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A pilot study of resistome characterization by using long read whole genome sequencing: from sheep faeces to soil fertilised with composted manure

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In sheep farming, the presence of antibiotic resistance genes (ARGs) in animal manure, and the composted manure may threaten environmental safety. Herein, we aim to better understand and characterize the resistome profiles in microbial communities found in two lamb feedlots. Total DNA extraction was performed using Quick-DNA™ HMW MagBead Kit (Zymo Research) from samples of pooled animal faeces (n=10), manure (n=4), and composted manure (n=4). Furthermore, samples from soil before (n=5) and after compost application (n=5) from one of the feedlots were also analysed. Metagenome sequencing was performed using a MinION device (Oxford Nanopore), with v14 chemistry and R10.4.1 flow cells, pooling previous DNA samples into one sample for each feedlot: animal faeces (n=3; an additional sample with sick lambs was also analysed), manure (n=2), composted manure (n=2), soil before and after compost application (n=2). We used the EPI2ME platform and ARMA (Antibiotic Resistance Mapping Application) pipeline to obtain gene annotation based on CARD database. Statistical analysis were performed using ResistoXplorer online software. Abundance in equivalent genome copies of ARGs per Gb of reads in a sample was calculated. A higher prevalence of tetracycline resistance genes (over 50% of the total ARGs), followed by drug pump efflux genes (around 30%) were found in faeces. In manure and soil, drug pump efflux genes were found predominant. Differential abundance analysis showed significant differences between feedlots at manure and composted manure level. However, no differences were found between samples from soil before and after compost application. Long reads enabled the detection of ARGs abundance in mobile elements such as plasmids or MGEs.

Prevalence of gastrointestinal parasitic infections in goat flocks in the Coastal Valley of Lima, Peru

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This study aimed to assess the prevalence of gastrointestinal parasites (GIP) and parasite burden in goats grazing stubbles from Lima, Peru. A total of 259 goat fecal samples were collected from 10 herds in two districts of Lima (Huaral and Aucallama) during winter 2023. The presence of GIP eggs/oocysts was determined using the sedimentation-flotation method and modified McMaster technique for counting. Descriptive statistics were used to establish parasite prevalence, and the Chi-square test was used to examine the association between prevalence and risk variables such as sex, and age. The data were processed using R software v. 4.3.1. The overall prevalence of GIP in the present study was 99.2 %; with prevalence of 98.8%, 44.4%, 34.6%, 6.2%, 1.9%, and 1.2% for *Eimeria* spp., Strongyle-type eggs (STE), *Skrjabinema* spp., *Moniezia* sp., *Trichuris* sp., and *Fasciola hepatica*, respectively. Maximum eggs/oocysts per gram (Epg/Opg) of *Eimeria* spp., STE; *Skrjabinema* spp. and *Trichuris* sp. were 26500, 16500, 400, and 50, respectively. Sex and age had a significant association ($p < 0.05$) with the presence of STE, where females over four years old had more prevalence. Likewise, there was an association ($p < 0.05$), between age and the presence of *Skrjabinema* spp where goats over four years old had more prevalence. *E. alijeivi*, *E. apsheronica*, *E. arloingi* and *E. caprina*, were the most frequent coccidia parasites. It was concluded that in the goat flocks of the Coastal Valley of Lima, the prevalence and parasite burden of *Eimeria* spp. was the highest, suggesting the need to implement parasite strategic control and prevention programs.