10/2014

☆ Febrile seizures (Feenstra, 2014)

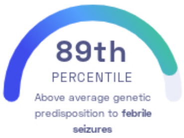
Bjarke Feenstra, et al.
Nature Genetics

Brain Infection

STUDY SUMMARY

Identification of 6 genetic variants associated with *febrile* seizures.

YOUR RESULT



89th
PERCENTILE
Above average genetic predisposition to **febrile seizures**

STUDY DESCRIPTION

Febrile seizures are fever-induced seizures that are common in small children.

In small children, high fevers can induce convulsions, causing uncontrollable shaking and loss of consciousness. This condition is known as *febrile* seizures and is a terrifying experience for many parents. However, *febrile* seizures are typically harmless and also quite common, affecting 2 - 9% (depending on ethnicity) of children before the age of 5. Because *febrile* seizures are caused by fever, they can occur after vaccinations. Fever is a relatively common response to vaccinations with the measles, mumps, and rubella (MMR) vaccine. Because little is known about genetic predisposition to *febrile* seizures, in particular in response to the MMR vaccine, this study examined genomes of nearly 9,000 children of European descent to identify contributing genetic factors. The study discovered 2 genetic variants associated with MMR-related *febrile* seizures and 4 more variants linked to *febrile* seizures in general. One of the identified variants is near a gene that plays a role in the immune response to viral infections. Another variant is near a gene that encodes for a *receptor* that is used by the measles virus to enter cells.

DID YOU KNOW?

Most children who have febrile seizures do not need treatment with drugs against seizures. The best way to respond to febrile seizures is to place the child on their side on a protected surface and watch them carefully. However, it's important to understand the reason for the fever and treat it accordingly.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to febrile seizures we summed up the effects of genetic variants that were linked to febrile seizures in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to febrile seizures. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to febrile seizures. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to febrile seizures. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for febrile seizures to be 2.21**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for febrile seizures is in the **89th percentile**. This means that it is higher than the polygenic scores 89% of people. We consider this to be an **above average genetic predisposition to febrile seizures**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

VARIANT ⓘ	YOUR GENOTYPE ⓘ	COMMENTS	EFFECT SIZE ⓘ	VARIANT FREQUENCY ⓘ	SIGNIFICANCE ⓘ
rs114444506_C NEW	**NA**	Febrile seizures overall	0.74 (-)	3%	3.70×10^{-20}
rs6432860_G NEW	**G / G**	Febrile seizures overall	0.29 (↑)	70%	2.20×10^{-16}
rs273259_A NEW	**A / A**	MMR-related febrile seizures	0.34 (↑)	70%	5.90×10^{-12}
rs11105468_A NEW	**T / A**	Febrile seizures overall	0.22 (↑)	29%	3.40×10^{-11}
rs1318653_T NEW	**T / T**	MMR-related febrile seizures	0.36 (↑)	77%	9.60×10^{-11}
rs3769955_T NEW	**C / C**	Febrile seizures overall	0.20 (-)	40%	3.10×10^{-10}

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.