

Hepatitis A virus molecular surveillance in Argentina after 11 years of universal vaccination.

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DESCRIPTION

Universal vaccination against hepatitis A virus (HAV) with a single dose in one-year-old children was implemented in Argentina in 2005.

Since then, the report of new cases steadily decreased almost 90%.

Prior vaccination, the only subgenotype isolated was IA.

In 2011 a new subgenotype IC was proposed which was isolated in 2012 in Argentina from environmental samples in Cordoba (Center). As National Reference Lab for Viral Hepatitis we support the intensive epidemiological surveillance in Argentina through molecular characterization of HAV variants. Serum and/or stool samples from 140 not vaccinated patients reported to the National Epidemiological Surveillance Lab System (SIVILA) between 2009-2016 whom were diagnosed with acute hepatitis and positive anti-HAV IgM antibodies (ELISA) were studied. VP1/2A junction were amplified, sequenced and analyzed with phylogenetic programs

PUBLIC HEALTH IMPACT

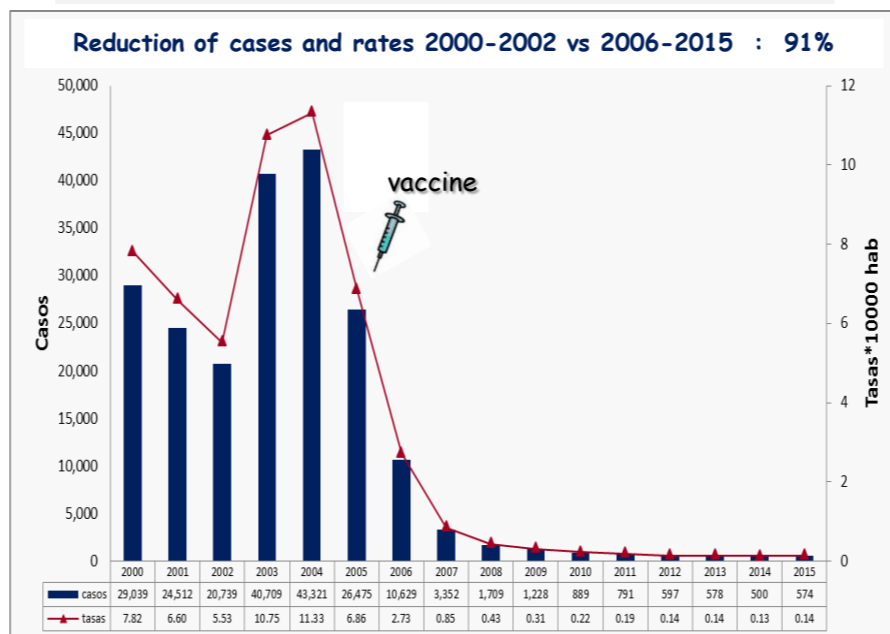
Subgenotype IA continued to be the main HAV circulating variant in locally acquired cases.

The intensive surveillance of this immuno-preventable disease allowed the detection of 2 subgenotype IC HAV variants from clinic samples and 1 subgenotype IIA variant imported from Africa.

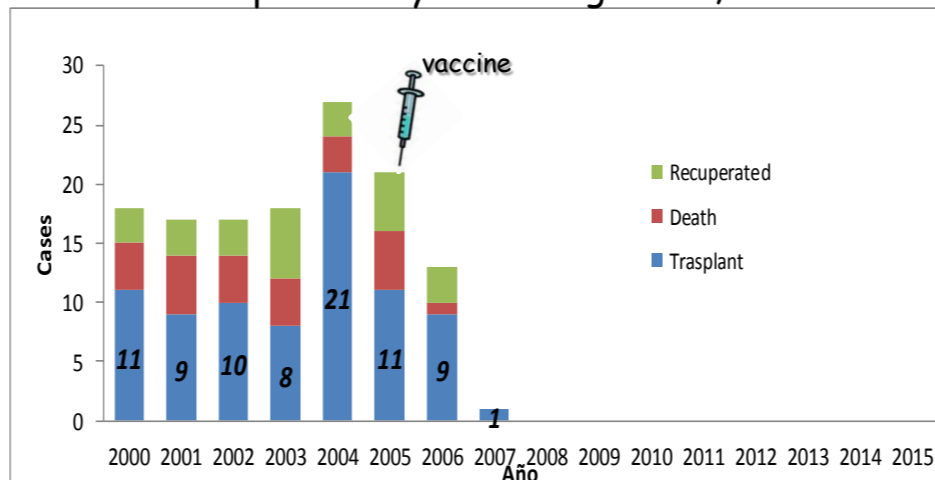
WHY IS THIS INNOVATIVE?

