J. KOSAE Vol. 23, No. E 1 (2007) pp. 1~9
Journal of Korean Society for Atmospheric Environment

Levels of Bioaerosols in Cattle Sheds and Nearby Farmers' Houses in Korea

Jung-Hwan Kang and Wan-Kuen Jo*
Department of Environmental Engineering, Kyungpook National University, Daegu, Republic of Korea
(Received 8 December 2006, accepted 12 February 2007)

Abstract

In Korea, there is only a limited amount of information currently available on the levels of airborne bacteria and fungi of cattle sheds, although certain portions of people are potentially exposed to these bioaerosols in cattle sheds. Accordingly, the current study measured them inside cattle sheds, inside and outside farmers' houses near the sheds, and/or inside residential houses far away from the sheds during winter, 2004 and summer, 2005. The airborne bacteria and fungi were detected in most samples in the cattle farmers' houses as well as in the cattle sheds. *Aspergillus*, *Cladosporium*, and *Penicillium*, which have been associated with adverse health effects, were three most prevalent fungal genera, and they took most of the total fungi (more than 69%). The microbial concentrations measured inside the cattle sheds were comparable to those in other reports. Nevertheless, the present arithmetic and geometric mean (GM) microbial concentrations exceeded the Korean guideline for total airborne bacteria at medical facilities (800 CFU m^{-3}), the current GM residential indoor concentrations at houses, and the residential indoor levels reported in other countries. The present findings suggest the need for a strategy to reduce Korean cattle farmers' exposure to these microorganisms. In contrast to the microbes, it is suggested that the cattle shed is not an important microenvironment for PM_{10} exposure. Two characteristics examined in this study (seasonal variation and summer survey period, i.e., temperature and humidity) were all important for the cattle farmers' occupational exposure to airborne microbes. The lack of constancy between highest and lowest concentrations of bioaerosols over the survey period further suggests the necessity of performing a long-term survey to better examine farmer exposure levels and their variability.

Key words : Total bacteria, Total fungi, Fungal genera, Occupational exposure, Season

1. INTRODUCTION

Although there is a benefit in that microorganisms are employed to control air pollutants through biofiltration technique (Arpacioglu *et al.*, 2002), there has been growing concern in recent decades about occupational exposure as well as environmental exposure to microbial aerosols because of their ubiquitous presence in nature and because of the related adverse health effects. In particular, cattle farming has been reported to be an occupation associated with potential exposure to bioaerosols (Adhikari *et al.*, 2004; Seedorf *et al.*, 1998). The bioaerosol lev-

* Corresponding author.
Tel : +82-53-950-6584, E-mail : wkjo@knu.ac.kr

els in cattle buildings were substantially higher in cattle sheds as compared to typical residential levels (Seedorf *et al.*, 1998; Dutkiewicz *et al.*, 1994; Larsson *et al.*, 1988), which could be due to various microbial growth substrates such as moldy livestock feeding materials, moldy hay, bedding for animals, and feces in the cattle sheds. Occupational exposure to the elevated bioaerosol levels may cause adverse health effects for cattle farmers. Several previous investigations have reported that exposure to large concentrations of airborne microbes is often associated with asthma and rhinitis (Beaumont, 1988), hypersensitivity pneumonitis (Siersted and Gravesen, 1993), and a number of other health effects, including infections (Ren *et al.*, 1999). In fact, certain studies (Westeel *et al.*, 2000; Dalphin *et al.*, 1998) reported consistently more respiratory symptoms and impaired levels of respiratory function among the dairy farmers compared to the control subjects. As such, the last decade has been characterized by a significant increase in the scientific database on occupational exposure to bioaerosols in many countries for the purpose of evaluating the relationship between exposure and health effects. Information about the occupational exposure of stock farmers can contribute to the decision for the need of any mitigation strategies in livestock sheds.

