

The use of Bioportal to analyse ORF 5 PRRS sequences in Spain



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INTRODUCTION

Porcine reproductive and respiratory syndrome virus (PRRSV) is one of the leading swine pathogens. The availability of sequence data from PRRSV from widespread geographic territories has enabled a better understanding of the fight against PRRS. The sequences don't provide any information unless we compare them within a farm, a company or a region level. During the last 6 years, Boehringer Ingelheim Vetmedica, Inc. (BIVI) in collaboration with UC Davis -and other institutions like Iowa State University- have improved the program Disease Bioportal to the particularities of PRRSV. BioPortal is a web-based system that can manage real time or near to real time a huge amount of data. Tools are available for spatio-temporal display, graphics, and phylogenetic analysis of the data. New introduction of isolates and the evolving dynamics of the virus can be monitored by the consistent sequence of the diagnosis. Thus, the aim of this work is monitoring the isolates in country level by using Bioportal.

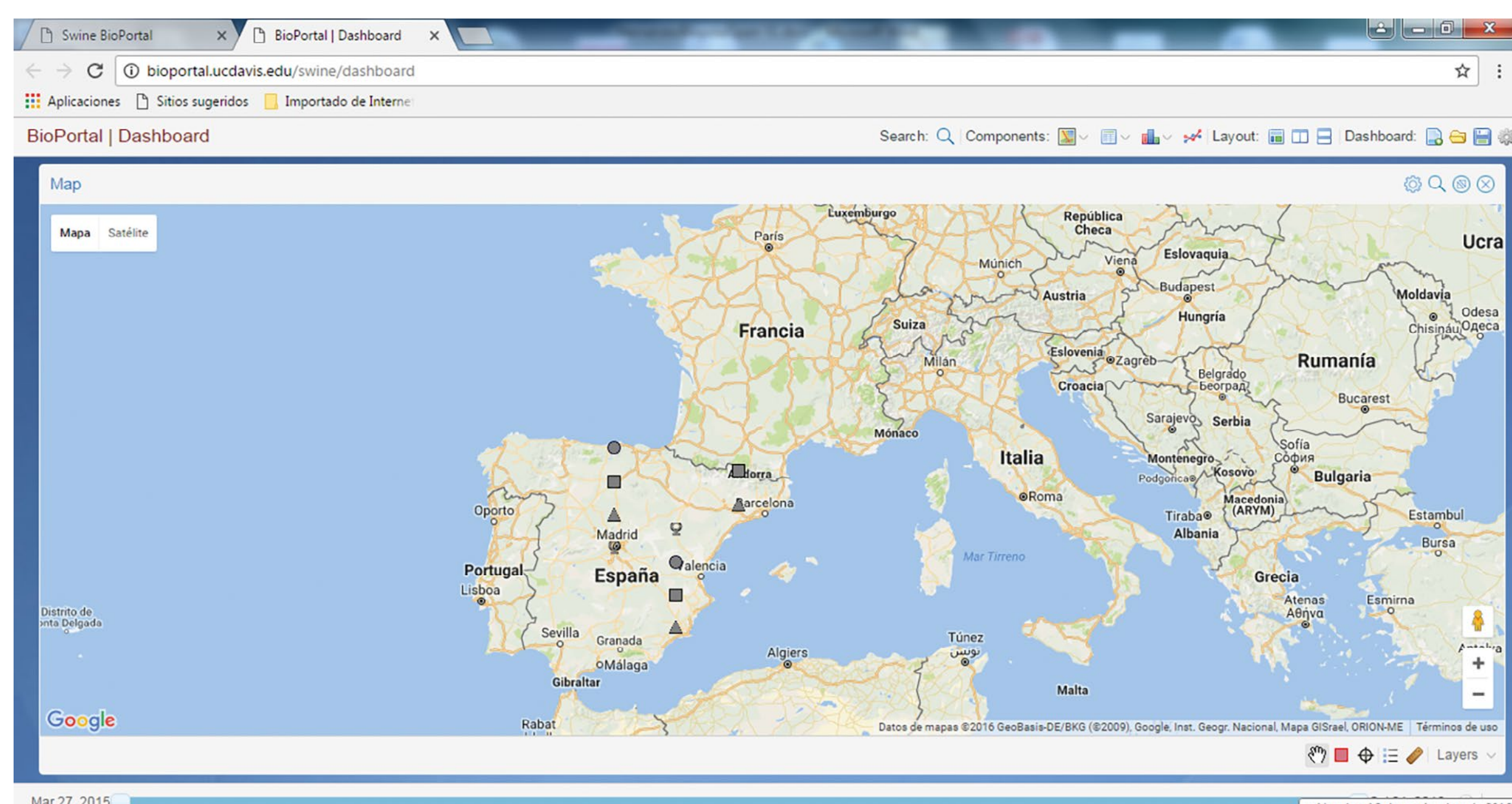
MATERIALS AND METHODS

Seven hundred and thirty six orf5 sequences were obtained from 39 different companies corresponding to 74 different farms across Spain. All the sequences were named to easily distinguish the sequences obtained in different areas (south of Spain, center of Spain or North of Spain), and production phases ("1": due to wean piglet, "2": weaner at the end of nursery, and "3": finisher or REC a gilt in the Gilt development unit(GDU)). The Disease BioPortal software (<http://bioportal.ucdavis.edu/>) was used to generate the phylogenetic trees and evaluate the genetic distances between the sequences. To determine that a sequence is different from other, we assumed the threshold of 2% even though there is no consensus in that point.

