

# Molecular epidemiology of adenovirus acute lower respiratory infections of children in the South Cone of South America (1991-1994)

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A collection of 165 adenovirus strains isolated from nasopharyngeal aspirates of children hospitalized for acute lower respiratory infection in Argentina, Chile, and Uruguay between 1991 and 1994 was studied by restriction enzyme analysis (work performed in the Department of Virology, University of Umea). Of the isolates, 71% (n = 117) were identified as members of subgenus B. Of these, 101 (61.2%) corresponded to genome type 7h, four (2.4%) to genome type 3p2, four (2.4%) to genome type 11 a, one (0.6%) to genome type 7b, and one (0.6%) to genome type 7c. Two isolates that were neutralized as serotype 3 and four isolates that were neutralized as serotype 7 exhibited novel BamHI cleavage profiles corresponding to three new genome types denominated 3x, 7i, and 7j. Subgenus C members represented 28.5% of all typed isolates. Five different genome types of Ad1, seven genome types of Ad2, and three genome types of Ad5 were identified of, which two, two, and one, respectively, were found to