Molecular dissection of respiratory syncytial virus infection

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A study published this week in *PLOS Medicine* reveals profound systemic dysregulation of the immune response induced by RSV infection in young children and suggest that molecular markers might be able to predict disease severity.

RSV is responsible for a substantial fraction of serious respiratory infections and deaths among young children worldwide and a top candidate for vaccine development.

A team of researchers led by Asuncion Mejias and Octavio Ramilo, both from The Research Institute at Nationwide Children's Hospital, and The Ohio State University College of Medicine, examined the global gene expression patterns in blood samples from four different cohorts of children who were hospitalized with lower respiratory tract infections.

They found that children who are ill with RSV infections have a characteristic gene expression pattern that is different not only from healthy children but also from children infected with either influenza virus or human rhinovirus, two other common causes of lower respiratory tract disease.

This pattern, which the researchers called the RSV biosignature, could reliably identify children with RSV infections in different settings. From it, they derived a genomic "severity score" that correlated with clinical indices of disease severity, and with length of hospitalization and need for supplemental oxygen.

The RSV biosignature also provided insights into the status of the immune system in the sick children: RSV infection was associated with elevated levels of some inflammation genes as well as suppression of non-specific immune system genes and reduced expression of specific B and T cell genes. This was particularly evident in infants under 6 months of age.

The authors conclude that "Blood RNA profiles of infants with RSV lower respiratory tract infections allow specific diagnosis, better understanding of disease pathogenesis, and assessment of disease severity" and say their study "opens new avenues for biomarker discovery and identification of potential therapeutic or preventive targets."

In an accompanying Perspective, Peter Openshaw agrees that "this study moves the field several steps towards the clinical use of transcriptomic profiling in the diagnosis and prognostication of children with acute respiratory infections" but also cautions that "the peripheral blood may not be telling the whole story and needs to be complemented by detailed studies of the response in the respiratory tract".

More information: Mejias A, Dimo B, Suarez NM, Garcia C, Suarez-Arrabal MC, et al. (2013) Whole Blood Gene Expression Profiles to Assess Pathogenesis and Disease Severity in Infants with Respiratory Syncytial Virus Infection. PLoS Med 10(11): e1001549. DOI: 10.1371/journal.pmed.1001549

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