ROCK RIVER LABORATORY, INC.
AGRICULTURAL ANALYSIS

# ENTEROBACTERIACEAE BACTERIA COUNTS VARY FOR US COMMERCIAL DAIRY DIETS FED DURING SUMMER MONTHS

2019 ADSA
POSTER # W158

J Goeser[1,2], J Becker[1], K Bryan[3], S Bascom[4], C Wacek-Driver[5], R Schmidt[6], C Stoffel[7], and N Michael[8]
(1)Rock River Laboratory, Inc.; (2)University of Wisconsin-Madison; (3)Chr. Hansen, Inc., Milwaukee, WI; (4)Phibro Animal Health Corp., Teaneck, NJ; (5)Forage Innovations, Bay City, WI, LLC;
(6)Lallemand Animal Nutrition, Milwaukee, WI; (7)Papillon-Ag, Easton, Maryland; (8)Arm & Hammer Animal Nutrition, Church & Dwight, Inc., Milwaukee, WI.

## INTRODUCTION:

Feed *Enterobacteriaceae* colony count per g (CFU/g) can be a bacterial contamination measure and the presence of Enterobacteria is generally undesirable (Pahlow et al., 2003). While US commercial dairy forage population data exists (Western et al., 2018), population data and descriptive statistics for commercial dairy TMR are unknown. The objective here was to determine if a food safety assay (3M™ Petrifilm™ *Enterobacteriaceae* count plate) was capable of culturing enterobacteria in TMR and determine if counts varied for commercial dairies.

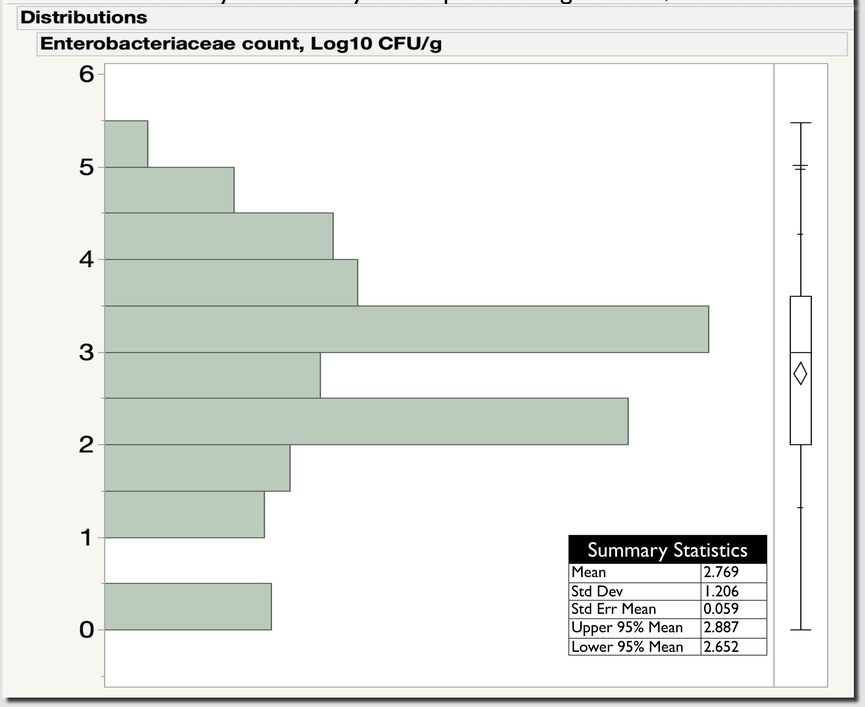
## MATERIALS AND METHODS:

Samples were collected (n=370), from April through September 2018, by US dairy industry professionals and submitted to Rock River Laboratory (Watertown, WI) for analysis. Samples were processed according to 3M™ Petrifilm™ instructions (2017, reference 6420/6421). This is the same procedure as that described to assess *Enterobacteriaceae* in forages by Western et al. (2018). In brief, 10g of TMR was blended into 90 mL Butterfield buffer, shaken and diluted 10, 100, 1000 and 10000-fold. 1mL of diluted solution was plated and incubated at 30C for 24h. Plates counts were manually counted and TMR CFU/g determined by multiplying plate count by plate dilution factor. A separate subsample (approximately 150 g) was dried, ground and analyzed for nutritive parameters by NIR to evaluate correlations with *Enterobacteriaceae* counts. TMR nutrition parameters were assessed by NIR.

## STATISTICAL ANALYSIS:

The bacterial count data were found to be not normally distributed, thus data were transformed using log10 transformation. The log10 transformed data were found to be normal using the continuous fit - normal function in JMP v14.0. Population statistics were evaluated using distribution function. Independent correlations between enterobacteria and nutrition parameters were evaluated using the response screening and multivariate methods functions in JMP v14.0.

Figure 1: Total mixed ration (TMR) *Enterobacteriaceae* count distribution, log10 CFU/g, for 370 TMR samples collected during summer 2018 from commercial US dairy farms. The y-axis represents log10 score, from 0 to 6.




## RESULTS AND DISCUSSION:

The resulting population statistics (log10 CFU/g) in TMR were then as follows: mean = 2.75, standard deviation = 1.18, coefficient of variation (CV) = 42.9%, minimum = zero, maximum = 5.02, and 15th and 85th percentiles = 1.67 and 3.95, respectively. The population distribution and quartile box plot is presented visually in Figure 1. Independent pairwise correlations were significant ($P<0.05$) for 11 NIR predicted nutritive parameters, with the largest r-values being water soluble carbohydrate (r=0.21), dry matter (r=0.18), and *in situ* rumen starch digestibility (3h; r= -0.18). The relationships between these nutrition and *Enterobacteriaceae* count correlations warrant further investigation to understand cause and effect.

## CONCLUSIONS:

The 3M™ Petrifilm™ proved capable of culturing *Enterobacteriaceae* colonies with TMR samples and log10 transformed data population statistics, with a CV greater than 40%, suggest variation exists in *Enterobacteriaceae* counts in TMR on commercial dairies. Further, the 15th percentile (1.67 log 10 cfu/g) may be considered a threshold for that which is achievable for commercial dairy TMR samples. Further research is warranted to investigate potential impact upon dairy cattle health and performance.

## REFERENCES:


- Pahlow, G., R.E. Muck, F. Driehuis, S. J.W.K Oude Elferink, and S.F. Spoelstra. 2003. Microbiology of Ensiling. Ch 2 in Silage Science and Technology. Ed. D.R. Buxton, R.E. Muck and J.H. Harrison. ASAS, CSSA, & SSSA, Madison, WI.
- M. Western, P. Hoffman, M. Windle. 2018. A survey of silage hygiene on Wisconsin dairy farms. Pg 118. Proc. XVIII International Silage Conference. Bonn, Germany.


## KEYWORDS:

Feed Contamination, Enterobacteria

## CORRESPONDING AUTHOR:

johngoeser@rockriverlab.com