

USING NEW BIOINFORMATIC AND EVOLUTIONARY TOOLS TO STUDY THE 2000-2001 FMDV EPIDEMICS IN ARGENTINA

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Introduction

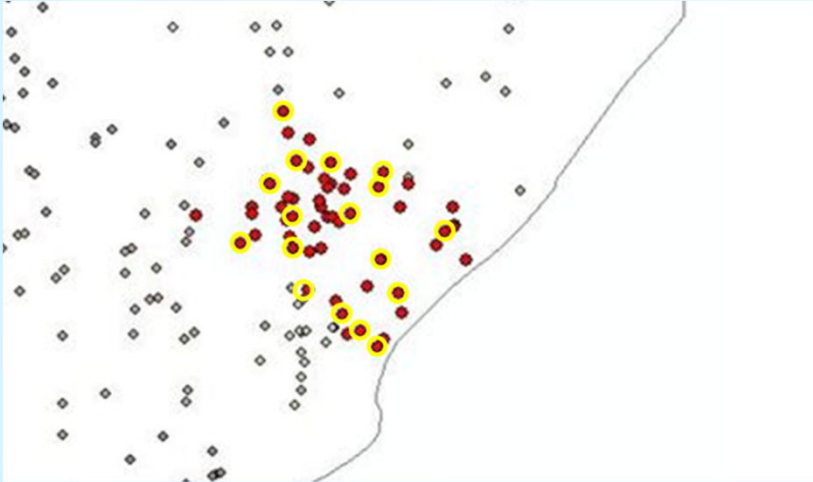
- RNA viruses, including FMDV, replicate with a high mutation rate and evolve rapidly during outbreaks.
- The last relevant FMD epidemic occurred in Argentina during 2000-2001.
- In this study, we applied a set of bioinformatic and evolutionary tools to understand the transmission of FMDV in the Mar Chiquita region

Goal:

Building capacity to analyze virus transmission pathways in the field.

Dataset

Mar Chiquita (50)



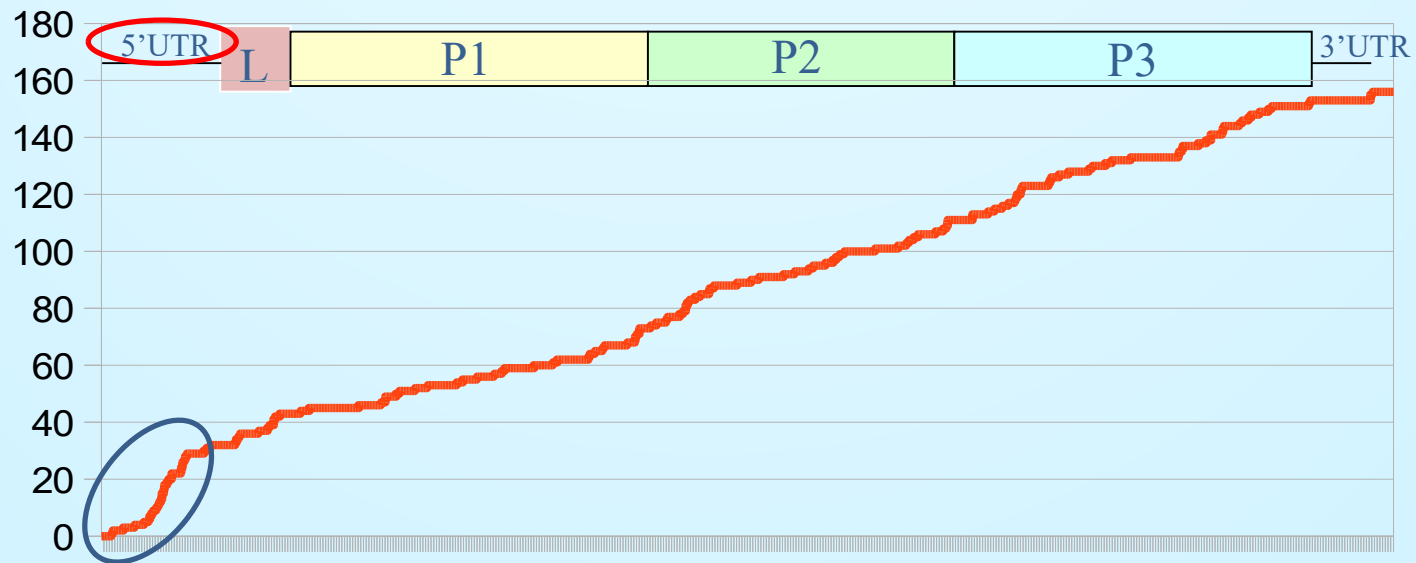
A2001 strain outbreaks: >2000



21 isolates collected across three months from locations that were no further than 40 km apart

