Alpine Goat and *Haemonchus contortus* infection

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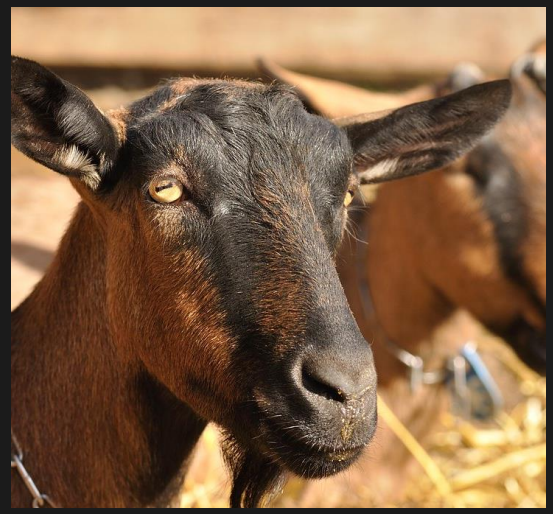
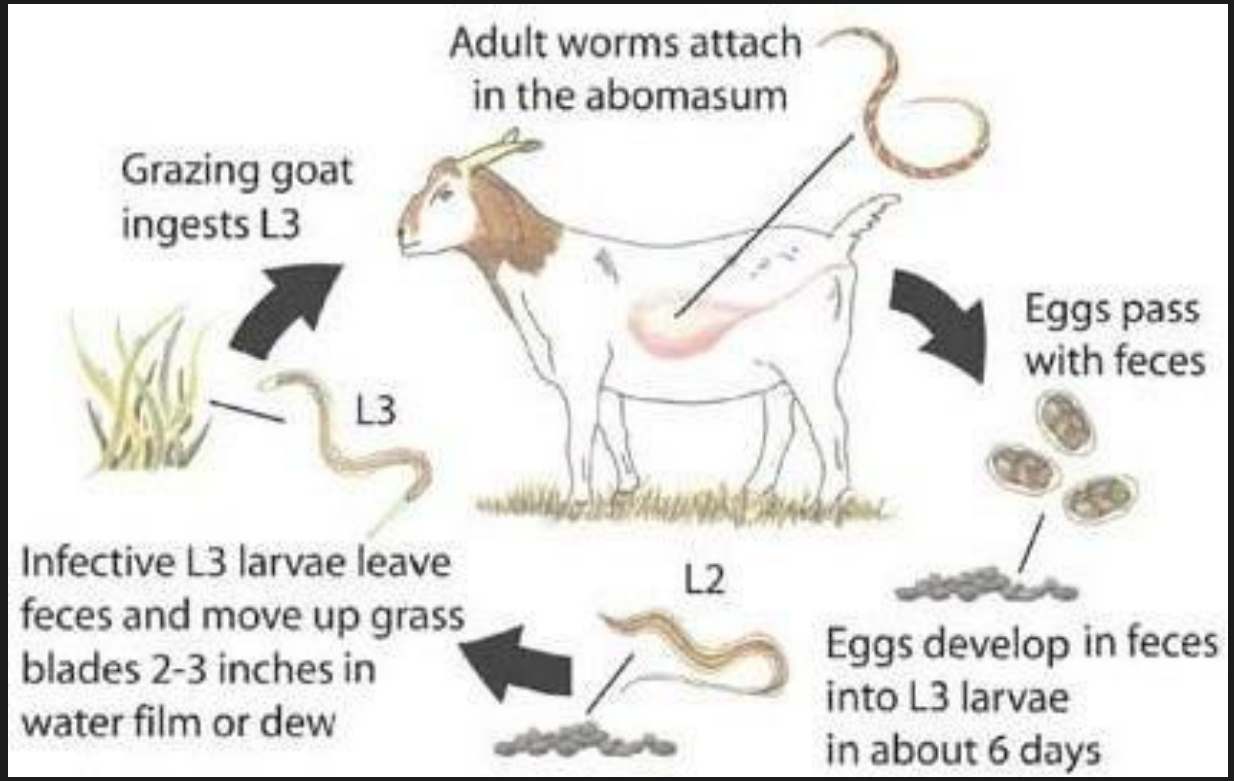
Haemonchus contortus

- *H. contortus* is a blood sucking parasite that can cost billions of dollars annually due to illness and death of domestic goat *Capra aegagrus hircus (Alpine goat)*.
- The barber pole worm is one of the most pathogenic nematodes of small ruminants.
- They cause anemia due to low iron and bottle jaw in domestic goat.
- Other symptoms noted in the host is weight loss, dysentery, leading to eventual death.
- *H. contortus* adults attach themselves to the abomasal mucosa wall of the host.
- Female nematodes may lay up to 10,000 eggs daily.



