P-22 **Bacterial community diversity in the rumen of sheep assessed by ARISA and DGGE fingerprinting methods.** C. Saro[a], M.J. Ranilla[a], A. Cifuentes[b], R. Rosselló-Mora[b], M.D. Carro[a]. [a]Dept. Producción Animal, Universidad de León, 24071 León, Spain. IGM (CSIC-ULE), Finca Marzanas s/n. 24346 Grulleros, León, Spain, [b]IMEDEA, Instituto Mediterráneo de Estudios Avanzados (UIB-CSIC). C/ Miquel Marqués, 21. 07190, Esporles, Illes Balears, Spain.

Automated ribosomal intergenic spacer analysis (ARISA) and the denaturing gradient gel electrophoresis (DGGE) are two of the most widely used techniques to assess microbial diversity. The aim of this study was to investigate the postprandial changes in bacterial communities in the solid (SOL) and liquid (LIQ) phases of the rumen in sheep fed two diets using ARISA and DGGE. Four rumen-fistulated sheep were used in a cross-over design. The two experimental diets had 70:30 forage:concentrate ratio with either alfalfa hay (AL) or grass hay (GR) as forage. Samples from the SOL and LIQ phases of the rumen were obtained from each sheep immediately before feeding (0 h) and 4 and 8 h post-feeding. With ARISA, mean values of total number of peaks ranged from 20.0 to 50.8 for SOL and from 38.5 to 52.0 for LIQ samples. With DGGE, mean values of total number of peaks ranged from 9.0 to 12.8 for SOL and from 8.8 to 14.3 for LIQ. When all samples were considered together, Shannon index ranged between 2.99 and 3.95 with ARISA, and between 2.11 and 2.61 with DGGE. Whereas no variations ($P>0.05$) in bacterial diversity over the postprandial period were detected either in SOL or LIQ with DGGE, ARISA showed a decrease ($P<0.05$) in the number of peaks in SOL samples at 4 h post-feeding compared with 0 and 8 h samplings. In LIQ samples, the number of peaks was lower ($P<0.05$) at 4 h post-feeding than that before feeding in GR-fed sheep, but no differences ($P=0.14$) were observed for AL diet. Both for SOL and LIQ samples, AL-fed sheep showed higher ($P<0.05$) number of peaks and Shannon index values than GR-fed sheep with both ARISA and DGGE. Despite of the lower number of bands detected by DGGE, it showed a clear discrimination among SOL and LIQ samples when dendrograms were constructed individually for each sheep. On the whole, ARISA was shown to be easier and less time-consuming than DGGE, and therefore more appropriate for the rapid analysis of a large number of samples. DGGE can detect major shifts in bacterial populations, but it might be not sensible enough to detect subtler changes in rumen bacterial communities.

P-23 **The impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and Rural Africa.** D. Cavalieri[12], M. Di Paola[3], M. Ramazzotti[2], J.B. Poullet[4], S. Massart[4], G. Pieraccini[2], P. Lionetti[3], C. De Filippo[1]. [1]Fondazione Edmund Mach, IASMA Research and Innovation Centre, Via E. Mach 1, 38010 San Michele all'Adige (Trento), Italy, [2]Department of Preclinical and Clinical Pharmacology, University of Florence, 50139 Firenze, Italy, [3]Department of Pediatrics, University of Florence, Meyer Children Hospital, Viale G. Pieraccini 24, 50139 Firenze, Italy, [4]DNAVision, Avenue George Lemaitre 25 - B-6041 Charleroi, Belgium.

NGS technologies are opening new frontiers in investigating human metagenome variation. We present results on how differences in diet and environment shaped gut microbial ecology in Europeans and Africans. We characterized the fecal microbiota of African children from Burkina Faso living in a rural village with a diet predominantly vegetarian, versus those living in an urban area, that maintains the consumption of cereals and legumes but introduces protein rich food (milk, meat, fish, egg) and European children living in an urban area with a typical western diet (Italy). The first key finding is that diet is the dominant factor in shaping gut microbiota. Burkina children from the rural village (BFR) are differentiated but closely related to the urban (BFU). All the Burkina gut microbiota profiles (BFR & BFU) cluster separately from EU. The second key finding is that BFR metagenome was significantly enriched in distinctive bacterial genera (*Xylanibacter*, *Prevotella*, *Treponema*) that might help to extract energy from the plant polysaccharides (abundant in the BFR children's fiber rich diet) while protecting them from inflammatory gut diseases. At the same time BFR also had decreased numbers of well-known pathogens compared with BFU and EU. The third key finding is that short chain fatty acids levels (SCFAs) are statistically much higher in Burkina children respect the European ones, and associated to the presence of sequences encoding for the enzymes needed to digest these fibers. In particular, propionic and butyric acids are nearly four times more abundant in BFR than in EU fecal samples ($p<0.001$). Interestingly SCFAs decrease in BFU respect to BFR probably due to depletion of SCFAs producing species, such as *Xylanibacter*. The observed different bacterial compositions are likely to have profound influences on the immune system, possibly explaining the absence of inflammatory bowel diseases, and allergies in African children and adults.