

Molecular characterization of Spike protein gene of Bovine Corona Virus strains

Background:

Bovine coronavirus (BCoV) is a worldwide viral infection that causes both respiratory and enteric diseases, including calf diarrhea (CD), winter dysentery (WD) in adults, and respiratory infections in cattle of all ages, resulting in enormous economic losses (Alenius et al., 1991; Bidokhti et al., 2009). Bovine coronavirus (BCoV) belongs to the family *Coronaviridae*, order *Nidovirales*, and possesses a single-stranded, non-segmented, positive sense RNA genome of 32 kb plus poly (A) tail in length, the longest genome among RNA viruses. The enveloped viral particles are pleomorphic to spherical in shape, helical in symmetry, and with a mean of about 120 nm in diameter. The nucleotide alignment of the S gene revealed a gap of 18 nucleotides within the S gene which was also found in human coronavirus strain OC43, supporting the recent proposal of a zoonotic spillover of BCoV (Brandao et al., 2006).

The S gene of BCoV has been considered as a target for molecular analysis in epidemiology study of this infection. Although several serological studies of BCoV infection among cattle farms in different regions of Sweden have been performed, just one molecular study was published in 2006.

Aim:

The purpose of this project is to study the molecular epidemiology of BCoV in Swedish dairy herds based on whole S1 subunit gene sequences.

Methods:

The samples were collected throughout Sweden since 2002. The training will be about principles of virology; including handling the clinical samples, genome extraction from clinical samples, RT-PCR, nested- or seminested- PCR, sequencing reaction, handling the sequencing machine, phylogenetic tree designation with softwares. Designing a real-time PCR based on the sequences is also included.

Significance:

Increased knowledge on sequences of the S gene of BCoV strains circulating in Sweden will help us trace the route of viral introduction to Sweden and understand the dynamics of viral circulation within Sweden.

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Location:

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Duration:

10-20 weeks

Period:

Starting from April-May 2010 to August-September 2010, after agreement.

References:

- Alenius, S., R. Niskanen, N. Juntti, and B. Larsson. 1991. Bovine Coronavirus as the Causative Agent of Winter Dysentery - Serological Evidence. *Acta Veterinaria Scandinavica* **32**:163-170.
- Bidokhti, M. R., M. Traven, N. Fall, U. Emanuelson, and S. Alenius. 2009. Reduced likelihood of bovine coronavirus and bovine respiratory syncytial virus infection on organic compared to conventional dairy farms. *Vet J.* **182**:436-40. Epub 2008 Oct 1.
- Brandao, P. E., F. Gregori, L. J. Richtzenhain, C. A. Rosales, L. Y. Villarreal, and J. A. Jerez. 2006. Molecular analysis of Brazilian strains of bovine coronavirus (BCoV) reveals a deletion within the hypervariable region of the S1 subunit of the spike glycoprotein also found in human coronavirus OC43. *Arch Virol.* **151**:1735-48. Epub 2006 Apr 3.