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Sepsis-associated acute respiratory distress syndrome (Guillen-Guio, 2020)

Beatriz Guillen-Guio, et al.
The Lancet Respiratory Medicine

Lungs | Infection | Inflammation

STUDY SUMMARY

Discovery of a variant in the FTL1 gene associated with susceptibility to sepsis-induced acute respiratory distress syndrome.

STUDY DESCRIPTION

Sepsis occurs when chemicals that are released in the bloodstream to fight an infection trigger inflammation throughout the body. Sepsis can be life-threatening and lead to long-term damage of many organs. If the lungs are affected, it can result in acute respiratory distress syndrome (ARDS), whereby fluids enter the lungs, making it extremely difficult to breathe. Individuals who survive ARDS are often left with permanent cognitive and physical impairment that is caused by organ damage due to insufficient oxygen supply. This genome-wide study examined nearly 2,000 individuals of European ancestry to better understand the genetic predisposition to developing ARDS in patients with sepsis. The study discovered one variant in the FTL1 gene. FTL1 encodes a *receptor* that plays an important role in the development and function of the body's vasculature.

DID YOU KNOW?

Sepsis is estimated to affect nearly 30 million individuals each year. Vulnerable populations include the elderly, pregnant women, and hospitalized patients.

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to sepsis-related ARDS. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to sepsis-related ARDS. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to sepsis-related ARDS. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

VARIANT	YOUR GENOTYPE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs9508032_T NEW	T / T	-0.49 (↓)	71%	5.20×10^{-8}