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Micro RNA profiling in maternal blood of women with preterm and term delivery

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Preterm birth (PTB) is a serious global health problem. The pathophysiological and molecular pathways involved in PTB are not fully understood. Highly conserved single stranded non-coding RNAs such as MicroRNAs (miRNAs) that are involved in gene regulation have been implicated in pregnancy associated diseases. The objective of this study is to characterize miRNAs expression in maternal circulation and to compare the expression profiles between women with spontaneous preterm and term delivery. The case control study involved 20 women with spontaneous preterm and term delivery. Total RNA extracted from maternal venous blood was used for miRNA profiling with the use of the Affymetrix GeneChip miRNA Array. Expression analysis of miRNAs in samples was performed using Affymetrix® Transcriptome Analysis Console (TAC). Real time quantitative polymerase chain reaction (RT-qPCR) was used to validate the microarray results. Microarray analysis in the maternal samples identified a total of 25 miRNAs differentially expressed between preterm versus term groups. We suggest that these miRNAs might be involved in the inflammatory and signaling pathway of PTB and its role in preterm birth complication warrant further investigation.

Biography

Immaculate Mbongo Langmia has completed her PhD at the University of Malaya and she is presently a Postdoctoral fellow at the same institution. She has published papers in reputed journals. Her research interests include molecular pharmacology (pharmacogenomics, pharmacogenetics) and clinical pharmacology (pharmacokinetics and drug metabolism).

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