PROFILING THE DIVERSITY OF THE VILLAGE CHICKEN FAECAL MICROBIOTA USING AMPLICON AND SHOTGUN

METAGENOMIC SEQUENCING DATA

ZULULAND

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BACKGROUND

- > Chickens have lived in rural villages throughout Africa and the Pacific for centuries and have adapted to the local environment and conditions.
- chicken gastrointestinal tract (GIT) consists of complex and diverse communities of microbiota that influence the metabolism, and production and health.
- > By classifying previously uncultivable microbiota and assessing compositional profiles, microbial population dynamics, and microbiota diversity in the chicken GIT, NGS-based metagenomic sequencing resolve limitations of conventional culture-dependant approaches.
- > Through the focused sequencing of 16S rRNA gene hypervariable areas, metataxonomics enables accurate bacterial taxonomic estimation.
- > Besides mapping of bacterial taxonomic abundances, the most difficult challenge in metagenomic studies is detection of individual genes contributing to functional attributes of microbiota, to address this issue, Shotgun metagenomic sequencing is the most suitable strategy.

OBJECTIVE

> Investigating the microbial community composition, diversity, and functional attributes of the indigenous chicken faecal microbiota using 16S rRNA amplicon sequencing and Shotgun metagenomic sequencing data from rural areas of Limpopo and KwaZulu-Natal Provinces.

METHODS

- > 85 Total indigenous village samples were collected using non-invasive sampling.
- Each sample was barcoded, and sequenced using the Illumina Miseq Platform Hiseq 2500 at 2 x 150 bp.
- > 16S rRNA and Shotgun metagenomic reads were received in fastq format.

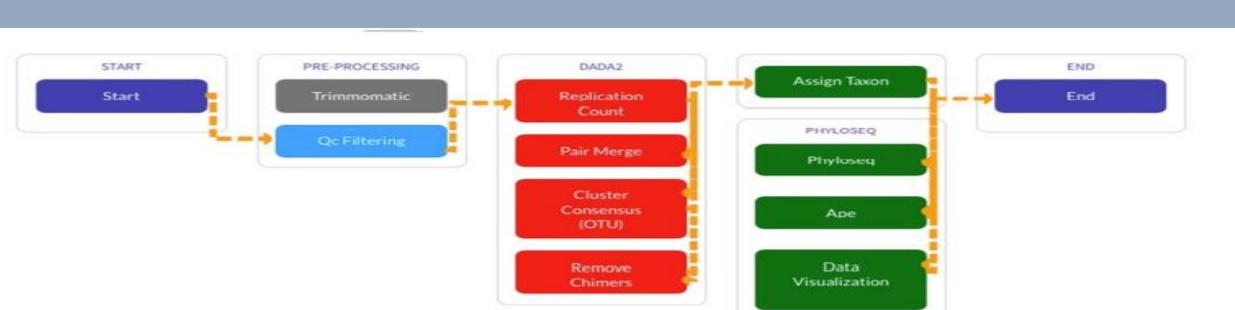


Figure 1: 16S rRNA analysis pipeline based on DADA2.

