

S554

Symposium

### **The gorilla gut microbiota**

**Objectives:** Little data are available about the gut microbiota in non-human primates. Thus, the objectives were to explore the prokaryotic and eukaryotic communities residing the intestinal tract of a wild gorilla and to detect eventual human pathogens present in gorilla. **Methods:** we have analysed a fecal sample of a wild western lowland gorilla. We tested 82 culture methods. Colonies were identified by MALDI-TOF Mass Spectrometry. In addition, 454 Pyrosequencing, targeting the 16S rRNA gene was used for comparison. Finally, to complete the repertoire, a specific-PCR for Archeae, Planctomyctes and 35 eukaryotic primer sets targeting the 18S rRNA gene and internal transcribed spacer gene were used to explore the occurrence of these organisms in the fecal sample. **Results:** Using culture methods, we tested 12,800 colonies and a total of 142 bacterial species were recovered belonging to 44 genera and 4 phyla. Moreover, a new genus: *Gorillea massiliensis* and 4 new species: *Bacillus marseillegorillensis*, *Microbacterium marseillegorillensis*, *Paenibacillus marseillegorillensis* and *Paenibacillus cameroungoreillensis* were found. Many potential human pathogens such as *Staphylococcus aureus*, *Proteus mirabilis*, *Klebsiella pneumoniae*, *Mycobacterium bolletii* and *Clostridium botulinum* were identified. Deep pyrosequencing enabled the detection of 11 phyla and 39 genera. However, the majority of reads assigned to Firmicutes (46.8%), Actinobacteria (20 %) and Bacteroidetes (18.6%). Planctomyctes and archaeal bacteria were also detected in this stool sample. Using the eukaryotic primers, 1,572 clones were sequenced resulting in the retrieval of 87 eukaryotic species, including 52 fungi, 10 protozoa, 4 nematodes and 21 plant species, of which 52, 6, 2 and 21 species, respectively, have never before been described in gorillas. We also provide the first molecular report of two human parasites (*Necator americanus* and *Oesophagostomum* spp.) in the fecal sample of a wild western gorilla as well as some pathogenic fungi. **Conclusion:** Our comprehensive prokaryotic and eukaryotic results showed that microbial diversity in gorilla gut is higher than this in human gut and confirm that it may act as reservoir for human pathogens.