Bedding strategies that promote udder health and milk quality by fostering a beneficial microbiome on organic dairy farms

A research and extension project funded by the USDA Organic Research and Extension Initiative

Investigators: John Barlow

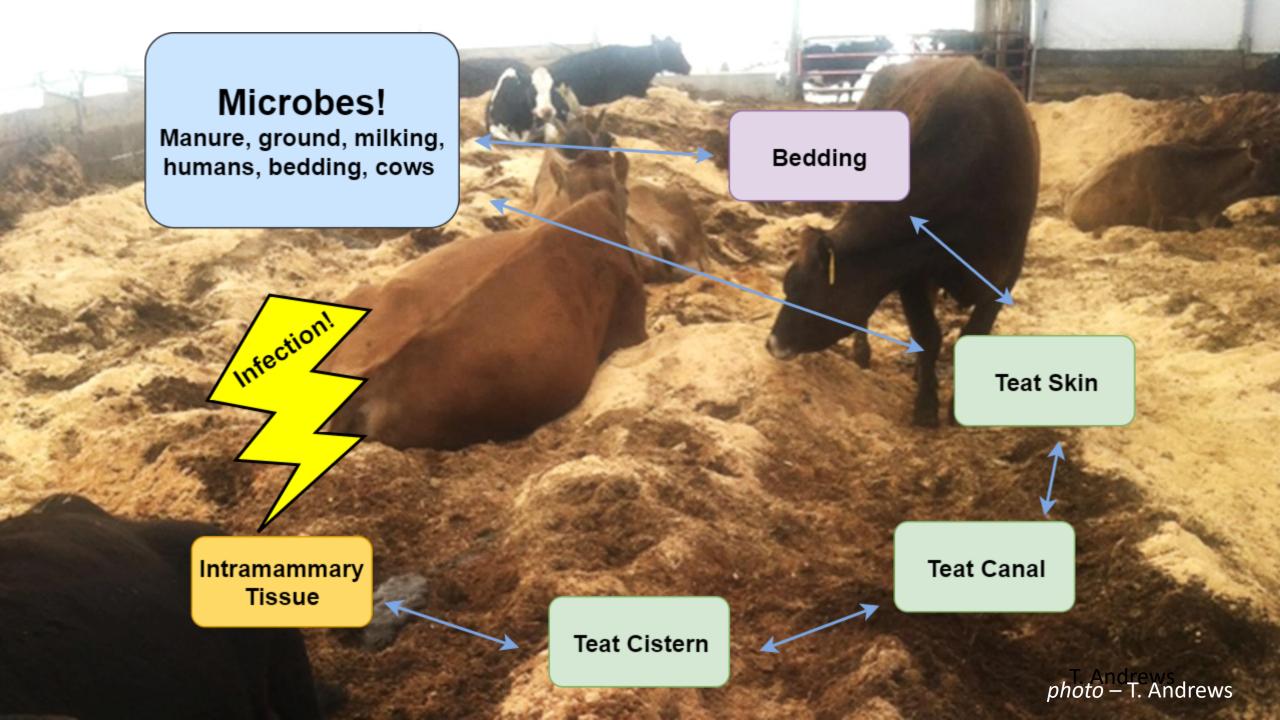
Deborah Neher

Jennifer Colby

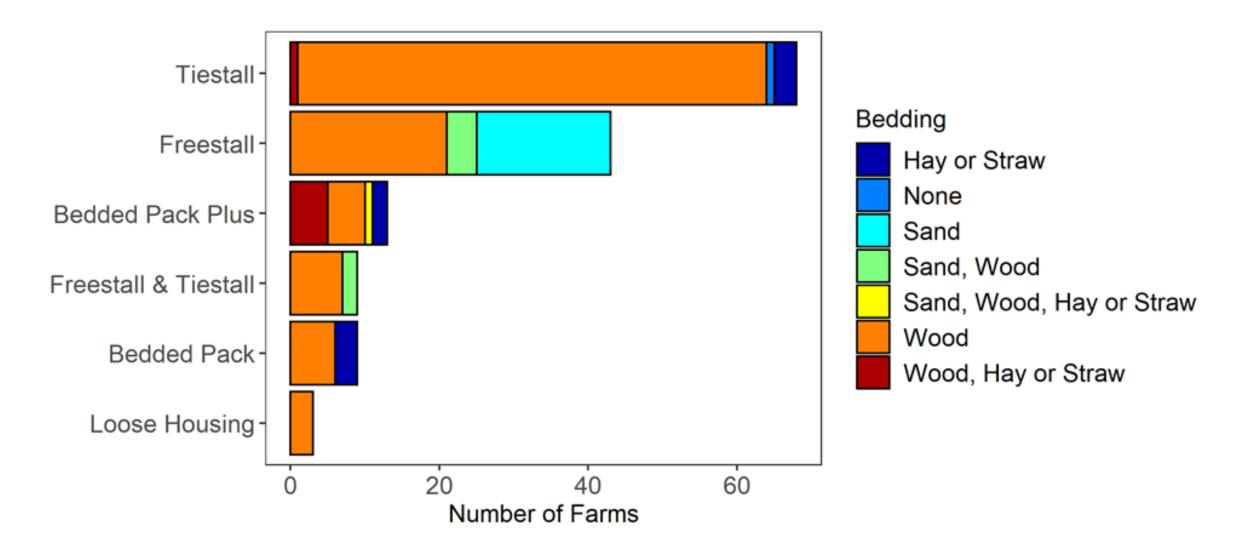
Juan Alvez

Tucker Andrews

Caitlin Jeffreys



"Survey design and implementation quantifies winter housing and bedding types used on Vermont organic dairy farms" Dairy industry Today, J Dairy Sci



10 herd longitudinal study – mastitis epidemiology culture-based

