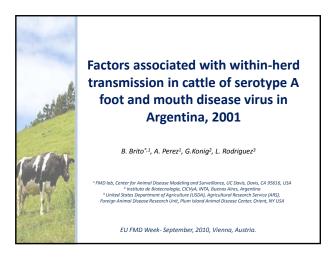
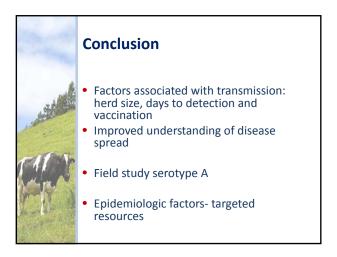
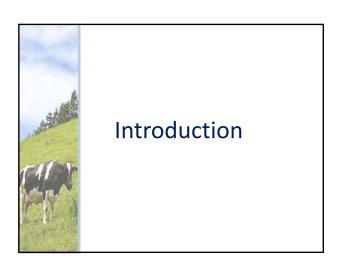
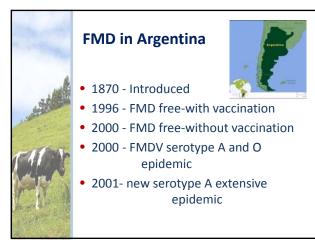
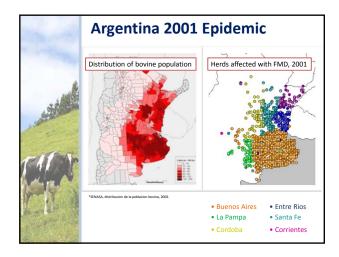
### Appendix 68

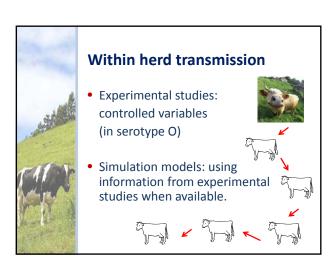








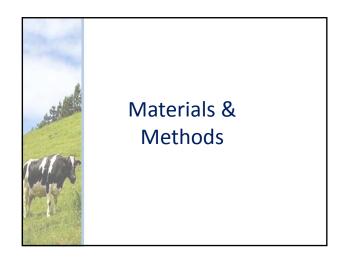






# **Objectives**

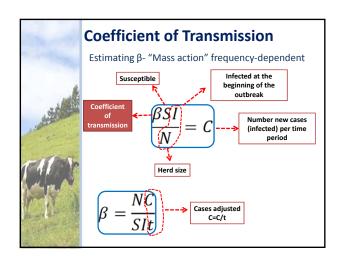
- To estimate the intra-herd transmission coefficient (β)
- To estimate the association with potential epidemiological factors for the disease.





#### **Database**

- Outbreak (case): herd officially recognized by SENASA as infected.
- Records: demographic variables and disease/dates records.

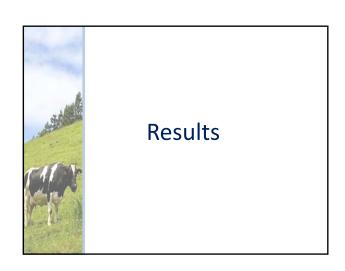


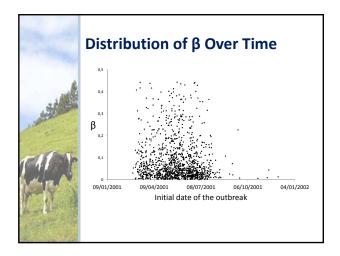
Multivariate logistic regression

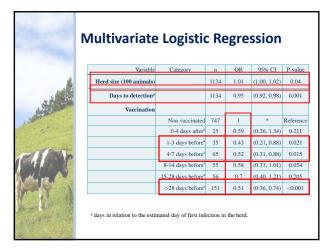
• Dependent variable: β categorized

1 = > β median
0 = ≤ β median
• Independent variables

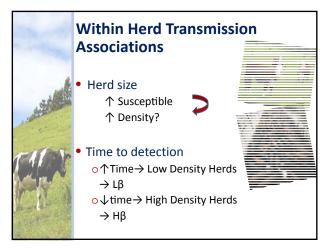
• Latitude and longitude
• Duration of the outbreak
• Herd size
• Days initial infection-detection
• Predominant age group
• Days initial infection-vaccination

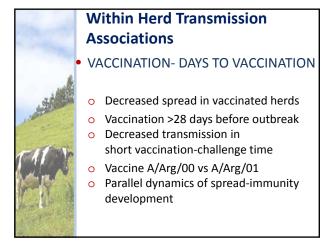


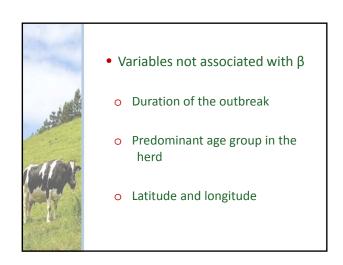














## **Conclusion**

- Improved understanding of mechanisms for disease spread
- SEROTYPE A
- Epidemiologic factors- targeted resources



# Acknowledgements

- Plum Island Animal Disease Center Research Participation Program fellowship, ORISE.
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