Research Project 3/10 Dr Ray Cursons

Final Lay Report

The Molecular Identification and Epidemiology of *Streptococcus equi* subsp. *equi*

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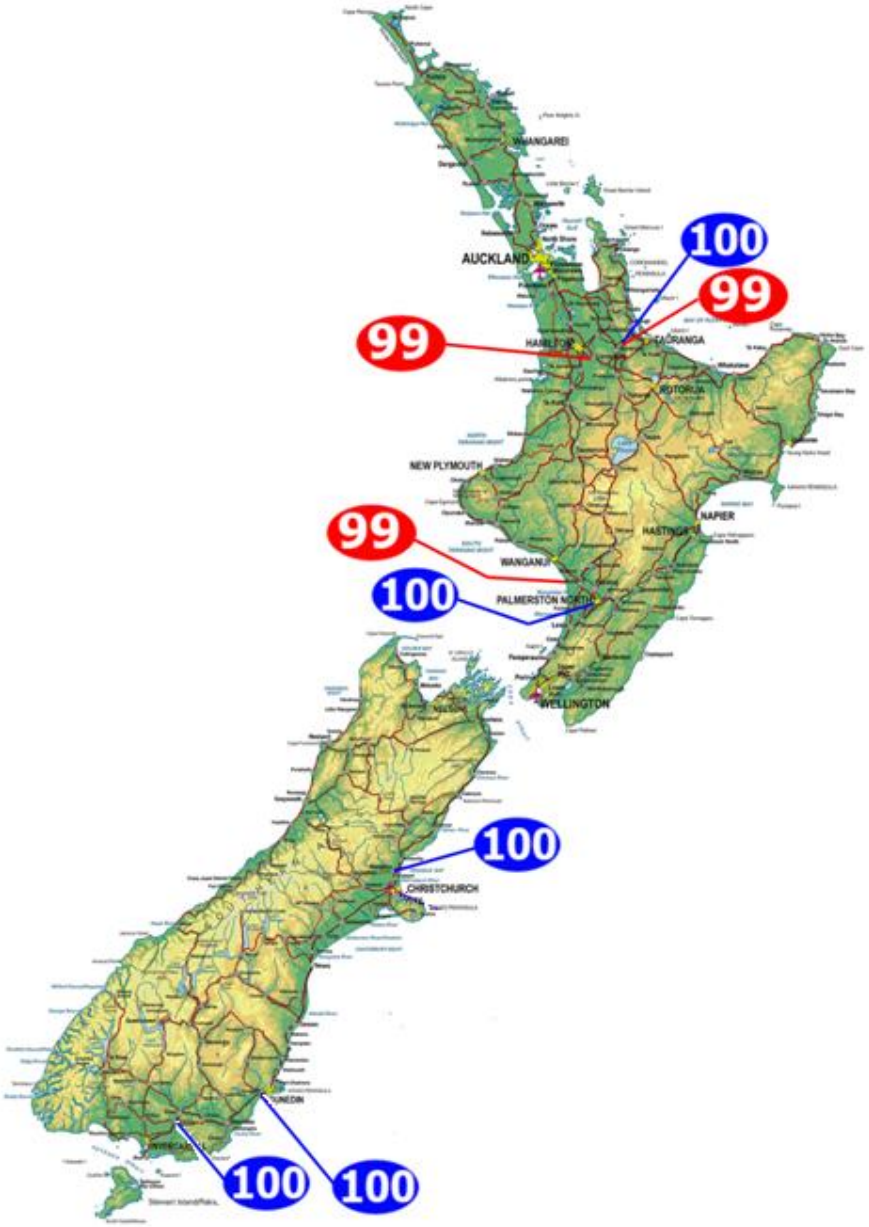
Final Lay Report

The disease strangles, which is caused by infection of horses with a bacterium called *Streptococcus equi* subsp. *equi* (S. equi), is one of the most frequently diagnosed, contagious disease of horses worldwide. The disease is characterized by abscesses in the neck that cause lymph nodes to become inflamed. The surrounding tissue becomes swollen and in very severe cases can "strangle" the airways of affected horses. When the abscesses burst the material from the draining abscess leads to a nasal discharge which is highly infectious and can contaminate pastures, barns and feed troughs. Strangles is further complicated because some infected horses may not totally clear the infection after treatment and can become carriers showing no signs of the disease.

The differential diagnosis of suspected strangles often results in the culture of multiple streptococci, namely *S. equi*, *S. equi* subsp. *zooepidemicus* (*S. zooepidemicus*) and *S. dysgalactiae* subsp. *equisimilis* (*S. equisimilis*). All three streptococci have implications in respiratory disease in horses. A multiplex PCR diagnostic test was developed to distinguish these Streptococcal species by identifying the presence of their DNA in a specimen. Comparison of culture verses PCR showed that the PCR detected approximately 30 % additional *S. equi* infections. The multiplex PCR had a diagnostic accuracy on field specimens of 100 % for *S. equi* and *S. zooepidemicus* and 99.3 % for *S. equisimilis*. These results are suggestive of a promising molecular diagnostic test for the rapid identification and differentiation of *S. equi*, *S. zooepidemicus* and *S. equisimilis*.

