A research team from China characterized the differentially expressed gene profiles in livers from biliary atresia (BA) patients. They found that RRAS gene and its related MAPK pathway are important regulatory modules in the pathogenesis of BA, which may serve as a novel prognostic marker for BA.

Biliary atresia (BA) is an inflammatory obliterative cholangiopathy with unknown etiology, leading to progressive fibrosis and cirrhosis. Microarray technology, emerged as an indispensable research tool for gene expression profiling, has been used to study the mechanism underlying BA, and allows the simultaneous analysis of thousands of transcripts within a single experiment. Some studies have been performed to investigate the gene expression profiling of livers from BA patients. However, none of them was designed to identify genes that play a key role in the pathogenesis and prognosis of BA.

A research article to be published on February 14, 2011 in the World Journal of Gastroenterology addresses this question. In this study, DNA microarrays for whole genome gene expression and bioinformatics analysis were used to characterize the differentially expressed gene patterns of normal livers and livers from BA patients at different ages, as well as to ascertain the genes and pathways that play a central role in the pathogenesis of BA. Furthermore, reverse-transcription polymerase chain reaction was performed to confirm the changes in selected genes. The relation between selected gene expression and prognosis of BA patients was also analyzed.
The results showed autoimmune response mediated by T lymphocytes may play a vital role in the pathogenesis of BA. The RRAS gene and its related MAPK pathway are important regulatory modules in the pathogenesis of BA, which may serve as a novel prognostic marker for BA.

By identifying genes and pathways playing a central role in the pathogenesis of BA, this study may represent a future strategy for therapeutic intervention in treatment of BA.


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