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MicroRNA profiling in women with threaten preterm labor

I Mbongo Langmia, Y Devi Apalasamy, S Zawiah Omar and **Z Mohamed**
University of Malaya, Malaysia

Preterm birth (PTB), which is defined as child birth before completion of 37 weeks of gestation is the largest single cause of neonatal mortality in the world. PTB is a multifactorial condition involving more than one biological pathway and until now, the molecular determinants of PTB have not been fully elucidated. Highly conserved single-stranded non-coding RNAs such as microRNAs (miRNA) that play important role in gene regulation have now been implicated in preterm birth complication. The objective of this study was to profile expression of microRNAs in women with preterm and term labor.

Materials & Methods: The study involved a total of 20 women (10 preterm and 10 term) with spontaneous preterm and term delivery. The miRNA profiles were measured in 3 mls of maternal blood using Affymetrix® GeneChip® miRNA 3.0 Array. Data were analyzed using Expression console software, Transcriptome Analysis Console (TAC) and IPA software. A fold change of >2 and a false-discovery rate of <20% was used to determine the most differentially expressed miRNAs.

Results: Thirty four microRNAs were found to be significantly different between women with preterm labor compared to term labor.

Conclusion: This study shows significantly different expression patterns of 34 microRNAs in women with preterm labor compared to term labor. These microRNAs may be involved in the mechanism that initiates preterm labor. Validation of these results in a lager sample size is ongoing. Specific microRNA regulators may have important roles for patient susceptibility to preterm birth.

Biography

Immaculate Langmia is a student at the University of Malaya in Malaysia. She obtained a master degree in pharmacy at the University of Teknologi MARA (UiTM) and a bachelor degree with honors in Biochemistry at the University of Buea (UB) in Cameroon. She has work experience as a research assistant at the Pharmacogenomics Laboratory, University Malaya. Presently her area of research focuses on genomics as well as pharmacogenomics, pharmacogenetics (drug metabolism) studies. She has been involved in research for the past few years with few publications in reputable journals. She is a member of Human Life Foundation (HLAF).

immapad2010@gmail.com

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