

Sand bedded freestall and compost bedded pack effects on cow hygiene, locomotion, and mastitis indicators



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ARTICLE INFO

Article history:

Received 24 January 2016

Received in revised form

4 June 2016

Accepted 6 June 2016

Keywords:

Sand bedded freestall barn

Compost bedded pack barn

Mastitis

Lameness

ABSTRACT

The objective of this study was to assess differences between compost bedded pack (CBP) and sand freestall barns (SFB) for mastitis indicators (herd clinical mastitis, SCC, high SCC prevalence (% of herd $\geq 200,000$ cells/mL SCC), and BTSCC), and locomotion, hygiene, and hock scores. This study was conducted on commercial Kentucky dairy farms using CBP ($n=8$) or SFB ($n=7$) as the primary lactating cow housing facility from May 2013 to May 2014. To indicate good management practices, eligible herds had to maintain a yearly mean SCC $< 300,000$ the year before enrollment in the study. Milk samples were collected from quarters that presented clinical signs of mastitis as identified by milking personnel. Each herd was visited biweekly ($n=26$ visits) over the study period. Each visit included evaluating 50 cows per herd for hygiene, locomotion, and hock scores. Somatic cell count (SCC) and high SCC prevalence (percentage of animals in each herd with a test day SCC $\geq 200,000$ cells/mL) were collected from Dairy Herd Information Association (DHI, Raleigh, NC). Bulk tank SCC from each pick up was gathered from each dairy's milk purchaser. Bulk tank SCC from each pick up for all Kentucky herds on DHI regardless of SCC or housing type from January 2013–2014 was requested from the Kentucky Milk Quality Safety Branch to determine differences among all bedding types without selecting for herds enrolled in DHI. Overall, no differences between 8 CBP and 7 SFB selected based on SCC existed for herd locomotion, hygiene, or hock health. No differences were observed for the main effects of housing, maximum temperature humidity index, or hygiene score on SCC, high SCC prevalence, clinical mastitis incidence, or bulk tank SCC for 8 CBP and 7 SFB Kentucky herds. Similarly, for Kentucky DHI herds, bulk tank SCC was not different among herds using CBP, freestall barns, and tie-stall barns. Herds using CBP alongside freestall barns had the lowest bulk tank SCC in Kentucky. These results indicate that, when managed properly, CBP can provide a housing environment comparable to SFB. Freestalls, tie-stalls, and compost bedded pack barns for all herds on DHI had similar bulk tank SCC.

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1. Introduction

The compost bedded pack barn (CBP) is a loose housing system without the stalls and partitions found in freestall and tiestall housing. Without stalls, the cows' resting and exercise areas are combined (Janni et al., 2006; Barberg et al., 2007a; Shane et al., 2010). Compost bedded pack barns require periodic bedding addition and twice daily tilling of the pack with a roto-tiller or cultivator (Janni et al., 2006; Barberg et al., 2007a; Black et al., 2013). Tilling incorporates manure and oxygen into the pack, promoting microbiological activity, heating, and drying of the pack (Janni et al., 2006). Heating and drying the pack provides a fresh, dry surface on which cattle can lie (Shane et al., 2010).

Inorganic materials, namely sand, have been considered the gold standard for freestall bedding (Bickert, 1999; Allen, 2007). Sand has five main qualities that make it the gold standard: 1) comfortable resting surface; 2) limited bacterial growth; 3) low initial moisture; 4) a cool lying surface; 5) reducing slippage in alleyways or stalls (Stowell and Inglis, 2000; Allen, 2007; Buli et al., 2010). Sand moves with the animal during lying, standing, and movement within the stall. This property reduces friction on the hocks and knees and increases resting area cushion for the animal (Bickert, 1999).

Similar to sand, compost moves with the animal and provides a comfortable lying and standing surface. Cows in compost bedded pack barns exhibited decreased lameness incidence compared to cows in low-profile cross-ventilated and naturally ventilated sand freestall barns (Lobeck et al., 2011). Similarly, New York researchers observed decreased lameness prevalence after transitioning to CBP, reducing total treatment costs to the dairy producer

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by \$33,000 (Petzen et al., 2009).

No adverse effects on somatic cell count (SCC) or high SCC prevalence (HSP; percentage of animals in each herd with a test day SCC $\geq 200,000$ cells/mL) in CBP have been reported in research compared to other housing systems. Mean SCC from October 2010 to March 2011 was $246,500 \pm 84,422$ cells/mL in Kentucky CBP housed cows ($n=47$ herds), below the 2010 state average of 313,000 cells/mL (Black et al., 2014). After transitioning to CBP in 2005, Minnesota dairy producers reported mean SCC as $325,000 \pm 172,000$ cells/mL, below the 2005 state average of 357,000 cells/mL. The average HSP decreased after moving into the CBP from previous housing facilities (35.4% before to 27.7% after, $P < 0.05$; Barberg et al., 2007b). However, this change cannot be attributed only to the facility type. Changes across time and other improvements in facilities or management also likely influenced HSP. Lobeck et al. (2011) noted HSP did not differ for CBP, naturally ventilated and cross-ventilated freestall barns studied at the same time period (33.4, 26.8, and 26.8%, respectively; $P \geq 0.05$).

To the authors' knowledge, no long-term study comparing CBP to other housing systems on cow hygiene, locomotion, and mastitis indicators currently exists. The objective of this study was to assess differences between compost bedded pack and sand freestall barns (SFB) for mastitis indicators (herd clinical mastitis, weighted average SCC, HSP, and bulk tank somatic cell count (BTSCC)), and locomotion, hygiene, and hock scores. A secondary objective of this study was to assess differences between housing systems in Kentucky in BTSCC from each pick up gathered from the Kentucky Milk Safety Branch.

2. Materials and methods

This study was conducted using data from Kentucky dairy farms with SFB ($n=7$) or CBP ($n=8$) from May 2013 to May 2014. All farms were assigned an identification number 1–15) that will be used from this point forward. All barns were used as the only housing facility for lactating cows. All herds on this study were enrolled in DHI. Enrollment in the study required herds to maintain a yearly mean DHI weighted SCC $< 300,000$ in the herd during the year before enrollment in the study to indicate good management practices were followed. Producers meeting these criteria were contacted and 7 SFB and 8 CBP producers agreed to participate in the study. Participating herds were fed a TMR and used mechanical ventilation to cool cows in the barn. Sand bedded freestalls had fresh sand added at least once every two weeks and were groomed daily. Compost bedded pack barns were tilled 1–2 times per day and bedding was added when compost moisture content reached 55–60%.

2.1. Data collection

An initial survey was conducted to ensure producers were following similar milking procedures. Performance records from DHI were collected with the permission of participating producers including: test day milk production (kg/cow), weighted average herd SCC (average of somatic cell count weighted by individual cow milk production; cells/mL (Fetrow et al., 1988)), HSP (%), and number of animals in the lactating herd. Bulk tank SCC from every milk pick-up was obtained from fluid-milk buyers with producer permission. Producers were provided a Tycon ProWeatherStation (model # TP1080WC; Tycon Systems, Buftdale, Utah) to record barn temperature and humidity, ambient temperature and humidity, and wind speed. Ambient temperature, humidity, wind speed, and precipitation data were collected from University of Kentucky's Weather Center stations nearest the farms.