For Korea, there is only a limited amount of information currently available on the levels of bioaerosols in cattle sheds. Although the number of cattle in Korea has slightly decreased, a large number of people are still occupationally involved in several types of livestock farming. According to the Korean national statistical office, the number of stock farmers was over 198,919 in 2003. The number of cattle, which is a major livestock in Korea, was 1,998,936 in 2003, and it was 2,125,601 in 1990. The airborne particle measured in livestock sheds also contains non-biological particles (Duchaine *et al.*, 2000; Donham *et al.*, 1989), which along with microbial particles, can induce a decrease in pulmonary functions (Donham *et al.*, 1989). Consequently, the present study measured the levels of respirable particulate matter $\leq 10\,\mu m$ in aerodynamic diameter (PM_{10}) as well airborne bacteria and fungi in Korean cattle sheds. Microbial study focuses on viable bacteria and fungi, that exist in the airborne state as single cells or clumps (Pastuszka *et al.*, 2000). The characteristics associated with the bioaerosol measurements included seasonal variation and summer survey period (seasonal rain-front period [SRFP] or no rain-front period [NRFP]). It is assumed that the two characteristics reflect the effects of relative humidity or temperature, which are important parameters for microbial growth (Ren *et al.*, 2001), on environmental microorganism levels. In addition, the current study measured the bioaerosols and PM_{10} in the indoor and outdoor air of farmers' houses located near the cattle sheds and the bioaerosols only in the outdoor and indoor air of residential houses located far away from any livestock sheds.

2. MATERIALS AND METHODS

2.1 Description of cattle sheds

The cattle sheds surveyed in the current study were located in Kyungsan province in southern Korea. Eighteen cattle sheds were visited, and 10 cattle sheds where the farmers granted permission to measure the bioaerosol levels were selected (Table 1). The cattle sheds varied according to shed size and the number of cattle. The shed areas and the densities (No. of cattle/100 m^2) observed in the 8 unselected sheds were included within the range of those values observed in the selected 10 sheds. The visitor for this survey reported that based on his personal judgment, the sheds were similar for certain environments, e.g. the ventilation, sanitary system, and the surroundings, although their size and density of cattle inside sheds are different (Table 1). Livestock food storage sheds were close to the livestock sheds. The sheds consisted of roofs and pillars, without any side walls for any season. As such, regardless of season, ventilation was excellent, even without any electric fans. Straw was spread on the concrete floor. The fecal materials and urine of cattle were mostly present during visits. The time interval for changing the straw in the livestock sheds was not constant.

Table 1. Information on cattle sheds surveyed in the current study.

No.	Site	Number of cattle		Shed area (m^2)	Density (No. of cattle/100 m^2)	
		Winter	Summer		Winter	Summer
1	Wachon, Kyungsan	101	110	1,157	8.7	9.5
2	Wachon, Kyungsan	21	21	198	10.6	10.6
3	Hayang, Kyungsan	15	12	165	9.0	7.3
4	Hayang, Kyungsan	25	32	496	5.0	6.5
5	Hayang, Kyungsan	12	12	198	6.1	6.1
6	Wachon, Kyungsan	22	29	473	4.7	6.1
7	Wachon, Kyungsan	51	42	727	7.0	5.8
8	Wachon, Kyungsan	13	13	101	12.9	12.9
9	Wachon, Kyungsan	52	19	827	6.3	2.3
10	Hayang, Kyungsan	25	17	331	7.6	5.1

2.2 Microbial sample analysis

Airborne bioaerosols were collected using single-stage Anderson samplers with 400 0.25-mm holes, drawing air at a flow rate of 28.3 l min^{-1}. The samplers were calibrated prior to and following the collection of each sample with a flow calibrator (DCL-H, Bios, Butler, NJ). The average of these two rates was then used as the sample flow rate for all the volume calculations. No samples departed more than 10% from the initial flow rate during the study.

Bioaerosol sampling was conducted for 0.5 to 2 min, following the method of Nevalainen *et al.* (1992), on nutrient media (specific to either fungi or bacteria) in Petri-dishes located on the impactor. Dichloran glycerol 18 agar (DG-18) was applied for fungi, with chloramphenicol added to inhibit baterial growth. Trypticase soy agar (TSA) was used for bacteria, with cycloheximide added to inhibit fungal growth. The DG-18 and TSA plates were incubated at room temperature for 3 to 5 days and 2 to 3 days, respectively, for proper growth of microbial colonies. The counts for the air sample plates were corrected for multiple impactions using the positive hole conversion method, and reported as colony forming units per cubic meter of air (CFU m^{-3}). The genera of certain cultures of fungi were identified based on their micro- and macromorphological characteristics, using standard taxonomic keys.