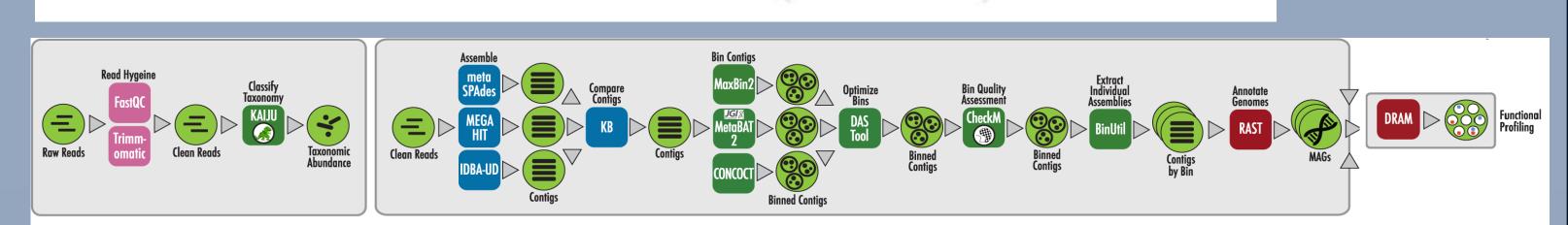
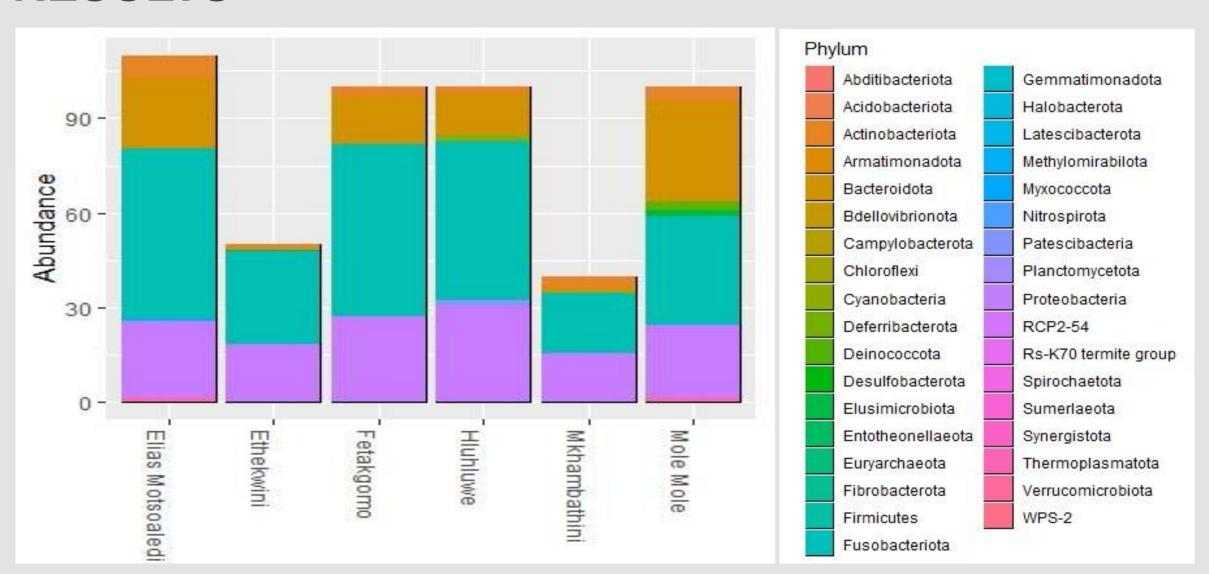
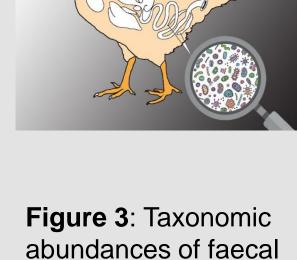


