

# **Alpaca Research Foundation Funding of New Studies for 2009-2010**

## **Newly Funded ARF Projects for 2009-2010**

### **Johne's Disease in Alpacas: Improved Detection and Prevalence of the Disease in Alpacas Presented to Veterinary Teaching Hospitals in the United States**

**One Year: \$15,702**

**Marie-Eve Fecteau, DVM, University of Pennsylvania School of Veterinary Medicine**

Johne's disease is a potentially devastating chronic intestinal infection of cattle, sheep, goats, alpacas, and wild ruminants caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP). The infection causes severe weight loss progressing to death in alpacas. Although the disease is characterized by diarrhea in cattle, infected alpacas frequently have normal fecal consistency and therefore may not be suspected as having Johne's disease. Because the infection is widespread in dairy cattle in the United States, the practice of feeding bovine colostrum to alpacas may be contributing to the spread of Johne's disease to alpacas. However, the disease can also be introduced into alpaca herds through the purchase of infected animals, or by contact of feces from infected animals of any of the susceptible species. This study will validate the use of a new, rapid sensitive PCR test to detect MAP in alpaca feces, and using this test, to estimate the extent of the MAP infection in alpacas in the United States. The prevalence of MAP will be studied by testing fecal samples from alpacas presented to 4 major veterinary teaching hospitals (Oregon State University, Cornell University, Tufts University, University of Pennsylvania).

### **Identifying Gross Chromosomal Rearrangements that Result in Infertility in Camelids**

**Two Years: \$52,548**

**Terje Raudsepp, PhD, Texas A and M University, Michelle Kutzler, DVM, PhD, Oregon State University and Polina Perelman, PhD, NCI, National Institutes of Health**

Birth defects affecting the development of the reproductive tract have been frequently described in alpacas. In females these defects include underdeveloped genitalia, narrowed vaginal passage, abnormal uterus, enlarged clitoris and double cervix, while various types of ambiguities in internal and external genitalia are found in both males and females. All conditions are associated with impaired fertility or infertility. Though very little is known about the causes of these abnormalities, it is proposed that, like in other species, chromosome rearrangements count for some. The normal number of chromosomes for alpacas is 74. At the time of conception, the gender of the animal is determined on the basis of its sex chromosomes - XX for a female and XY for a male. Thus, sex chromosome abnormalities such as 73,XO (Turner's syndrome) and 74, XX/XY (freemartin) result in abnormal sexual development and infertility. Birth defects and/or abnormal development of the female reproductive tract can be caused also be other chromosome abnormalities of which 74,XX-minute (Minute chromosome syndrome) is among the few known so far. This lack of knowledge is largely because alpacas (and other camelids) have high number of chromosomes and some of these, especially the smallest chromosomes, are

very difficult to study. Therefore, the aim of this research proposal is to use traditional chromosome analysis methods in combination with new molecular tools to improve the characterization of chromosomal abnormalities that underlie impaired fertility in female and male alpacas.

### **Investigation of a Novel Respiratory Coronavirus in Alpacas; Diagnostic Test Development and Initial Prevalence Assessment**

**One Year: \$16,690**

**Beate M. Crossley, DVM, California Animal Health and Food Safety Laboratory, UC Davis**

A disease, called 'alpaca respiratory syndrome' (ARS) was first recognized in the United States in June 2007. A novel coronavirus was isolated from lung tissue of an affected animal. Preliminary serological studies from alpacas in 6 states have shown a strong association between a positive disease history and the presence of antibody suggesting the isolated virus is associated with ARS. To learn more about the virus, whole genome sequence analysis was performed and the resulting nucleotide sequence was compared to a previously recognized coronavirus causing diarrhea in alpacas. Genetic analysis of the virus demonstrates that even though both viruses belong in the family of coronaviruses, they are associated with different serological and phylogenetic groups within the *Coronaviridae*, making the respiratory alpaca coronavirus a unique virus. The focus of this study is to develop and validate a diagnostic test, which will be used to determine the prevalence of the respiratory coronavirus in alpacas. Alpaca age, clinical history, gender, and management history will be queried for a possible association with prevalence and clinical findings.

### **Segregation Analysis and Molecular Characterization of Black and Brown Phenotypes in Alpaca**

**Two Years: \$30,000**

**Carlo Renieri, DVM University of Camerino, Italy**

Coat colour is an important parameter in the selection of alpaca, especially in animals bred for fine fibre production. White, black and different shades of brown are the phenotypes preferred for textile production. Naturally coloured fibre is especially appreciated by the textile industry for manufacturing of ecologically sustainable and organic products. An estimated 20% of coloured wool is presently produced in Peru and very limited information is available about the genetic basis of coat colour in alpaca. In this context, a collaboration between the University of Camerino (Italy) and the Peruvian INIA (National Institute of Agronomic Research) was established in 2006 in order to improve the knowledge on alpaca genetics. Several research topics were defined, such as coat colour, fleece type, quantitative parameters, and population structure. The present project aims to contribute to the research on coat colour and its main objectives are: a) to analyse the phenotypes of the offspring from black x black, black x brown and brown x brown crosses; b) to characterise the gene *ASIP*, one of the genes most likely to be involved in the explanation of both black and brown phenotypes. The ultimate goal of this research is to provide the basis for the development of a marker assisted breeding programme for coat colour in alpaca.

## **Sequencing of BVDV Strains Isolated From Persistently Infected Alpacas**

**One Year: \$12,650**

**John D. Neill, PhD, National Animal Disease Center, Ames Iowa**

Bovine viral diarrhea virus (BVDV) is a common but economically important pathogen of cattle. Only in the last few years have these viruses been recognized to infect and cause disease in alpacas and other New World camelid species. There has been an increase in reports of BVDV in alpaca herds, as well as crias being found that are persistently infected with the virus. There is some evidence that BVDV strains isolated from alpacas grow only poorly in bovine cells suggesting that there are adaptive changes within the genomes of these viruses that allow them to grow efficiently in alpacas. In addition, in some instances, it appears that diagnosis of BVDV infection in alpaca may be hindered by changes that have occurred within the BVDV genome. The goal of this project is to sequence the genomic RNA from BVDV strains isolated from alpacas and compare them to BVDV strains isolated from cattle. This analysis should lead to the identification of changes that allow adaptation to the camelid host. This in turn will lead to the development of new alpaca-specific reagents that will better diagnosis of BVDV in alpaca.