2.3 Study strategy

The current study measured the airborne bacterial and fungal concentrations inside 10 cattle sheds 30 times (three visits per shed) during winter, 2004 and 40 times (four visits per shed) during summer, 2005. The same cattle sheds were included in both the summer and winter studies. The summer period for the cattle shed surveys was subdivided into two periods (SRFP and NRFP). The majority of bioaerosol samples were taken from the middle of the facilities and houses at breathing height, predominantly between noon and 14:00 on weekdays (Monday thru Friday). The bioaerosol samples were collected without controlling any indoor environmental conditions. However, five environmental conditions (PM_{10}, shed area, number of cattle, temperature, and relative humidity) were measured or recorded during, prior to, or right after the bioaerosol sampling. The PM_{10} concentrations were measured during the winter sampling period only, using a PM_{10} monitor (Model EPAM-5000, Environmental Devices Corporation, Plaistow, New Hampshire) previously calibrated by a low-volume air sampling system (MiniVOL portable sampler, Air Metrics, Springfield, Oregon). Right after the cattle-shed sampling, the bioaerosols and PM_{10} were also measured in the indoor and outdoor air of farmers' houses located within 50 m of the cattle sheds during both the winter and summer. Additionally, for summer only the bioaerosols were measured in the outdoor and indoor air of residential houses located at least 500 meters from any livestock sheds in order to examine the effects of proximity to livestock sheds on the bio-

aerosol levels in the houses.

2.4 Statistical analyses

Data were analyzed using the SAS program (Version 8) on a personal computer. The Shapiro-Wilk statistical test was employed to evaluate the normality of the data. The data were compared for seasonal variation and summer survey period, and proximity effects on residential levels, using a one-tailed paired t-test for normally-distributed data or a nonparametric test (Wilcoxon Rank-Sum Test) for non-normally-distributed data. The GM and geometric standard deviation (GSD) were used to characterize the log-normally distributed data, when this was indicated by the Shapiro-Wilk statistical test. The criterion for significance in the procedures was $p < 0.05$.

3. RESULTS

3.1 Occurrence levels of airborne microbes

Table 2 exhibits the occurrence levels of airborne microbes identified in cattle sheds and cattle farmers' houses. The occurrence levels included the total bacteria and total fungi counts, along with the levels of the four most prevalent fungal genera typically detected in many occupational as well as nonoccupational environments (Adhikari *et al.*, 2004; Hong *et al.*, 2003; Huang *et al.*, 2002; Ren *et al.*, 2001). The total bacteria and total fungi were detected for most samples, whereas the fungal genera were not. For most of the fungal genera, the occurrence levels were usually higher in the summer than in the winter. The occurrence levels for *Alternaria* were much lower when compared to those of the other three fungal genera. The occurrence levels for the other three fungal genera (*Aspergillus*, *Cladosporium*, and *Penicillium*) ranged from 60 to 100%. Since for *Alternaria*, no reliable information was expected due to their low prevalence, the current study focused on the three most prevalent fungal genera, along with the total bacteria and the total fungi.

Table 2. Occurrence (%) of airborne bacteria and fungi identified inside cattle sheds, and inside and outside farmer's house according to season.

Bioaerosol	Sample type	Cattle shed		Farmer's house	
		Winter	Summer	Winter	Summer
Total bacteria	Indoor	100	100	100	100
	Outdoor	–	–	100	100
Total fungi	Indoor	97	100	100	100
	Outdoor	–	–	100	100
Alternaria	Indoor	13	35	30	47
	Outdoor	–	–	50	69
Aspergillus	Indoor	67	100	93	93
	Outdoor	–	–	80	97
Cladosporium	Indoor	97	100	100	100
	Outdoor	–	–	100	100
Penicillium	Indoor	60	89	77	93
	Outdoor	–	–	67	97

Note. Number of samples: N=30 for cattle-winter-indoor, N=40 for cattle-summer-indoor, N=30 for farmer's house-winter-indoor, N=37 for farmer's house-summer-indoor, N=30 for farmer's house-winter-outdoor, N=37 for farmer's house-summer-outdoor; "–", not measured; The "occurrence level" was calculated by dividing the number of samples that the matched microorganisms were detected, by the number of total samples colleted during the sampling periods.