During the study, 178 ± 108 and 84 ± 37 cows were housed in

CBP and SFB at each visit, respectively. The DHI reported mean daily milk production over the year was 33.69 ± 4.29 and 32.15 ± 4.83 kg per cow per day for CBP and SFB, respectively. All farmers pre and post-dipped their cows with iodine based (pre: 7 herds; post: 10 herds), chlorine based (pre: 4 herds; post: 2 herds), peroxide based (pre: 4 herds; post: none), or a mixture of lactic acid, phosphoric acid, and sodium chlorite (pre: none; post: 3 herds) teat dips. Cloth or paper towels were used to dry the teats of cows from all herds before milking unit attachment. Cows were milked in herringbone ($n=7$), parallel ($n=4$), and parabone ($n=2$) parlors. Seven herds milked twice daily, 4 herds milked 3 times per day except during the summer, and 2 herds milked 3 times per day continuously. Although milking frequency and parlor type differed, milking management and yield were similar between CBP and SFB groups.

2.2. Herd locomotion, hygiene, and hock health

The same observer scored locomotion, hygiene, and hock lesions (48 ± 5 cows) at all visits on all farms. Locomotion was assessed using the 5-point scoring system by Sprecher et al., (1997) where: 1=sound, 2=mildly lame, 3=moderately lame, 4=lame, and 5=severely lame. Observations were collected by encouraging the animal to move on a concrete surface, such as the feed alley or parlor exit, and evaluating the leg movement and back arch. Locomotion scores ≥ 3 were classified as clinically lame, with scores ≥ 4 classified severely lame. Hygiene evaluation of the lower legs, upper leg and flank, and udder was conducted using the 4-point system by Cook and Reinemann (2007) where: 1=clean, 2=moderate dirt, 3=plaques of dirt with hair visible and 4=confluent plaques of dirt with no hair visible. Hocks were evaluated as 1=no swelling or missing hair, 2=no swelling with missing hair, and 3=swelling or lesion through hide (Nocek, 2010).

2.3. Barn analysis

Surface temperature was collected in three stalls in each row of freestalls from the center of the back one-third of the stall using an infrared thermometer (accuracy of ± 1 °C; Fluke, model 62, Everett, WA, USA). The observer stood behind the stall and pointed the laser light at the center of the stall (Fig. 1(a) and (b)). The temperature was recorded when the digital readout no longer fluctuated. Each CBP was divided into 9 evenly distributed sections. At the center of each section, the observer collected surface temperature using the same infrared thermometer (Fig. 1(c)). The observer pointed the laser light at the center of the section. The temperature was recorded when the digital readout no longer fluctuated.

2.4. Clinical mastitis identification and collection

All participating farmers were provided a kit including alcohol soaked cotton balls in a sealed container, sterile sample collection tubes (14 mL tube with snap top, Fisher Scientific Company LLC, Hanover Park, IL, USA), a laminated instruction sheet, and a binder containing recording material. The instruction sheet included steps for aseptic milk collection and a mastitis severity guide from Hogan et al., (1989a). Mastitis severity was reported as 1=abnormal milk (flakes, clots, or watery appearance) without swelling of the affected quarter, 2=normal or abnormal milk and swelling of the affected quarter, or 3=abnormal milk, swelling of the affected quarter, and systemic signs (fever, reduced rumen function, dehydration, weakness, depression, loss of appetite, or rapid pulse; Bramley et al., 1996; Hogan et al., 1989a). Each producer was trained on taking mastitis samples and recording

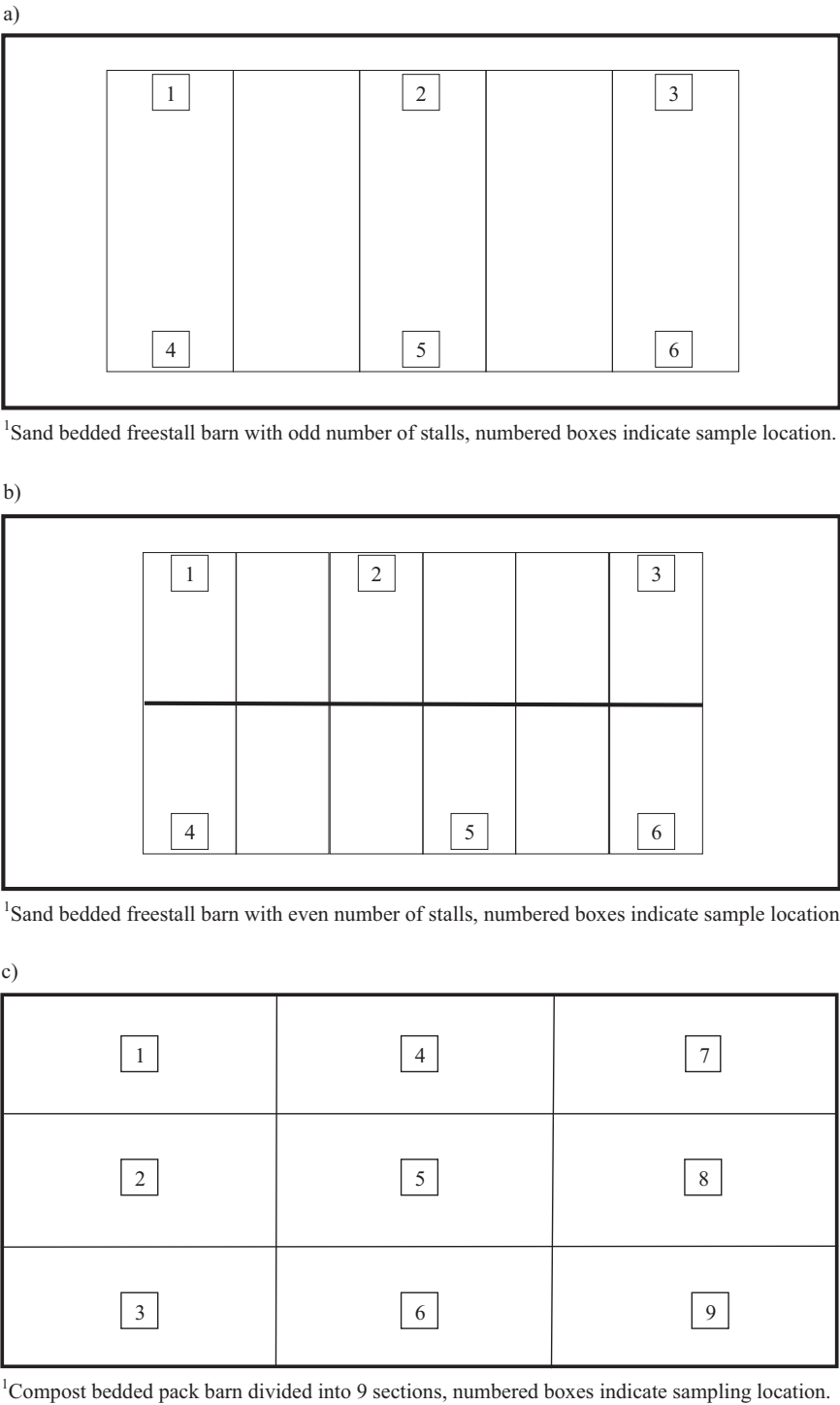


Fig. 1. Sampling locations for resting area surface temperature in sand bedded freestalls (a and b) and compost bedded pack barns (c).¹Sand bedded freestall barn with odd number of stalls, numbered boxes indicate sample location. ¹Sand bedded freestall with even number of stalls, numbered boxes indicate sample location. ¹Compost bedded pack barn divided into 9 sections, numbered boxes indicate sampling location.

information at the initial visit. Producers were instructed to take a sample when first signs of mastitis were identified by milking staff before treatment. Ideally, only 1 sample was taken per case of mastitis. If more than 1 case of mastitis was reported for a single cow within a 14 d period and the same pathogen was isolated from both samples, a new case was not reported. If a new pathogen was isolated, a new mastitis case was reported. Samples were frozen following milking and picked-up for culturing at each visit. Samples were stored in a –18 °C freezer at the University of Kentucky until culturing the week following each visit.

