

HUNT-One Health

Enabling human-animal health studies

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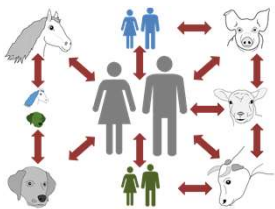
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Overview

- HUNT-One Health (H1H) is a data repository project to increase the cross-institutional and cross-disciplinary collaborations via a One Health metagenomics approach, and promote sustainable reuse of samples and datasets to improve the research on health- and well-being of animals and humans.
- HUNT-One Health project is an animal focused One Health project, from the demographic of the human population-wide health study HUNT (the Nord-Trøndelag Health Study)

Introduction

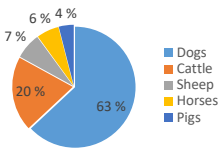
- This project will provide biological material and sequence datasets researchers can use to study the link of health in animals and humans
- Gut and Fecal microbiota is important for maintaining microbial balance, and help the organisms with nutrient digestion and fermentation, immune-development, and a range of other essential functions
- The fecal microbiota from one organism can interact with other organisms' microbiota via contamination of food and water, direct contact
- The fecal microbiota contains a plethora of microorganisms, including bacteria, protozoa, fungi, parasites as well as viral particles from eukaryotes and bacteria (bacteriophages)
- Systematic sampling of fecal samples from animals from the same demographic of the HUNT participants, could provide unique opportunity to link members of the microbiota and genetic traits of these with other animals and humans
- Improved understanding of the fecal microbiota, of all is possible with new sequence technology and metagenomics tools
- This One Health project aim to facilitate cross-institutional and cross-disciplinary One-Health research by systematic collection of samples, gathering of metadata and systematic processing of samples with subsequent high quality shotgun-DNA-sequencing of fecal samples from companion and production animals
- The repository aims to facilitate One Health-related research including studies on how human and animals exchange zoonotic pathogens, e.g. DNA-viruses, by enabling access to data and material in the project



Hunt One Health enabling researchers to study the link of health in animals and humans

Methods

Animal owners participated actively in sampling and provided dried fecal cards from approx. 3000 companion and production animals from 2017 to 2019 (Fig. 1).



Animal owners provided dried fecal cards from 3000 animals for this sample and data repository project (63% dogs, 20% cattle, 7% sheep, 6% horse and 4% pigs).



Animal stool samples were applied onto standardized sample-cards by the animal owners according to a simple protocol, dried briefly before shipped and frozen.

A pilot study DNA isolation was performed on punched-out discs from the sample cards, followed by 150PE shotgun sequencing on Novaseq sequence platform (Illumina) to verify the suitability of the fecal card samples for deep-shotgun sequencing

Spiked fecal card samples with known microbiota was tested on different available DNA-extraction platforms and procedures were selected that allowed satisfactory sequence data generation, whilst at the same time enabling a complete-as-possible picture of all genetic material in the samples by ensuring rigorous homogenization of samples

To aid in assessment of quality of the datasets, metagenomic classifier through Kraken, for preliminary assessment of the presence of bacterial phyla, and virus in these sequence datasets

The Norwegian Veterinary Institute's activities encompass the entire chain from plants, via animal feed, fish, animals and food for human consumption.

Results

Samples generated typically sequence datasets of 15-20 mill good quality reads

Raw-data and processed clean data from samples are available from the project and is stored securely on the HuntCloud (NTNU)

Hunt One Health-project is currently performing key statistics and quality control of the generated datasets, including initial classification of the datasets

We present relevant preliminary results below, which indicate that there are also sequence information that cover DNA from the viromes in these datasets.

Additional health and demographic data is available for owners enrolled in the HUNT4 project, allowing link with human data and samples. Access to data or samples is managed through a data admission committee (DAK).

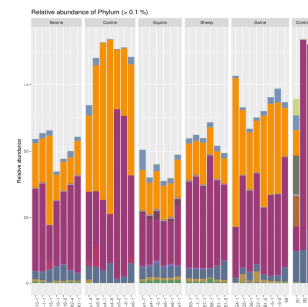


Figure showing the bacterial phyla in the shot-gun sequence dataset from fecal samples from a random number of samples from different animal

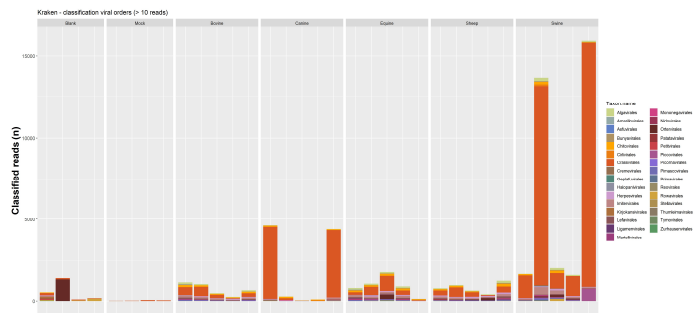


Figure of the abundance of viral orders after performing a Kraken-classification of the sequence data, indicating that a number of sequence data from different virus orders are present in these randomly selected sequence datasets from different animal hosts

Conclusions

H1H data and the collection of biological samples, may be for virome investigations of animals and potential link with humans. Our preliminary classification results indicate presence of virus in the sequence datasets. By re-using non-targeted metagenome deep-sequencing data, we believe the stage is set to initiate a number of One Health investigations that include research on DNA-virus*

Visit www.huntenhelse.no for more information

Acknowledgements

This project was funded by the Norwegian Ministry of Agriculture and Food, and various other contributors*