3.2 Bioaerosol and PM_{10} concentrations inside cattle sheds

The airborne microbial and PM_{10} concentrations inside the cattle sheds for two seasons (winter and summer) are summarized in Table 3. For the two seasons, the bacterial and fungal concentrations ranged from 71 to 3.1×10^4 CFU m^{-3} and from less than 1 to 1.3×10^4 CFU m^{-3}, respectively. Regardless of the season, the concentration order of individual fungal genera was *Cladosporium*, *Aspergillus*, and *Penicillium* in a descending order. According to their GM values, the three fungal genera (*Aspergillus*, *Cladosporium*, and *Penicillium*) consisted of 69 and 80% of the total fungi for winter and summer, respectively. All the microbial concentrations inside the cattle sheds were significantly higher in the summer than in the winter. The GM bacterial concentration was 5.3×10^3 CFU m^{-3} for the summer, whereas it was 3.9×10^3 CFU m^{-3} for the winter. For total fungi, the GM concentration was 3.1×10^3 CFU m^{-3} and 1.0×10^3 CFU m^{-3} for the summer and winter, respectively. Meanwhile, the wintertime PM_{10} concentration ranged from 9 to 98 μg m^{-3}. As expected, the ambient temperature and

Table 3. Summary of bioaerosol (CFU m^{-3}) and PM_{10} ($\mu g\ m^{-3}$) concentrations, temperature (Temp, °C), and relative humidity (RH, %) measured inside cattle sheds according to season.

Bioaerosol/ PM_{10}/ Temp/RH	Winter					Summer					Summer/ Winter[a]
	GM	GSD	Mean	Min	Max	GM	GSD	Mean	Min	Max	
Total viable bacteria	3946	2.7	5986	572	21194	5312	4.8	12224	71	30707	**1.3**
Total viable fungi	1029	2.6	1529	ND	4926	3093	2.4	4090	141	12508	**3.0**
Aspergillus	164	2.5	188	ND	1770	532	2.7	815	74	4032	**3.3**
Cladosporium	526	3.6	989	ND	2030	1260	3.3	2264	ND	9885	**2.4**
Penicillium	129	2.6	137	ND	892	332	2.1	389	77	1924	**2.6**
PM_{10}	35	21	35	9	98	NA	NA	NA	NA	NA	NA
Temp	NC	2.7	6.2	1.1	13.0	NC	3.7	30.7	23.3	39.3	**5.0**
RH	NC	10	24	8	59	NC	14	75	50	100	**3.1**

Note. Number of samples: N=30 for winter, N=40 for summer; For the temperature and RH, the arithmetic standard deviation is presented instead of the geometric standard deviation (GSD) value; min, minimum; max, maximum; NA, not available; ND, not detected (minimum detection limit, 1 CFU m^{-3}); NC, not calculated.

[a]GM concentration ratios for summer air to winter air; boldface indicates that data sets for two seasons were significantly different at $p<0.05$ or close to 0.05 (<0.07).

Table 4. GM bioaerosol concentration (CFU m^{-3}), temperature (Temp, °C), and relative humidity (RH, %) measured during seasonal rain-front period (SRFP) and No rain-front period (NRFP) for cattle shed samples.

Bioaerosol/ Temp/RH	SRFP	NRFP	SRFP/NRFP
Total bacteria	9754 (5.8)	5058 (2.9)	**1.93**
Total fungi	4104 (2.1)	2756 (2.1)	**1.49**
Aspergillus	537 (2.2)	626 (3.0)	0.86
Cladosporium	2294 (2.4)	752 (2.7)	**3.05**
Penicillium	419 (3.1)	343 (2.2)	1.22
Temp	28.6 (3.2)	32.6 (2.3)	0.88
RH	82 (12)	69 (11)	**1.19**

Note. Number of samples: N=20 for SRFP, N=20 for NRFP; Values in parentheses are GSD; For the temperature and RH, the arithmetic mean and standard deviation are presented instead of the GM and GSD values, respectively; boldface indicates that data sets between SRFP and NRFP were significantly different at $p<0.05$ or close to 0.05 (<0.07).

humidity were substantially higher in the summer than in the winter.