2.5. Clinical mastitis culturing

Clinical mastitis culturing occurred at the University of Kentucky Animal and Food Sciences Department microbiology laboratory. Samples were thawed at room temperature and plated in duplicate. A 0.1 mL sample was inoculated onto one half of a Difco (BD Diagnostic Systems, Detroit, MI) Columbia blood esculin agar plate with 5% calf's blood using a plastic L-shaped agar spreader and repeated on the other half of the plate. Plates were incubated for 48 h at 37 °C followed by bacterial growth observation. Use of

colony morphology and hemolytic characteristic analysis allowed for tentative bacteria identification on the primary culture medium. Mastitis pathogen isolates were placed in brain-heart-infusion broth and incubated for 24 h at 37 °C. Heat fixing of 10 µL of each broth culture to a microscope slide was conducted, followed by gram staining. Slides were examined under a microscope for Gram-negative and Gram-positive identification and all isolates were further evaluated by Vitek 2 Compact (bioMérieux, Durham, NC). A milk sample returning ≥ 3 colony types was deemed contaminated and not investigated further. A milk sample with at least 1 colony on each duplicate was considered a causative mastitis pathogen. A milk sample with no growth present on either duplicate was considered a no growth.

3. Statistical analysis

3.1. Inclusion criteria

All analyses including DHI data required a minimum of 6 DHI tests on file for the study period. One CBP herd was excluded from analyses because of lack of DHI data (< 6 tests for the year). Two farmers on DHI test declined participation in the SCC analysis provided by DHI as an additional service. Consequently, 1 SFB and 1 CBP herd was excluded from HSP and SCC analyses because of lack of somatic cell data from DHI. To include herds that were consistently sampling clinical mastitis cases, producer reported clinical mastitis incidence (RCMI) analyses required 13 weeks of data. Four CBP and 4 SFB herds were excluded from the RCMI analyses because of lack of clinical mastitis data (< 13 weeks of data for the year).

3.2. Herd information

The MEANS procedure of SAS 9.3 (SAS Inst. Inc., Cary, NC) was used to determine mean number of lactating animals, DHI test day milk yield, DHI weighted average SCC, BTSCC, and stocking density for each herd. The MEANS procedure of SAS was also used to create a herd mean locomotion, hygiene, and hock score and the BTSCC for each herd at each visit period. The means were included in the MIXED analyses in SAS comparing variables between barn types. The FREQ procedure of SAS was used to determine the percentage of cows in each herd and barn type with hock scores of 1, sound cows, clinical lameness, and severe lameness.

3.3. Housing comparison

The MIXED procedure of SAS was used to develop all models for all barn type comparison analyses. Somatic cell count and HSP data for 12 herds across the study were adjusted for 5th and 95th percentiles to remove outliers. Reported clinical mastitis incidence data for 8 herds across the study were adjusted for 5th and 95th percentiles to remove outliers. Explanatory variables for locomotion, hygiene, and hock score included barn type and maximum ambient temperature humidity index (THI) group. Temperature humidity index was calculated using the following formula (NOAA, 1976): $\text{THI} = \text{temperature } (^{\circ}\text{F}) - (0.55 - (0.55 * \text{relative humidity}/100)) * (\text{temperature } (^{\circ}\text{F}) - 58.8)$.

Temperature humidity index was adjusted for 5th and 95th percentiles to remove outliers using the UNIVARIATE procedure of SAS. Adjusted THI data was grouped as cool or warm, defined as \leq or $>$ the median THI of 66.30, respectively. Locomotion, hygiene, and hock scores were compared as a herd mean for each farm and visit across time. Variables were repeated by visit with farm as subject. Stepwise backward elimination was used to remove non-significant interactions ($P \geq 0.05$). All main effects remained in the

model regardless of significance. The model generated LSMeans (\pm SE) for locomotion, hygiene, and hock scores for each barn type and THI period.

Bulk tank SCC and DHI weighted average herd SCC explanatory variables were barn type, THI period, mean herd hygiene score, and all 2-way interactions. Variables were repeated by visit with herd as subject. Stepwise backward elimination was used to remove non-significant interactions ($P \geq 0.05$). All main effects remained in the model regardless of significance. The model generated LSMeans (\pm SE) for BTSCC and DHI weighted average herd SCC for each barn type and THI period.

High SCC prevalence and RCMI explanatory variables were barn type, maximum ambient THI period, mean herd hygiene score, and all 2-way interactions. High SCC prevalence and RCMI were calculated as a herd percentage for each visit period. High SCC prevalence was the % of the herd with a DHI SCC $\geq 200,000$ cells/mL at each visit period (Barberg et al., 2007b; Lobeck et al., 2011). Reported clinical mastitis incidence was calculated as a herd percentage for each week as follows: $\text{RCMI} = (\text{number of isolates over 2-wk period}/\text{number of animals in herd})/2$. Variables were repeated by visit with herd as subject. Stepwise backward elimination was used to remove non-significant 2-way interactions ($P \geq 0.05$). All main effects remained in the model regardless of significance. The model generated LSMeans (\pm SE) for HSP and RCMI for each barn type and THI period.

3.4. Mastitis pathogens

To determine differences in proportion of clinical pathogens, χ^2 analyses were conducted using the FREQ procedure of SAS at a $P < 0.05$ significance level. Nine groups of pathogens were included in the analysis: no growth, coagulase negative staphylococci (CNS), environmental streptococci, *Escherichia coli*, *Klebsiella* spp., *Staphylococcus aureus*, yeast species, other Gram-negative species, and other Gram-positive species. To determine differences in mastitis severity, χ^2 analyses were conducted using the FREQ procedure of SAS at a $P < 0.05$ significance level.

3.5. Yearly changes

The GLM procedure of SAS was used to determine differences between CBP and SFB at each visit. Hygiene score, locomotion score, lying surface temperature ($^{\circ}\text{C}$), DHI weighted average herd SCC (cells/mL), and BTSCC (cells/mL) were included in the analyses, with the LSMeans (\pm SE) for each barn type compared by each visit. Tukey's test for multiple comparisons was used with a $P < 0.05$ significance level.

