

markers p53, Ki67 and MCM7 positively correlated with neoplastic progression.

Main limitations: The raft cultures were established from a small number of horses.

Conclusion: Established 3D raft cultures authentically reflect major features of corresponding *ex vivo* material, thus constituting a valuable new research model for the study of EcPV2 infection and viral-induced neoplasia in the horse.

Ethical animal research: Research ethics committee oversight not currently required by this journal: the study was performed on archived material collected previously during clinical procedures.

Informed consent: Owners gave informed consent for use of samples for research.

Competing interests: None declared.

Source of funding: The study was funded by Vetsuisse Faculty University of Zurich's competitive Joint Appointments.

Other pathogens

Oral Presentations

43 | Seroprevalence of equine piroplasmiasis, equine infectious anaemia and equine influenza in zebras and rhinoceros from Kenya and Tanzania

P. Bolfa¹; S. Marchi¹; P. Kanyari²; J. Keyyu³ and C. Issel⁴

¹Department of Biomedical Sciences, Ross University School of Veterinary Medicine, St. Kitts, West Indies; ²Department of Pathology, Microbiology and Parasitology, Faculty of Veterinary Medicine, College of Agriculture and Veterinary Sciences, University of Nairobi, Kenya; ³Tanzania Wildlife Research Institute, Arusha, Tanzania; and ⁴Department of Veterinary Science, Gluck Equine Research Center, University of Kentucky, Lexington, KY, USA.

Email: pompeibolfa@gmail.com

Background: Limited information exists regarding prevalence of major infectious diseases (OIE equine listed) in members of the *Perissodactyla* order, like wild equids (*Equus grevyi*) and rhinoceros (black - *Diceros bicornis* and white - *Ceratotherium simum*).

Objectives: To perform a serological survey in Kenya and Tanzania national parks and national reserves on zebras and rhinoceros and investigate the seroprevalence of Equine Infectious Anaemia Virus (EIAV) combined with a survey on equine piroplasmiasis (both *Theileria equi* and *Babesia caballi*) and equine influenza (EI) and compare two EIAV ELISAs.

Study design: Retrospective serosurvey.

Methods: Sera (fresh or banked), from 284 animals were tested (135 females, 149 males including 69 rhinoceros, 215 zebras) from 8 locations in Kenya and 3 locations in Tanzania using commercially available ELISA kits. Two kits from different manufacturers were employed for EIAV testing.

Results: Rhinoceros showed no serological evidence of previous exposure to any of the tested diseases. All zebra samples were negative for evidence of exposure to EIAV. Piroplasmiasis was found in all regions ranging from 3.9% for *B. caballi* to 94.2% for *T. equi*. EI seroprevalence in zebras was 9.3% (N=20), all from Serengeti, Tanzania.

Main limitations: Limited sample size and lack of animal history.

Conclusions: EIAV might not be present or has a very low prevalence in wild African *Perissodactyla* from Kenya and Tanzania. The seroprevalence of equine piroplasmiasis in our study is in line with previous reports in the area, with reactions against the antigens used probably representing exposure to closely related organisms. Almost 10% of the tested Grevy's zebra had previous exposure to Type A influenza viruses, suggesting they could represent a potential reservoir for this virus.

Ethical animal research: Samples were provided by Tanzania Wildlife Research Institute, with approval from Wildlife Research Ethics Committee of TAWIRI and by Kenya Wildlife Service

Informed consent: Not applicable.

Competing interests: None declared.

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44 | Topography of the respiratory, oral, and guttural pouch bacterial and fungal microbiotas in horses

S. Bond¹; C. McMullen¹; E. Timsit^{1,2} and R. Léguillette¹

¹Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada; and ²I&D Pharma Departement, Ceva Santé Animale, Libourne, France.

Email: stephaniebond88@gmail.com

Background: Respiratory disease has a large economic impact on the equine industry. It has been reported that the equine lower respiratory tract microbiota is different in states of health and disease; however, the bacterial and fungal composition of the healthy equine respiratory tract has not been studied in detail.

Objective: To characterise the bacterial and fungal microbiotas present along the upper and lower equine respiratory tract.

Study design: Prospective, controlled, cohort study.

Methods: Eleven upper and lower respiratory tract anatomical locations were sampled in 11 healthy Argentinian Thoroughbred horses from the same herd using a combination of swabs, protected specimen brushes, and saline washes. DNA was extracted from each sample and negative control, and the 16S rRNA gene (V4) and ITS2 region were sequenced. Community composition, alpha-diversity, and beta-diversity were compared among sampling locations.

Results: Fungal species richness and diversity was highest in the nostrils. There was more spatial heterogeneity in bacterial composition than fungal communities. The pharyngeal and arytenoid microbiotas were most similar to the distal tracheal bacterial and