Recombination and variability

- RDP4 – No signal



Temporal signal



Virus Evolution, 2016, 2(1): vew007

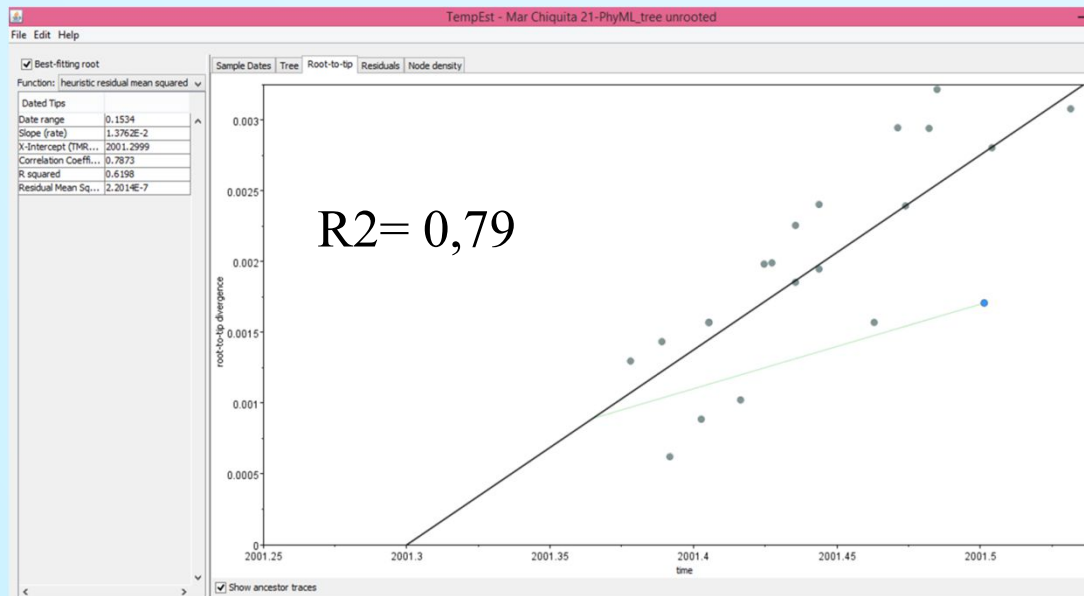
doi: 10.1093/ve/vew007
Resources

Exploring the temporal structure of heterochronous sequences using **TempEst** (formerly Path-O-Gen)

Andrew Rambaut,^{1,2,*}† Tommy T. Lam,³ Luiz Max Carvalho,¹ and Oliver G. Pybus^{4,‡}

Dynamic regression to estimate temporal and genetic divergence.