The summertime bioaerosol concentrations were significantly higher during SRFP than during NRFP (Table 4). The ratio of SRFP to NRFP was about 2 and 1.5 for the bacterial and total fungal concentrations, respectively; additionally, it ranged from about 1 to 3 for the fungal genera. The relative humidity was significantly higher for SRFP than for NRFP, while the temperature was similar.

3.3 Bioaerosol and PM_{10} concentrations inside and outside farmers' houses

Table 5 presents the bioaerosol and PM_{10} concentrations measured inside and outside the farmers' houses near the cattle sheds and residential houses far away from them for two seasons (winter and summer). Similar to the cattle sheds, the three fungal genera (*Aspergillus*, *Cladosporium*, and *Penicillium*) took most of the fungi (72 and 77% in the nearby farmers' houses for winter and summer, respectively, and 73% in the far-away houses). The airborne bacterial levels were lower inside the nearby houses (GM values of 2.6×10^3 and 1.8×10^3 CFU m^{-3} for winter and summer, respectively) than inside the cattle sheds (GM values of 3.9×10^3 and 5.3×10^3 CFU m^{-3} for winter and summer, respectively) (Table 3). However, for the fungal concentrations, the difference was not significant. The GM total fungal levels inside the nearby houses were 793 and 2.7×10^3 CFU m^{-3} for the winter and summer, respectively, whereas for the cattle sheds they were 1.0×10^3 and 3.1×10^3 CFU m^{-3} (Table 3) for the winter and summer. Like the bacterial concentrations, the PM_{10} concentrations were lower inside the nearby houses (GM value of 26 $\mu g\ m^{-3}$) than inside the cattle sheds (GM value of 35 $\mu g\ m^{-3}$). Meanwhile, the microbial concentrations were slightly or significantly higher in the nearby farm-

Table 5. GM bioaerosol (CFU m^{-3}) and PM_{10} ($\mu g\ m^{-3}$) concentrations, temperature (Temp, °C), and relative humidity (RH, %) measured inside and outside farmers' houses near cattle sheds and other far-away houses according to season.

Bioaerosol/ PM_{10}/ Temp/RH	Season	Farmers' house					Far-away house		
		In	Out	S/W[a] In	S/W[a] Out	In/Out[b]	In	Out	In/Out[b]
Total viable bacteria	Winter	2572	1161	**0.68**	0.90	**2.22**	NA	NA	NA
	Summer	1758	1043			**1.69**	1435	552	**2.60**
Total viable fungi	Winter	793	445	**3.40**	**3.58**	**1.78**	NA	NA	NA
	Summer	2695	1593			**1.69**	1606	1131	**1.42**
Aspergillus	Winter	195	51	**2.07**	**3.47**	**3.82**	NA	NA	NA
	Summer	403	177			**2.28**	184	115	**1.60**
Cladosporium	Winter	271	294	**5.08**	**3.62**	0.92	NA	NA	NA
	Summer	1376	1065			1.29	673	615	1.09
Penicillium	Winter	102	39	**2.92**	**4.79**	**2.62**	NA	NA	NA
	Summer	298	187			**1.59**	314	140	**2.24**
PM_{10}	Winter	26	25	NA	NA	1.04	NA	NA	NA
	Summer	NA	NA			NA	NA	NA	NA
Temp	Winter	14.0	8.2	**2.07**	**3.78**	**1.71**	NA	NA	NA
	Summer	29.0	31.3			0.94	30.1	32.2	0.93
RH	Winter	39	23	**1.95**	**3.26**	**1.70**	NA	NA	NA
	Summer	76	75			1.01	71	69	1.03

Note. Number of samples: N=30 for farmer-in-winter, N=37 for farmer-in-summer, N=30 for farmer-out-winter, N=37 for farmer-out-summer, N=36 for far-away-in-summer, N=36 for far-away-out-summer; For the temperature and RH, the arithmetic mean and standard deviation are presented instead of the geometric mean (GM) and geometric standard deviation (GSD) values, respectively; min, minimum; max, maximum; NA, not available; ND, not detected (minimum detection limit, 1 CFU m^{-3}).

