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Δccr5 Genotype Is Associated with Mild Form of Nephropathia Epidemica

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Abstract

 Nephropathia Epidemica (NE), a mild form of hemorrhagic fever with renal syndrome (HFRS) and linked to hantavirus infection, is endemic in the Republic of Tatarstan. Several genetic markers of HFRS severity have been identified previously, including human leukocyte antigen (HLA) complexes and nucleotide polymorphism in the tumor necrosis factor alpha (TNFα) gene. Still, our understanding of the genetic markers of NE severity remains incomplete. The frequency of the C–C chemokine receptor type 5 (CCR5) gene wild type and gene with 32-base-pair deletion (Δ32CCR5) genotypes in 98 NE samples and 592 controls was analyzed using PCR. Along with the serum levels of 94 analytes, a lack of differences in the CCR5 genotype distribution between NE cases and the general population suggests that the CCR5 genotype does not affect susceptibility to hantavirus infection. However, in NE cases, significant variation in the serum levels of the host matrix metalloproteases between functional CCR5 homozygous and Δ32CCR5 heterozygous patients was detected. Also, the oliguric phase was longer, while thrombocyte counts were lower in functional CCR5 homozygous as compared to heterozygous NE cases. Our data, for the first time, presents the potential role of the CCR5 receptor genotype in NE pathogenesis. Our data suggests that NE pathogenesis in functional CCR5 homozygous and heterozygous NE patients differs, where homozygous cases may have more disintegration of the extracellular matrix and potentially more severe disease.

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Keywords

CCR5, Cytokines, Hemorrhagic fever with renal syndrome, Matrix metalloprotease, Nephropathia epidemica, Δ32CCR5

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