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The relative abundance of bacterial genera present in faecal samples from children with single *T. Appl Environ Microbiol* 2009 75: 7537–7541. trichiura infections and 21 of the 30 uninfected children received anthelmintic treatment. 20. trichiura infections. A study of the effects of H. 39. P=0.025). lumbricoides infection. (1987) Predisposition to Trichuris trichiura infection in humans. While similar organisms are common inhabitants of ruminants [26] to our knowledge they have never been observed at such abundant proportions in human faecal samples from Western subjects. It should be acknowledged also that we cannot rule out the possibility that differences between our Ecuadorian cohort and individuals from the Western world might be influenced by methodological differences in sample storage and processing steps such as DNA extraction and PCR primer bias. Furthermore, the apparent predominance of *Prevotella* spp. Wu S, Li RW, Li W, Beshah E, Dawson HD, et al. (2008) Impact of long-term treatment with ivermectin on geohelminth infections in Esmeraldas Province, Ecuador. There were no significant differences between the two groups in the proportional abundances of the bacterial genera identified. Olsen A (2007) Efficacy and safety of drug combinations in the treatment of schistosomiasis, soil-transmitted helminthiasis, lymphatic filariasis and onchocerciasis. Furthermore, the most abundant organism in our Ecuadorian dataset was the Firmicutes species *Faecalibacterium prausnitzii* (16.6% of total sequences recovered), which has previously been reported to be one of the most abundant organisms in individuals from the Western/industrialised world [24] and has also received much attention recently as a potentially anti-inflammatory species [25]. Chimeras were removed using Perseus software [22], as implemented in mothur. Despite these broad similarities there was also some evidence for the development of distinct microbiota structures in the rural Ecuadorian population sampled for the current study. 15. We selected for further evaluation a total of 121 of these children who met the study inclusion criteria: belonging to one of the 3 infection groups as described above, aged 8 to 14 years, had taken neither antibiotics in the previous month nor anthelmintic treatment in the previous 3 months before the start of the study, and were afebrile and asymptomatic at the time of sampling. (2010) Exploitation of the intestinal microflora by the parasitic nematode *Trichuris muris*. (2013) Patent Human Infections with the Whipworm, *Trichuris trichiura*. Are Not Associated with Alterations in the Faecal Microbiota. Future studies should focus on the effects of T. In the present study we tested the hypothesis that STH infections of humans affect the composition of faecal microbiota and that anthelmintic treatment would revert this altered microbiota composition towards that observed in uninfected controls. Anthelmintic treatment of children with T. Both drugs are extremely safe at the doses used [18],[19]. We were unable to detect an effect of concurrent T. trichiura infection (Figure 5). BMC Bioinformatics 12: 38. Nucleic Acids Res 41: D8–D20. To minimise PCR nucleotide insertion mistakes, a high fidelity Taq polymerase (AccuPrime™, Invitrogen, Carlsbad, USA) was used, and samples were amplified in quadruplicate reactions with 20 cycles each and then pooled. The Jaccard calculator ignores relative abundance of each OTU and instead examines the level of overlap in community membership by simply observing presence or absence of each OTU across all of the samples. 7. Eckburg PB, Bik EM, Bernstein CN, Purdom E, Dethlefsen L, et al. We observed a decreased proportional abundance of a few bacterial genera from the Clostridia class of Firmicutes and a reduced bacterial diversity among children with mixed infections compared to the other two groups, indicating a possible specific effect of A. We also observed mixed infections with A. The proportions of OTUs belonging to different bacterial genera among children infected with single T. 21. Nature 486: 207–214. All children with single T. Experimental infections with *Trichuris suis* in 7 pigs showed a disturbed microbiota in the proximal colon at 21 [12] and 53 [14] weeks following infection that was associated with changes in the abundance of approximately 13% of bacterial genera and particularly with declines in the relative abundance of *Fibrobacter* and *Ruminococcus*, although these were not reflected in changes in diversity indices at the genus level [12]. 