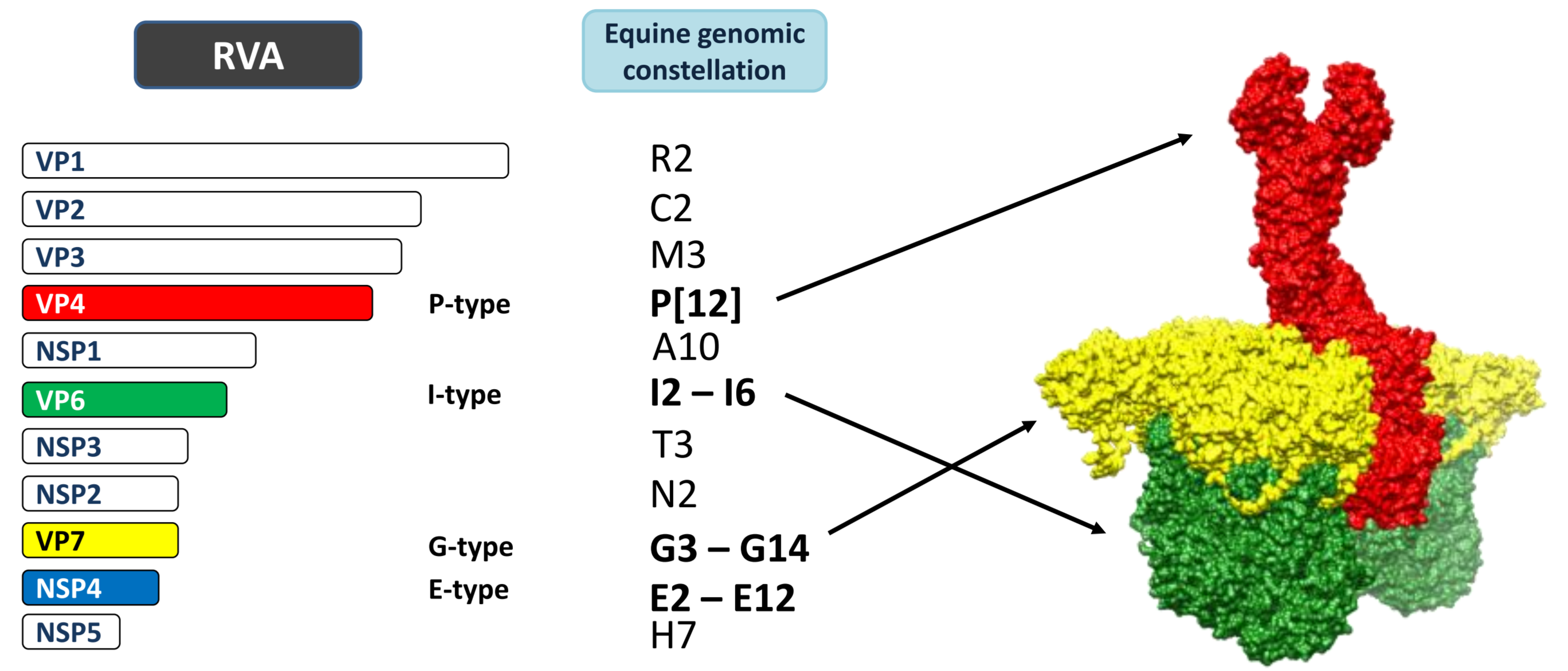


# Worldwide evolution of equine RVA: Four voices, one story

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## Introduction

- Rotavirus group A (RVA) is classified into G- and P- genotype according to the nucleotide sequence of both VP7 and VP8 genes. Moreover, the VP6 and NSP4 nucleotide sequence are used to classify the I-type (subgroup antigen) and the E-type (toxin antigen).
- The full genome sequence of equine RVA strains demonstrate that the equine RVA possess a constant genome constellation. Phylogenetic studies showed that RVA strains from different continent are grouped in different lineages.
- Phylogenetics studies suggest that equine RVA cluster with geographical structure.



## Objective

In this work, we used a Bayesian approach, together with all the information that was available in databases, to study the evolution of equine RVA.

## Material and Methods

- All sequences are available at genbank database.
- Alignments were done in ClustalW and the edition were carried out with Bioedit.
- Maximum likelihood tree and likelihood mapping were carried out in IQ-Tree 1.5.5 software (2017), [www.iqtree.org](http://www.iqtree.org)
- Bayesian analysis were carried out in BEAST 1.8.3 (2007), <http://tree.bio.ed.ac.uk>
- The all trees were visualized and edited with FigTree 1.4.3.

