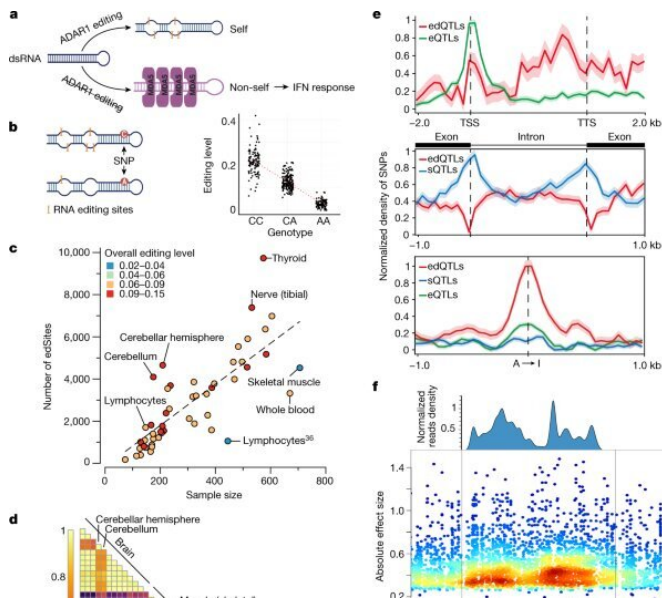


Genetic variants that dampen A-to-I RNA editing associated with increased risk of autoimmune disorders

18 August 2022, by Bob Yirka



RNA edQTL map in human tissues. Credit: *Nature* (2022). DOI: 10.1038/s41586-022-05052-x

A team of researchers at Stanford University, working with two colleagues from Fudan University and another from the Broad Institute of MIT and Harvard, has found evidence suggesting that genetic variants that dampen A-to-I RNA editing can be associated with an increased risk of autoimmune disorders. In their paper published in the journal *Nature*, the group describes how they analyzed genetic expression data from tissue samples collected from hundreds of human donors to identify genetic variants that affect RNA editing and what they learned by doing so. Kaur Alasoo, with the University of Tartu in Estonia, has published a News & Views piece in the same journal issue outlining the work done by the team on this new effort.

Prior research has shown that genetic variants can increase the risk of a person developing certain diseases. In some cases, they do so by impacting RNA—such variants can result in the production of more or less than is the normal case, or in differences in transcribed sequences. In the latter case, such differences can lead to problems with amino-acid sequencing.

Variants have also been found to exert influence on RNA molecules as they undergo A-to-I RNA editing, which is a process that involves subunits of RNA undergoing changes from adenosine to inosine. In this new effort, the researchers looked into the possibility of an association between these kinds of variants and autoimmune disorders.

The work by the team involved pulling data from the Genotype-Tissue Expression catalog and filtering it to find examples of variants that impact RNA editing. In so doing, they found data from tissue of 838 human donors with such variants. In analyzing the variants, they found that they had an impact on the binding strength between adenosine deaminase and RNAs.

The researchers next found that the variants were common in people who had [autoimmune diseases](#), such as lupus. And finally, they found that the same variants seemed to have stronger associations with such diseases than with variants involved in gene splicing. They conclude by suggesting that the type of gene variants that they observed, which lead to dampening of A-to-I RNA editing, appear to be associated with an increased risk of autoimmune disorders.

More information: Qin Li et al, RNA editing underlies genetic risk of common inflammatory diseases, *Nature* (2022). DOI: [10.1038/s41586-022-05052-x](https://doi.org/10.1038/s41586-022-05052-x)

Kaur Alasoo, Genetic variants that edit risk of autoimmune diseases, *Nature* (2022). DOI: [10.1038/d41586-022-01641-y](https://doi.org/10.1038/d41586-022-01641-y)

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