

Porcine Reproductive and Respiratory Syndrome: Is this the Resident Virus or is it a New Introduction?



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INTRODUCTION

Veterinarians are challenged with the question, "Is this the resident virus, or a new introduction?" following the receipt of Porcine Reproductive and Respiratory Syndrome (PRRS) positive test results. With sequencing and comparison to previous viral isolates, various rules of thumb (typically 2% or 3% heterology) are often applied to attempt to make the determination. This is a case report from a 5000 sow herd, in a high density area of the United States, which illustrates the importance of evaluating more of the contextual evidence.

MATERIALS AND METHODS

The herd was infected with a virulent PRRS virus in late 2010. In early 2011, the herd underwent elimination by loading the farm with gilts, closing the herd and mass vaccinating with a modified live vaccine. In late 2012, PRRS virus was detected in due to wean piglet and onsite finishing samples with 1.8% and 2.2% heterology to the 2010 isolate, respectively and 1% different from each other. Participation in the local PRRS area/regional control program (ARC) allowed additional information to be assessed for this determination.

RESULTS

Using the rule of thumb would result in determining that these 2012 isolates were the same as the previous resident virus. Other available evidence gives a compelling argument to conclude that there was a successful elimination and a new introduction of a similar virus from a neighboring farm. Specifically:

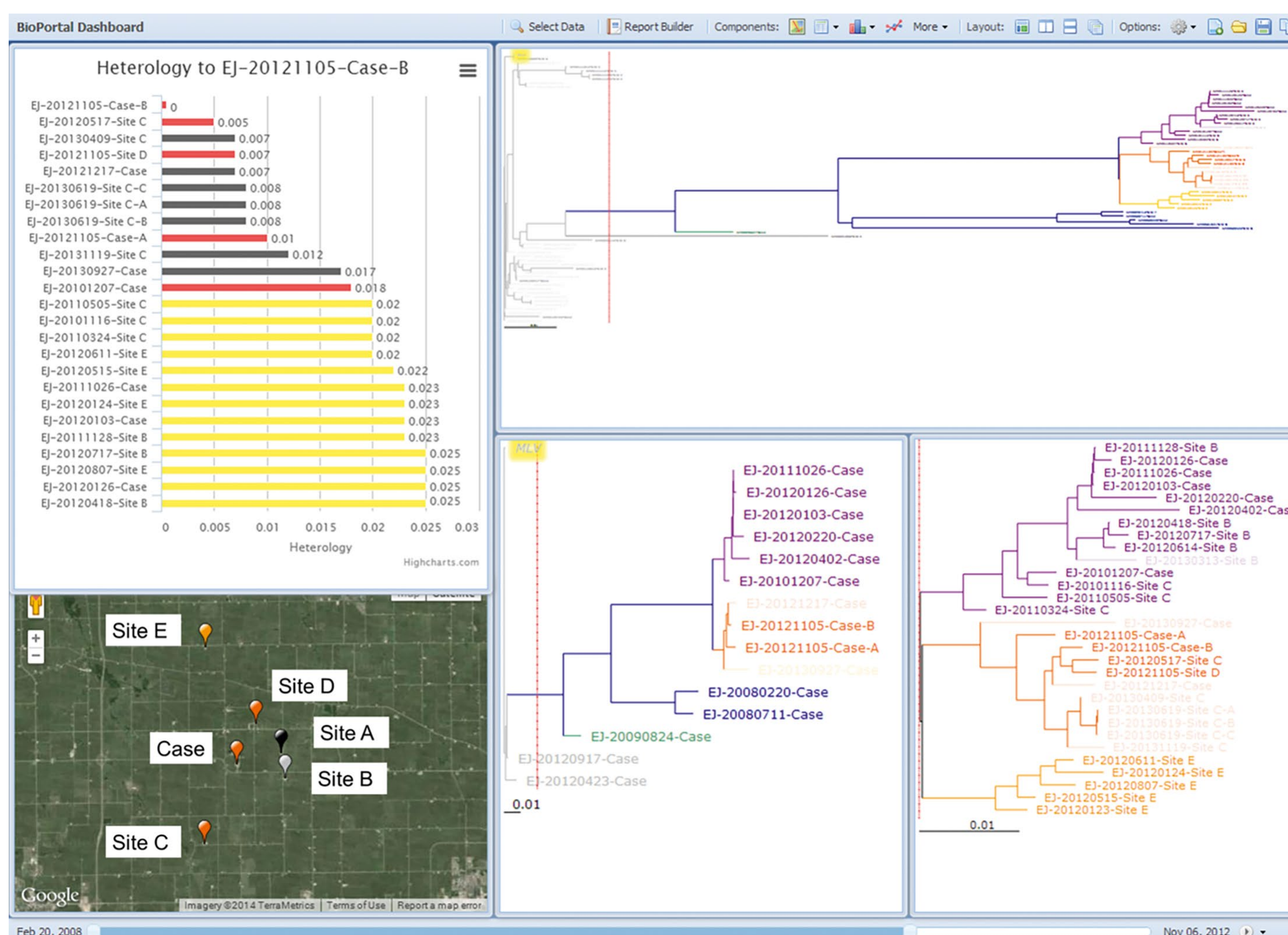
- Similar viruses were circulating in this region since December of 2010, giving credence to lateral spread.
- A neighboring farm (Site D – 2.54 km) also detected a similar (0.7 – 1.3%) virus on the same day. (Figure 1: EJ-20121105-Site D)
- Another similar (0.5 – 1.2%) virus had been found 7 months prior at site C (Case – 4.8 km and Site D – 7.34 km). (Figure 1: EJ-20120517-Site C)

DISCUSSION AND CONCLUSION

Without the information from the ARC, the rule of thumb alone allows the producer to conclude a failure of the elimination plan or in execution of the plan rather than a breach in biosecurity. This perception would no doubt inform future PRRS control decisions on the farm and in the area.

Figure 1: Disease BioPortal# Dashboard

Disease BioPortal Dashboard including: heterology pareto (upper left), Map of local cluster of farms including case site (lower left), phylogenetic tree of all isolates from cluster (upper right) with a closer view of pertinent isolates (lower right) and a phylogenetic tree of isolates from the Case herd (lower middle). The time slider is scrolled back to the day following the outbreak, thereby making all subsequent isolates either pale or grey in the figure. Note: isolates are labeled EJ (system) – YearMonthDate-Site-isolate (A, B, etc. in instances where more than one isolate was sequenced on the same day at the same site).



#The Disease BioPortal is operated and maintained by the University of California, Davis (<http://cadms.ucdavis.edu/>)

