

Recombination, reassortment, and many-to-one genotypes in natural arenavirus infections

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Abstract

Mutation, recombination, and reassortment generate virus particles with variable genotypes, some of which may be better adapted to infect a new host, resist drug treatment, or escape immune pressure. The arenaviruses are a family of viruses that package a large (L) and small (S) genome segment. Arenaviruses infect mammals and snakes and are associated with fatal disease in both groups of animals. Although recombination and reassortment are well documented in some virus families, neither process has been observed in natural arenavirus infections. In this study, we documented a surprising degree of genetic diversity in arenavirus-infected snakes. Instead of one or two viral species or quasispecies, individual animals harbored complex populations of viral genotypes composed of up to 5 S and 11 L genotypes, which replicated as stable ensembles in culture. S and L segment genotype accumulation was not balanced and a particular S segment genotype dominated, both in individual animals and at a population level. Numerous instances of recombination and reassortment were detected. Some recombinant segments had unusual organizations with 2 intergenic regions.

Keywords: