

# Research Notes

Arm & Hammer Animal and Food Production



## Analysis of clostridia populations in feed samples.

### INTRODUCTION

*Clostridium* are spore forming bacteria which commonly reside in soils and the gastrointestinal tract and have been associated with enteric disease such as hemorrhagic bowel syndrome (HBS) in ruminants.

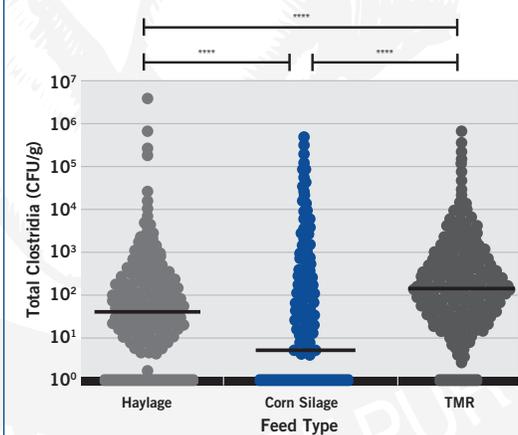
HBS has been associated with *C. perfringens* Toxin Type A. *Clostridium sordellii* and *Clostridium septicum* can also produce toxins that can negatively impact gut health. Other clostridia commonly isolated from dairy feed, fecal and rumen samples include *Clostridium beijerinckii* and *Clostridium bifermentans*. *Clostridium beijerinckii* and *Clostridium bifermentans* are known industrially to produce byproducts such as acetone, butanol and 1,3 propanediol. These end products are antimicrobial and have been shown to negatively impact rumen function.

Over the past several years ARM & HAMMER™ has quantified and characterized clostridia organisms from TMR (n=2,760), corn silage (n=866) and haylage (n=577) samples from 457 farms across 31 states!<sup>1</sup>

### RESULTS

- The dominant clostridia species detected in feed samples have been identified as *C. perfringens*, *C. beijerinckii* and *C. bifermentans*<sup>2</sup>
- Clostridia loads in feed samples have correlated to clostridia loads in fecal samples
- Lower clostridia counts in feed can be deceiving and given the large daily intake of dairy cattle can be a risk to health and performance. For example:
  - o 100 CFU/g clostridia in TMR X 454 grams/lbs. X 100 lbs. TMR/head/day
  - o 4,540,000 CFU total clostridia daily challenge per head
- TMR samples have significantly higher clostridia levels than fermented feeds (Fig. 1).

**FIGURE 1:** Total clostridia enumeration results from Haylage, Corn Silage and TMR samples. Each circle represents an individual sample and black lines represent means (\*\*\*\* =  $P$ -value<0.0001).

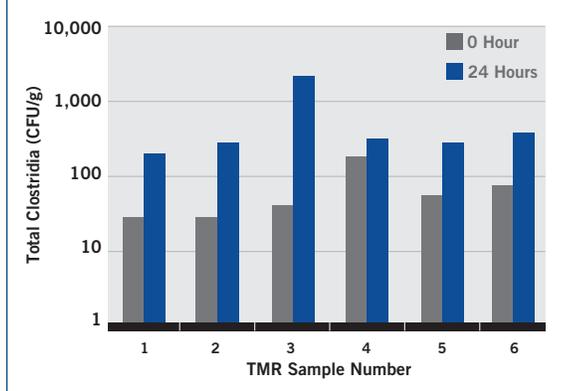


- Previous data has indicated specific reasons for the higher levels of clostridia in TMR:
  - o Other sources of clostridial contamination
    - Commodities
    - Water
    - Whey
    - Dirt or fecal matter
  - o Clostridia growth<sup>3</sup> (Fig. 2)
    - Clostridia are capable of growing in a feed matrix

## SUMMARY

Major clostridia populations (*C. perfringens*, *C. beijerinckii* and *C. bifermentans*) are commonly found in fermented feeds and TMR samples. High levels of these populations have been shown to negatively impact rumen function. These organisms are commonly found at higher levels in TMRs compared to fermented feeds due to contamination from other TMR ingredients, dirt/manure and/or clostridia out-growth in the TMR.

**FIGURE 2:** Total clostridia enumeration results from TMR samples. Blue bars indicate initial clostridia count and gray bars indicate clostridia counts after 24 hours in a simulated feed out phase environment.



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1 Rehberger TG, Thompson JS. Pathogenic Bacterial Levels in US Silages. 2020. American Dairy Science Association, Midwest American Society of Animal Science. Omaha, Neb.

2 March TL, Thompson JS, Teal RF, Smith AH, Rehberger TG. Survey of *Clostridium* populations in Dairy Cattle Feed Samples across the United States. 2018. Symposium on Gut Health in Production of Food Animals. St Louis, Mo.

3 Bretl VG, Thompson JS, March TL, Smith AH, Rehberger TG. 2018. The proliferation of *Clostridium* species in Total Mixed Ration after 24 hours Heat Challenge. 2018. Symposium on Gut Health in Production of Food Animals. St Louis, Mo.

