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# The association of housing environment on teat skin staphylococcal populations

Veterinary Research Scholars Program
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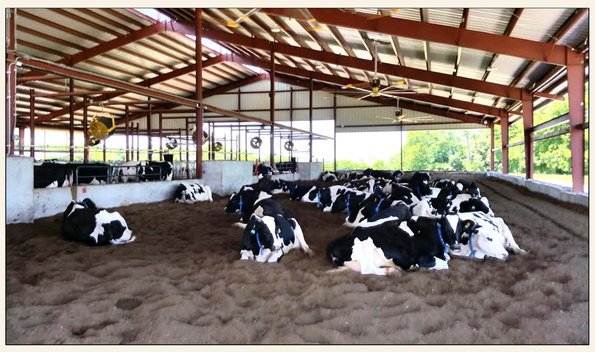
## Background

Mastitis prevention is an ongoing field of research aimed at minimizing the prevalence of the disease on dairy farms. Teat skin colonization has been found to be a risk factor for staphylococcal mastitis in dairy cattle. Though research points to deep-bedded new sand as being the best choice for lactating dairy cow bedding, compost bedded pack housing offers the following benefits: improved cow comfort, cleanliness, decreased somatic cell count, and low investment costs.[1] However, staphylococcal colonization of teat skin on cows housed in these systems has not been evaluated.

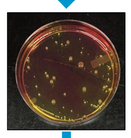
**The purpose of this study was to determine whether housing dairy cattle in new sand bedded free-stalls (n = 10) or compost bedded pack barns (n = 10) was associated with staphylococcal populations on teat skin.**



Sand-bedded free stall housing (top) versus compost bedded pack housing (bottom)

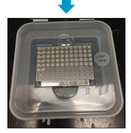
## Materials & Methods

Samples were collected from teat skin surfaces before and after pre-milking teat disinfection (1 composite sample containing skin swabs from one teat of 10 randomly selected animals in each herd before and after teat disinfection [n = 40 samples]).

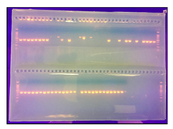


Swabs were placed in peptone water, diluted 1:10, plated on mannitol salt agar and incubated at 37°C for 24 hours.

After 24 hours, 10 staphylococcal colonies, including at least one of each morphologically distinct colony type, from each of the plates were sub-cultured on Columbia Blood Agar (CBA). The plates were reread at 48 hours and any new colonies (up to 10) were sub-cultured on CBA.



Initial bacterial speciation was performed using matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry.[2]



Isolates that were not identified by MALDI-TOF were speciated using PCR amplification and sequencing of a portion of either the *rpoB*[3] or *tuf*[4] gene.

The proportions of samples positive for a given culture result were compared between groups using the Fisher's Exact test with significance declared at $P < 0.05$.

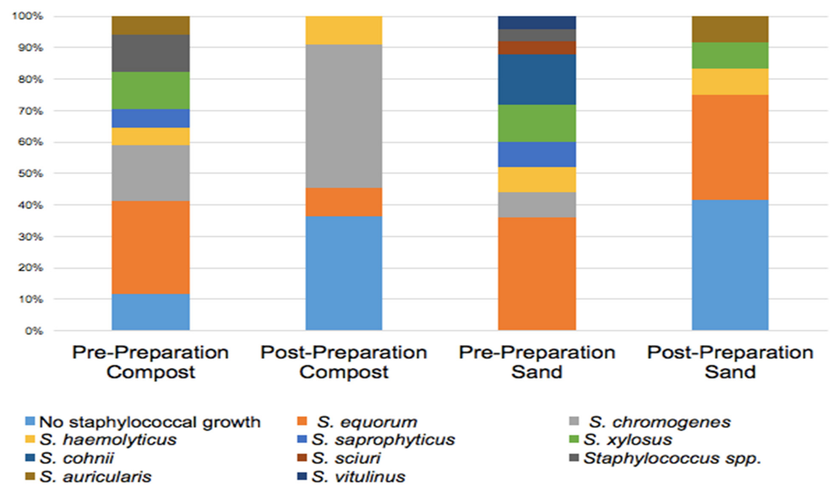



Figure 1. Comparison of the percentages of different staphylococcal species found in teat swabbing samples before and after pre-milking teat disinfection by group.

## Results

*Staphylococcus equorum* was the most common species identified in sand herds (n = 13). *Staphylococcus chromogenes* was the most common species indentified in compost herds (n = 8). *Staphylococcus vitulinus, Staphylococcus sciuri,* and *Staphylococcus cohnii* were only present in samples collected before pre-milking teat disinfection of cows housed on new sand bedded free-stalls.

There was significantly more samples culture negative for staphylococci after pre-milking disinfection (n = 5) than before (n = 0) in the compost herds ($P < 0.01$). There was significantly more *S. chromogenes* in the compost herds (n = 5) after pre-milking teat disinfection than in sand herds at the same time point (n = 0) ($P = 0.01$). The number of staphylococcal species (1 or >1) isolated within herd was not detectably different between groups ($P \geq 0.30$).

## Conclusions

Overall, no clear relationship was found between bedding type and the prevalence of different staphylococcal species on teat skin. These data suggest that pre-milking preparation of the teat is effective at reducing the number of staphylococci on teat skin prior to milking.

Additional samples, including bulk tank milk and bedding samples, are also being cultured for staphylococcal species. The outcome of these studies will aid in better understanding the relationship between staphylococcal species and housing environments on the dairy farm and inform future studies on management factors that influence the prevalence of staphylococcal intramammary infection.

## Acknowledgements

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## References

[1]Black et al., *J Dairy Sci.* 2013;96(12):8060. [2]Cameron et al., J Dairy Sci. 2017;100(3):2137. [3]Drancourt et al., J Clin Microbiol. 2002;40(4):1333. [4]Hwang et al., J Clin Microbiol 2011;49(12):4142