[a]GM concentration ratios for summer air to winter air; boldface indicates that data sets for two seasons were significantly different at $p<0.05$ or close to 0.05 (<0.07).

[b]GM concentration ratios for inside air to outside air; boldface indicates that data sets for inside air and outside air were significantly different at $p<0.05$.

ers' houses than in the far-away houses.

The bacterial concentrations inside the nearby farmers' houses were significantly lower for the summer than for the winter, whereas the reverse was true for the fungal concentrations. In addition, regardless of the proximity to the cattle sheds, most residential indoor microbial concentrations were significantly higher than the outdoor microbial concentrations, suggesting that there was an indoor source (s) for the microbes. The indoor temperature at the nearby farmers' houses was significantly higher than the outdoor temperature during the winter, whereas the difference was similar during the summer.

4. DISCUSSION

4.1 Cattle farmers' exposure level to bioaerosol and PM_{10}

The current study evaluated the levels of airborne bacteria and fungi in cattle sheds, along with PM_{10}. The airborne bacteria and fungi were detected in most samples in cattle farmers' houses as well as in the cattle sheds. *Aspergillus*, *Cladosporium*, and *Penicillium* were three most prevalent fungal genera, which were consistent with previous studies conducted in other environments (Adhikari *et al.*, 2004; Hong *et al.*, 2003; Ren *et al.*, 2001). The three fungal genera took most of the fungi. The prevalent

bacterial (arithmetic [AM] mean values of 6.0×10^3 and 1.2×10^4 CFU m^{-3} for winter and summer, respectively) and fungal (AM values of 1.5×10^3 and 4.1×10^3 CFU m^{-3} for winter and summer, respectively) concentrations measured inside cattle sheds are comparable to those in other reports, such as an AM bacterial value of 2.0×10^4 CFU m^{-3} in Northern European cattle sheds (Seedorf *et al.*, 1998), bacterial concentrations ranging from 165 to 2.2×10^3 CFU m^{-3} in Indian cattle sheds (Adhikari *et al.*, 2004), and an AM fungal concentration of 6.3×10^3 CFU m^{-3} in Northern European cattle sheds (Seedorf *et al.*, 1998). However, the cattle-shed levels reported in the current study are lower than other livestock shed levels reported in Northern Europe. It was reported that in Northern Europe the AM bacterial values inside poultry and swine buildings were 2.69×10^6 and 1.3×10^5 CFU m^{-3}, respectively, and the AM fungal aerosol concentrations 5.0×10^3 and 1.0×10^4 CFU m^{-3} (Seedorf *et al.*, 1998). Nevertheless, the present AM and GM bacterial concentrations exceeded the Korean guidelines for total airborne bacteria (800 CFU m^{-3}), the current GM residential indoor concentrations at houses located far away from any livestock sheds, and the residential indoor levels reported in other countries (Pastuszka *et al.*, 2000; Li and Hsu, 1997; DeKoster and Thorne, 1995). Several previous studies (Pastuszka *et al.*, 2000; Li and Hsu, 1997; DeKoster and Thorne, 1995) reported that most residential indoor bioaerosol concentrations were less than 10^3 CFU m^{-3}. Meanwhile, the present indoor microbial levels at farmers' houses still exceeded the present far-away residential indoor concentrations and the Korean guidelines, although they were similar to or lower than the indoor levels for the cattle sheds. Exposure to these microbes including the current three most prevalent fungal genera (*Aspergillus*, *Cladosporium*, and *Penicillium*) has been strongly associated with allergic respiratory diseases, such as asthma (Ostro *et al.*, 2001; Ross *et al.*, 2000; Halonen *et al.*, 1997). Consequently, the present findings suggest the need for a reducing strategy for cattle farmers' exposure to the microorganisms. Similar to the airborne microbial concentrations, the PM_{10} concentrations inside the cattle sheds were higher than those inside the nearby houses. However, the GM PM_{10} concentration inside the cattle sheds was substantially lower than the Korean annual standard of 70 μg m^{-3} and the American annual standard of 50 μg m^{-3} for PM_{10}. Accordingly, it is concluded that contrary to the airborne microbes, the cattle shed is not an important microenvironment for PM_{10} exposure.