5 bedded pack herds5 tiestall herds

Monthly samples from 35 cows per herd from December 2019 to March 2020

Collected

4,212 quarter milk and teat swab samples from 1,536 quarters of 384 cows aerobic culture and quarter SCC of milk samples cow level SCC and production from farm DHIA records teat swab samples processed for marker gene analysis quarter milk samples processed for marker gene analysis

10 herd longitudinal study – mastitis epidemiology culture-based

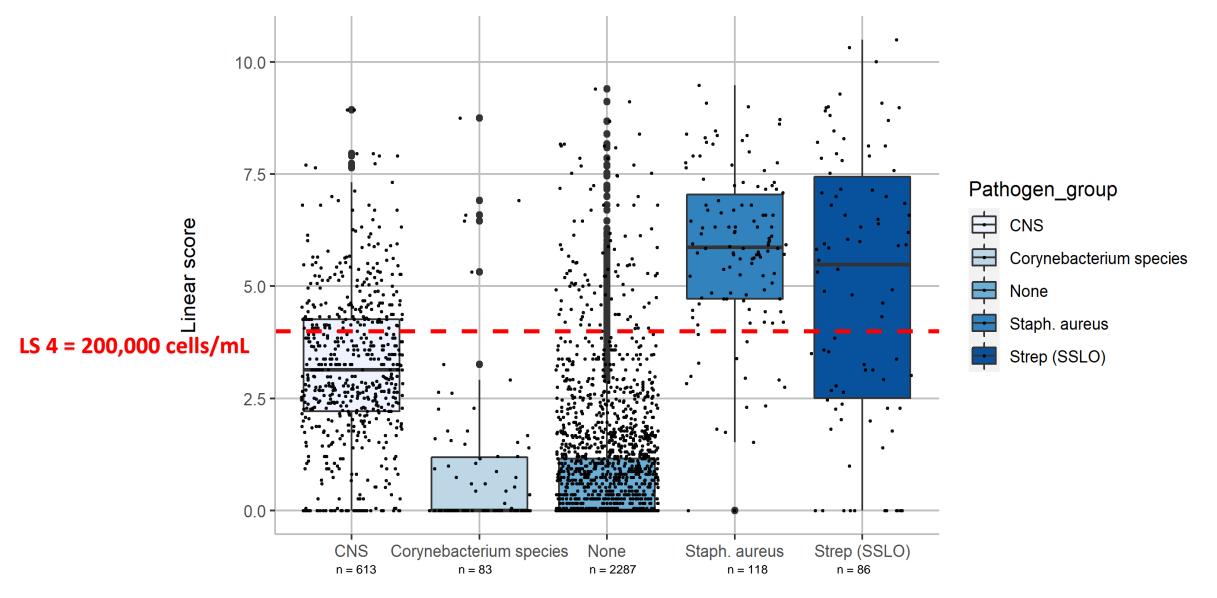
Table 2: Presumptive species identification of isolates saved from the 10-herd longitudinal field
study

