



# SERUM MICRORNAs IN BUFFALO COWS: POTENTIAL BIOMARKERS OF PREGNANCY



VIDEO INTERVIEW  
Paolo Manini & Francesco Lipariti (2019)



**Abstract** In recent decades, interest in buffalo breeding has largely increased worldwide thus focusing the attention on this species as a dairy purpose animal. Problems related to long calving interval, late puberty and seasonal anestrus hamper reproductive efficiency in this species.

Early pregnancy diagnosis is important to shorten the calving interval and increase lifetime production on dairy animals. MicroRNAs have recently emerged as key molecules in fertilization of several species even though in buffalo, few previous studies have investigated miRNAs. The aim of this research was to identify the best miRNA reference in serum among miR-191, miR-25-3p, SNORD44, and SNORD48.

Consequently, assess the expression levels of miR-103, miR-200b, miR-301a, miR-423-5p, miR-375, miR-451 and miR-452 involved in buffalo progesterone-maturation oocyte and pregnancy. Interestingly, we found that all the miRNAs analyzed at 40 days after artificial insemination were differentially expressed among pregnant and non-pregnant buffalo.

**TESISTA**  
Michela Capurro

**RELATORE**  
dr Danilo Zampini

**CORRELATORI**  
dr Gabriella Guelfi  
dr Raoul Ciappelloni

## BACKGROUND

Reproductive efficiency is the primary factor affecting productivity. Failure to become pregnant leads to a negative impact on reproductive performances in the dairy industry and causes important economic losses ... [1]



<https://vimeo.com/128129079>

Animation – **MicroRNAs** (by Katharina Petsche)

Biogenesis and functions of microRNAs within the cell. MicroRNAs are small RNA molecules that regulate gene expression and have a big impact on many biological processes.

## EXPERIMENTAL PROCEDURE

**Animal selection and study design.** Fifteen lactating Italian Mediterranean buffalo cows were included in the present study... [2]

**Serum sample collection and preparation.** Blood was withdrawn at D0, D25 and D40 from AI and C buffaloes... [3]

**Computational prediction of miRNAs and pathway enrichment analysis.** Kyoto Encyclopedia of Genes and Genomes was used to identify the genes involved in buffalo progesterone mediated oocyte maturation... [4]

**Total RNA isolation, reverse transcription, and qPCR amplification.** Total RNA, including miRNAs, extracted ... [5]



<https://youtu.be/RynQM1kVJk>



Sequenza LNA microRNA technologies

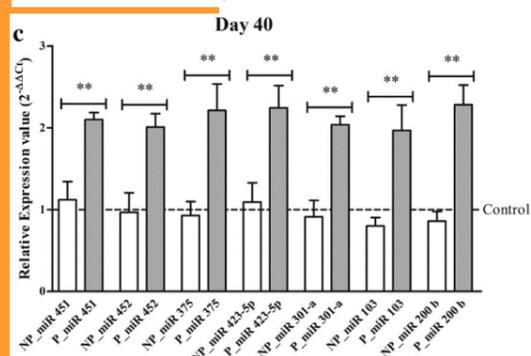
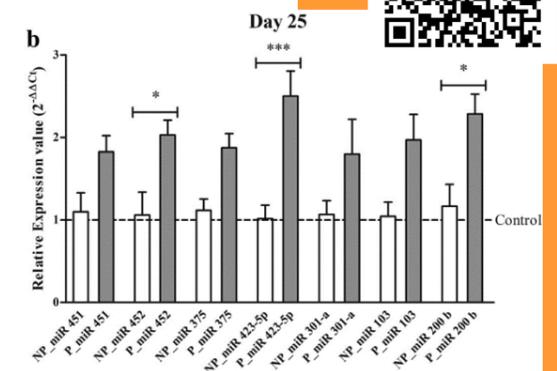
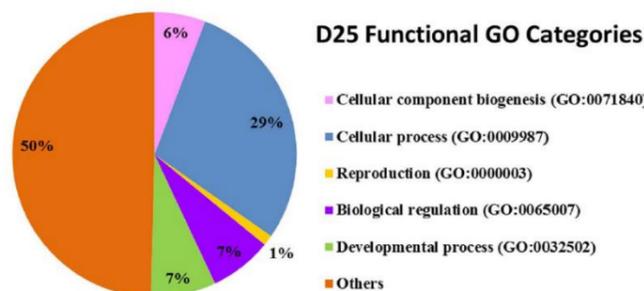
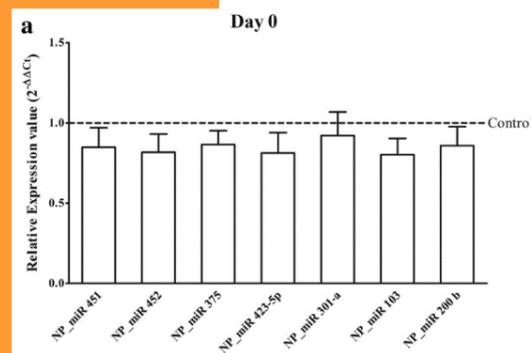


## RESULTS

**Analysis of stability of candidate reference miRNAs.** [6]

### MicroRNA detection and differential expression analysis

A D25 miR-452, miR-423-5p, miR-200b are differentially expressed between P and NP groups. While a D40 in P groups all miRNAs are upregulated. differentially expressed between P and NP groups. While a D40 in P groups all miRNAs are upregulated. [7]



Differentially expressed miRNAs integrated to target genes using miRDB and related to their functional groups using Gene ontology.

## DISCUSSION

Data suggest that there could exist a relationship between miRNAs investigated and pregnancy outcome in buffaloes. In conclusion, this study may be considered a first step for gaining further insight into miRNAs biological function in buffalo reproduction. However, miRNA-mediated repression of the uterine transcriptome in pregnancy is not entirely clear and further investigation is required to explore the functional implications of miRNAs in a successful pregnancy.



This work is licensed under a Creative Commons Attribution-ShareAlike 4.0 International License.



This work is licensed under a Creative Commons Attribution 4.0 International License.