

GENETIC AND ENVIRONMENTAL RISK FACTORS ASSOCIATED WITH EBV SEROCONVERSION

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Background

EBV infects 90-95% of the world's population. Why 5% remain uninfected throughout life is unknown. Genetic and behavioural factors may be involved but defining the relative contributions of such factors is challenging due to confounding and reverse causality [1].

Methods

Mendelian randomisation (MR) is a technique for identifying causal factors in complex situations [2]. To identify EBV infection risk factors, we applied MR to data obtained from 8422 individuals within the UK biobank, genomically deemed to have white ancestry and for whom EBV status was known.

Results

GWAS identified two novel genetic loci (rs1210063 and rs71449058) associated with EBV serostatus. Using MR we confirmed educational attainment, number of sexual partners, and smoking as causal risk factors for EBV serostatus.

Conclusions

Our study highlights the power of MR to decipher complex webs of risk factors and determine which are causal for the acquisition of infectious diseases. The factors identified for EBV will help inform future vaccine deployment by determining individuals at greater risk of infection.

[1] Winter, Joanne R et al., 2020, *Journal of global health* vol. 10

[2] Davies N M, Holmes M V, Davey Smith G., 2018, *BMJ* issue 8161