Posters

31. Exploring equine atypical myopathy through *in vitro* toxicity tests

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Equine atypical myopathy (AM) is a seasonal intoxication of grazing equids. In Europe, this poisoning is linked with the ingestion of toxins contained in the seeds and seedlings of the sycamore maple tree (*Acer pseudoplatanus*). Once ingested, one of the incriminated toxins, hypoglycin A (HGA), is metabolized into methylenecyclopropylacetyl-CoA (MCPA-CoA) which inhibits several steps of the fatty acid *ß*-oxidation cycle. This inhibition results in a general decrease in mitochondrial respiration, as determined by high-resolution respirometry (HRR) previously applied to muscle samples taken from cases of AM. The severe impairment of mitochondrial bioenergetics may explain the high rate of mortality observed: about 74% of horses with AM die, most within the first two days of signs of poisoning. To this day, the mechanism of toxicity is not completely elucidated.
With the purpose of improving our understanding of the pathological process and to assess therapeutic candidates, we performed *in vitro* assays using equine skeletal myoblasts cultured from muscle biopsies and subjected them to toxins involved in AM. Through HRR, toxicity and viability assays, we have established that equine skeletal myoblasts do respond the toxic metabolite MCPA. Indeed, a severe depression in mitochondrial respiration as well as cytotoxic responses were recorded after MCPA addition, rendering cell culture and *in vitro* assays interesting perspectives for further pathophysiological explorations of the condition.

32. The middle ear microbiota in healthy dogs is similar to that of the external ear canal

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Background - Otitis media can be a consequence of chronic otitis externa and could represent a perpetuating factor. Sparse information is available concerning the normal microbiota of middle ear. Aim – To compare the tympanic bulla (TB) microbiota with the external ear canal (EEC) microbiota in healthy dogs.
Material and methods - Six healthy experimental Beagle dogs were selected based on the absence of otitis externa, negative cytology and bacterial aerobic culture from the TB. Samples from the EEC and TB were collected directly after death using a total ear canal ablation and lateral bulla osteotomy. The hypervariable segment V1-V3 of the 16S rDNA was amplified and sequenced with a MiSeq Illumina sequence carried out by the Mothur software using the SILVA database. EEC DNA extracts of healthy client owned dogs from the study of Ngo *et al*. was used for the comparison.
Results – In Beagles, a significant difference ($P = 0.009$) for Chao1 richness index between the right and left EEC, but no significant differences between EEC and TB microbiota for Chao1 richness index ($P = 0.6544$), Simpson evenness index ($P = 0.4328$) and the reciprocal Simpson alpha diversity ($P = 0.4313$) was noted (Kruskal-Wallis test). A significant clustering ($P < 0,0001$) was observed between EEC of Beagles and client owned dogs (AMOVA).
Conclusions – The microbiota profile is similar in the EEC and TB in Beagles. The microbiota of the EEC of Beagles differs significantly from the one of healthy client owned dogs, suggesting involvement of environmental factors.