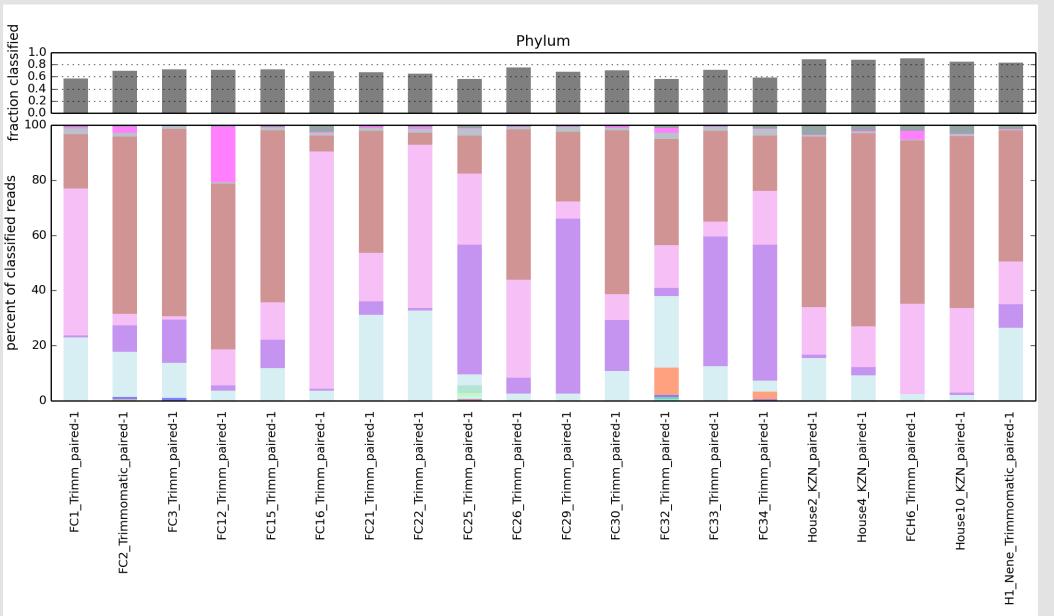
Figure 2: Shotgun metagenomic analysis pipeline based on the KBase platform.

RESULTS





microbiome from Limpopo and KwaZulu Natal districts based on 16S rRNA amplicon sequencing.



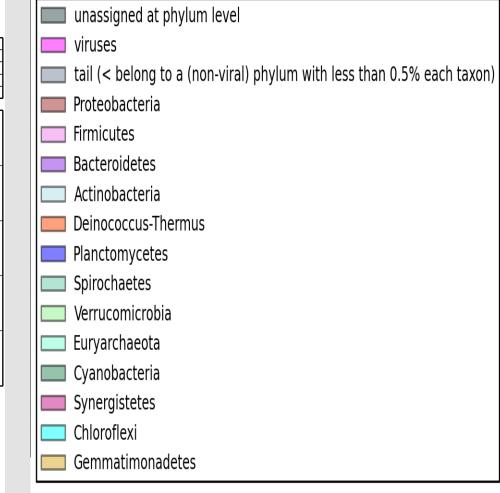


Figure 4: Taxonomic abundances of faecal microbiome from Limpopo and KwaZulu Natal districts based on Shotgun metagenomic sequencing.