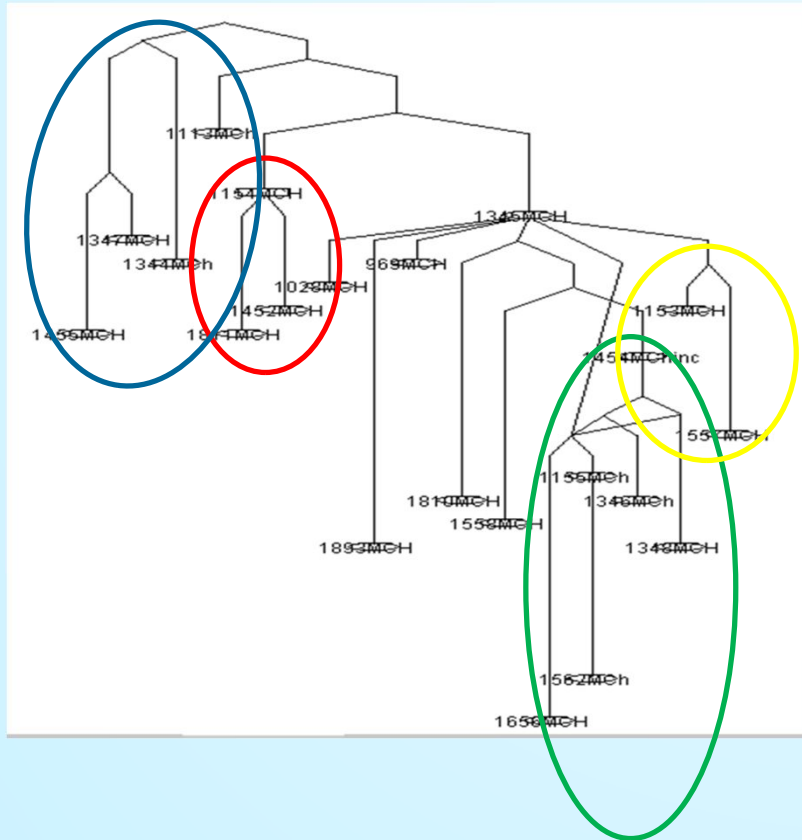
Molecular phylogenies
Temporal dataset



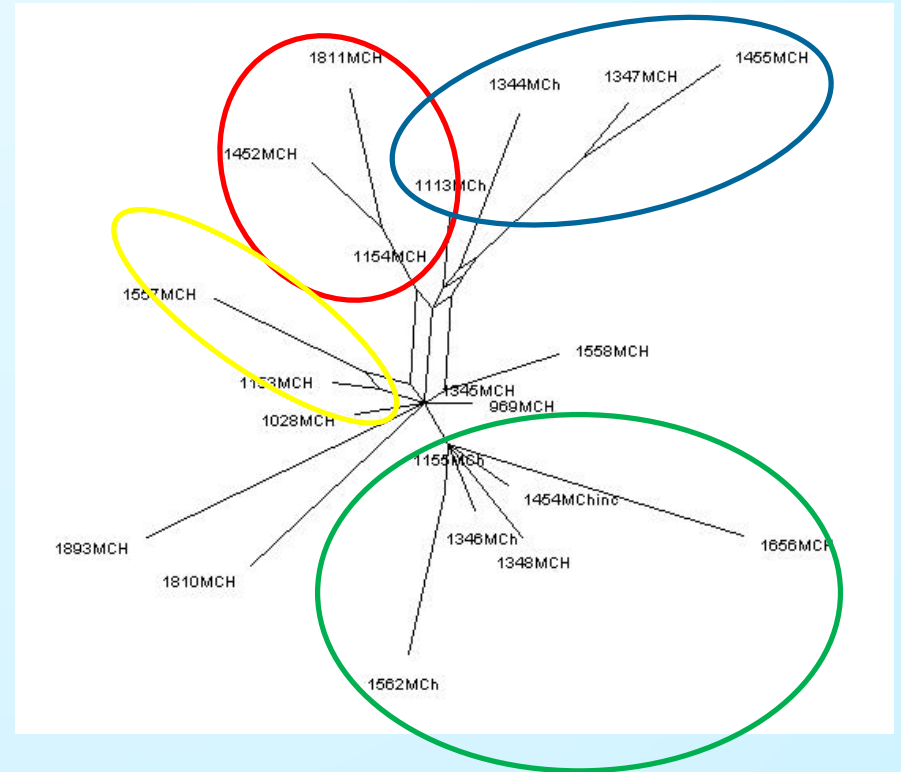
The results showed that the virus evolved at a rate of 9×10^{-4} substitutions per site per year (similar to previously reported rates estimated from viruses collected over a small time window).

Haplotype network

TCS



Split Tree



BEAST: Partition-Models

Partition

No

X UTR-Poliprotein

Evolutionary Model

TN93 X

SRD06 X

Codon(1+2;3)

