

---

**Equine respiratory viruses: looking for the new players**  
**Magda Dunowska<sup>1</sup>, Kaylyn McBrearty<sup>1</sup> and Patrick Biggs<sup>1</sup>**  
*Massey University, Palmerston North, New Zealand*

---

*Funding: (ET3) This project was funded by the New Zealand Equine Trust 2008-2010 \$64,750*

---

**Background:** Several viruses have been associated with equine respiratory disease worldwide. Of these, Equine herpes viruses types 1, 4, 2 and 5 (EHV-1, EHV-4, EHV-2 and EHV-5), Equine rhinitis viruses A and B (ERAV and ERBV), and equine adenoviruses are present in New Zealand. The past surveys were based on traditional methods of virus detection, including virus isolation, PCR and serology. As such, only culturable viruses, or viruses with known sequence data, could be identified and any novel viruses would have escaped detection.

**Objective:** The objectives of the current project were two-fold:

- 1) To update our knowledge of which equine respiratory viruses circulate in New Zealand, and whether or not there is an association between viral infections and respiratory disease in sampled horses.
- 2) To detect any potentially novel equine respiratory viruses that may be present in New Zealand.

**Methods:** nasal swabs were collected from horses with respiratory disease ( $n=52$ ) and from clinically normal horses ( $n=33$ ) from the Manawatu and Hawkes Bay regions. All samples were tested for the presence of EHV- 1, EHV-2, EHV-4, EHV-5, ERAV, ERBV and adenoviruses by PCR. The PCR results were confirmed by dot-blot hybridization with virus-specific DIG labelled probes. In addition, virus isolation in three different cell types was performed on samples from horses with respiratory disease.

**Results:** One or more viruses were identified in samples collected from 41 of 52 (79%) horses with respiratory disease, and from 2 of 33 (6%) clinically normal horses. The most common viruses identified were EHV-5 and EHV-2, followed by EHV-4, and EHV-1. In addition, a sample enriched for viral sequences, prepared from pooled nasal swabs from horses with respiratory disease, was submitted for next generation sequencing (ngs) at the Massey Genome Centre. The ngs generated 37.4 mln sequences. These data will be used to search for any new viruses that might have been present in the samples, but were not identified using traditional methods.