BioMed Research International

Special Issue on

New Insight into Pathogenesis of Neonatal Diseases: Application of the Whole-Genome Studies

CALL FOR PAPERS

The development of medicine has resulted in an increased survival of newborns. However, the improved survival of infants has led to an increased rate of morbidities among very low birth weight infants, hypoxic-ischemic term infants, or children with birth defects. It is an interesting and still partly unanswered issue which factors from the prenatal and perinatal periods are of crucial importance in the survival of infants and then the development of long term complications.

Evaluation of genetic background of neonatal problems is difficult; however, rapid development of molecular diagnostic methods increases their applications in neonatology. For example, new, less invasive methods of DNA sampling such as buccal swabs are possible now, making this type of studies more suitable for newborns and acceptable by the Ethics Committee and parents.

Most of clinically relevant problems in neonatology can be recognized as complex diseases, and their pathogenesis depends on the interaction of a susceptible host with a multitude of environmental risk factors. Nowadays, the major approach in the identification of the genetic background of complex diseases is based on positional cloning and candidate gene approach. This can be achieved by GWAS (genome wide association study) and genome wide linkage analysis and functional studies. The new tool, DNA microarray, allows for the analysis of expression of practically all human genes. Computational methods for analysing vast amounts of data are being developed and quantitative tools for analysing networks are now available. Microarrays could be used for studying associations between genetic variations and the occurrence of diseases, searching for disease susceptibility markers, molecular karyotyping, and pharmacogenomics. The greatest advantage of this method is that it enables in one experiment the assessment of a great number of genetic factors, although only a small amount of blood is necessary for testing, which is very important in neonates. Another important issue which can contribute to the phenotype variation of complex diseases and traits is epigenetics. Methods for evaluation of DNA methylation have been introduced to neonatology too.

Identification of factors involved in the pathogenesis of diseases could help developing new and innovative treatments and allow the targeting of a "high-risk" subpopulations reducing unnecessary exposure to potentially harmful therapies.

The purpose of this special issue is to publish research papers as well as review articles addressing recent advances on understanding of neonatal pathologies. Original contributions that are not yet published or that are not currently under review by other journals or peer-reviewed conferences are sought.

Potential topics include, but are not limited to:

- GWAS and genome wide linkage analyses in neonatology
- The results of genome expression profiling in neonatology
- Methylation studies in neonatology
- Histone modifications and microRNA studies in neonatology
- Experimental studies of functional genomics
- Animal studies with application of whole-genome analysis related to neonatal diseases
- Epigenetic-based diagnostics in neonatology
- Genome-based diagnostics in NICU
- Recent advances in genome-based diagnostics to identify biosignatures of neonatal diseases
- Next-generation sequencing-based diagnostics in neonatology

Authors can submit their manuscripts via the Manuscript Tracking System at http://mts.hindawi.com/submit/journals/bmri/pediatrics/pnd/.

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