Molecular Clock

Strict X

Relaxed

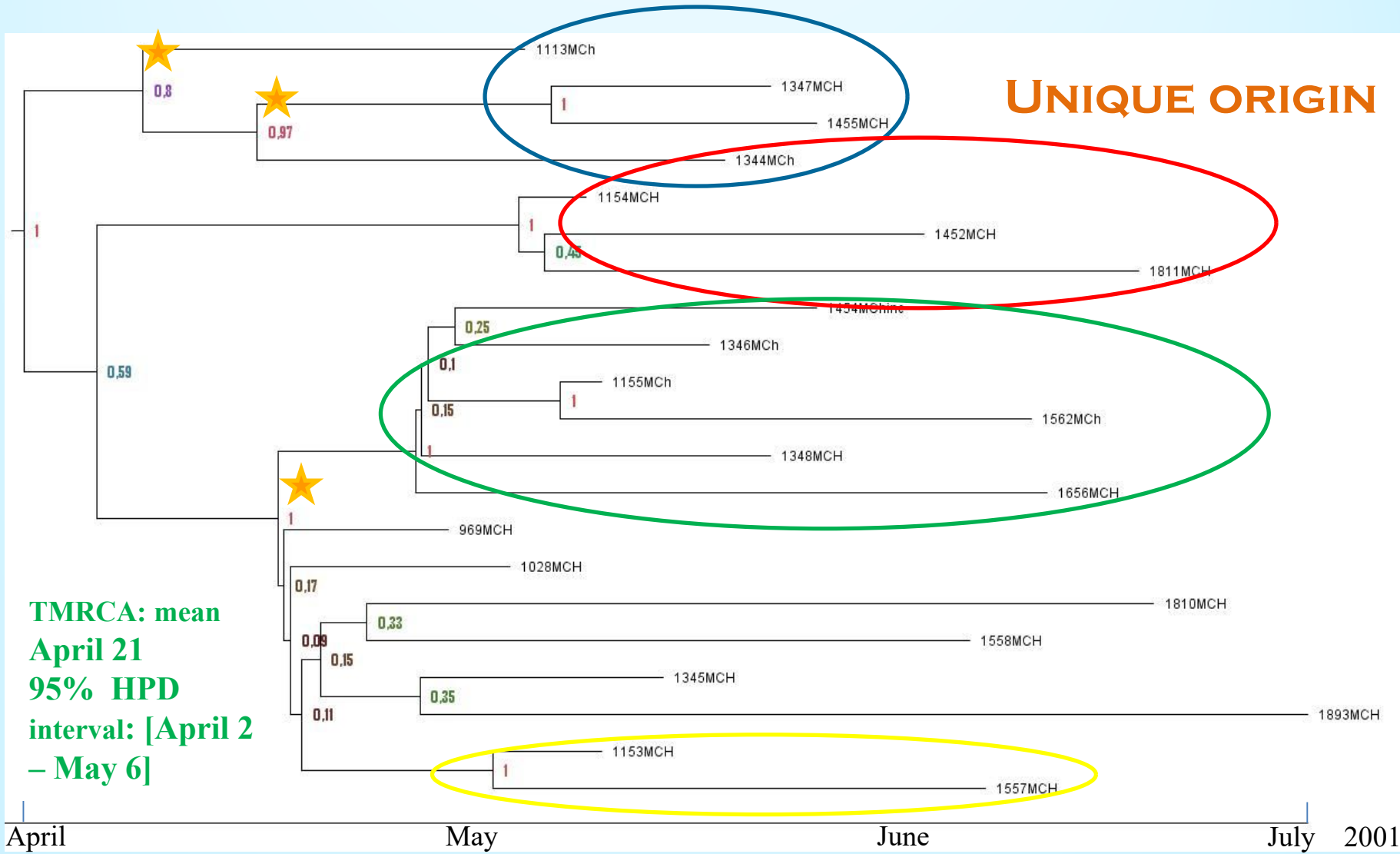
Uncorrelated
Log Normal

Coalescent

PS/SS

	A	B	C	D
1	Marginal Likelihood	10 steps	20 steps	40 steps
2	WGS-TN93			
3	Strict clock			
4	PS	-12650,55	-12647,92	-12647,78
5	SS	-12647,28	-12647,03	-12647,66
6	UncorrelatedLogNormal			
7	PS	-12675,73	-12649,25	-12651,1
8	SS	-12651,92	-12648,15	-12651,85
9	UTR-PP TN93			
10	SC-SC			
11	PS	-12675,7	-12673,75	
12	SS	-12671,52	-12672,73	
13	SC-UnLN			
14	PS	-12700,81	-12672,55	
15	SS	-12674,88	-12671,78	
16	UnLN-SC			
17	PS	-12681,79	-12675,23	
18	SS	-12672,99	-12673,39	
19	UnLN-UnLN			
20	PS	-12674,77	-12672,7	
21	SS	-12671,94	-12671,95	
22	UTR-PP TN93-SRD06			
23	SC-SC (I)			
24	PS	-12643,72	-12636,86	-12636,49
25	SS	-12636,69	-12635,6	-12636,37
26	SC (I)			
27	PS		-12636,1	
28	SS		-12634,9	
29	SC-UnLN (j)			
30	PS	-12643,03	-12637,05	
31	SS	-12635,63	-12635,49	
32	UnLN-SC (K)			
33	PS	-12640,97	-12636,5	-12637,08
34	SS	-12635,72	-12632,52	-12637,18
35	UnLN-UnLN (L)			
36	PS	-12649,66	-12636,87	
37	SS	-12637,06	-12635,62	