Currently there are 128 recorded strains of *S. equi* throughout the world. This strain discrimination is based on differences in the DNA sequence of the *S. equi* SeM gene. Sequencing of the SeM gene allows identification of current circulating *S. equi* strains and will aid in the recognition of newly emerging strains of *S. equi*. We identified two novel strains in New Zealand (SeM allele 99 and 100). SeM Allele 100 had a higher prevalence rate then 99, appearing on both islands of New Zealand. SeM allele 99 only appeared on the North Island. The dominance of SeM allele 100 needs to be further accessed with more isolates.

On completion of this work Olivia has received her MSc with first class honours and has been invited as one of forty international participants to the Havemeyer Workshop entitled "Getting to Grips with Strangles and other Streptococcal Diseases 2012" which precedes the 9th International Conference on Equine Infectious Diseases in Kentucky, USA.



Distribution of NZ *S. equi* strains (SeM alleles 99 and 100)

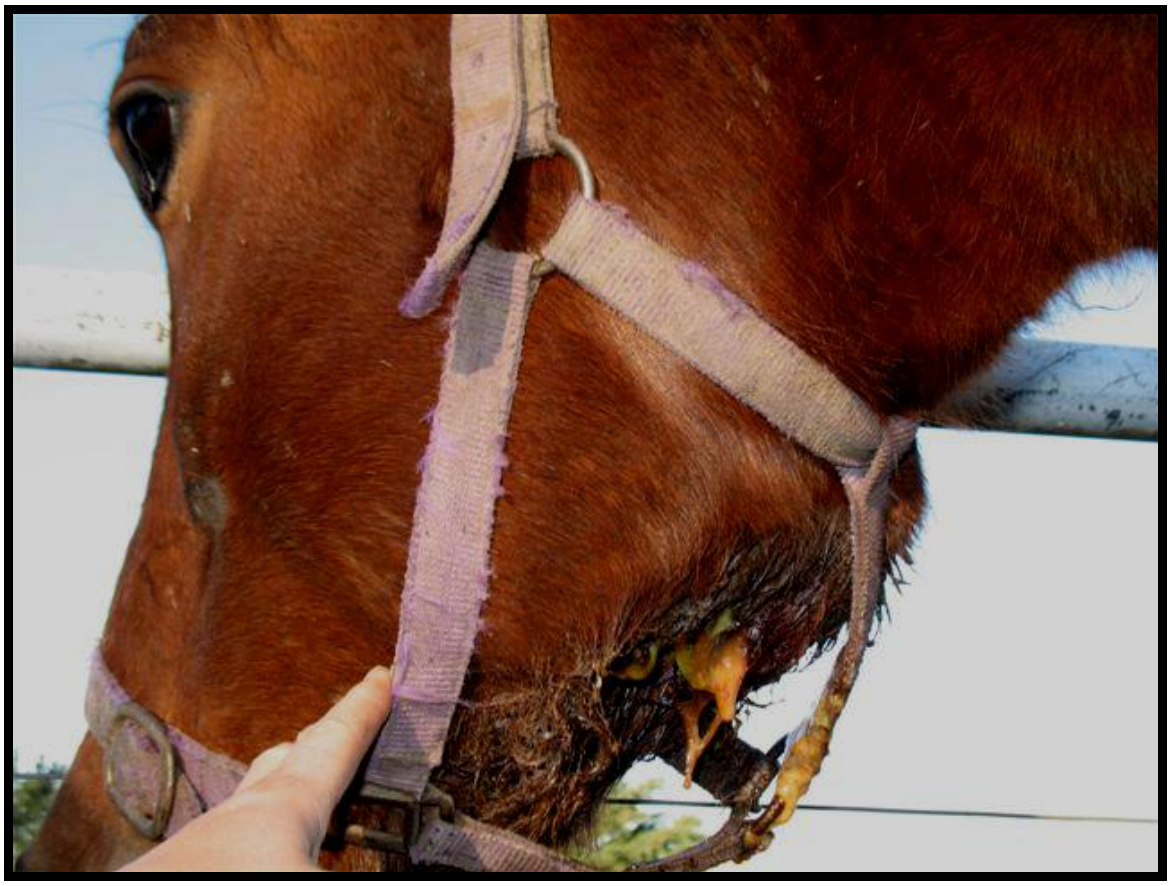


Photo supplied by New Zealand veterinarian Rebecca Sutorius