RESULTS

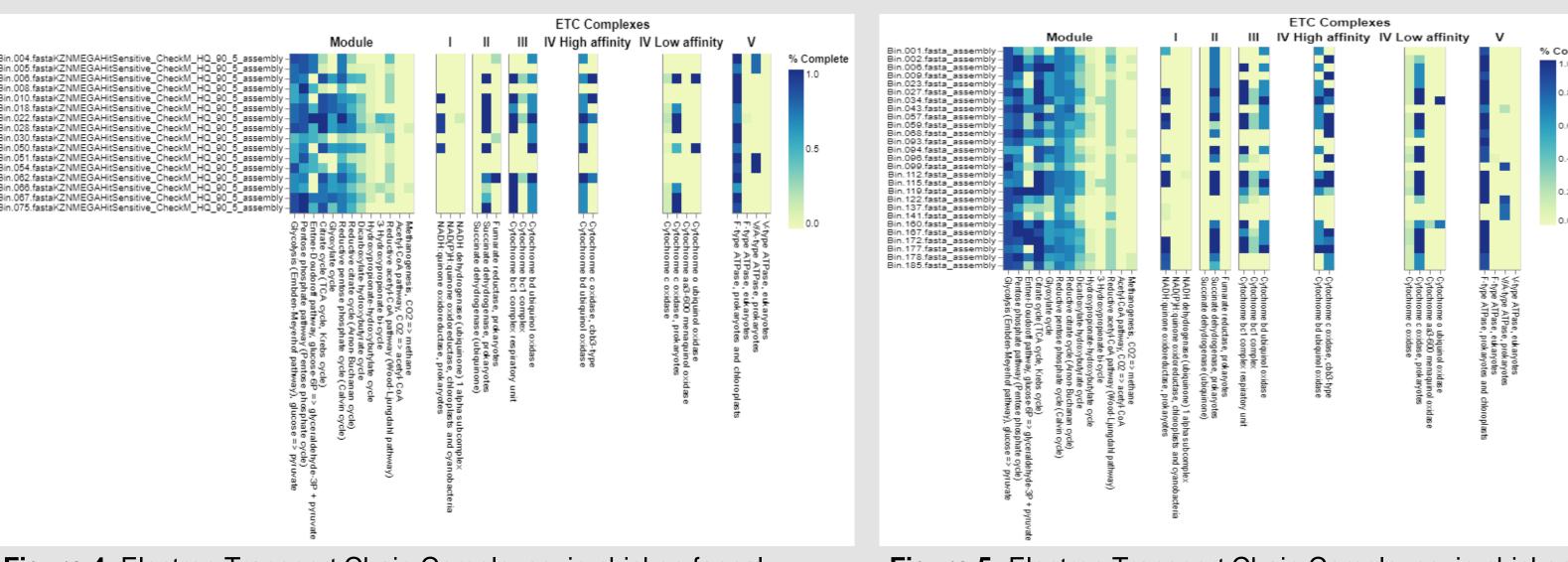


Figure 4: Electron Transport Chain Complexes, in chicken faecal microbiota from KwaZulu-Natal.

Figure 5: Electron Transport Chain Complexes, in chicken faecal microbiota from Limpopo.

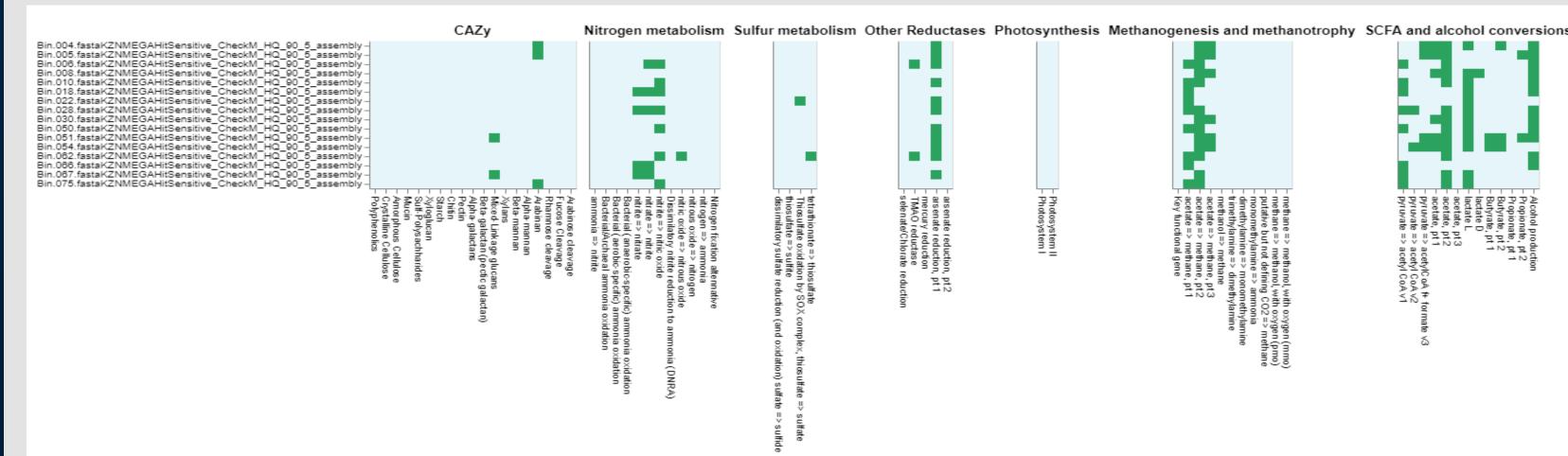


Figure 6: Metabolic function attributes, in chicken faecal microbiota from KwaZulu-Natal