Research

- The barber pole worm also develops ways to induce depression in the host immune response.
- Gene expression plays a major role in response to an attack from a parasite or pathogen.
- The microbiome helps modulate response to internal and external environmental stimuli.
- Good health vs infection of selected wethers through microbial flora and bloodwork.



Life cycle of Haemonchus contortus. (Courtesy: pinterest.com)

Hypothesis

What determines immune response in domestic goat?

The host genome produces an immune response due to the presence of parasites in the form of gene expression. The microbiome also produces an immune response. Therefore, the immune response is expressed through genes exhibited by the host genome and its microbiome to the parasite.

Objective

Analyze

Analyze the different responses to different treatment types by gene expression and metagenomic analyses.

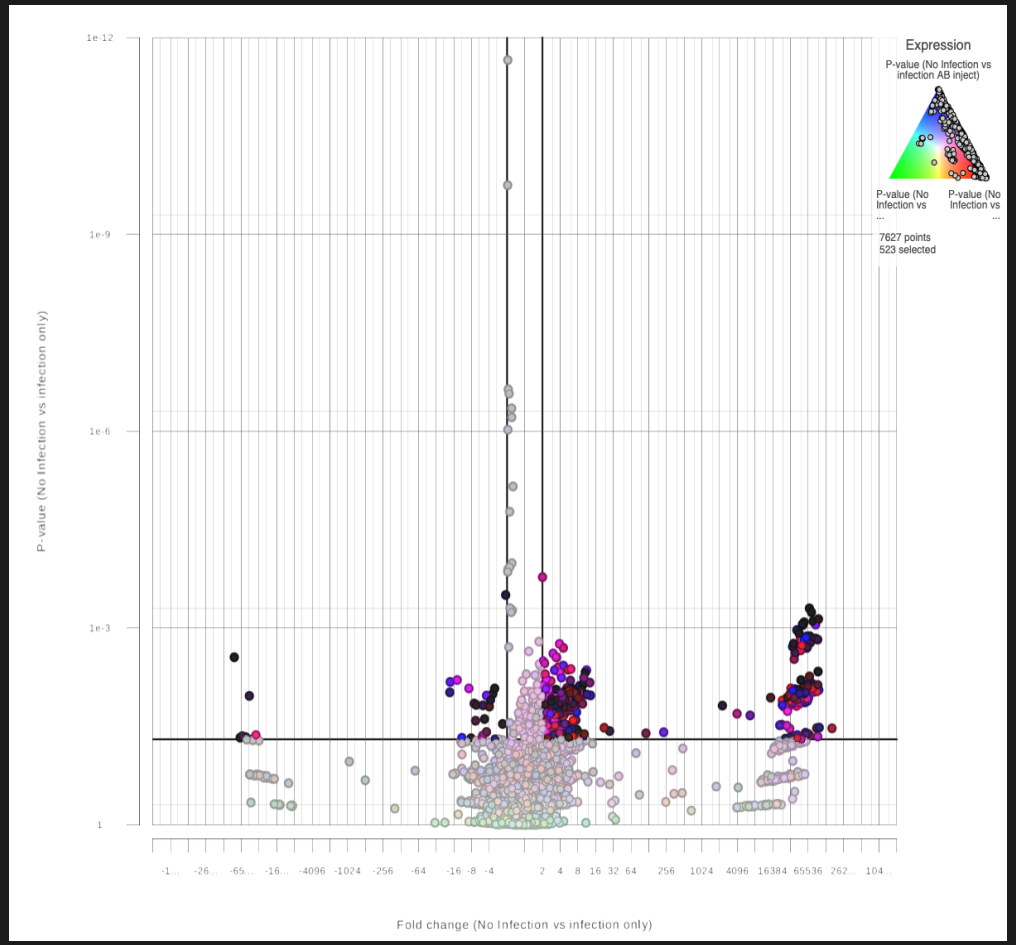
Identify

Identify genes expressed from the treatment 7 (dpi).