18. NCBI resource coordinators et al (2013) Database resources of the National Center for Biotechnology Information. See Table S1 for full barcode and primer sequences. lumbricoides reside in the small intestine while those of T. Funding for AWW, SJS, JP and sequencing was provided by the Wellcome Trust (grant number, WT076964). Reina Ortiz M, Schreiber F, Benitez S, Broncano N, Chico ME, et al. (2010) Chronic intestinal helminth infections are associated with immune hyposensitiveness and induction of a regulatory network. Moncayo AL, Vaca M, Erazo S, Oviedo G, Rodriguez A, et al. *Trichuris* spp. 33. P=0.047: Clostridial cluster IX, mixed 0.6% vs. (2012) Worm Burden-Dependent Disruption of the Porcine Colon Microbiota by *Trichuris suis* Infection. trichiura on intestinal microbiota may be persistent, such studies should collect samples at various time points after treatment and several control groups to control for past exposures may be appropriate. A 500 mg aliquot of stool was placed in a 2 ml microtube and an equal volume of 90% ethanol was added. trichiura. Following these data cleaning steps a median of 2286 sequences remained per sample. Polymerase chain reaction (PCR) was used to amplify variable regions 3 to 5 (V3-V5) of the 16 S rRNA gene. Steinmann P, Utzinger J, Du ZW, Jiang JY, Chen JX, et al. We did not detect any other “classic” overt bacterial pathogens such as *Salmonella* spp., *Yersinia enterocolitica*, *Vibrio cholerae*, *Staphylococcus aureus*, and *Aeromonas hydrophila*. Walker AW, Ince J, Duncan SH, Webster LM, Holtrop G, et al. trichiura ova and although patent infections were not established, there was some evidence of clinical improvement in four out of the five monkeys investigated [15]. T. (2008) *Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. Errors bars show standard deviation from the mean. A sample of uninfected children and those with T. trichiura on diarrhoea could have been mediated through immune mechanisms rather than through changes in microbiota, with the latter being a consequence of the resolution of diarrhoea rather than a direct effect of the parasites. (2011) Effects of chronic ascariasis and trichuriasis on cytokine production and gene expression in human blood: a cross-sectional study. lumbricoides, could potentially drive the development of an altered faecal microbiota profile, with reduced proportional abundances of some members of the Clostridia class, an increase in streptococci (in some individuals) and reduced overall diversity. Streptococci are not typically dominant in health, indicating that the microbiota was particularly disturbed in these individuals. trichiura only, sampled 21 days post treatment [N=14], C = uninfected children before treatment [N=21], F = uninfected children from Group C, sampled 21 days post treatment [N=21]. One mechanism is through the induction of immune regulatory cytokines such as IL-10, which are increased during chronic infections in humans [7],[8]. The effect of anthelmintic treatment per se was evaluated by comparing paired samples from uninfected children before and after treatment. lumbricoides. trichiura are localised to the sites of parasite colonisation. Comparisons of the microbiota at different taxonomic levels showed no statistically significant differences in composition between uninfected children and those with T. coli strains using just short fragments of the 16 S rRNA gene we could not determine the presence or absence of these potential pathogens. For example, the fourth most abundant OTU was most similar to a member of the *Succinivibrio* genus of the gamma-proteobacteria (median abundance of 3.1%, interquartile range 0.4% to 6.2%, maximum of 27.4%) (Table S3). (2009) Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. As a result, the faecal samples collected in this study do not necessarily represent the microbiota of the caecum/mucosa, the principal site of colonisation of T. trichiura. Our inability to detect an effect of T. A clinical correlate of an experimental observation. We hypothesised that patent T. trichiura infections, only 2 (12%) had heavy parasite burdens ( $\geq 10,000$  eggs per gram [epg] of stool) [39] and the majority (59%) had moderate parasite burdens (1,000–9,999 epg). Downstream data analysis was performed using the mothur software package [21]. Costello EK, Lauber CL, Hamady M, Fierer N, Gordon JI, et al. Bacterial community profiles in faecal samples were studied by 454 pyrosequencing of 16 S rRNA genes. trichiura infections would be associated with altered faecal microbiota and that anthelmintic treatment would induce a microbiota resembling more closely that observed in uninfected individuals. 