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Genetic variants associated with susceptibility of Ashkenazi Jews to West Nile virus infection

N. Bisharat[1], N. Danial-Farran[2], S. Eghbaria[1], N. Schwartz[3]

[1]Medicine D, Emek Medical Centre, Afula, Israel ; [2]Genetics, Emek Medical Centre, Afula, Israel ;

[3]Clinical Research unit, Emek Medical Centre, Afula, Israel

Objectives: The epidemiology of West Nile virus (WNV) in Israel is different from other neighbouring countries in the Middle East where disease burden has been minimal. We hypothesized that the Israeli Jewish population is genetically predisposed to WNV infection and symptomatic disease.

Methods: We analyzed a cohort of patients with symptomatic WNV infection (n=47), asymptomatic WNV-positive (n=50) and WNV-negative (n=89) controls, for 9 genetic variants that has been suggested to be associated with susceptibility to WNV among North American populations. The association of single nucleotide polymorphism (SNPs) with WNV infection and or symptomatic infection was tested at the allele level and at the genotype level (assuming dominant and recessive models)

Results: Nearly 90% of the patients suffering from symptomatic WNV infection were Ashkenazi Jews. Four SNPs were significantly more frequent among WNV infected than non-infected individuals, rs7280422 (*MX1*), rs3213545 (*OASL*), rs10774671 (*OAS1*), and rs2298771 (*SCN1A*). Three SNPs were found to be associated with symptomatic infection, rs7280422 (*MX1*) [OR=2.3 (95%CI: 1.2-4.4), P=0.008], rs25651 (*ANPEP*) [OR= 1.9 (95% CI: 1.02-3.6) P=0.01], and rs2066786 (*RFC1*) [dominant model, OR=6.2 (95% CI: 2.5-15.3), P<0.0001].

Conclusion: Genetic polymorphism may play a significant role in susceptibility to WNV infection and symptomatic disease among Ashkenazi Jews.