Whole-genome shotgun metagenomic analysis revealed gut microbiome changes in beef cattle under endophyte-infected tall fescue toxicosis

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Introduction

Gut microbiome correlates strongly to hosts’ health in livestock. In cattle, the rumen and the gut microbiome are critical to digestion, affecting the meat production rate.

Tall fescue (Lolium arundinaceum), a perennial grass commonly infected with an endophyte, is grown on over 14 million hectares in the Southeastern US. The fungal endophyte results in high concentrations of ergot alkaloids, inducing fescue toxicosis. The economic losses to the forage-based livestock industry are estimated to be 3.5 billion dollars.

Gut microbiota is directly related to animal nutrition and health, affecting every aspect of animal physiology. Although the cattle rumen microbiome has been studied extensively, the fecal microbiota and its response to ergovaline are not well understood.

Here, we performed the first comprehensive study of the gut microbiome in the context and beef cattle toxicosis.

Methods

A total of 16 fecal samples were collected from 3 cows and 5 heifers at the beginning and the end of a 30-day tall fescue seed feeding experiments. These cattle were genotyped at XKR4 and DRD2 genes, known loci to affect tall fescue toxicosis susceptibility. Four animals were susceptible, and four were resistant. We made whole-genome shotgun metagenomic sequencing libraries and sequenced them on an Illumina NovaSeq6000 machine. We applied a standard pipeline for data preprocessing, including read filtering and trimming, de novo metagenome assembly, taxonomy annotation, abundance quantification. LEfSe was used to determine the differential taxonomy composition before and after treatment. The microbial genetic pathways were analyzed with HUMANN2. Our gut microbiome profiles were also compared with the rumen metagenomes in the public domain.

Experiment Design

A total of 16 fecal samples were collected from 3 cows and 5 heifers at the beginning and the end of a 30-day tall fescue seed feeding experiments. These cattle were genotyped at XKR4 and DRD2 genes, known loci to affect tall fescue toxicosis susceptibility. The body-weight of the cattle was measured every week as a phenotype.

Recovery rate of body weight

The recovery rate of heifers obviously overwhelms cow’s, but it may also has relation with the fact that heifers are growing up. Sus is abbreviation for “susceptible” and Tol is abbreviation for “tolerant.”

Practical contig-level genome drafts

In this study, we generated a total of 157 Gbp of metagenomic sequences, with 65.4 million high-quality reads per sample. Host and viral sequence contaminations were removed before performing de novo assembly of the microbial contigs. The reference assembly contains 16,580,560 microbial contigs with a total metagenome length of 13.1 Gbp. Gene annotation analysis identified a total of 21,950,894 bacterial genes in the gut microbiome after redundancy removal using CDHIT. We aligned the microbial reads from all 16 individual samples to our reference gut microbiome metagenome assembly, and the average mapping rate is 91.7%.

The reads-mapping percentages were plotted for seven draft metagenome assemblies (after, before, susceptible, tolerant, cow, heifer, and all cattle).

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