12. 36. Bryant MP, Small N (1956) Characteristics of two new genera of anaerobic curved rods isolated from the rumen of cattle. 24. Human Microbiome Project Consortium (2012) Structure, function and diversity of the healthy human microbiome. are natural parasites of a wide variety of different mammalian hosts [32]. To evaluate the effects of anthelmintic treatment on intestinal microbiota, all 17 children in the T. suis infection of pigs, there are marked changes in the large intestinal mucosa at 21 days after infection, characterised by a catarrhal enteritis [12] with oedema coincident with the emergence of larvae at the mucosal surface. trichiura only, and mixed infections with T. Summers RW, Elliott DE, Urban JF Jr, Thompson RA, Weinstock JV (2005) *Trichuris suis* therapy for active ulcerative colitis: a randomized controlled trial. trichiura on faecal microbiota - we did this by comparing microbiota composition between children infected with T. (2012) Alterations in the Porcine Colon Microbiota Induced by the Gastrointestinal Nematode *Trichuris suis*. 30. Suputtamongkol Y, Premasathian N, Bhumnuang K, Waywa D, Nilganuwong S, et al. Our results also catalogue the microbiota of rural Ecuadorians and indicate differences with individuals from more urban industrialised societies. trichiura on faecal microbiota could not be explained by infection intensity. 40. Curr Opin Gastroenterol 28: 63–69. lumbricoides infection because significant differences also between children with mixed infections and those infected with T. trichiura on microbiota; mixed infections - presence of A. However, it is possible that we missed delayed effects on faecal microbiota that might have been detected at a later sampling point. Families with blue background belong to the Firmicutes phylum, red = Bacteroidetes, green = Proteobacteria, yellow = Spirochaetes (mostly *Treponema* spp.), trichiura-only infection group and 21 of the 30 children in the Uninfected group received albendazole 400 mg twice daily for 3 days and a single dose of 200 µg/kg of ivermectin. Analyzed the data: AWW PJ. The presence of other known starch/fibre fermenters such as *Succinivibrio* species and *Sarcina ventriculi*, which is more commonly found in the guts of vegetarians [27], in these Ecuadorian children also supports the hypothesis that diet is a key driver of their microbiota development. trichiura in humans, the presence of parasites are not associated with marked histologic changes [6] except among symptomatic children with high parasite burdens (i.e. the *Trichuris* dysentery syndrome) [6]. Phylogenetic classifications were assigned to each OTU at all taxonomic levels from Phylum to Genus using the reference Ribosomal Database Project database (RDP) provided in mothur. Cluster dendrogram, generated with the Jaccard calculator in the mothur software package, showing similarity in community membership at the OTU-level between faecal samples from different study groups. Surrounding bar charts show the microbiota composition at the genus level for each sample. Zoetendal EG, von Wright A, Vilpponen-Salmela T, Ben-Amor K, Akkermans AD, et al. Following treatment none of the children had evidence of any STH infection at 7 and 21 days following treatment, indicating that the treatment regimen cured all T. Our results widen sampling to children living in rural Ecuador, and indicate that there are distinctive microbial signatures associated with these individuals. Although the sample size of this study was relatively large in comparison to previous studies of human faecal microbiota, it is clear that we have sufficient power for detecting only relatively large perturbations in faecal microbiota and limited power for more subtle alterations that could still have significant immunological effects in the human host. Sampling at 7 and 21 days was chosen to document cure of STH infections and 21 days for measurement of faecal microbiota. Young VB (2012) The intestinal microbiota in health and disease. trichiura but no other STH parasite in all stool samples [specific effects of T. in other developing world cohorts] [35],[36] suggests intriguing large-scale differences in microbiota composition between individuals from urban, industrialised societies and those from rural areas of less-developed regions, which is clearly worthy of further investigation. *Epidemiol Infect* 98: 65–71. Can J Gastroenterol 18: 175–7. 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