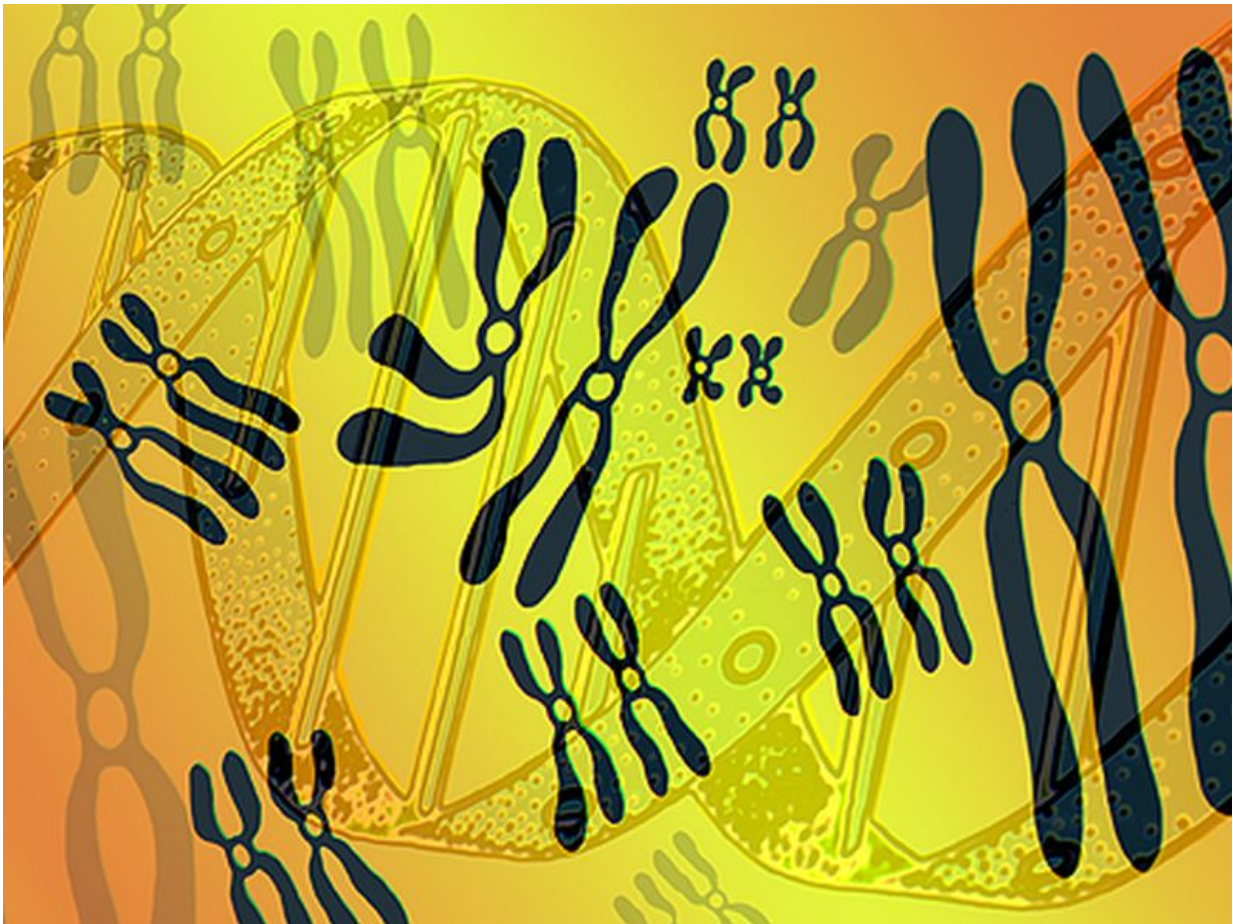


Gene expression may predict response to methotrexate in RA

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(HealthDay)—For patients with rheumatoid arthritis (RA), increased

baseline gene expression of *p21*, *caspase 3*, and runt-related transcription factor (*RUNX*)2 in the peripheral blood may be associated with improved clinical response to methotrexate (MTX), according to a study published online July 25 in the *International Journal of Rheumatic Diseases*.

Elena V. Tchetina, Ph.D., from the Nasonova Research Institute of Rheumatology in Moscow, and colleagues examined 26 control subjects and 40 patients with RA to determine the potential of baseline gene [expression](#) in the whole blood of disease-modifying anti-rheumatic drug-naïve RA patients for predicting response to MTX.

The researchers found that significant increases in joint space narrowing score (JSN) accompanied decreases in [disease activity](#) at the end of the study. Expressions of the Unc-51-like kinase1 (*ULK1*) and matrix metalloproteinase (*MMP-9*) [genes](#) were positively associated with the level of C-reactive protein; *MMP-9* expression correlated with Disease Activity Score of 28 joints (DAS28) and swollen joint count. There was a positive correlation for baseline tumor necrosis factor α gene expression with JSN at the end of follow-up, while correlations were seen for *p21*, *caspase 3*, and *RUNX2* with Δ DAS28 values.

"Our results suggest that the expressions of *MMP-9* and *ULK1* might be associated with disease activity," the authors write. "Increased baseline gene expressions of *RUNX2*, *p21*, and *caspase 3* in the peripheral blood might predict better responses to MTX therapy."

More information: [Abstract](#)
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