3.6. Additional analyses

To examine a broader sample of herd, an additional analysis was conducted using BTSCC from all herds in Kentucky enrolled in DHI from January 2013 to January 2014 ($n=240$ farms). In this analysis, all herds were included regardless of management. The BTSCC data was collected from the Kentucky Milk Safety Branch. The Kentucky Dairy Development Council provided information on the housing system of each herd. Housing facilities were identified as compost bedded pack barns ($n=36$), freestall barns ($n=92$), tie-stall barns ($n=56$), conventional bedded pack barns ($n=6$), or no housing (pasture based; $n=24$). Some dairy producers used multiple types of housing. One subset of mixed housing was included in the analysis as compost bedded pack barn with freestall housing ($n=14$). All other housing combinations were referred to as mixed housing ($n=12$). The GLM procedure of SAS was used to determine the differences in BTSCC among all housing types in Kentucky using the DHI management system. The

LSMeans (\pm SE) for each housing type was compared for the period between January 2013 and January 2014. Tukey's test for multiple comparisons was used with a $P < 0.05$ significance level.

4. Results and discussion

4.1. Herd background information

Yearly mean (\pm SD) daily milk yield, DHI weighted average SCC, BTSCC, total cow resting area, and stocking density for each co-operating herd are reported in Table 1.

4.2. Lying Surface

Lying surface temperature was not different between barn types over the year (17.81 ± 9.03 °C and 16.12 ± 8.52 °C for CBP and SFB, respectively; $P=0.95$). Yearly variations in surface temperatures were not different between both barn types and were similar to ambient temperatures. Given that CBP exhibit internal temperatures greater than the ambient temperature (Black et al., 2013; Eckelkamp et al., 2016), the surface temperature similarity with SFB indicates that the high internal temperature may not adversely affect CBP housed cattle. Lying surface temperature may assist with conductive cooling or heating of dairy cattle (Ortiz et al., 2014; Perano, 2014). Sand bedding is a non-insulator, maintaining a cool surface temperature even in warm ambient temperatures (Stowell and Inglis, 2000). In a previous Kentucky study, CBP surface temperatures remained near ambient temperatures (9.9 ± 9.4 and 10.5 ± 8.0 °C for surface and ambient temperature, respectively). This was achieved through evaporative cooling of the compost surface coupled with barn ventilation (Black et al., 2013). Study results indicate that Kentucky CBP and SFB provided surface temperatures that would allow animals to experience similar heat abatement or heat acquisition. Similar

surface temperature, allowing for a comfortable resting area, and freedom from physical restraints such as stall dividers, brisket boards, and neck rails may make CBP a more attractive option for producers with good management skills.

5. Cow measures

5.1. Hock health

Overall, LSMean (\pm SE) of hock scores were not different between barn types (1.00 ± 0.00 for both housing types; $P=0.12$; Table 2). In each barn type, the highest mean herd hock score was 1.06 and 1.07 in CBP and SFB, respectively. The lack of difference may be because of the soft surface of both the CBP and the SFB. Sand allows movement with the animal, reducing friction on the hocks and increasing the cushion provided to the cow (Bickert, 1999). Van Gastelen et al. (2011) reported decreasing hock injuries with softer, dryer bedding ($r = -0.41$; $P=0.05$) such as shavings and sand instead of mattresses or other solid surfaces. Compost bedded pack barns maintain a soft and dry lying surface, which may be why hock health was maintained in the current study. Barberg et al., (2007b); Lobeck et al., (2011) noted 3.8–25.1% of animals housed within CBP experienced hock lesions. Klaas et al. (2010) reported no hock or body lesions on cows housed in Israeli compost barns. These studies corroborate the hock health witnessed in the current study.

5.2. Locomotion

Herd locomotion score (LSMeans \pm SE) was not different between CBP (2.22 ± 0.05) and SFB (2.27 ± 0.06) ($P=0.58$; Table 2). In CBP, 27.44% of animals were scored as 1 (sound) and the same score was observed in 28.79% of cows in SFB. The highest percentage of cows were scored mildly lame (score 2) for both barn

Table 1
Mean (\pm SD) lactating herd number, Dairy Herd Information Association herd somatic cell count (DHI weighted average SCC), bulk tank somatic cell count (BTSCC), available cow resting area, and stocking density for 8 compost bedded pack and 7 sand bedded freestall Kentucky herds from May 2013 to May 2014.^a

Farm code	Number of DHI tests	Number of lactating cows	Test d milk yield (kg/cow/d)	DHI SCC (x 1000 cell/mL)	BTSCC (x 1000 cells/mL)	Lying area		Stocking density (%)
						Compost (total m ²)	Freestall (total stall #)	
1	12	205 (\pm 27)	36 (\pm 6)	160 (\pm 68)	150 (\pm 42)	1858		103 (\pm 14)
2	5	455 (\pm 23)	37 (\pm 1)	180 (\pm 31)	174 (\pm 18)	4496		94 (\pm 5)
3	13	160 (\pm 15)	31 (\pm 3)	206 (\pm 63)	224 (\pm 69)	1561		95 (\pm 9)
4 ^b	7	120 (\pm 13)	36 (\pm 2)	–	227 (\pm 47)	1081		88 (\pm 11)
5	12	102 (\pm 12)	30 (\pm 3)	290 (\pm 107)	261 (\pm 106)	1137		84 (\pm 10)
6	11	90 (\pm 14)	37 (\pm 4)	241 (\pm 102)	264 (\pm 83)	892		93 (\pm 15)
7	6	112 (\pm 5)	32 (\pm 3)	314 (\pm 99)	284 (\pm 84)	1117		93 (\pm 4)
8	8	212 (\pm 14)	33 (\pm 1)	366 (\pm 71)	335 (\pm 90)	2323		85 (\pm 5)
CBP ^c	9	182 (\pm 120)	34 (\pm 3)	251 (\pm 75)	240 (\pm 60)	1808 (\pm 1186)		92 (\pm 6)
9	7	44 (\pm 4)	35 (\pm 3)	106 (\pm 22)	119 (\pm 33)		51	86 (\pm 7)
10	12	59 (\pm 4)	28 (\pm 3)	128 (\pm 80)	123 (\pm 48)		66	89 (\pm 5)
11 ^c	3	111 (\pm 32)	38 (\pm 3)	–	181 (\pm 64)		136	81 (\pm 23)
12	6	151 (\pm 8)	36 (\pm 2)	270 (\pm 27)	218 (\pm 38)		150 ^d	114 (\pm 11)
13	6	49 (\pm 8)	29 (\pm 3)	268 (\pm 83)	269 (\pm 110)		60	82 (\pm 14)
14	12	94 (\pm 4)	28 (\pm 3)	236 (\pm 69)	283 (\pm 42)		118	80 (\pm 3)
15	10	98 (\pm 9)	37 (\pm 2)	371 (\pm 74)	299 (\pm 52)		112	87 (\pm 8)
SFB ^e	8	87 (\pm 39)	33 (\pm 4)	230 (\pm 99)	213 (\pm 75)		99 (\pm 40)	88 (\pm 12)

^a Lactating cow number, test d milk yield, DHI weighted average herd SCC, bulk tank SCC, and stocking density reported as the mean number across the study period for the available DHI tests.