Epidemiological surveillance at a molecular level is essential to study changes in the viral circulation pattern, detection of vaccine escape variants and take measures for the control and prevention of HAV infection.

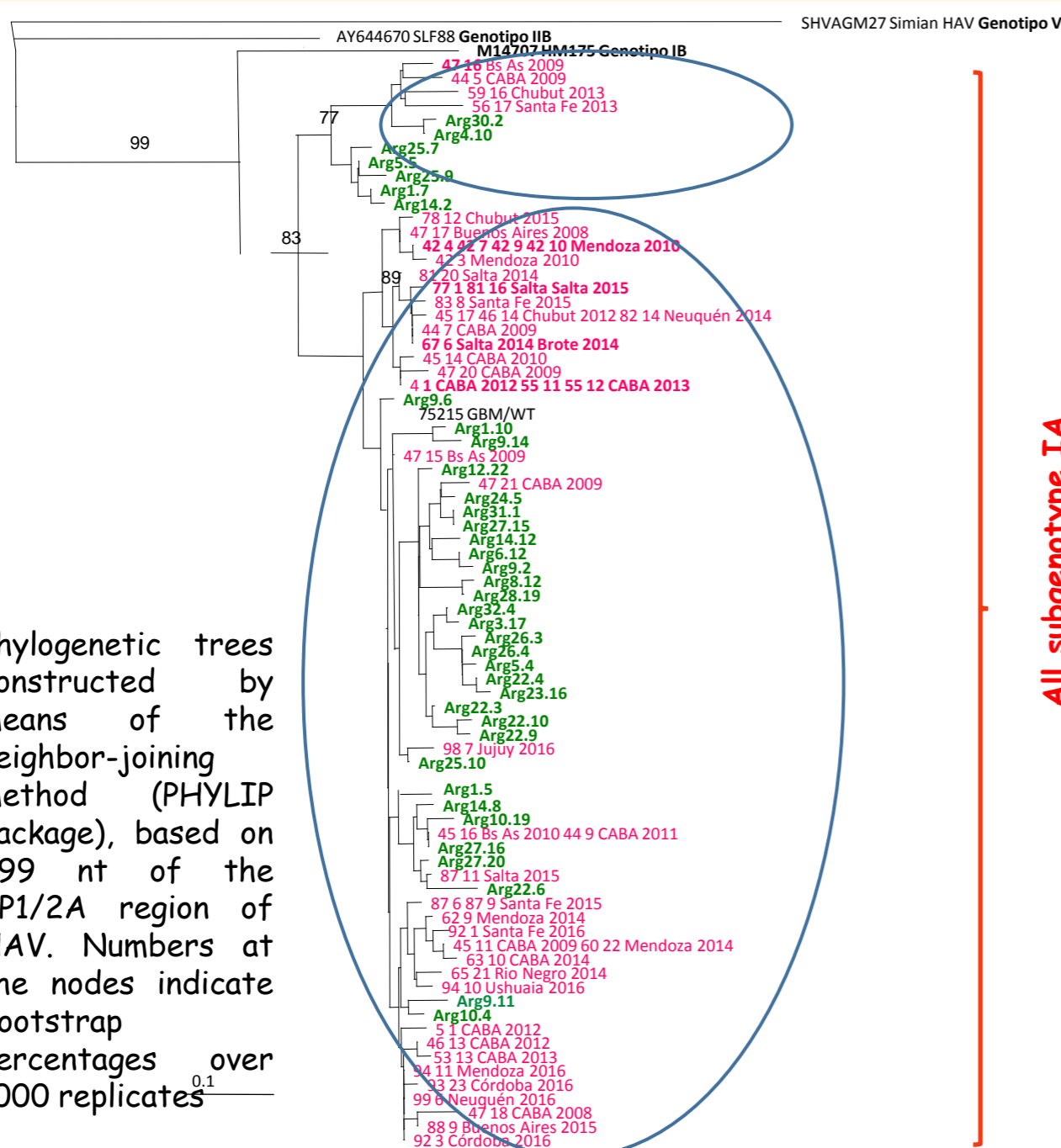
Hepatitis A and unespecified Hepatitis. Cases and Rates. 2006-2015