4.2 Bioaerosol levels according to season and summer survey period

The summertime microbial concentrations measured inside cattle sheds were significantly higher than the wintertime values. The number of cattle would not be an important parameter for the seasonal concentration difference, since the total number of cattle inside 10 sheds was similar between the two seasons (337 and 307 for the winter and summer, respectively) (Table 1). Similarly, the ventilation rate would not influence the seasonal difference, since as described in the earlier section the cattle sheds were kept a maximum ventilation rate even during winter. Rather, air temperature and humidity would result in the seasonal concentration difference, since the higher environmental temperature and relative humidity measured during the summer favor microbial growth (Ren *et al.*, 2001). Meanwhile, the higher bioaerosol concentration during SRFP as compared with NRFP would mainly be due to high humidity, since the relative humidity was significantly higher for SRFP than for NRFP, but the temperature was similar.

However, the seasonal concentration difference is not consistent with that of swine buildings studied in Quebec, Canada (Duchaine *et al.*, 2000). Similar to Korea, Quebec has a wide range of ambient temperatures between winter and summer. In contrast to the Korean cattle sheds, the swine sheds were kept at a minimal ventilation rate during winter and at their maximum during summer. As such, the low winter ventilations could increase the airborne bacterial concentrations inside the swine sheds, thereby possibly exceeding the negative winter temperature effects on the bacterial growth.

Similarly, the fungal concentrations inside the

houses near the cattle sheds were significantly higher in summer than in winter. Conversely, the bacterial concentrations inside the nearby farmers' houses were higher in the winter than in the summer, although the outdoor concentrations were similar. The farmers' houses were kept at a minimal ventilation rate during cold winter and at their maximum during hot summer, whereas the cattle sheds were kept at a maximum ventilation rate even during winter. Moreover, as compared to the residential outdoor concentrations, the elevated residential indoor bacterial concentrations suggested that there was an indoor source for the microbes at the farmers' houses. Accordingly, it is assumed that at the farmers' houses, for the winter the positive effect of low ventilation on indoor bacterial levels would exceed the negative effect of low temperature on the bacterial growth. Meanwhile, the high geometric standard deviations (>2.0) and wide range of bacterial and fungal concentrations inside the cattle sheds suggest that there was a substantial temporal variation in the bioaerosol levels during the survey periods. Furthermore, this substantial variation suggests the necessity of performing a longitudinal survey to better examine farmer exposure levels and their variability.

ACKNOWLEDGEMENTS

The current study could not have been accomplished without the dedicated support of the farmers of 10 cattle sheds, who granted permission to measure the bioaerosol levels in their cattle sheds. The authors wish to thank two graduate students (J.Y. Lee and S.H. Shin) from the Department of Environmental Engineering, Kyungpook National University (KNU), for their sample preparation and/or collecting. This work was supported by a Grant from KNU.

REFERENCES

Adhikari, A., M.M. Sen, S. Gupta-Bhattacharya, and S. Chanda (2004) Volumetric assessment of airborne fungi in two sections of a rural indoor dairy cattle shed. Environ. International 29, 1071-1078.

Arpacioglu, B.C., J.C. Kim, and E.R. Allen (2002) Control of odor emissions using biofiltration: a case study of dimethyl disulfide. J. KOSAE 18, 153-163.

Beaumont, F. (1988) Clinical manifestations of pulmonary Aspergillus infections. Mycoses 31, 15-20.

Dalphin, J.C., A. Dubiez, E. Monnet, D. Gora, V. Westeel, D. Pernet, J.C. Polio, R. Gibey, J.J. Laplante, and A. Depierre (1998) Prevalence of asthma and respiratory symptoms in dairy farmers in the French province of the Doubs. Am. J. Respir. Crit. Care Med. 158, 1493-1498.

DeKoster, J.A. and P.S. Thorne (1995) Bioaerosol concentrations in noncompliant, complaint and intervention homes in the Midwest. Am. Ind. Hyg. Assoc. J. 56, 576-580.

Donham, K., P. Haglind, R. Peterson, R. Rylander, and L. Belin (1989) Environmental and health studies of farm workers in Swedish swine confinement buildings. Br. J. Ind. Med. 46, 31-37.

