

Quantification of microbial populations in organic and inorganic dairy cattle bedding materials

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Introduction: Mastitis

- Most economically important disease in the dairy industry
- Route of infection is usually the teat canal
- Modern, well managed dairy farms
 - Environmental pathogens are primarily pathogens
 - Live in the environment, including **bedding**
- Priority is to minimize exposure

Introduction: Prior research

- Dairy cattle: 40 to 65% lying time
 - Direct teat skin exposure to pathogens in bedding
- Mastitis causing organisms in bedding
 - Many different bedding materials
 - Compared and contrasted
 - Studied in controlled experiments and on farm
 - Bacterial enumeration methods well established

Hypothesis

- Populations of **environment mastitis** causing organisms vary among bedding types

Objective

- Quantify differences in microbial populations of four different bedding types used in dairy barns
 - Deep-bedded New Sand (NS)
 - Deep-bedded Recycled Sand (RS)
 - Deep-bedded Organic Solids (DBOS)
 - Shallow-bedded organic solids over mattresses with a foam core (SBOS)

Materials and Methods: Facilities

- University of Wisconsin Marshfield Agricultural Research Station (MARS)
 - 128 freestalls divided into four equal quadrants of 32 stalls each designed for bedding trials



Materials and Methods: Treatment

- Treatment in our study is Pen
 - Deep-bedded New Sand (NS)
 - Deep-bedded Recycled Sand (RS)
 - McLanahan screw type separator
 - Deep-bedded Organic Solids (DBOS)
 - Recycled on farm using screen press
 - Shallow-bedded organic solids over mattresses with a foam core (SBOS)
- New bedding added twice weekly
 - Tuesday and Friday



Materials and Methods: Timeline

- Data was collected for 12 months
 - January to December 2013
- Bacterial populations
 - Used bedding
 - Weekly on Fridays prior to adding new bedding
 - Clean bedding
 - Every 28 days on Fridays

Materials and Methods: Sampling

- Used bedding was sampled before addition of new bedding
 - 4 randomly assigned positions within each of 4 randomly assigned stalls within each treatment pen
 - Sampled weekly each Friday
- Unused bedding culture
 - Sampled every 28 days prior to use



Culture Procedure and Statistics

- Bedding Culture Procedure
 - Ohio Agricultural Research and Development Center, Mastitis Laboratory SOP
- CFU/g bedding
 - Normalized as $\text{Log}_{10}(\text{Count} + 1)$
- Bedding counts nicely distributed
- SAS PROC MIXED Repeated Measures Analysis
- Bedding Cultures
 - $Y_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + e_i$
 - Y_i is the \log_{10} (CFU count + 1) for
 - sample i
 - pen X_{i1}
 - date X_{i2}

Results:

Bacterial Populations in Bedding

Table. Bacteria isolated from different dairy cattle bedding types (\log_{10} CFU/g)

Bedding material	Gram-negative	Coliform	<i>Klebsiella</i>	<i>Streptococci</i> spp.
NS	4.72 ^a	3.59 ^a	2.41 ^a	6.88 ^a
RS	5.25 ^b	4.10 ^b	3.19 ^b	7.21 ^b
SBOS	5.81 ^c	4.08 ^b	2.74 ^{ab}	8.16 ^c
DBOS	6.83 ^d	5.70 ^c	5.05 ^c	7.08 ^{ab}

^{a,b,c,d}Values with different letters in the same column differ significantly ($P \leq 0.02$).

SAS 9.3 PROC MIXED with Repeated Measures

Preliminary Conclusions

- Mastitis pathogen populations
 - Gram-negatives fewest in NS, most in DBOS
 - *Streptococci* spp. fewest in NS and DBOS, most in SBOS
- Part of a clinical trial analyzing associations of
 - Bacterial populations in bedding
 - Bacterial populations on teat skin
 - Subclinical and Clinical Mastitis
 - Quarters nested within cows
- More analysis to be performed

Research support

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