^b Farm 4 and farm 11 did not take advantage of the DHI somatic cell count service and had no somatic cell count data for the study period.

^c CBP=mean (\pm SD) for all compost bedded pack barns: lactating cow number, test d milk yield, DHI weighted average herd SCC, bulk tank SCC, and stocking density reported across the study period for the available DHI tests.

^d Farm I underwent a renovation during the study period, increasing available stalls from 100 to 150. Stocking density was calculated using 100 stalls from May 18, 2013 to February 20, 2014 and 150 stalls from March 6, 2014 to April 30, 2014.

^e SFB=mean (\pm SD) for all sand bedded freestall barns: lactating cow number, test d milk yield, DHI weighted average herd SCC, bulk tank SCC, and stocking density reported across the study period for the available DHI tests.

Table 2

Comparison of LSMeans (\pm SE) for locomotion, hygiene, and hock scores observed on 48 ± 5 cows per herd per visit period across 26 visits from May 2013 to May 2014 for 8 compost bedded pack and 7 sand bedded freestall barns in Kentucky.^a

Variable	Compost bedded pack barns (n = 8)	Sand bedded freestall barns (n = 7)	P value
Hock score ^b	1.00 (\pm 0.00)	1.00 (\pm 0.00)	0.12
Locomotion score ^c	2.22 (\pm 0.05)	2.27 (\pm 0.06)	0.58
Hygiene score ^d	2.19 (\pm 0.05)	2.26 (\pm 0.06)	0.38

^a A single observer conducted all scoring at each visit period. Visual observation was used to collect hock, locomotion, and hygiene scores. All locomotion scoring observed with cows walking on concrete flooring. All results were obtained using the MIXED procedure of SAS with visit period as the repeated measure.

^b Hock score (Nocek, 2010) where 1=no swelling or hair missing, 2=moderately swelling with missing hair, 3 = swelling or lesion through the hide.

^c Locomotion score (Sprecher et al., 1997) where 1=normal, 2=mildly lame, 3=moderately lame, 4=lame, and 5=severely lame. All locomotion scoring conducted with cows walking on concrete flooring.

^d Hygiene score on udder, upper leg and flank, and lower leg (Cook and Reinemann, 2007) where 1=clean, 2=moderate dirt, 3=plaques of dirt with hair visible, and 4= confluent plaques of dirt with no hair visible.

types (33.31% and 30.42% for CBP and SFB, respectively). Percent of cows in each barn type scored clinically lame (score ≥ 3) were 39.24% and 40.80% in CBP and SFB, respectively. Percent of cows in each barn type scored severely lame (score ≥ 4) were 10.71% and 13.33% in CBP and SFB, respectively. No differences between barn types at each visit period were observed ($P=0.99$).

These results differed from other research, as the softer walking and standing surface of CBP has been thought to reduce lameness prevalence when compared to SFB. Black et al. (2013) reported 69.3% of all cows housed in Kentucky CBP as sound versus 27.44% in the current study with lower clinical (11.9%) and severe lameness prevalence (5.0%). The differences between the two studies may be linked to the variation in visits, with Black et al. (2013) visiting each herd once whereas the current study required bi-weekly visits over a year. With biweekly visits, chronically lame cows may have influenced the higher percentage of clinically and severely lame animals because all lameness events were considered independent of each other. Black et al. (2013) also had more herds on their study than the current study (42 vs 8), potentially resulting in the lower lameness percent over all herds. Shane et al., (2010); Barberg et al., (2007b); Lobeck et al., (2011) all reported low lameness prevalence in CBP 4.4–9.1% of herds). Lobeck et al., (2011) also found CBP housed cows had lower lameness than SFB housed cows (4.4 vs 14.5%, respectively). Although the current study did not see reduced lameness in CBP, the similarity between systems indicated that the animals were similarly affected by CBP and SFB. As SFB are the gold standard of housing, not only for lower bedding bacterial load but also for improved cow comfort, these results are indicative of a good housing option.

5.3. Hygiene

No differences were observed between mean herd rear cow hygiene score between CBP (2.19 ± 0.05) and SFB (2.26 ± 0.06 ; $P=0.38$; Table 2). This indicates that animals in both systems remained clean throughout the study. Black et al. (2013) reported a similar mean herd hygiene score of 2.2 ± 0.7 ($n=1699$) for CBP in Kentucky. Shane et al., (2010) reported a mean herd hygiene score of 3.1 (range 2.2–3.8) for all cows housed in CBP using several different bedding materials. A slightly lower mean hygiene score (2.7 ± 0.2) was reported by Barberg et al., (2007b) for cows housed in CBP in Minnesota. The differences in hygiene throughout CBP studies were likely because of varying bedding types (Shane et al., 2010) and the strict inclusion criteria of SCC $< 300,000$ cells/mL on the current study. Compost bedded pack barns and SFB that are

not well managed may house cows with higher hygiene scores, indicating dirtier cows.

A slight increase in hygiene score occurred in the current study in the cooler THI period (below the median THI; 2.27 ± 0.04) compared to the warmer THI period (above the median THI; 2.20 ± 0.04 ; $P=0.02$). However, the interaction between barn type and THI period was not significant ($P=0.76$). The increase in hygiene score in the cooler THI period was 0.07 higher than the warm THI period and may not have biological significance. Both hygiene scores were within the range of 2–3, indicating splashes of manure, but no solid areas of manure. No differences were observed between barn types over time ($P=0.99$). Lobeck et al. (2011) reported that animals housed in CBP exhibited greater overall hygiene score than cross-ventilated and naturally ventilated SFB (3.18, 2.83, and 2.77; $P=0.02$ and $P=0.01$, respectively). The greater overall hygiene score was likely because of greater winter hygiene scores in CBP than in cross-ventilated and naturally ventilated SFB ($P=0.01$ and $P=0.03$, respectively). Producers reported difficulty keeping CBP at optimal moisture and temperature in winter (Lobeck et al., 2011). The moisture content of CBP increases over the cooler months of the year (Barberg et al., 2007b; Eckelkamp et al., 2016). Increased moisture content allows material to adhere more easily to animals, increasing hygiene score. This reinforces the need to maintain barns with low moisture contents throughout the year.

6. Mastitis indicators

6.1. Somatic cell count

Compost bedded pack and SFB both had yearly LSMeans (\pm SE) DHI weighted average SCC of $241,716 \pm 21,450$ and $228,796 \pm 22,761$ cells/mL respectively ($P=0.69$; Table 3). Herd mean SCC was not affected by THI period or hygiene scores ($P \geq 0.05$). Sand bedded freestall barns were below the 2013 Kentucky state average of 237,000 cells/mL with CBP slightly above the state average. Both barn types in Kentucky had SCC above the 2013 national average SCC of 199,000 cells/mL (Norman and Walton, 2013). Animals housed within CBP and SFB had mean SCC below 250,000 cells/mL. Lost milk production occurs at SCC $> 200,000$ cells/mL, which is also the cutoff for subclinical infections (Bramley et al., 1996). Although the mean SCC for the herds on the current study was above 250,000 cells/mL, it could be because of a few cows with a high SCC while the rest of the herd maintained a SCC $\leq 200,000$ cells/mL. For this reason, HSP, discussed below, is a better indicator of the animals in the herd with subclinical mastitis infections.

