

Genome type analysis of South American adenoviruses of subgenus C collected over a 7-year period

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A collection of 148 adenovirus strains of subgenus C collected in Argentina, Chile, and Uruguay were studied by restriction enzyme analysis of genomic DNA with endonucleases Bam HI, Bgl II, Bst EII, Eco RI, Hind III, Kpn I, and Sma I. Only strains corresponding to serotypes 1, 2, and 5 were identified representing both already described and new genome types. The most frequently detected type was Ad 2 followed by Ad 1 and Ad 5. Three different genomic variants of both Ad 1 and Ad 5 were discriminated. Ad 2 with 9 genome types exhibited the greatest variability. Novel profiles emerged only in strains corresponding to this serotype by restriction with Bgl II and Bst EII. The circulation of prototype-like strains of Ad 1 throughout the study period is noteworthy. Thirty-six of 43 strains corresponded to genome type D 1. Clearly, one genome type of each serotype predominated over the 7-year period (Ad 1 D 1, n=36; Ad 2 D 5, n=32, and Ad 5 D 36, n=17). Some genomic variants were detected spo