Domesticated equines have fundamental differences in faecal microbial concentrations

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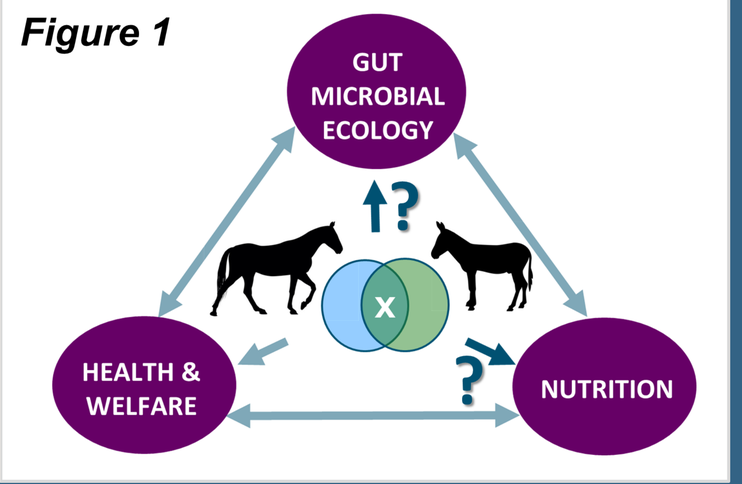
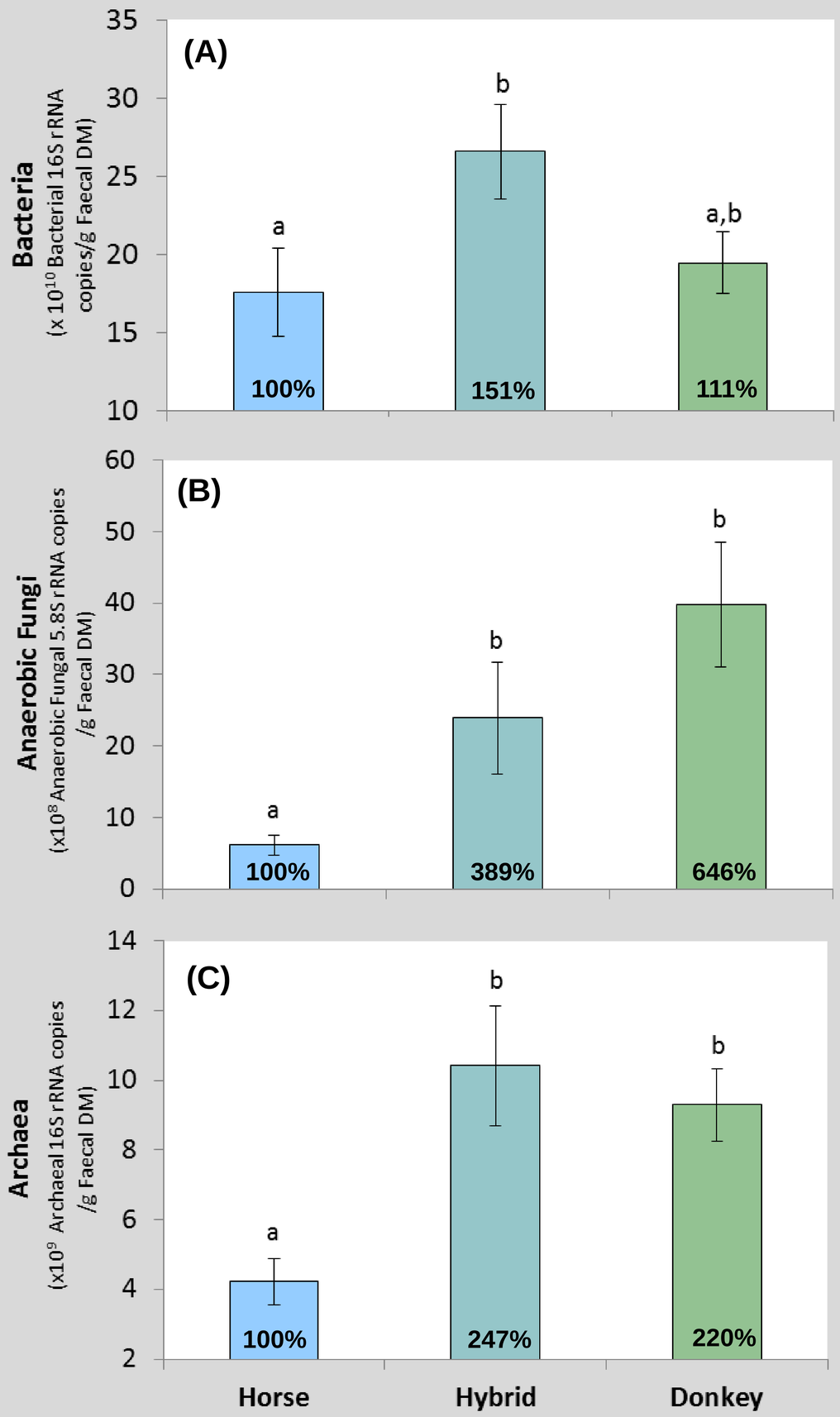
Background & Objective

- Nutritional studies have shown that horses and donkeys differ, with donkeys having a higher dry matter digestibility (DMD) of dietary material and a longer gut retention time of dietary particles[1,2].
- As analysis of the equine gut microbiome to date has primarily focussed on horses[3], however, it is unclear to what extent these differences are mediated by differences in the physiology and/or hindgut microbiota of these domesticated equines (*Figure 1*).
- **A preliminary study was therefore conducted in order to assess the faecal concentrations of bacteria, archaea and anaerobic fungi in horses, donkeys and hybrids (mules & hinnies)** .

Figure 1



▼***Figure 2***: Faecal concentrations of bacteria (A), anaerobic fungi (B) and archaea (C). Averages and the SEM are shown. Within each plot, superscripts indicate significant differences (P<0.05) and the percentage of the horse mean value is shown for each equine group.



Conclusions

- **All microbial concentrations were affected by equine group (*Figure 2*), and the greatest differences observed were in terms of the anaerobic fungi.**
- **A six-fold higher anaerobic fungal concentration in donkeys relative to horses suggests that these potent fibre degrading organisms contribute to the previously reported higher DMD of dietary material in donkeys relative to horses.**

Materials & Methods

- Fresh faecal samples were collected from healthy 4-25 year old animals with no known history of gut-related problems (donkeys & hybrids n=18; horses, n = 17).
- For each equine group a representative animal size range was used, with animals sourced from multiple locations. The majority of the animals sampled had a predominantly pasture based diet.
- Faecal samples were freeze-dried and ground, and then DNA extracted using a customised Maxwell method (Promega)[4]. Concentrations of bacteria, archaea and anaerobic fungi were determined using established quantitative PCR methods[4,5].
- Data were analysed on a dry matter basis after Log_{10} transformation using a one-way ANOVA with equine group as a single independent factor and a Tukey post-hoc test.

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