Compare

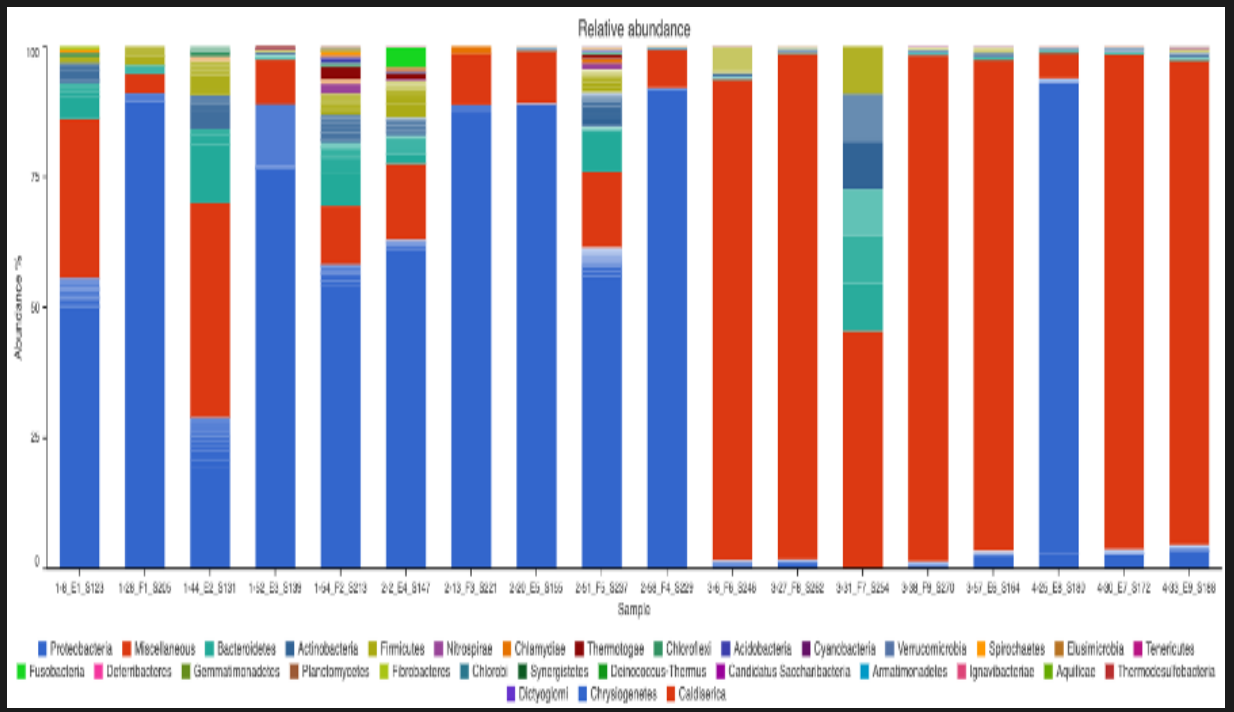
Compare microbial flora presence after 7 and 21 (dpi) in quantitative terms of abundance and diversity to determine the differences of health of the goat wethers.

