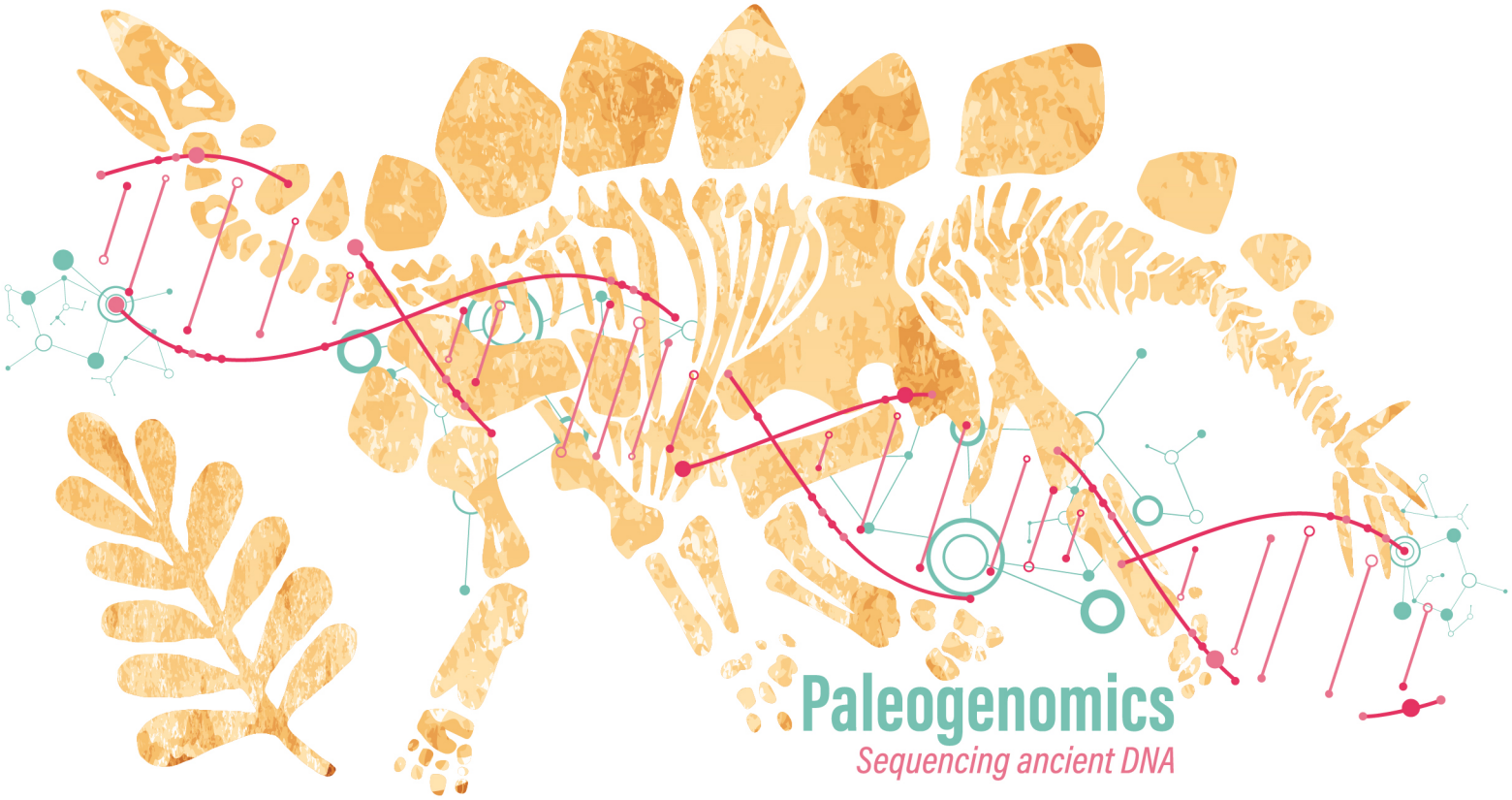

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MIRNA EXPRESSION PROFILE DIFFERS BETWEEN CHICKEN LINES WITH DIFFERENT GROWTH RATES

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Abstract:
Chicken has been domesticated for over 8000 years, but it was in the last 50 years that selection for quantitative traits, such as growth, feed efficiency, and meat quality, led to increased phenotypic changes. In these 5 decades, the growth rate increased by over 400%. Recent studies have shown different epigenetic changes in the methylation patterns among red jungle fowl and domestic chickens. Considering broilers, several genotypes have been selected including those related to different growth rates, which may affect meat quality and the appearance of muscle disorders. Therefore, to verify if the miRNAs expression is involved with chicken growth pattern, we evaluated the pectoral major muscle (PMM) microRNA profile in a fast-growth commercial broiler line (Ross) and in a medium-growth paternal broiler line developed by Embrapa (TT). A total of 18 male broilers with 28 days of age (10 from TT and 8 from Ross) was used for the sequencing analysis. RNA extraction was performed with Trizol (ThermoFisher Scientific), followed by purification with RNeasy Mini kit (Qiagen). Libraries were prepared with the QIAseq miRNA Library kit (Qiagen). Sequencing was performed in the NextSeq equipment (Illumina) with a single-end protocol (1x75bp). Reads were submitted to quality control (Trimmomatic), mapping (bowtie + miRDeep2), and miRNA identification and counting (miRDeep2). miRNA expression analysis was performed using limma package from R and those with FDR ≤ 0.05 were considered differentially expressed (DE). miRNAs target genes were predicted with sRNAtoolbox and functional annotation was performed using DAVID, String, and Biomart tools. A total of 142 miRNAs were detected using all samples, and 15 were DE between the two lines. Five miRNAs were upregulated in the TT (gga-miR-499-5p, gga-miR-181a-3p, gga-miR-133c-3p, gga-miR-1a-3p, gga-miR-30a-5p) and 10 were upregulated in the Ross (gga-miR-132a-3p, gga-miR-146b-5p, gga-miR-219b, gga-miR-29a-3p, gga-miR-29c-3p, gga-miR-223, gga-miR-146b-3p, gga-miR-27b-3p, gga-miR-146a-5p, gga-miR-1729-5p). While the upregulated miRNAs in the TT line have essential roles on muscle development (gga-miR-1a-3p), myogenesis (gga-miR-499 and gga-miR-1a) and satellite cell activation (gga-miR-499 and gga-miR-30), those upregulated in the Ross line are involved in muscle development (gga-miR-29, gga-miR-146b), angiogenesis (gga-miR-27b), lipid and glicose metabolism (gga-miR-27b, gga-miR-219, gga-miR-1729) and inflammation (gga-miR-132a, gga-miR-223, gga-miR-219). A total of 544 genes was predicted as targets for the 15 DE miRNAs. When these target genes were evaluated, several of them were related to the biological processes previously mentioned. Therefore, we identified miRNAs DE in the PMM between the two lines that are probably involved in the difference in their growth intensities, which may explain the increase in the occurrence of pectoral disorders in fast-growing lines in the last decade.
Palavras-chave: broilers; small RNAs; sequencing; non -coding RNAs; muscle

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