		number saved isolates associated with an				
	number ALL	intramammary				
Presumptive pathogen ID*	saved isolates	infection				
Coagulase-negative Staphylococci	780					
Streptococcus "like" spp. (Gram-positive catalase-						
negative cocci)	200	175				
Staphylococcus aureus (Gram-positive catalase-positive						
coagulase-positive cocci)	145	137				
Corynebacterium spp. (Gram-positive pleomorphic rods)	146	115				
Bacillus spp.	8	1				
Gram-negative coliform	8	6				
Gram-negative non-coliform	10	7				
Serratia spp.	1	1				
Unidentified yeast	3	2				
Unknown	28	23				
Total	1329	1181				
* groups of pathogens most frequently observed in bold font						

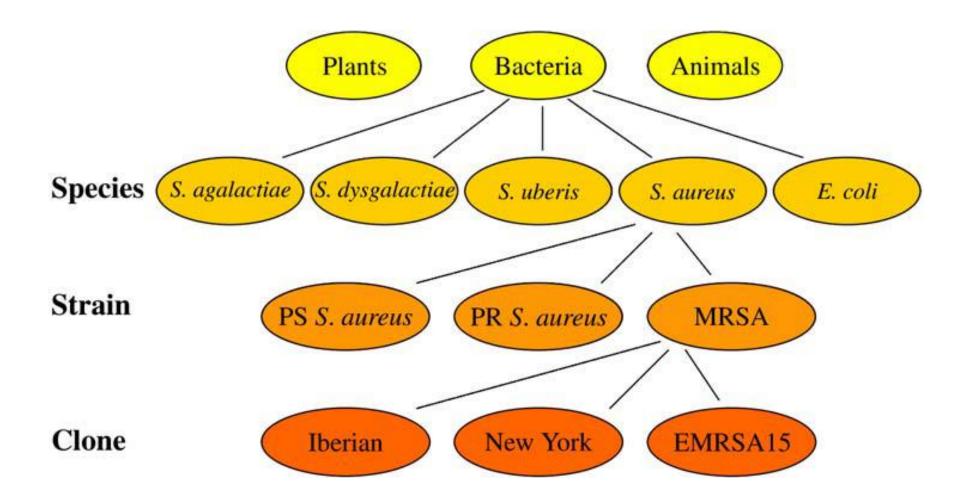
60% of isolates from infections are non-aureus Staphylococci