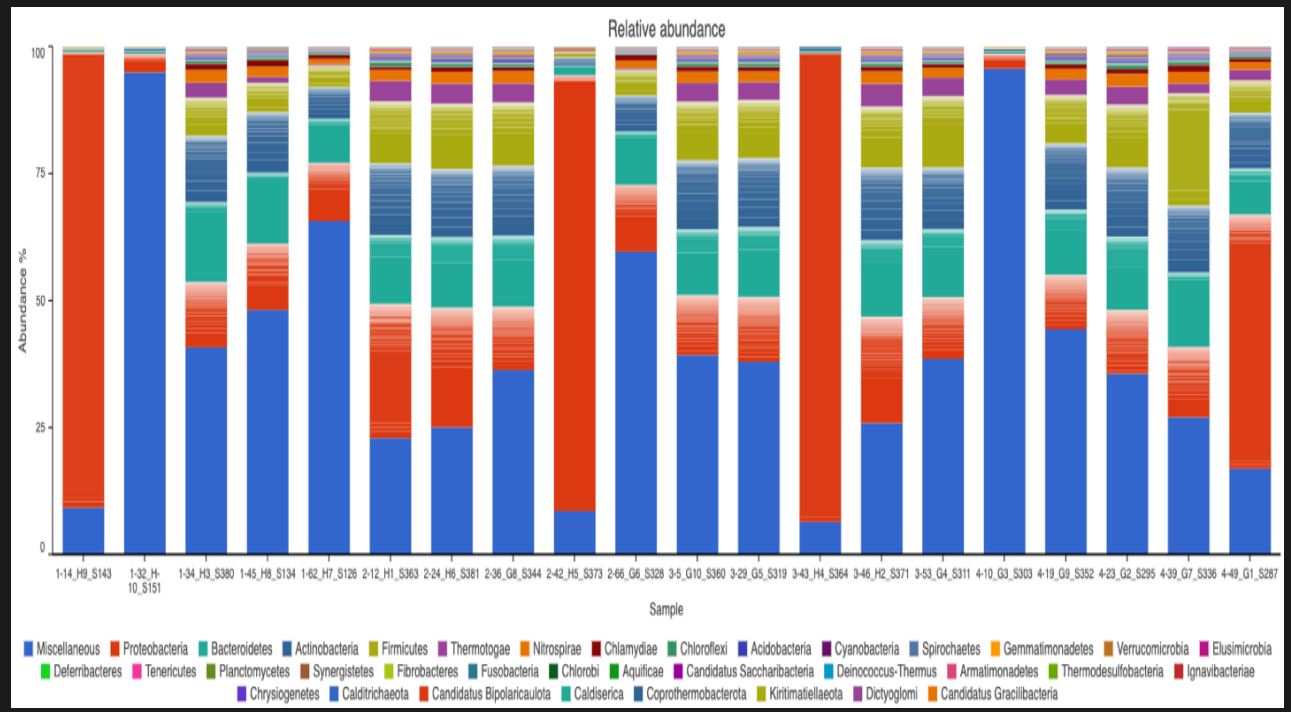
Data/Observations



- A Volcano plot for 19/20 blood samples indicating likely significant expression of genes (* = p < 0.05) based on treatment type of *Capra hircus* following STAR alignment and GSA differential analysis for transcript sequences of 7627 identified genes expressed on 7 dpi. The fold change indicates downregulated (* = < -2), no change (NC; * = > -2, * = < 2), and upregulated (* = > 2) gene distribution when comparing No Infection samples to infection only samples when expressed against a Numeric Triad of P-values for No Infection vs Infection only (green), No Infection vs Infection ZA inject (red) and No Infection vs infection AB inject (blue).

Data/Observations





- Relative Abundance of OTUs on 7 dpi for 18 samples. The first number before each sample ID identifying the treatment type (1- No infection, 2- Infection only, 3- Infection ZA inject, and 4- Infection AB inject).

Relative Abundance of OTUs on 21 dpi for 20 samples. The first number before each sample ID identifying the treatment type (1- No infection, 2- Infection only, 3- Infection ZA inject, and 4- Infection AB inject).

Conclusion

- Through gene expression and microbial flora structure during infection with the barber pole worm, examination presents there are significant differences in the gene expression effects.
- The abundance and diversity of the group of organisms studied increased as the subject is older and exposed to the environment longer.
- This implies *H. contortus* does effectively change and disrupt the internal habitat health of the subject host.
- *Firmicutes/Bacteroidetes* (F/B) microbial flora ratio can indicate host health status.
- High *Firmicutes* and Low *Bacteroidetes* suggest microbial imbalance that implies impaired insulin sensitivity causing a dysregulation of immunity, and increased inflammation
- Low F/B ratio indicates decreased diversity of the microbiome compared to healthy companion without infection of *H. contortus*.

Acknowledgements

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