

# QRT-PCR EVALUATION OF SELECTED MICRORNAS' EXPRESSIONS IN THE AMNIOTIC FLUID AND CHORIONIC VILLUS SAMPLES FROM DOWN SYNDROME PREGNANCIES

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## INTRODUCTION

Trisomy 21, responsible for 95% of Down syndrome cases, is the most common viable aneuploidy. Prenatal diagnosis is based on genetic tests conducted on samples obtained by invasive procedures (1, 2, 3).

## OBJECTIVES AND BACKGROUND

Here we show preliminary data on the expression of hsa-miR-371-3 placenta specific cluster and of 5 microRNAs mapped on chromosome 21 (hsa-miR-99a, hsa-let-7c, hsa-miR-125b-2, hsa-miR-155, hsa-miR-802).

## MATERIALS AND METHODS

Biological material obtained by amniocentesis and chorionic villous sampling, was preserved in RNA later at -80°C until further usage. microRNA quantification was performed using dedicated TaqMan assays on synthesized cDNAs using a two-step Cells-to-Ct kit. The changes that occurred in microRNA expression were calculated using the  $\Delta\Delta C_t$  method.

## RESULTS

We found statistically significant changes in the expression of three microRNAs (one belonging the miR-371-3 cluster, the other two mapped on chromosome 21)

in aneuploid samples compared to euploid samples. We found significant differences between microRNAs' expression in samples obtained from male fetus vs. female fetus pregnancies. Data regarding the transcriptional profiles, primary microRNAs respectively, are provided by these microRNAs, through an advanced putative mechanism that explains the results.

## CONCLUSIONS

The significance of our data is also discussed in terms of utility for antenatal diagnosis.

## REFERENCES

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