Fulminant Hepatitis by HAV. Argentina, 2000-2015

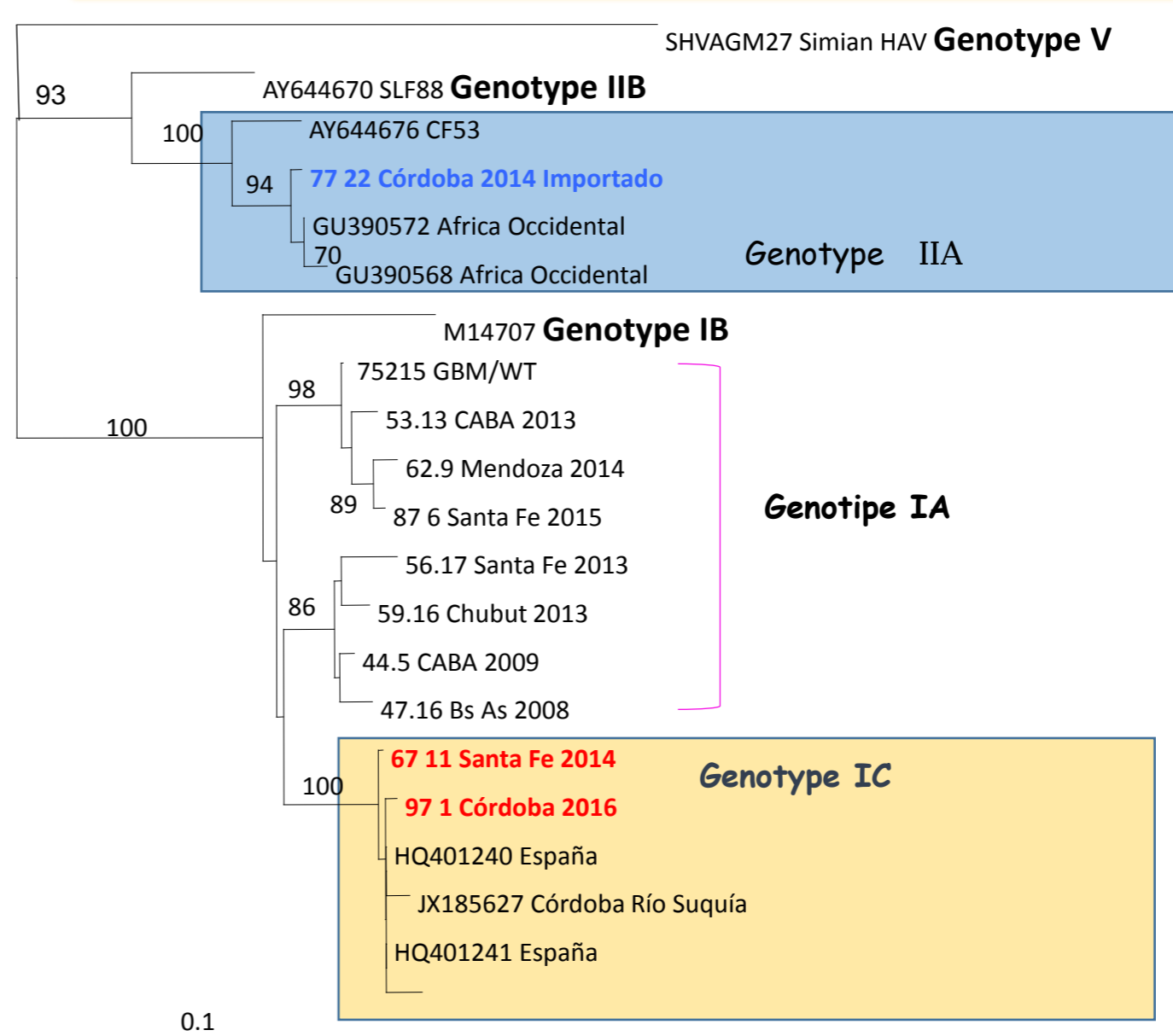


SUBGENOTYPE IA CIRCULANT VARIANTS



Phylogenetic trees constructed by means of the neighbor-joining method (PHYLIP package), based on 299 nt of the VP1/2A region of HAV. Numbers at the nodes indicate bootstrap percentages over 1000 replicates

NEW VARIANTS



- ✓ Between 2009 and 2016, 75 HAV variants from different geographical areas of Argentina were molecularly characterized analyzing VP1/2A junction region.
- ✓ Within these variants, 72 belonged to subgenotype IA and presented a dissimilar nucleic acid sequence compared with variants reported prior to vaccine implementation.
- ✓ Identical sequences corresponded to related cases : outbreaks in Mendoza (Center west) (2009) and Salta (North west) (2014/2015) and 2 cases in Esquel (South west) (2012); but also were observed in geographic and temporal not related events.
- ✓ In addition, 1 subgenotype IIA HAV variant from an imported case from Africa (2014) and 2 variants belonging to subgenotype IC one from an autochthonous case in Santa Fe (Center east) (2014) and the other from a probably-imported case from Ecuador (2016) were isolated

CONFLICTS OF INTEREST

NONE

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