Immune cells' gene expression may predict flu susceptibility

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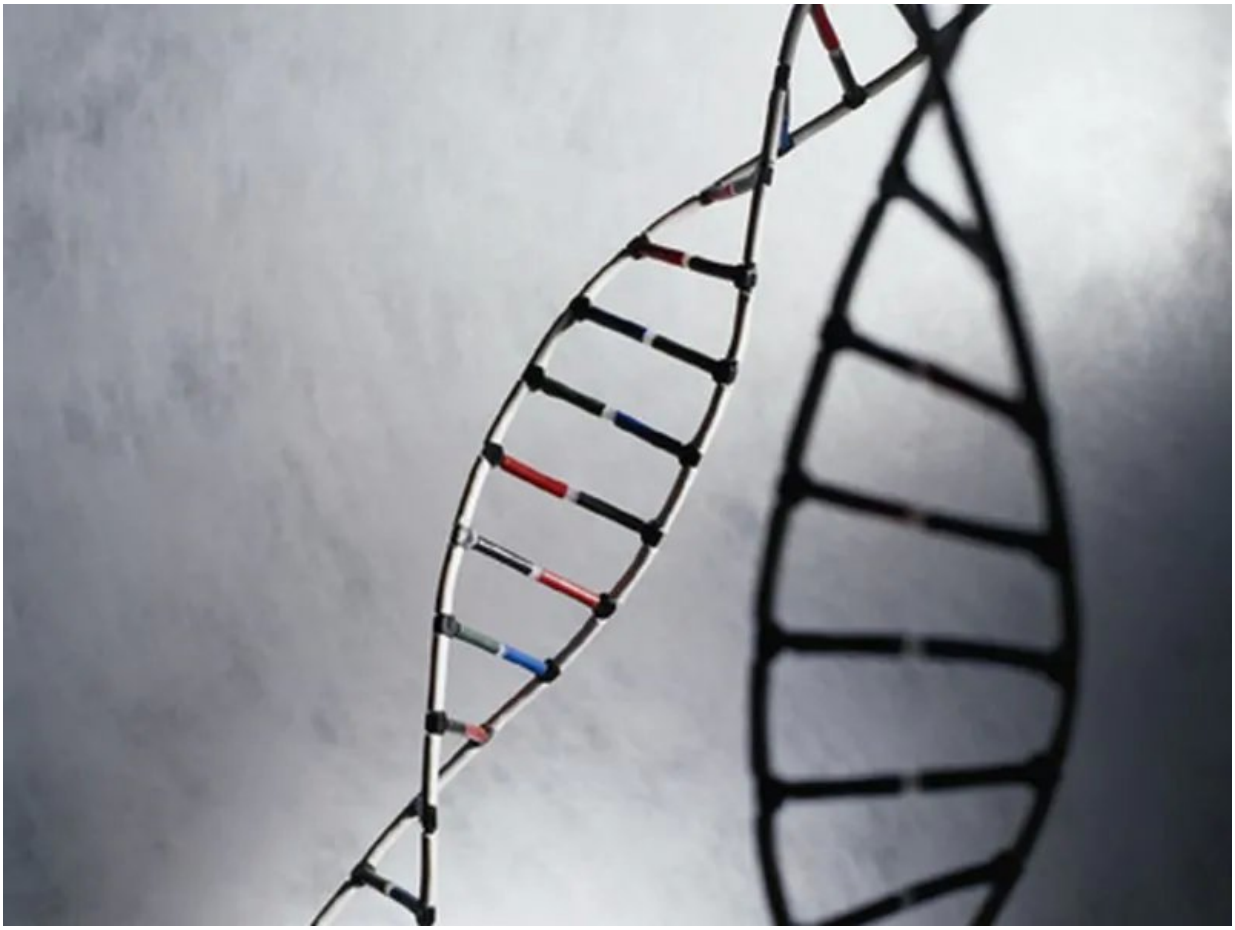

(HealthDay)—*KLRD1*-expressing natural killer cells may be a biomarker

for influenza susceptibility, according to a study published recently in *Genome Medicine*.

Erika Bongen, from the Stanford University School of Medicine in California, and colleagues estimated immune cell proportions from whole blood transcriptome data in four independent influenza challenge studies. Immune cell proportions were compared between symptomatic shedders and asymptomatic non-shedders across three discovery cohorts before influenza inoculation, and results were tested in a held-out validation challenge cohort.

The researchers found that natural killer cells were significantly lower in symptomatic shedders at baseline in all cohorts. In symptomatic shedders, hematopoietic stem and progenitor cells were significantly higher at baseline in discovery cohorts and higher, but not significantly higher, in the validation cohort. *KLRD1*, a gene associated with natural killer cells, was expressed at lower levels in symptomatic shedders at baseline in discovery and validation cohorts. Furthermore, *KLRD1* expression at baseline was negatively correlated with influenza infection symptom severity.

"It will be crucial to understand the role of natural killer cells' protection so that we can potentially leverage that in designing better flu vaccines," a coauthor said in a statement. "Since we see that natural killer cells are protective across different strains, maybe that would be a path to a universal flu vaccine."

More information: Abstract/Full Text

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