

# Molecular epidemiology of Human Adenovirus in Asturias (2011–2023)

Santiago melon<sup>1</sup>, Marta Alvarez-Arguelles<sup>1</sup>, José María González Alba<sup>1</sup>, Susana Rojo<sup>1</sup>, Jose Boga<sup>1</sup>, Zulema Pérez-Martínez<sup>1</sup>, Costanza Gómez-deOña<sup>1</sup>, Cristina Ochoa-Varela<sup>1</sup>, and Mercedes Rodríguez-Pérez<sup>1</sup>

<sup>1</sup>Hospital Universitario Central de Asturias Laboratorio de Medicina

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## Abstract

Human Adenoviruses (HAdV) are implicated in multiples pathologies causing mild to severe disease. The predominant genotypes detected in association with disease differ among different countries or regions, and change over time. In Spain and elsewhere little is known about the molecular epidemiology of HAdV. From a total of 250 HAdV, members of five species were present: A (1), B (126), C (87), D (27) and E (9). The most found genotypes were B3 (119), C2 (48), C1 (29) and D8 (26). Genotypes E4, C5, C6, B7, A31, B35 and D56 were also detected. HAdV diversity increases over the years until the B3 genotype displaces all other types in 2016 and 2023. HAdV detected in Asturias were similar to those already described in other countries, no new local genotype were observed. Genotypes 1-7 were more frequent in children under 15 years of age, while types 8-56 were more frequent in the elderly. Multiple HAdV introductions must have occurred given that only small transmission clades can be inferred. The diversity of the epidemic increased with the years until it disappeared one year periodically. The COVID-19 epidemic accelerated the loss of diversity suggesting that interventions during the pandemic were able to reduce HAdV transmission.

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