No differences in SCC were observed between barn types over time ($P=0.58$; Fig. 2). The lowest SCC in both barns occurred when lying surface and ambient temperatures were lowest. Dohoo and Meek, (1982); Morse et al., (1988) both reported SCC decreasing at lower THI, which would occur at lower ambient temperatures. Researchers suggested that heat stress played a role in increased SCC. Eckelkamp et al. (2016) reported a similar relationship occurred in CBP, with SCC increasing with increasing THI. The SCC results from the current study suggest that ambient temperature similarly affects animals housed in CBP and SFB.

The LSMeans (\pm SE) of HSP were 21.8 ± 2.0 and 19.4 ± 2.1 for CBP and SFB, respectively ($P=0.43$; Table 3). High SCC prevalence was not affected by THI period or hygiene scores ($P \geq 0.05$). High SCC prevalence was a measure of subclinical mastitis prevalence within the herd. These results indicate that over the year, on average 20% of each herd had subclinical mastitis. These animals would be experiencing production losses and potentially pain or discomfort (Bramley et al., 1996). In the most recent NAHMS study,

Table 3
Comparison of LSMeans (\pm SE) for Dairy Herd Information Association herd weighted average somatic cell count, high SCC prevalence, reported incidence of clinical mastitis, and bulk tank somatic cell count for 26 visits from May 2013 to May 2014 for compost bedded pack and sand bedded freestall barns in Kentucky.

Variable	Compost bedded pack barns mean (\pm SE) cows ^a = 190 \pm 146		Sand bedded freestall barns mean (\pm SE) cows ^a = 65 \pm 25		P value
Herd somatic cell count ^b (\times 1000 cells/mL)	242 (\pm 21)		229 (\pm 23)		0.69
High SCC prevalence ^c	22 (\pm 2)		19 (\pm 2)		0.43
Reported clinical mastitis incidence ^d	1.2 (\pm 0.1)		1.2 (\pm 0.1)		0.90
Pathogen isolated ^e	total new cases=212 total isolates=214 Number of isolates ^f		total new cases=87 total isolates=88 Number of isolates ^f		
		Percent of total isolates		Percent of total isolates	
No growth	41		21		23.9
<i>Escherichia coli</i>	62		19		21.6
Environmental streptococci	36		17		19.3
Klebsiella species	3		4		4.5
Yeast species	7		3		3.4
<i>Staphylococcus aureus</i>	11		6		6.8
Coagulase negative staphylococci	17		4		4.5
Other Gram-negative species ^g	29		6		6.8
Other Gram-positive species ^h	8		8		9.1
Severity score ⁱ	Number of cases	Percent of total cases	Number of cases	Percent of total cases	
1	147	69.3	33	37.9	
2	60	28.3	36	41.4	
3	5	2.4	18	20.7	
Bulk tank somatic cell count ^j (\times 1000 cells/mL)	230 (\pm 19)		205 (\pm 20)		0.38

^a Mean population of cows at each sample period throughout the study.

^b Dairy Herd Information Association weighted average somatic cell count reported as \times 1000 cells/mL. Seven compost bedded pack and 6 sand bedded freestall barns were included in this analysis.

^c High SCC prevalence derived from the Dairy Herd Information Association reported as the % of the herd with somatic cell counts \geq 200,000 cells/mL. Seven compost bedded pack and 6 sand bedded freestall barns were included in this analysis.

^d Reported clinical mastitis incidence collected from cooperating farmers and reported as % of the herd infected per week. Total mastitis incidence was calculated for each visit period then divided by the number of lactating animals in the herd. The herd incidence was divided by 2 creating a weekly herd incidence. Four compost bedded pack and 3 sand bedded freestall barns were included in this analysis.

^e Causative pathogens isolated from reported clinical mastitis cases from cows housed in 4 compost bedded pack and 3 sand bedded freestall barns.

^f One to two isolates were possible per sample, with \geq 3 isolates per sample categorized as contaminated.

^g Other Gram-negative species consisted of *Achromobacter xylosoxidans*, *Acinetobacter lwoffii*, *Brevundimonas* species, *Chryseobacterium indologenes*, *Citrobacter koseri*, *Enterobacter* species, *Pasturella* species, *Proteus mirabilis*, *Pseudomonas luteola*, *Rhizobium radiobacter*, *Salmonella* species, *Serratia marcescens*, *Sphingomonas paucimobilis*, and *Stenotrophomonas maltophilia*.

^h Other Gram-positive species consisted of *Arcanobacterium pyogenes*, *Bacillus circulans*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus pumilus*, *Kocuria rosea*, *Kocuria varians*, *Lactococcus lactis*, *Lactococcus garvieae*, *Microbacterium* species, and *Paenibacillus amylolyticus*.

ⁱ Mastitis severity was reported as 1=abnormal milk (flakes, clots, or watery appearance) without swelling of the affected quarter, 2=normal or abnormal milk and swelling of the affected quarter, or 3=abnormal milk, swelling of the affected quarter, and systemic signs (fever, reduced rumen function, dehydration, weakness, depression, loss of appetite, or rapid pulse) (Hogan et al., 1989a; Bramley et al., 1996).

^j Bulk tank somatic cell count collected from cooperating farm milk cooperatives and marketers over the study period reported as \times 1000 cells/mL. Eight compost bedded pack barns and 7 sand bedded freestall barns were included in this analysis.

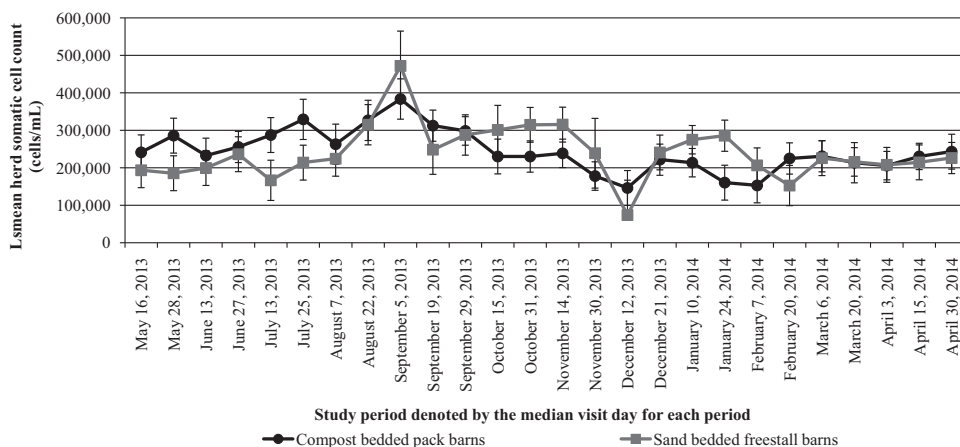


Fig. 2. LSMeans (\pm SE) Dairy Herd Information Association herd somatic cell count (cells/mL) for 7 compost bedded pack and 6 sand bedded freestall barns at each visit period (n=26) from May 2013 to May 2014 derived using the GLM procedure in SAS.¹ The difference between compost bedded pack and sand bedded freestall barns at each visit period was not significantly different (P=0.58). However, the variation between visit periods over the year was significant (P=0.04).

researchers reported mean high SCC cows constituted $41.1 \pm 3.9\%$ of all US dairy herds (USDA, 2007). The percentages in the current study are much lower than the NAHMS study. This may indicate

that animals had above average udder health in the current study, which may be partially attributed to the inclusion criteria. Like the current study, Lobeck et al. (2011) showed no difference in HSP

among CBP, cross-ventilated, or naturally ventilated SFB (33.4, 26.8, and 26.8%, respectively; $P \geq 0.05$). The lack of HSP difference between well-managed CBP and SFB are encouraging for producers considering CBP. The similarity indicates that CBP and SFB provide an environment for cattle that equally affects subclinical mastitis when good management is observed. Limiting the study to herds with DHI SCC < 300,000 for the year before enrollment does introduce a bias toward well-managed herds into the current study. Compost bedded pack barns and SFB that do not follow best management practices may not experience the same results as those discussed above.

