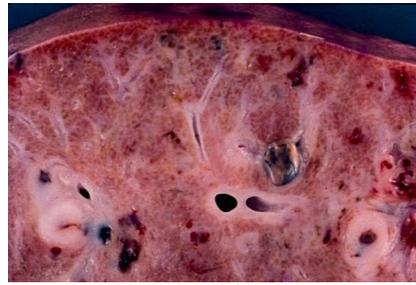


Molecular characterization of gut microbiome of fasciolosis infected cattle with comparison to healthy cattle



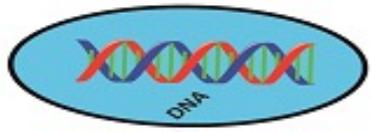
Fasciolosis infected cattle



Fasciolosis infected cattle liver



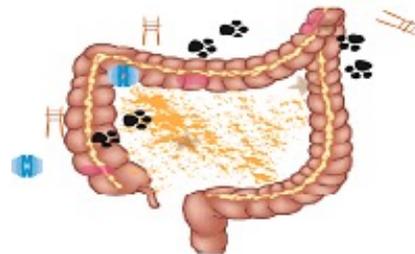
Gut microbiota



Amplification of V3 +
V4 region of 16S rRNA



High throughput
Sequencing



Gut microbial dysbiosis

Introduction

Parasitic infestation fasciolosis affect the health of dairy animal as well as decrease the milk production. Acute infection can cause abdominal pain, hepatomegaly, intermittent fever, urticaria, and weight loss due to liver damage. It has been hypothesized that there is gut microbial dysbiosis in fasciolosis. Considering the significant impact of the intestinal microbiome on animal health it is considered as one of the main health and milk production concerns of the animal around the globe.

Diagnosis:

The fasciolosis infection is diagnosed by examining stool (fecal) specimens under a microscope by sedimentation technique. The diagnosis is confirmed if Fasciola eggs are seen. More than one specimen used to examine to find the parasite.

Sign and Symptoms:

Acute infection can cause abdominal pain, hepatomegaly, intermittent fever, urticaria, , and weight loss due to liver damage.

Results:

Phylum

Firmicutes, Bacteroidetes

Family

ruminococcaceae and enterobacteriaceae, lactobacillaceae and veillonellaceae.

Genus

Bifidobacterium Shigella, Prevotella_9 and Dialister

Species

prevotella copri and Escherichia coli.

The findings of the current study provided a basic foundation to understand gut microbiota in treatment of fasciolosis , disease pathway, mechanism, and probiotic development.

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