PHYLOGENETIC ASSESSMENT OF FULL-SEQUENCED SEROTYPE A FOOT AND MOUTH DISEASE VIRUSES FROM ARGENTINA, 2001

Gustavo S. Cabanne, Andrés Perez, Aitana Takebe Heras, María Soledad García Nuñez, Claudia Pérez, Eduardo Maredei, Leandro Biscaldi, Elisa Carrillo, Luis Rodriguez and Guido König















Introduction

- The FMDV produce a devastating epizootic that affected the Argentine herd in 2000-2002.
- The A Argentina 2001 FMDV strain is considered the responsible for most of the 2561 outbreaks that affected the country during the epizootia.
 - Unvaccinated and vaccinated animals were affected by the disease.



Sampling

- A location with good epidemiologically information, high attack rate, limited duration over time was selected to conduct the analysis (Mar Chiquita from Buenos Aires province).
- The protocol for the selection of samples made use of a factorial design to stratify the selection, so that samples are representative of the temporal and spatial distribution of outbreaks, attack rate and vaccination status.
 - Sixteen samples were selected from 41 outbreaks occured from May to July 2001 with viral isolates and good epidemiological data.





The FMD virus was introduced once in Mar Chiquita and all the subsequent outbreaks derived from the index case (first outbreak in Mar Chiquita).

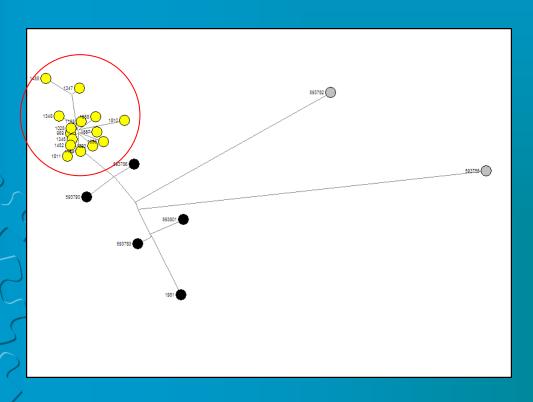
The genetic evolution of the virus is related to the spatial, temporal, demographic or immunological characteristics of the infected herd.



Materials and Methods

- Protocols and primers to produce seven overlapping PCR products were designed and 45 primers were selected with the aim of obtaining a full genome FMDV sequence of each isolate.
- Phylogenetic analyses were completed with MEGA, Model Test, PAUP, Phy-ML, Split tree and Network software.
- Association between virus evolution and selected epidemiological factors was assessed using Mantel correlaion technique.

- 15 complete genome secuenced were already obtained
- As expected they group together and showed a cluster association among them

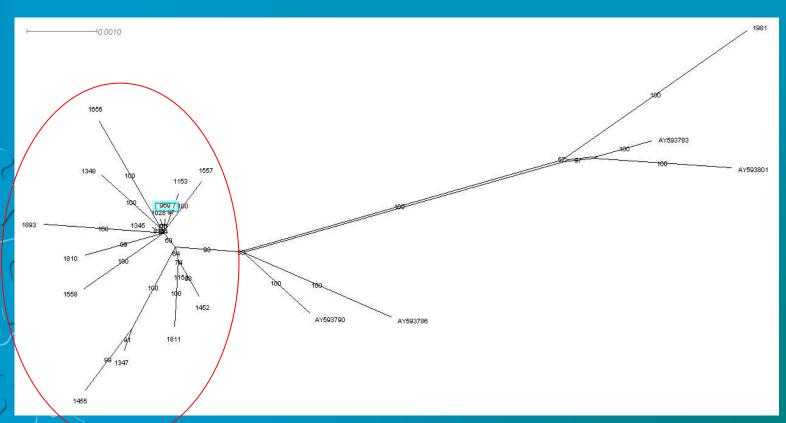


- Mar Chiquita
- A 2001
- Other A virus

Median Joining Network analysis

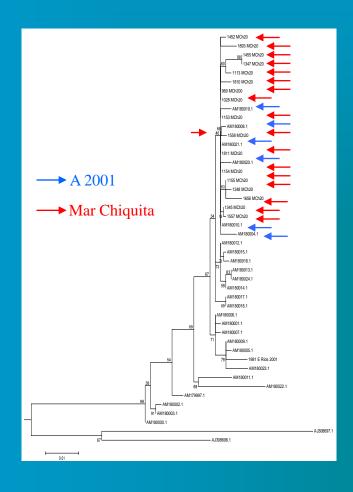


Split decompositioin network, with bootstrap (100x). Complete genome





- Genealogical analysis of Vp1 sequences
- ML tree made in PHYML (as obtained in Modeltest), using model GTR +I +G. Bosstrap values has a low support.





Multiple correlation performed in program FSTAT with 10000 permutations.

Independent variable	Partial correlation coef.	Significance.
DGEO	-0.173386	0.148
DTIME	0.036112	0.758

No dependence of genetic to geographic distance or time between premises.



Conclusion

- Multiple introduction of FMDV in Mar Chiquita?
- No correlation with time or distance?

Support:

- •SCA ARS-INTA, Argentina Agreement Number 58-1940-7-124F:
- Developing predicting tools for prevention of FMD
- •PAE 37206-PICT 33 : Estudio de la evolución molecular del VFA utilizando el brote Argentino correspondiente a la cepa A Argentina 2001 como modelo
- •PE Fiebre Aftosa-Modulo 8 Epidemiología Molecular



