

# Putting autoimmune disease genetic links to the test

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Credit: NIH

Studies of autoimmune and inflammatory diseases have identified hundreds of genetic regions thought to be associated with these conditions. At the same time, studies of expression quantitative trait loci (eQTLs) have revealed the abundance of inherited variations in gene expression levels in the normal human population. While it is widely believed that the majority of disease-associated loci influence disease risk through regulatory variations in gene expression, this hypothesis has not been formally tested by verifying whether most of genetic loci influencing disease risk are also detectable as eQTLs. In an effort to

examine this hypothesis, investigators at BWH and their colleagues took approximately 270 genetic loci associated with seven diseases and tried to map them back to causal genes using eQTLs in key immune cells.

They report their results in *Nature Genetics*.

The team was able to resolve 55 of these associations to candidate genes with strong statistical consistency with variations of baseline [gene expression](#) in unstimulated immune cells. However, this is only a small fraction - about 25 percent - of the [genetic loci](#) examined. For the rest, the researchers did not observe any signal in the eQTL data that were consistent with autoimmune disease associations despite the fact that disease-relevant cell populations are easier to access from blood samples compared to other disease.

"Abundant caution must be exercised before pathological relevance is inferred for an observed eQTL simply on the basis of proximity to a disease association," the authors write. "Strong-evidence of a shared genetic effect should therefore be established before time-consuming and costly experimental dissection of such effects is undertaken."

**More information:** Sung Chun et al, Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types, *Nature Genetics* (2017). [DOI: 10.1038/ng.3795](https://doi.org/10.1038/ng.3795)

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