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Characterising the taxonomic composition of children and livestock gut microbiomes and of environmental samples and the potential role for household-level microbiome sharing in western Kenya

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Abstract

Background Humans and animals living in close proximity may share microbiome constituents at the household level because of daily domestic contact. Such sharing could affect enteric and metabolic functions of the gut microbiome of humans and livestock living in such households. We sought to characterise the microbiome of children, cattle, chickens, and environmental surfaces within households in western Kenya to determine the degree of microbiome sharing.

Methods We randomly selected households that were part of ongoing syndromic disease surveillance programme with at least one child under 5 years, one cow, and one chicken in the Lwak region of western Kenya. Trained field teams obtained informed consent and during household visits they took samples of stools from up to two children aged 5 years or younger, a healthy cow belonging to the household, a cloacal swab from a household chicken, and environmental swabs of living areas and kitchen surfaces. Samples were refrigerated immediately after collection and transported to a laboratory where they were frozen and subsequently had DNA extracted. DNA from samples was sequenced for 16S ribosomal RNA and 16S rRNA sequences were clustered into operational taxonomic units (OTUs). We analysed and compared the microbial community profiles of human, cow, chicken, and environmental samples to determine their composition and relationship.

Findings A principal coordinates analysis of taxonomic profiles showed that each sample type (ie, human, cow, chicken, and environmental samples) was associated with a distinct microbial composition. Children who shared a household had greater similarity in their microbiome compositions than did children from different households. We also noted a slightly greater degree of similarity in the microbiome composition of children and cows sharing a household than in children and cows from different households, but this pattern did not reach statistical significance. We also noted that the diversity of gut microbiomes in children increased with age.

Interpretation Exchange of microbiome components may occur at the household level, but the extent to which this takes place remains poorly understood. Further investigation should focus on the role of shared pathogens or non-pathogenic microbes and implications for growth, development, and disease status across species.

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Declaration of interests

We declare no conflicts of interest.

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