RESULTS

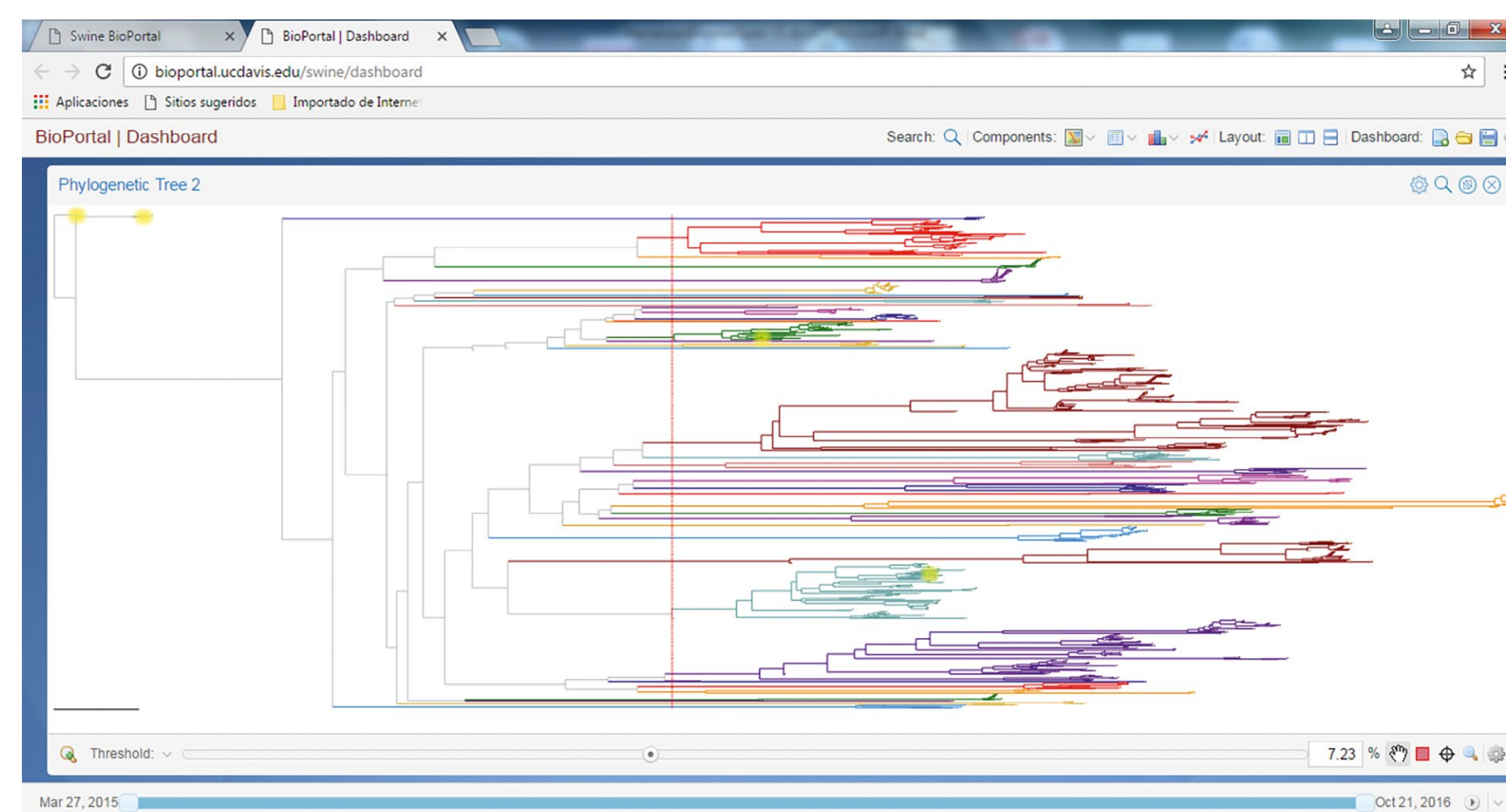
Overall, 44% of the sequences came from due to wean piglets and are presented in the maps in Bioportal as a triangle (sow farm). 47% of the sequences came from the piglets at the end of the nursery represented in the map as a square. Only 4.9% and 3.2% came from the finishers (represented as a circle) and the gilts (represented as a combination of a circle and a triangle), respectively.

Figure 1: Simulation map, representing the locations where the sequences were obtained within Spain.



We were able to find all the relevant PRRSV modified live vaccine strains in Spanish market even though the vaccination program implemented was based on BI vaccines. Rerouting the phylogenetic tree to the first isolate found in Europe Lelystad (1991) we found that the nearest wild isolate found in our data base was one found in a finishing unit in the south of Spain and was 7.23% different from the Lelystad. If we go to the last isolate within the tree we found an isolate coming from a sow farm that was 17.42% different to the Lelystad. This result can suggest us an annual evolution of the virus between 0.29 and 0.69% been similar (0.5% annual evolution) to the ones showed in other studies¹.

Figure 2: Phylogenetic tree of the % of heterology between Lelystad strain and the BI Spanish data base.



DISCUSSION AND CONCLUSION

Farms selected for this study were well representative for Spanish conditions. Current technologies allow for cheaper and faster results in diverse fields of knowledge as sequencing, mapping and information processing/sharing, and that we at Boehringer Ingelheim and UC Davis with this Bioportal is leading the swine industry in terms of technological advancement. All relevant PRRS MLVs can be found in the field. Bioportal will be able to monitor the strains within a farm, company a region even in a country as in this study is showed.

REFERENCES

1. E. Mateu et al; Virus research 2006

