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

*Samuel Miño, María Barrandeguy, Viviana Parreño*

mina.samuel@inta.gob.ar

---

**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 IQTree 1.5.5 software (2017), [www.iqtree.org](http://tree.bio.ed.ac.uk).
- Bayesian analysis were carried out in BEAST 1.8.3 (2007), [http://tree.bio.ed.ac.uk](http://tree.bio.ed.ac.uk).
- The all trees were visualized and edited with FigTree 1.4.3.

---

**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.

---

**Table 1. Mutation rate of the equine variable genes.**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genotype</th>
<th>μ</th>
<th>CV</th>
</tr>
</thead>
<tbody>
<tr>
<td>VP7</td>
<td>G3</td>
<td>1.69 x10^-4</td>
<td>0.401</td>
</tr>
<tr>
<td></td>
<td>G14</td>
<td>4.94 x10^-4</td>
<td>1.150</td>
</tr>
<tr>
<td>VP8</td>
<td>P[12]</td>
<td>5.65 x10^-4</td>
<td>2.105</td>
</tr>
<tr>
<td></td>
<td>I6</td>
<td>3.56 x10^-4</td>
<td>0.888</td>
</tr>
<tr>
<td>VP6</td>
<td>E12</td>
<td>3.93 x10^-4</td>
<td>0.414</td>
</tr>
<tr>
<td>NSP4</td>
<td>E12</td>
<td>4.93 x10^-4</td>
<td>0.338</td>
</tr>
</tbody>
</table>

μ: Mutation rate expressed in substitution/site/year.
CV: Coefficient of variation