### G3

### G14

### I6

### I2

### E12

Only in South America

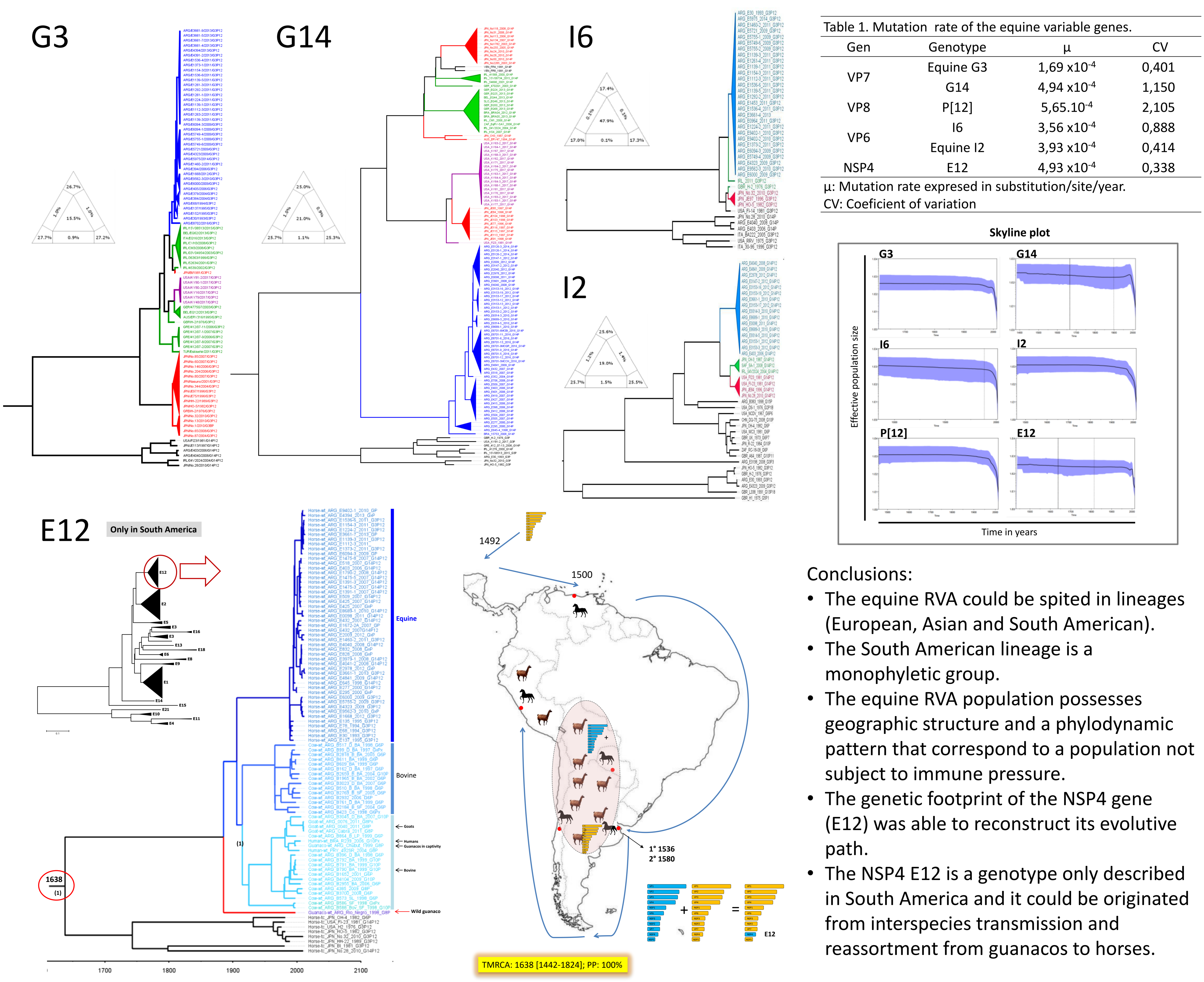
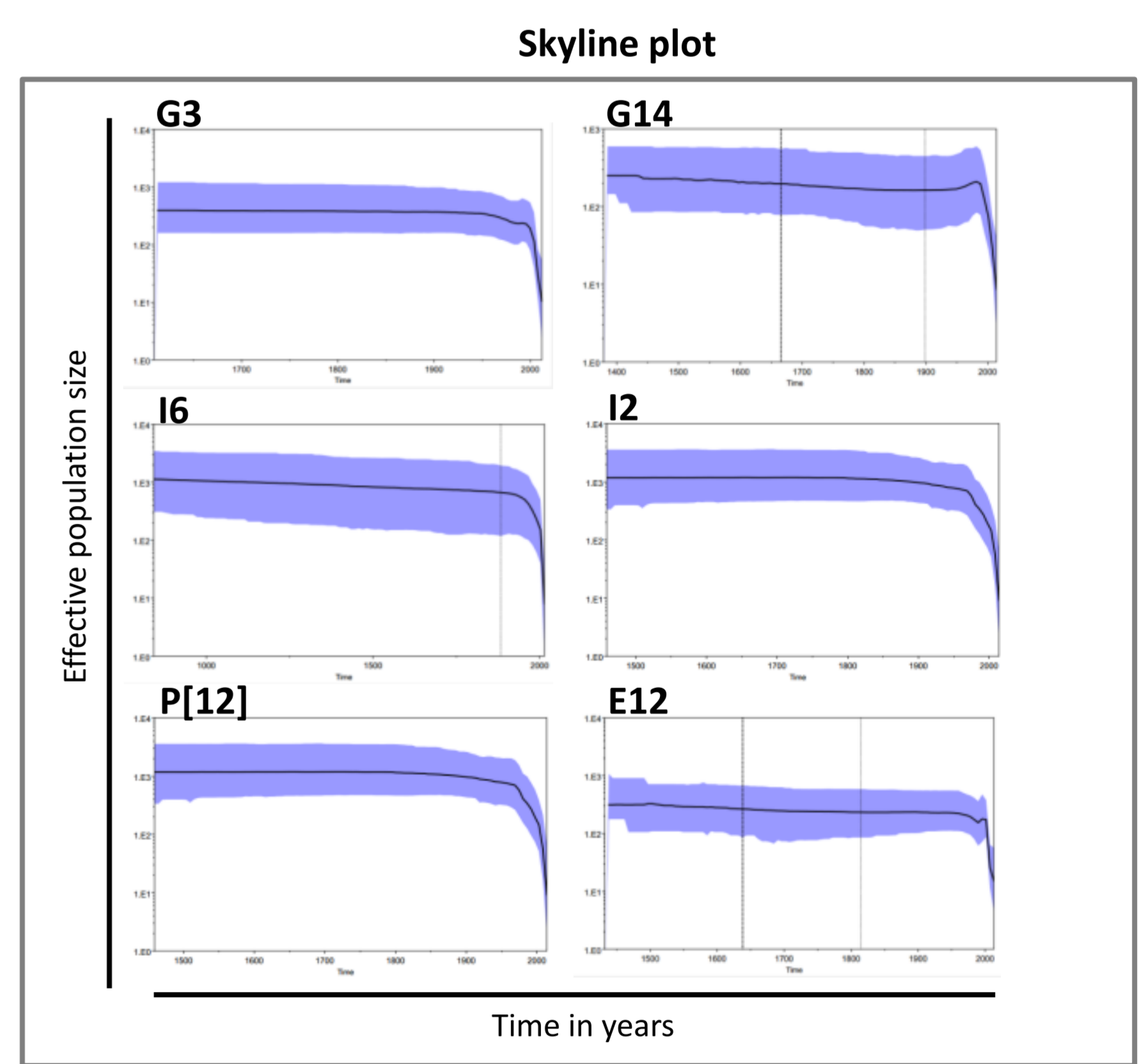


Table 1. Mutation rate of the equine variable genes.

Gen	Genotype	$\mu$	CV
VP7	Equine G3	$1,69 \times 10^{-4}$	0,401
	G14	$4,94 \times 10^{-4}$	1,150
VP8	P[12]	$5,65 \cdot 10^{-4}$	2,105
	I6	$3,56 \times 10^{-4}$	0,888
VP6	Equine I2	$3,93 \times 10^{-4}$	0,414
	E12	$4,93 \times 10^{-4}$	0,338

$\mu$ : Mutation rate expressed in substitution/site/year.  
 CV: Coefficient of variation



## Conclusions:

- The equine RVA could be spited in lineages (European, Asian and South American).
- The South American lineage is a monophyletic group.
- The equine RVA population possesses geographic structure and a phylodynamic pattern that correspond to a population not subject to immune pressure.
- The genetic footprint of the NSP4 gene (E12) was able to reconstruct its evolutive path.
- The NSP4 E12 is a genotype only described in South America and it could be originated from interspecies transmission and reassortment from guanacos to horses.