Research team identifies a new genetic variant associated with acute respiratory distress

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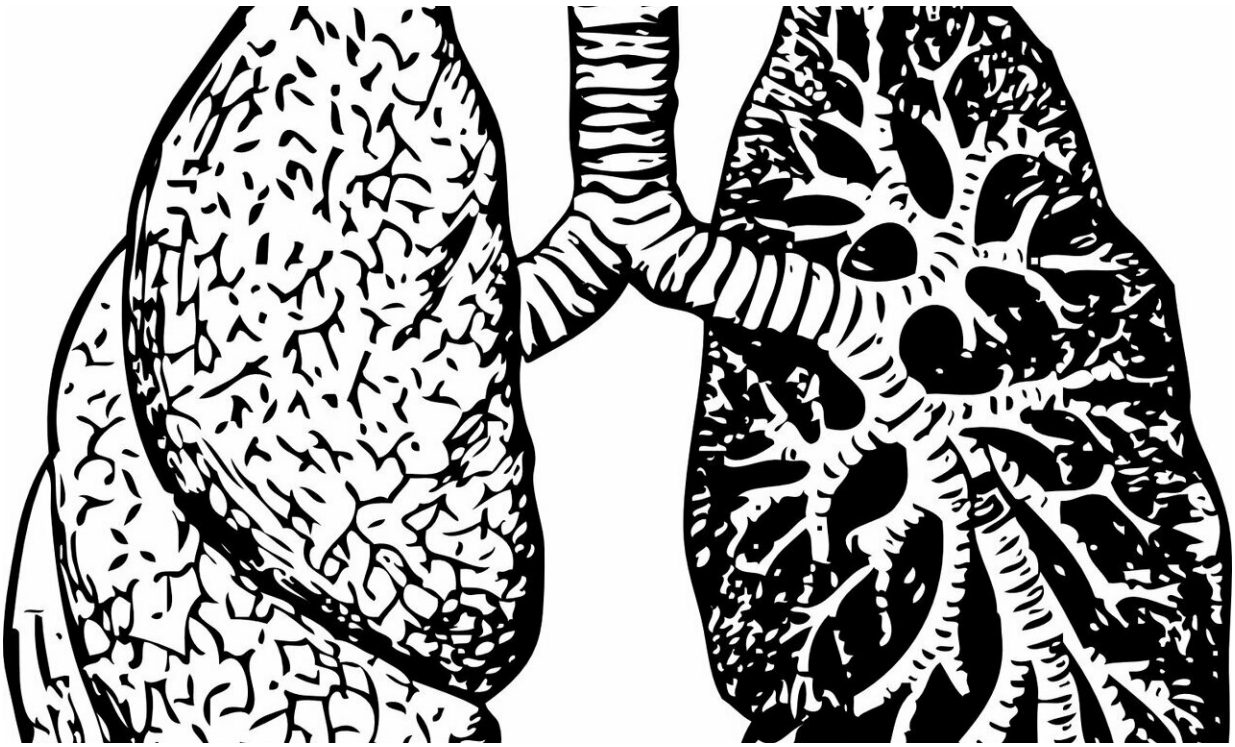

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An international collaboration including Javier Belda, professor of surgery at the University of Valencia, has reported a new genetic variant associated with acute respiratory distress syndrome (ARDS). The work,

with a sample of more than 2,000 patients, has been published in the *Intensive Care Medicine Experimental* journal.

ARDS is one of the main causes of mortality in adults admitted to intensive care units. Previous studies have shown the existence of genetic variants involved in susceptibility for this syndrome.

The researchers sought to identify new genes involved in the susceptibility to ARDS induced by sepsis. For this, three candidate genes were prioritised, and a single nucleotide polymorphism of the FLT1 gene was associated with ARDS.

Javier Belda, co-author of the study, says, "The identification of genes associated with respiratory distress syndrome allows us in the clinic to advance treatment decisions to the patient, which brings us closer to a personalised or precision medicine."

The work included a sample of more than 2,000 participants. The first study of association and recognition of the genes involved was carried out among 225 patients with ARDS induced by sepsis and 899 controls based on the population. Finally, the findings were validated in an independent sample of 661 cases of ARDS induced by sepsis and 234 risk controls.

The researchers identified a genetic variant of the vascular endothelial growth factor receptor FLT1 as a new susceptibility gene for ARDS and have shown that the integration of genomic data can be a valid procedure to identify new susceptibility genes.

More information: undefined undefined et al. A vascular endothelial growth factor receptor gene variant is associated with susceptibility to acute respiratory distress syndrome, *Intensive Care Medicine Experimental* (2018). DOI: 10.1186/s40635-018-0181-6