on an improved K-mer scheme (PLEK), Coding Potential Assessment Tool (CPAT) and Coding-Non-Coding Index (CNCI) were used to predict the coding potential of the transcripts and those which were common to the programs were considered potentially new lncRNAs. Furthermore, to improve the confidence, Pfam database was used to verify if the identified transcripts had known protein domains. A total of 871 potential new lncRNAs were identified, of which 699 were intronic lncRNAs, 169 were intergenic, two were antisense and one was a potential new isomorph. Intronic lncRNAs accounted for a high proportion (80%) of the identified lncRNA candidates, distributed across all chromosomes, with most of the new lncRNAs located on chromosome 1. Among them, we identified new intronic lncRNAs, potentially regulating the expression of the genes *IGF1R* (Insulin-like Growth Factor 1 Receptor), *IGF2BP1* (insulin-like growth factor 2 mRNA-binding protein 1), *SOX5* (SRY-Box Transcription Factor 5) and *FOXO1* (Forkhead Box O1), which are involved on fetal growth and development. In this study, lncRNAs in swine fetuses at 35 days of pregnancy were identified, showing the importance of this RNA class on fetal development. Furthermore, new lncRNAs were predicted, which improve the knowledge about lncRNAs in swine. These findings will also help future research on the role of lncRNAs in reproduction, not only in swine, but also in other species.
Palavras-chave: bioinformatics; exon; intronic; ;

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