Inferred tree



Next steps

- Obtain a detailed transmission tree.
- Use more complex models including the location of every infected and noninfected herd.
- Compare the results with a pure epidemiological model.
- Get more practice with these tools and develop the capacity to interpret the analysis.

Thank you!

Transmisión

Red filogenética o Red de haplotipos

- **Secuencias**
- Datación temporal
- Localización geográfica

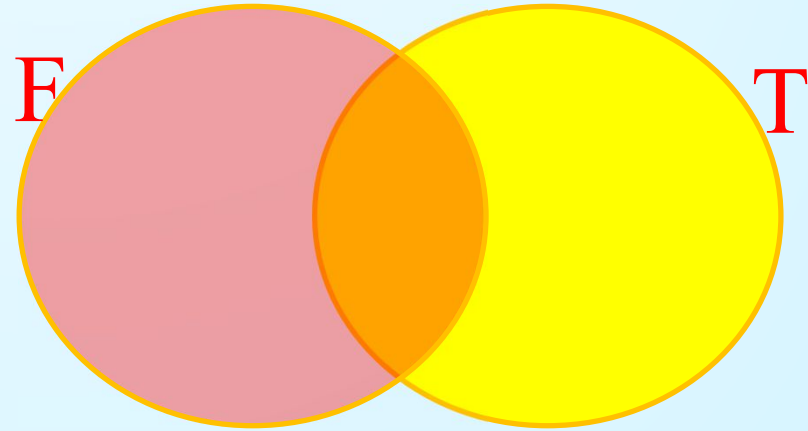
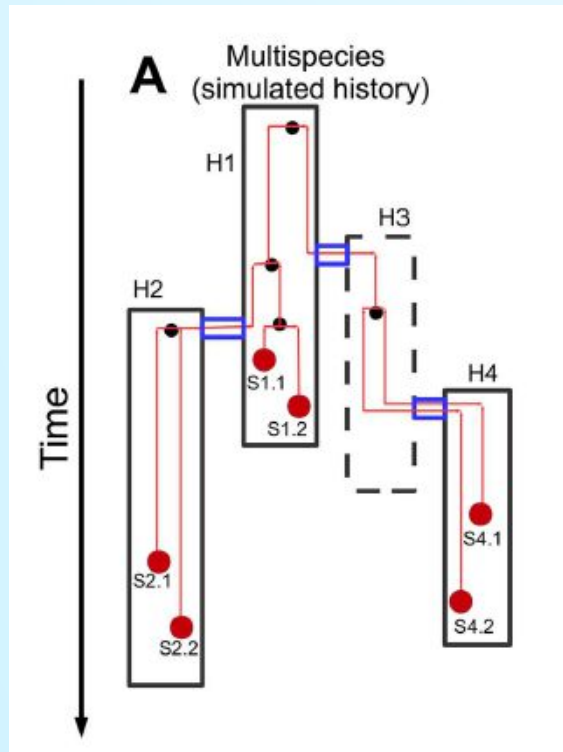
TCS
Split Tree

Análisis filogeográfico o filodinámico

- Señal filogenética
- Señal temporal
- Recombinación
- Variabilidad
- Modelos evolutivos
- Reloj Molecular
- Dinámica poblacional

BEAST

Árboles de transmisión



- Evolución intrahospedador
- Historia epidemiológica

PLOS COMPUTATIONAL BIOLOGY

RESEARCH ARTICLE

Beastlier

Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set

Matthew Hall^{1,2*}, Mark Woolhouse^{1,2}, Andrew Rambaut^{1,2,3}

PLOS COMPUTATIONAL BIOLOGY

RESEARCH ARTICLE

SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent

Nicola De Maio^{1,2*}, Chieh-Hsi Wu², Daniel J Wilson^{1,2,3}