European Respiratory Society
Annual Congress 2012

Abstract Group: 2.1. Acute Critical Care

Keyword 1: Circulation **Keyword 2:** Sepsis **Keyword 3:** Critically ill patients

Title: Serum microRNA signatures identified by Solexa sequencing predict sepsis patients mortality: A prospective observational study

Dr. Huijuan 6322 Wang wanghuijuan301@gmail.com MD [1,2,3], Dr. Pengjun 6323 Zhang zhangpj301@gmail.com MD [4], Prof. Weijun 6324 Chen chenwj@genomics.org.cn [5], Prof. Dan 6325 Feng fddd@263.net MD [6], Mrs. Yanhong 6326 Jia yang8625@mail.nankai.edu.cn [3] and Prof. Lixin 6327 Xie xielx@263.net MD [1,3]. [1] Department of Respiratory Medicine, Hainan Branch of Chinese PLA General Hospital, Sanya, Hainan Province, China, 572013 ; [2] Medical College, Nankai University Medical College, Tianjin, China, 30071 ; [3] Department of Respiratory Medicine, Chinese PLA General Hospital, Beijing, China, 100853 ; [4] Department of Clinical Biochemistry, Chinese PLA General Hospital, Beijing, China, 100853 ; [5] Chinese Academy of Sciences, Beijing Institute of Genomics, Beijing, China and [6] Department of Medical Statistics, Chinese PLA General Hospital, Beijing, China .

Body: Background: Sepsis is the leading cause of death in Intensive Care Unit. Novel biomarkers and targets of treatment were still needed to improve the mortality. Our goal of the prospective study was to investigate if serum miRNAs identified in genome-wide scans could predict sepsis mortality. Methodology/Principal findings: 214 sepsis patients participated in the study. Solexa sequencing followed by qRT-PCR were used to test for differences in the levels of miRNAs between survivors and non-survivors of sepsis patients. miR-223, miR-15a, miR-16, miR-122, miR-193* and miR-483-5p were significantly differentially expressed, and the area under curve of the six miRNAs predictive mortality value ranged from 0.610 (95%CI, 0.523-0.697) to 0.790 (95%CI, 0.719-0.861). Logistic regression analysis showed that sepsis stage, APACHE II score, miR-15a, miR-16, miR-193b* and miR-483-5p were correlated to the death of sepsis and area under curve of the six variables predictive value was 0.950 (95% Confident interval, 0.919-0.982), which was much higher than APACHE II score, SOFA score, and procalcitonin with area under curve of 0.782 (95% CI, 0.712-0.851), 0.752 (95% CI, 0.672-0.832) and 0.689 (95% CI, 0.611-0.784), respectively. When the cut off point set at 0.526, the predictive value of the six variables provided a 85.2% sensitivity and a 90.4% specificity. In addition, miR-193b* had highest odds ratio of 9.23(95% CI, 1.20-71.16). Conclusion/Significance: Six miRNAs expression profiles could be used to predict septic mortality. The predictive value was better than the indictors that used in clinical.