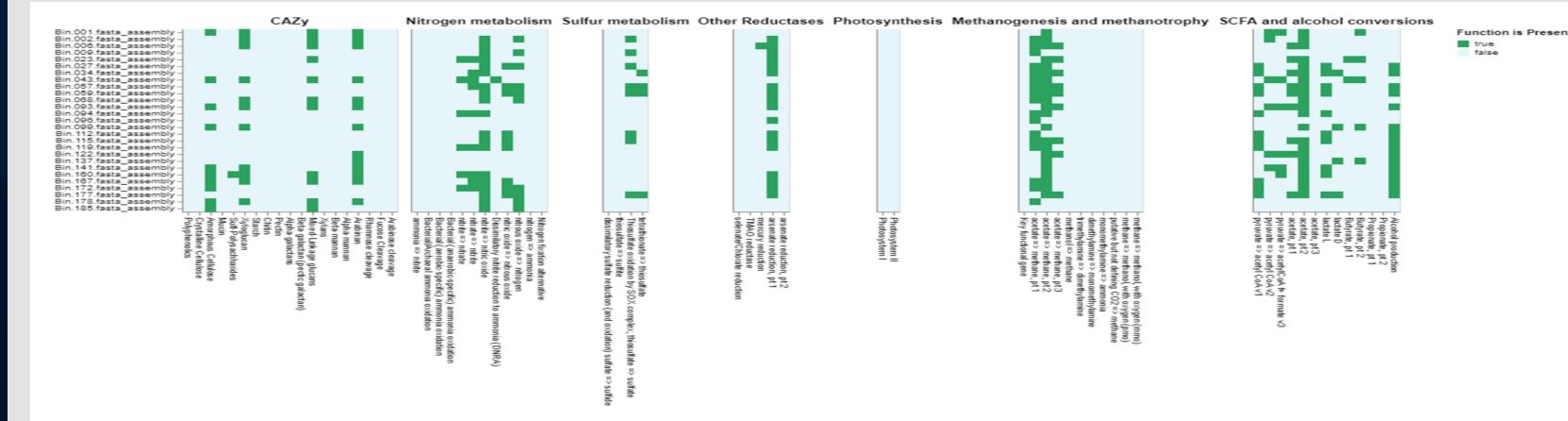


Figure 7: Metabolic function attributes, in chicken faecal microbiota from Limpopo.

DISCUSSION

- According to 16S rRNA sequencing analysis, Limpopo has highest abundances of, Firmicutes, Actinobacteria and Proteobacteria respectively, whereas KwaZulu – Natal has highest abundances of Firmicutes, Proteobacteria and Actinobacteria.
- > According to Shotgun Metagenomic analysis, Limpopo and KwaZulu Natal, both have high abundances of Proteobacteria, Firmicutes, and Actinobacteria and there's an uncharacterized viral population within the Limpopo province.
- > ETC complexes for both provinces varies greatly, signifying diversity of microbiota involved in ETC complexes.
- Metabolic functions based on DRAM, vary between Limpopo and KwaZulu Natal, signifying differences in production environments since these chickens are scavengers.

CONCLUSION

- > Shotgun metagenomic sequencing and the NGS platforms improve the scope of gut microbiome studies, allowing for detailed functional profiling of samples and detection of even viral populations within microbiome communities.
- > Differences in production environments is evident, signifying differences in microbiome involved in metabolism which could be possible if village chickens scavenge on varied feedstuffs available in their production environments.

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