Describing biosynthetic gene clusters of dairy cattle uterine microbiomes associated with anti-metritis properties

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Introduction

Uterine disease perturbs fertility thereby causing economic losses to the dairy enterprise worldwide. About 25-40% of dairy cattle develop metritis postpartum (Sheldon et al., 2009). 16S rRNA amplicon sequencing taxonomic identification of the endometrial microbiome signatures differentiate cattle harboring uterine disease (Becker et al., 2023), particularly at 7 and 10 days postpartum (DPP), before clinical signs of metritis are evident (Tasara et al., 2023). It is hypothesized that predominating bacterial strains inhabiting the healthy bovine uterus postpartum elucidate antimicrobial molecules that hinder pathogens causing endometritis. This study aims to describe predictive biosynthetic gene clusters (BGCs) present in the healthy bovine endometrial microbiome that may be protective against metritis.

Materials and methods

Publicly available metagenomic sequences from dairy cattle uterine microbiomes were assessed. Raw metagenomic sequences from 7 and 10 DPP of 10 healthy and 10 metritis cows (diagnosed at 21DPP) were co-assembled into contiguous sequences within test groups, using the MEGAHIT bioinformatic tool. Reconstructed genomic fragments were assessed using Prodigal gene finding algorithm to predict protein coding BGCs. Secondary metabolism gene families of predicted BGCs were identified using hidden Markov models in AntiSMASH, characterizing potential biological/bacteriocin activity.

Results

BGC frequencies and putative secondary metabolites were assessed in healthy and metritis groups at 7DPP and 10DPP. Our systematic approach revealed 64, 109, 90 and 122 BGCs within the metritis 7DPP, healthy 7DPP, metritis 10DPP, and healthy 10DPP groups, respectively. Assessment of secondary metabolite gene families suggested the presence of microcin J25 lasso peptides, a purported antimicrobial secondary metabolite, within the identified BGCs.

Significance

Dairy cattle that developed metritis have lower levels of predictive antimicrobial BGCs compared to healthy animals. Additional genomic and phenotypic analysis is warranted to further characterize the antimicrobial properties of the microbiota inhabiting the bovine reproductive tract microbiome postpartum.