6.2. Bulk tank somatic cell count

In the current study, no effect of barn type, ambient maximum THI period, and hygiene score or their interactions occurred for BTSCC ($P \geq 0.05$). Mean BTSCC remained below 300,000 cells/mL for both barn types ($229,582 \pm 18,478$ and $205,131 \pm 19,581$ cells/mL for CBP and SFB, respectively; $P=0.38$; Table 3). No differences were observed between barn types over time ($P=0.63$). Herd SCC was a monthly snapshot of herd performance, whereas BTSCC was a constant measure in all herds recorded with every milk load pick-up. Bulk tank SCC may be a more accurate representation of what occurred in each barn type on a herd level.

Similar results were observed when all herds on DHI were compared (Fig. 3). Producers using a mixture of CBP and freestall barns had the lowest BTSCC ($227,695 \pm 22,706$ cells/mL), followed by mixed ($258,252 \pm 24,526$ cells/mL), CBP ($259,193 \pm 14,160$ cells/mL) freestall barns ($259,478 \pm 8,857$ cells/mL), and tie-stall barns ($260,411 \pm 11,353$ cells/mL; $P \geq 0.05$). Bedded pack barns and pasture were different from the mixture of CBP and freestall barns ($303,612 \pm 34,685$, $316,896 \pm 17,342$, and $227,695 \pm 22,706$ cells/mL, respectively; $P < 0.05$). In Kentucky, many producers use CBP as special needs housing for lame cows, or cows with difficulty lying in stalls. This practice may improve the increase lying time and limiting lying in alleyways, resulting in decreased BTSCC for all herds using this practice in Kentucky.

In a national study, freestall, tiestall, loose housing, and pasture based systems were used on 52.9, 26.9, 13.9, and 6.3% of all operations, respectively ($n=1013$ dairies in 21 states). Housing was related to BTSCC ($P=0.01$). In all housing systems, most herds had BTSCC between 200,000 to 400,000 cells/mL, with a greater percentage of pasture-based herds having BTSCC over 400,000 cells/mL (32.3% pasture, 12.3% freestall, 24.6% loose housing, and

19.3% tiestalls; USDA, 2007). Sand, mattress, and newspaper bedding decreased BTSCC ($P=0.02$, 0.006, and < 0.001 , respectively). Like the current study, pasture based systems had a greater BTSCC than freestall, CBP, tiestall, CBP and freestall, and other mixed housing types ($P < 0.05$). Pasture based systems lying surfaces are more susceptible to changes in ambient weather conditions than housed herds. Lack of shelter from the elements and unmanaged lying surfaces may be the cause of the greater BTSCC in these herds.

7. Clinical mastitis

7.1. Clinical mastitis

Clinical mastitis incidence was measured by producer reported clinical mastitis incidence (RCMI). The LSMeans (\pm SE) of RCMI were 1.2 ± 0.1 and $1.2 \pm 0.1\%$ per week for CBP and SFB, respectively ($P=0.90$; Table 3). Reported clinical mastitis incidence was not affected by THI period or hygiene scores ($P \geq 0.05$). Canadian researchers reported incidence rate of clinical mastitis over 3 barn types and 101 farms (Olde Riekerink et al., 2008). No differences were reported between tie-stalls, freestalls, or other housing (including straw yards and pasture-based herds) when all pathogens isolated from samples were considered ($P \geq 0.05$). The Canadian results, coupled with those from the current study, indicate that udder health can be maintained in CBP as well as it is maintained in SFB, the gold standard of dairy housing.

7.2. Causative pathogen

The distribution of udder pathogen isolates (% of total isolates) were not different between CBP and SFB (Table 3; $P=0.15$). Plates that were identified as No Growth (no growth occurred in the media) constituted 19.2% and 23.9% in CBP and SFB, respectively. The highest percentages of pathogens isolated in CBP and SFB were *E. coli* (CBP: 29.0%, $n=62$ isolates; SFB: 21.6%, $n=19$ isolates) followed by environmental streptococci (CBP: 16.8%, $n=36$ isolates; SFB: 19.3%, $n=17$ isolates). Barberg et al., (2007a); Black et al., (2014) noted *Streptococcus* spp. made up a larger portion of the bedding bacterial population than coliform species 20.6–39.4% vs. 10.7–1.9% for environmental streptococci and coliforms). Hogan et al., (1989b) reported that inorganic bedding materials still supported high levels of streptococci growth ($> 6 \log_{10}$ cfu/g), similar to those reported in the current study.

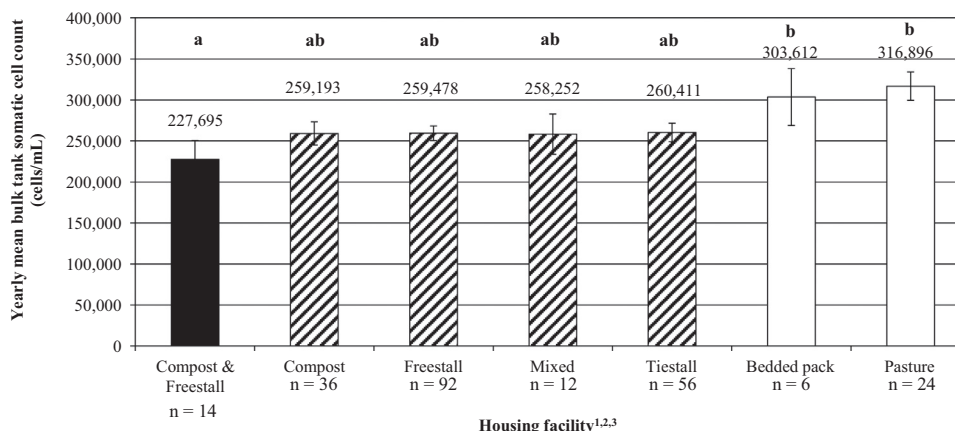


Fig. 3. Sampling locations for resting area surface temperature in sand bedded freestalls (a and b) and compost bedded pack barns (c).¹Freestall barns were bedded with limestone (1 farm), mattresses (16 farms), mattresses & waterbeds (2 farms), waterbeds (3 farms), sand (32 farms), wood sawdust (26 farms), wood shavings (6 farms), or undefined bedding (6 farms).²Mixed housing included: compost bedded pack & tiestall barn housing, pasture & freestall barn housing, pasture & bedded pack barn housing, pasture and compost bedded pack barn housing.³Tiestall barns were bedded with mattresses top dressed with sawdust (55 farms) or undefined bedding (1 farm).