Duchaine, C., Y. Grimard, and Y. Cormier (2000) Influence of Building Maintenance, environmental factors, and seasons on airborne contaminants of swine confinement buildings. Am. Ind. Hyg. Assoc. J. 61, 56-63.

Dutkiewicz, J., Z.J.H. Pomorski, J. Sitkowska, E. Krysinska-Traczyk, C. Skorska, Z. Prazmo, G. Cholewa, and H. Wojtowicz (1994) Airborne microorganisms and endotoxin in animal houses. Grana. 33, 85-90.

Halonen, M., D.A. Stern, A.L. Wright, L.M. Taussig, and F.D. Martinez (1997) Alternaria as a major allergen for asthma in children raised in a desert environment. Am. J. Respir. Crit. Care Med. 155, 1356-1361.

Hong, J.B., Y.H. Chung, and Y.H. Chang (2003) Distribution of hospital airborne microorganisms in Seoul, Korea. Kor. J. Environ. Heal. 29, 1-7.

Huang, C.Y., C.C. Lee, F.C. Li, Y.P. Ma, and H.J.J. Su (2002) The seasonal distribution of bioaerosols in municipal landfill sites: a 3-yr study. Atmos. Environ. 36, 4385-4395.

Larsson, K., P. Malmberg, A. Eklund, L. Belin, and E. Blaschke (1988) Expsoure to microorganisms, airway inflammatory changes and immune reactions in asymptomatic dairy farmers. Int. Arch.

Allergy Appl. Immun. 87, 127-133.

Li, S.H. and L.Y. Hsu (1997) Airborne fungus allergen in association with residential characteristics in atopic and control children in a subtropical region. Arch. Env. Health 52, 72-79.

Nevalainen, A., J. Pastuszka, F. Liebhaber, and K. Willeke (1992) Performance of bioaerosol samplers: collection characteristics and sampler design considerations. Atmos. Environ. 26A, 531-540.

Ostro, B., M. Lipsett, J. Mann, H. Braxton-Owens, and M. White (2001) Air pollution and exacerbation of asthma in African-American children in Los Angeles. Epidemiol. 12, 200-208.

Pastuszka, J.S., U. kyaw Tha Paw, D.O. Lis, A. Wlazło, and K. Ulfig (2000) Bacterial and fungal aerosol in indoor environment in Upper Silesia, Poland. Atmos. Environ. 34, 3833-3842.

Ren, P., T.M. Jankun, and B.P. Leaderer (1999) Comparisons of seasonal fungal prevalence in indoor and outdoor air and in house dusts of dwellings in one Northeast American county. J. Expos. Anal. Environ. Epidemiol. 9, 560-568.

Ren, P., T.M. Jankun, K. Belanger, M.B. Bracken, and B.P. Leaderer (2001) The relation between fungal propagules in indoor air and home characteristics. Allergy 56, 419-424.

Ross, M.A., L. Curtis, P.A. Scheff, D.O. Hryhorczuk, V. Ramakrishnan, R.A. Wadden, and V.W. Persky (2000) Association of asthma symptoms and severity with indoor bioaerosols. Allergy 55, 705-711.

Seedorf, J., J. Hartung, M. Schröder, K.H. Linkert, V.R. Phillips, M.R. Holden, R.W. Sneath, J.L. Short, R.P. White, S. Pedersen, H. Takai, J.O. Johnsen, J.H.M. Metz, P.W.G. Groot Koerkamp, G.H. Uenk, and C.M. Wathes (1998) Concentrations and emissions of airborne endotoxins and microorganisms in livestock buildings in Northern Europe. J. Agric. Engng. Res. 70, 97-109.

Siersted, H.C. and S. Gravesen (1993) Extrinsic allergic alveolitis after exposure to the yeast Ehodotorula rubra. Allergy 48, 298-299.

Westeel, V., S. Julien, C. De Champs, J.C. Polio, F. Mauny, R. Gibey, J.J. Laplante, J.M. Aiache, A. Depierre, and J.C. Dalphin (2000) Relationships of immunoglobulins E and G sensitization to respiratory function in dairy farmers. Eur. Respir. J. 16, 886-892.