Species
identification
ongoing with Dr.
Pamela Adkins at U
of Missouri

Linear score by pathogen type

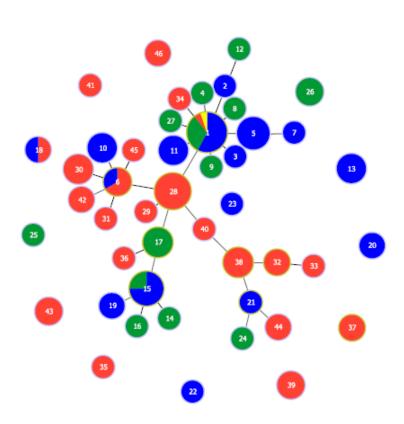


Pathogen type



From Zadoks and Schukken 2006

PLOS ONE



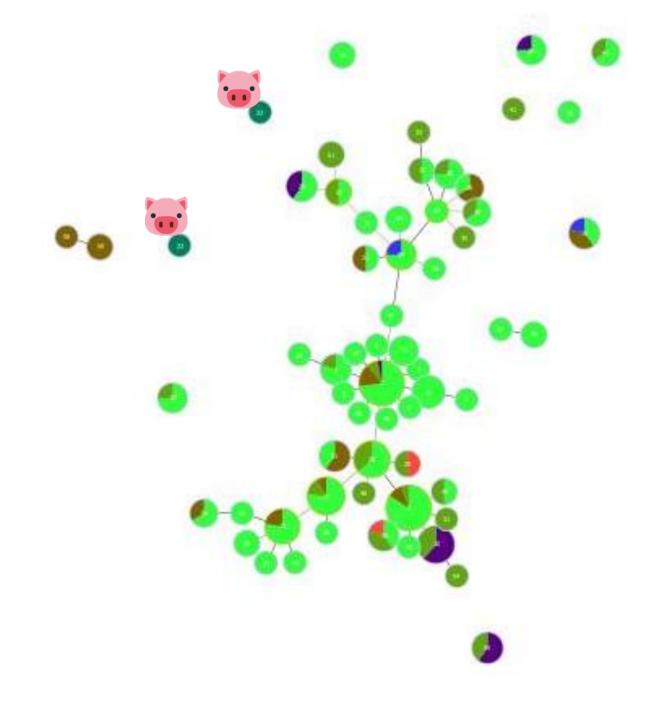
RESEARCH ARTICLE

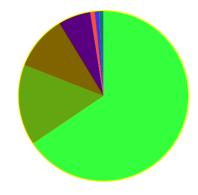
Characterization of genetic diversity and population structure within *Staphylococcus* chromogenes by multilocus sequence typing

Rebeca Huebner¹, Robert Mugabio² , Gabriella Hetesy² , Lawrence Fox³, Sarne De Vlieghero⁴, Anneleen De Visscher⁴ , John W. Barlowo² , George Sensabaugh¹

70% of non-aureus Staphylococci isolates from our current study are *Staphylococcus chromogenes*

Sources





Cow IMI (n=158, 66%)

Teat skin (n=137, 15%)

Milking System (n=25, 10%)

Other cow skin (n=15, 6%)

Barn environment (n=2, 1%)

Cheese (n=2, 1%)

Pigs (n=2, 1%)

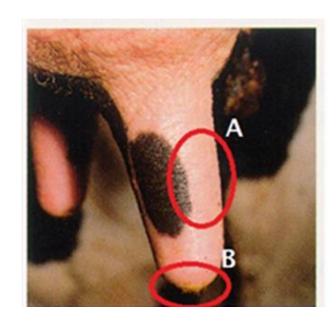
10 herd longitudinal study – mastitis epidemiology marker gene experiments

Table 3: Number of quarters meeting the infection status definitions included in the source data files for samples selection for the marker gene metagenomic experiments

	never infected (NNN)	became infected (NYY)	became infected and recovered (NYN)	always infected (YYY)
Bedded pack herds	191	36	38	91
Tiestall herds	196	42	43	73
Total	387	78	81	164

Study Design

- Collected skin swab samples from 8 lactating Holstein cows at the UVM Teaching herd
 50 cow herd, housed in tie-stalls, milked in a parlor, all milkers wear nitrile gloves,
 chlorhexidine pre- and post-milking teat disinfectant
 - 4 cows with composite milk SCC < 60,000 cells/mL for 5 consecutive months
 - 4 cows with composite milk SCC >280,000 cells/mL for 4 to 5 consecutive months
- Swabbed Three locations: teat barrel (TB), teat end (TE), streak canal (SC)
- 96 total samples
- Samples stored -20°C for up to 4 weeks



Screening assay



Quantify the number of isolates observed per total cfu/ml plated

Simultaneous antagonism assay



Quantify the size of the zone of inhibition for each isolate



Controls

Test plate

"Bedding strategies that promote udder health and milk quality by fostering a beneficial microbiome on organic dairy farms."

John Barlow

Deborah Neher

Thomas Weicht

Tucker Andrews

Caitlin Jeffrey

Asa Hurd

Juan Alvez

Jenn Colby

Hannah Rich

Sarah Flack

Rachel Gilker

Brian Jerose

Pamela Adkins

Noah Fierer

Sandra Godden

Myles Goodrich

Annie Claghorn

Tyler Webb

John Cleary

Funded by the USDA Organic Research and Extension Initiative – grant #2018-51300-28561







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@UVM_BarlowLab



@barlow_lab_uvm

staphylococcus chromogenes	174	
staphylococcus simulans	23	
staphylococcus haemolyticus	21	
staphylococcus species	14	
staphylococcus warneri	8	
staphylococcus equorum	4	
staphylococcus xylosus	2	
staphylococcus auricularis	1	
staphylococcus capitis	1	
staphylococcus devriesei	1	
staphylococcus hominis	1	
staphylococcus saprophyticus	1	
staphylococcus sciuri	1	