7.3. *Staphylococcus* spp

constituted the second largest distinct group of causative pathogens in SFB (11.3%; $n=10$ isolates) and CBP (13.0%; $n=28$). *Staphylococcus aureus* comprised a 6.8% of isolates in SFB housed cows ($n=6$ isolates) compared to 5.1% of isolates in CBP housed cows ($n=11$ isolates). Coagulase negative staphylococci made up a larger percentage of isolates in CBP housed cows (7.9%; $n=17$ isolates) compared to SFB housed cows (4.5%; $n=4$ isolates). Hogan et al., (1989a) observed clinical mastitis in 9 low SCC Ohio herds housed in freestalls similar to the current study. Hogan et al., (1989a) reported the same hierarchy as CBP in the current study of causative pathogen starting with coliforms (29.7%), environmental streptococci (25.2%), CNS (5.4%), and *Staph. aureus* (1.7%). In a Canadian study, CNS was the third most often isolated pathogen in freestall barns (0.68%) following *S. aureus* and *Klebsiella* spp. (Olde Riekerink et al., 2008). The high percentage of CNS isolates reported in research and the current study indicated that CNS has become a pathogen of concern, in Kentucky and other areas in North America. Coagulase negative staphylococci comprise the natural skin flora of heifers and are opportunistic pathogens (White et al., 1989; Bramley et al., 1996). Increasing incidence of CNS may indicate that improved management of other causative pathogens is allowing opportunistic pathogens to cause more clinical mastitis cases.

7.4. *Klebsiella* spp

in the current study constituted a small percentage of causative pathogens in CBP housed cows (1.4%; $n=3$ isolates) and SFB housed cows (4.5%; $n=4$ isolates). The number of *Klebsiella* spp. isolates in the current study was similar between housing types. However, *Klebsiella* spp. as a percent of total isolates was greater in SFB housed cows (4.5 vs. 1.4%). Newman and Kowalski, (1973) suggested that green sawdust bedding increased *Klebsiella* species and mastitis incidence when compared to sand bedding. However, Verbist et al., (2011) reported that most *Klebsiella pneumoniae* was isolated from feces (125 isolates) and not from used sawdust bedding (20 isolates) or unused sawdust bedding (6 isolates) and concluded that *K. pneumoniae* could be prevalent in the environment without causing mastitis. Verbist et al., (2011) conclusion supports the observations found in the current study.

Other Gram-negative species constituted 13.5% ($n=29$ isolates) in CBP housed cows compared to 6.8% ($n=6$ isolates) in SFB housed cows. Other Gram-negative species isolated included: *Achromobacter xylosoxidans*, *Acinetobacter lwoffii*, *Brevundimonas* species, *Chryseobacterium indologenes*, *Citrobacter koseri*, *Enterobacter* species, *Pasturella* species, *Proteus mirabilis*, *Pseudomonas luteola*, *Rhizobium radiobacter*, *Salmonella* species, *Serratia marcescens*, *Sphingomonas paucimobilis*, and *Stenotrophomonas maltophilia*. Other Gram-positive species constituted 3.7% ($n=8$ isolates) in CBP housed cows compared to 9.1% ($n=8$ isolates) in SFB housed cows. Other Gram-positive species included *Arcanobacterium pyogenes*, *Bacillus circulans*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus pumilus*, *Kocuria rosea*, *Kocuria varians*, *Lactococcus lactis*, *Lactococcus garvieae*, *Microbacterium* species, and *Paenibacillus amylolyticus*.

7.5. Clinical mastitis infection severity

Mastitis infection severity was different between CBP and SFB (Table 3, $P<0.001$). Variance may have occurred between farms based on milking staffs' interpretation of the severity scale. Severity score of 1 (abnormal milk but no swelling) made up the highest percentage of scores for CBP (69.3% and 37.9% of scores for CBP and SFB, respectively). The severity score of 2 (abnormal milk

with swelling) made up the highest percentage of scores for SFB (28.3% and 41.4% of scores for CBP and SFB, respectively). The largest difference was the severity score of 3 (systemic signs). The most severe cases of mastitis were most often seen in SFB (20.7% of scores) compared to CBP (2.4%). In SFB, 50.0% ($n=9$ isolates) of the cases scored as 3 were caused by *E. coli*. Similarly, in CBP 66.7% ($n=4$ isolates) of the cases scored as 3 were caused by *E. coli*. Similar results were reported by Bradley and Green (2001) with 67.4% of mastitis cases recorded as severity 1, 26.4% as severity 2, and 6.2% as severity 3. Of those scored severity 3, *E. coli* was more likely to be the causative agent (16.0% of 81 *E. coli* cases scored 3) than all other mastitis causative agents (5.0% of 221 other mastitis cases scored 3). Coliforms caused acute or peracute mastitis with occasional subclinical infections. Typically, coliforms cause no extensive damage and the decrease in milk production may be less noticeable than other mastitis causing pathogens. In some instances, endotoxemia from coliform mastitis may cause death within a few days (Jain, 1979). These results emphasize the importance of managing environmental mastitis pathogens regardless of bedding type.

8. Conclusion

Well managed (BTSCC <300,000 cells/mL previous year) compost bedded pack and sand bedded freestall barns were not significantly different in hock health, locomotion score, and cow hygiene, regardless of ambient maximum THI period. Similarly, no significant differences were observed between housing types in high SCC prevalence, clinical mastitis incidence, herd SCC, and BTSCC. The BTSCC from herds across Kentucky returned lower counts for CBP, freestall barns, and tie-stall barns and mixtures of the housing systems than conventional bedded pack barns and cows housed solely on pasture. This study validates producers' observations of similar SCC and mastitis prevalence in CBP compared to SFB. However, the higher percentage of systemic mastitis in SFB and the lower initial construction investment cost may make CBP a more desirable housing option. The inclusion criteria limited the findings to well-managed herds, CBP and SFB herds that are not following best management practices may not experience the same results as those mentioned above.

Conflict

We wish to confirm that there are no known conflicts of interest associated with this publication and there has been no significant financial support for this work that could have influenced its outcome.

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Acknowledgements

The authors would like to thank the cooperating Kentucky farmers who made this study possible. We would also like to thank Jessica Lowe, Mickayla Myers, Jamie Leistner, Grace Nation, and Summer Miller for all of their help in the lab and on farm visits. We would like to thank Amanda Stone, Barbara Wadsworth, Bettie Kawonga, Derek Nolan, Karmella Dolecheck, Katie Holzhausen, Lauren Mayo, Maegan Weatherly, Mathew Borchers, Nicky Tsai, and Stefani Garbacik for all of their help with editing. We also wish to thank the cooperating county agents and the Kentucky Dairy Development Council for their assistance in gaining farmer

cooperation and their support of this project. Finally, we would like to thank the Kentucky Agricultural Development Fund, Southern Sustainable Agriculture Research & Education, the United States Department of Agriculture Natural Resources Conservation Service, and the United States Department of Agriculture for funding that supported this research effort.

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