

Are Bovine Respiratory Syncytial Virus (BRSV) vaccine strains still aligned with circulating BRSV field strains?

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INTRODUCTION

Bovine Respiratory Syncytial Virus (BRSV) is spread in cattle herds worldwide and is considered one of the most important etiological agents involved in Bovine Respiratory Disease Complex (BRDC).

We conducted an updated phylogenetic analysis to study the evolution of circulating BRSV strains in the field during the last 30 years.

OBJECTIVE

The objective of the phylogenetic analysis is to study BRSV evolution during the last 30 years. Two vaccine strains were also included in the analysis in order to understand the diversity between the field strains and the ones used for prophylactic measures.

MATERIALS AND METHODS

Nucleotide sequences based on a partial sequence of the G protein of 272 strains were collected from Genbank and aligned using ClustalW and manually optimized. The best DNA model was determined using MEGA X and Maximum Likelihood phylogenetic tree (Tamura Nei model, and 500 bootstrap values as statistical support) were constructed using PhyML software implemented in Geneious Prime.

BRSV is constantly evolving throughout the years. Despite this, the vaccine strains present in Bovilis[®] Bovipast[®] RSP and Bovilis[®] INtranasal RSP[®] Live still belong to the same genetic group as the predominant strains currently circulating in the field.



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RESULTS

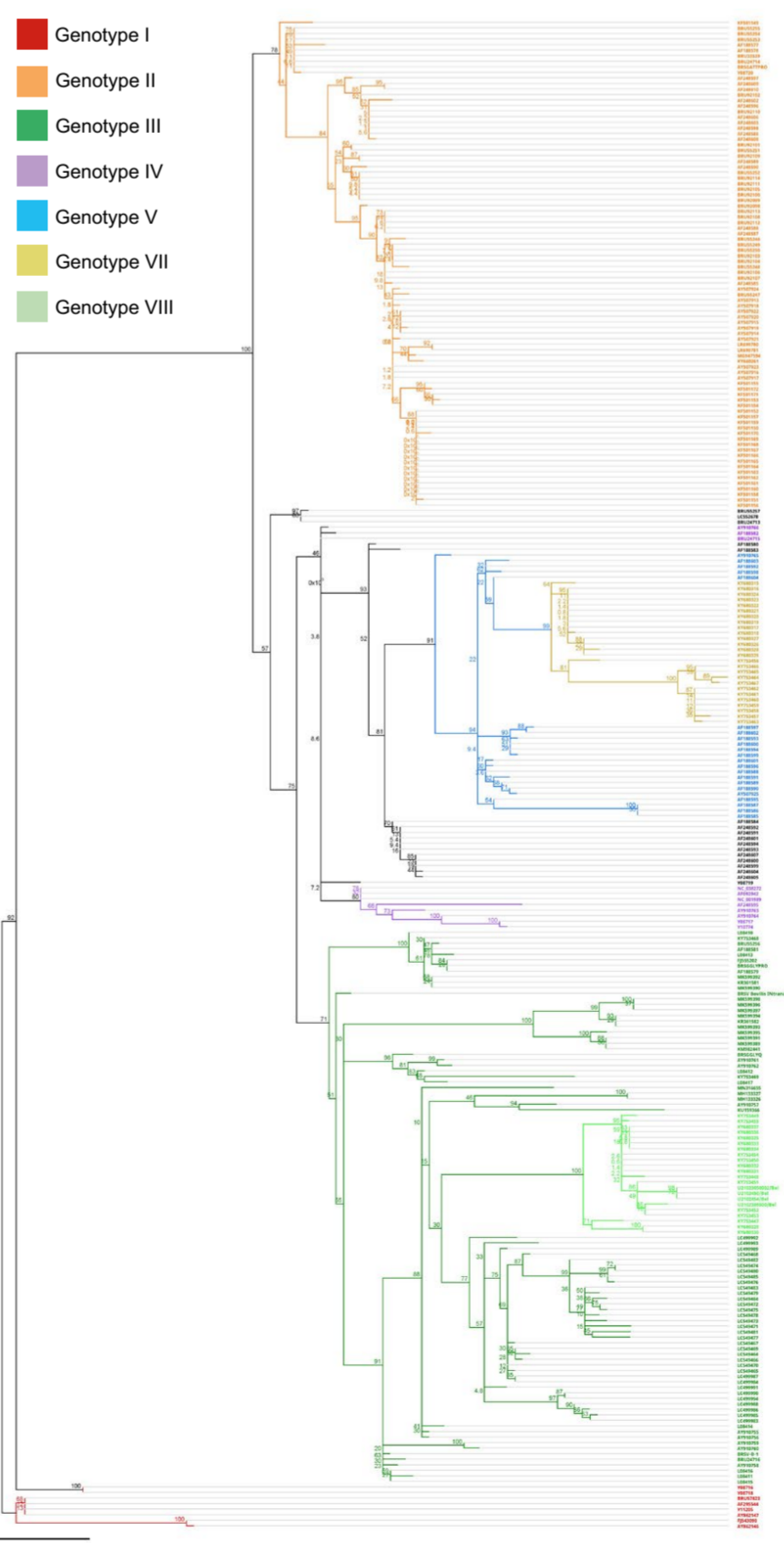
There are 8 genetic BRSV groups. Unlike in the past (Valarcher 2000), those are no longer geographically specific.

The most recent circulating strains in the field seem to belong to the genetic group II (Norway, Croatia, Italy), group III (Brazil, Turkey, China), VII (Croatia, Italy) and VIII (subgroup of III, Italy, Croatia, Belgium). Some other diverging groups were identified and could possibly be classified as new clusters.

The vaccine strains present in Bovilis[®] Bovipast[®] RSP and Bovilis[®] INtranasal RSP[®] Live belong to the same genetic group as the predominant strains currently circulating in the field.

FIGURE 1. Phylogenetic tree constructed by using the highly variable region of the G gene. TN93 model was calculated as the best model for this analysis. Bootstrap statistical support is marked on main branch nodes. GenBank accession numbers of isolates are provided in branches, and BRSV lineages of isolates are indicated in colors.

PhyML, ML, Bootstraps = 500, Model: TN93, G protein 320 nucleotides



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