

Use of *in silico* approach for identification of miRNAs content in buffalo

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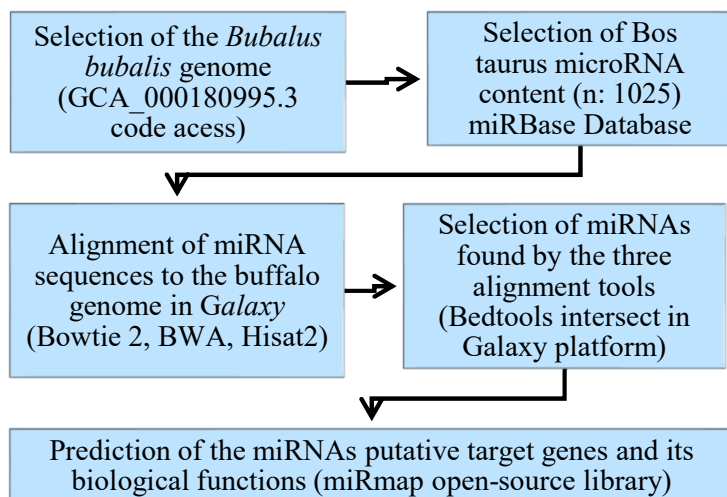
Introduction

- The miRNAs are short molecules involved in the post-transcriptional regulation of gene transcripts in several metabolic pathways.
- Due its regulative role, elucidate the content of miRNAs in different tissues can be used to study the gene expression mechanisms.
- The use of bioinformatic tools are low cost and available strategy for identifying miRNAs, particularly in species with few transcriptomic data available on open access platforms such as buffaloes (*Bubalus bubalis*).

Main Goal

- This work aims to carry out an *in silico* approach to identify homologous miRNAs between cattle (*Bos taurus*) and buffaloes, through the mapping of miRNAs sequences from cattle to the buffalo genome.

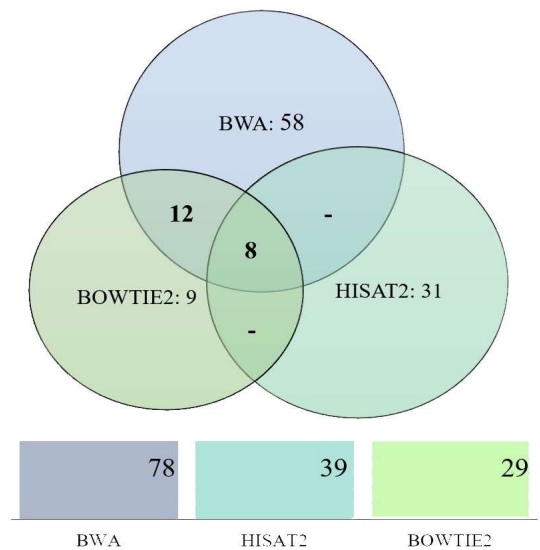
Methods



Conclusions

- In conclusion, the *in silico* approach used herein was able to find homologous miRNAs in cattle and buffalo, the increment of transcriptomic data may further reveal that the miRNA content shared by these species may be more extensive than this initial evaluation showed to be.

Results and Discussion



- Alignment results: 29 (2.83%) miRNAs were identified using Bowtie2, 78 (7.71%) using BWA and 39 (3.74%) using Hisat2. From that, the miRNAs sequences obtained were superimposed and 8 miRNAs were simultaneously aligned by the three softwares (*bta-miR-11975*, *bta-miR-214*, *bta-miR-7865*, *bta-miR-1343-5p*, *bta-miR-10185-5p*, *bta-miR-2449*, *bta-miR-12030* and *bta-miR-11976*).
- Next, was identified the putative target genes of the 8 miRNAs, thus only 3 miRNAs were available in the miRmap library: *bta-miR-2449* regulates at least 33 target genes, *bta-miR-214* at least 32 genes and *bta-miR-1343-5p* at least 8 target genes. The biological functions of target genes were related to immune and inflammatory response, female fertility, fetal development and lipid metabolism.
- In summary, 8 homologous miRNAs with identical sequences were identified between buffalo and cattle, whose biological functions may also be conserved. Studies comparing cichlid fishes (X et al. 2019. *Sci Rep*, 9: 13848) and human and murine oocytes (B et al. *Biol Reprod*, 95: 1–13) indicated that miRNA content among species may be conserved, therefore, we suggest that a comparative alignment with cattle related specie may be useful as an initial screening of miRNAs in buffalo.
- Due to the molecular complexity the identification of miRNA content and its associated targets in tissues and species is still challenge, to achieve that the development and improvement of bioinformatic tools, as well as the generation of transcriptomic data are required.