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☆ Podoconiosis (Tekola Ayele, 2012)

Fasil Tekola Ayele, et al.

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Inflammation

STUDY SUMMARY

Identification of a genomic region associated with susceptibility to developing podoconiosis.

STUDY DESCRIPTION


Podoconiosis is a disease that many people may have never heard of, yet in some communities across the globe, nearly 1 in 20 individuals are affected. The disease predominantly affects farmers and people that walk barefoot on red-clay soil formed from volcanic rock that is found in tropical Africa, Central and South America, and north India. Scientists think that red-clay soil contains large amounts of minerals which are absorbed through the skin of the feet. This induces a reaction of the immune system that leads to the characteristic swelling of the feet. Genetics is thought to contribute over 60% to a person's risk of developing podoconiosis. This genome-wide study examined nearly 400 individuals from southern Ethiopia to identify genetic variants associated with podoconiosis, and found a significant association with the HLA-DQA1 region, that has an important function in the immune system.

DID YOU KNOW?

The World Health Organization believes that it is possible to eradicate podoconiosis. Efforts to increase the availability of shoes, and the further development of roads, are seen as key strategies to control the disease.

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to podoconiosis. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to podoconiosis. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to podoconiosis. 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 ^⓪	YOUR GENOTYPE ^⓪	EFFECT SIZE ^⓪	VARIANT FREQUENCY ^⓪	SIGNIFICANCE ^⓪
rs17612868_T 	A / T	0.78 (↑)	42%	3.44×10^{-8}