

# JC polyomavirus circulation in one-year surveillance in wastewater in Santiago, Chile

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Human polyomavirus JC (JCPyV) is a widely distributed viral agent and because of its high resistance against environmental conditions it is frequently recovered from diverse sources of water and is considered a good marker for human pollution. Phylogenetic analysis of JCPyV isolated in different parts of the world has revealed 7 genotypes, which have been associated with specific populations or ethnic groups. This feature has been used to trace pre-historic and historic human migration patterns across the world. Although there are many reports describing genotypes distribution around the world, data on JCPyV genotypes in the southernmost areas of South America are scarce. The goal of this study is to detect and characterize the JCPyV that circulates in Santiago, Chile using sewage samples from wastewater treatment plants (WWTP). Sewage samples were obtained monthly during 1 year from three WWTPs which together process about 80% of wastewater generated in the city of Santiago, Chile. Our results show that JCPyV profusely circulates in Santiago, Chile, because it was detected in 80.56% of the samples, reinforcing the use of JCPyV as a feasible marker to assess human environmental pollution. JCPyV was detected in high frequency in influents and effluents samples, with the largest WWTPs showing the highest percentage of detection and viral loads. In the phylogenetic analysis the Chilean sequences clustered mainly with genotype 2A (Asian genotype). This is similar to that previously reported from Buenos Aires, Argentina and divergent to data from Brazil, where the circulation of European subtypes 1 and 4 and African subtypes 3 and 6 has been described.