AIR-BORNE MICROBE NUMBERS IN DIFFERENT HOUSING CONDITIONS OF REARING PIGS

Pavičić, Ž., Balenović, T., Popović, M., Valpotić, I., Biuk-Rudan, N., Valpotić, H. and Ekert Kabalin, A.

SUMMARY

The aim of this investigation was to determine the degree in which different housing systems and population size, with monitoring of primary microclimatic conditions, influence the number of airborne microorganisms in piglet nurseries. The investigation extended through three production cycles totaling 150 days in two different nurseries with full capacity of piglets per turn. Nursery A was 180 m^2 in size equipped with 16 pens with full floors and bedding area of 8 m^2 estimated for 20 piglets. Nursery B was 280 m^2 in size equipped with 60 one story cages with 3 m^2 of slated floors estimated for 10 piglets. Fifteen air samplings were performed in equal weekly intervals in every 45-day turn with the use of SAS 100^{TM} (PBI International, Italy) device and Testo and Dräger (Germany) device for the control of microclimatic conditions. Air was sampled onto growth medium for the isolation of mezophylic, hemolytic, coliform bacteria and fungi. The numbers of bacteria and fungi were determined in the laboratory with standard analytical methods. According to acquired results significantly higher microbe numbers were recorded in nursery A in relation to nursery B. However, total microbe numbers in both nurseries did not exceed 10^4 CFU/m^3 ensuring beneficial conditions to overall piglet health status. The use of bedding can cause an increase of airborne microbes in the nursery but by achieving optimal microclimatic conditions and acceptable number of animals per floor space it does not negatively affect production results and welfare of weaned piglets.

Key words: piglets, nursery**,** floor and cage housing system, airborne microbes

INTRODUCTION

Pig welfare in intensive production is significantly dependant on technological housing solutions, which along with animal numbers influence hygienic air quality. Therefore, beside control of primary microclimatic conditions (temperature, humidity, air flow speed and harmful gases) the investigation of total number and species of microbes in pig facilities is of utmost importance hence the air can serve as a reservoir of primary and potentially pathogenic microbes significant in the etiology of infectious and allergic diseases (Wathes, 1994). Many studies have been published recently regarding air hygiene in pig facilities with the use of current devices like SAS 100^{TM} (Pavičić et al., 2006). Nonetheless, maximum concentrations of microbe numbers allowed have not been standardized to this day, mostly because of different housing systems and population density (Baekbo, 1998; Pavičić et al., 2006). Therefore, every study from this field represents a reliable contribution for establishing reference values in individual technologic housing systems, most notably with current measuring methods and prescribed animal numbers per unit of housing space.

MATERIALS AND METHODS

The investigation was conducted through three production cycles totaling 150 days in two different nurseries with full piglet capacities per turn. Nursery A was 180 m^2 in size equipped with 16 pens with full floors and bedding area of 8 m^2 estimated for 20 piglets. Nursery B was 280 m^2 in size equipped with 60 one story cages with 3 m^2 of slated floors estimated for 10 piglets. Air exchange in both facilities was based on negative pressure ventilation. Fifteen air samplings were performed with SAS 100^{TM} (PBI International, Italy) device in each 45 day turn in identical weekly intervals. Samples were taken from 9 diametrically different locations in the level of animal biozone. Nutrient agar, blood agar and Sabourdaud maltose agar was used for the isolation of mezophylic, hemolytic and coliform bacteria, respectively. After the incubation period the colonies were counted with an electric counter and the number obtained was expressed in m^3 (CFU/m^3) of air. Isolated bacteria and fungi were identified by microscope and API tests (Bio Mérieux, France). Control of primary microclimatic conditions: temperature, relative humidity, airflow speed and ammonia concentration was performed after every air sampling with portable digital devices (Testo and Dräger, Germany). The acquired data was subjected to basic statistical analysis with Statistica 7.1 (StatSoft Inc., 2005) software, and eventual significant differences in average bacteria and fungi numbers between two nurseries were recorded. Microclimatic parameters were calculated as mean values.

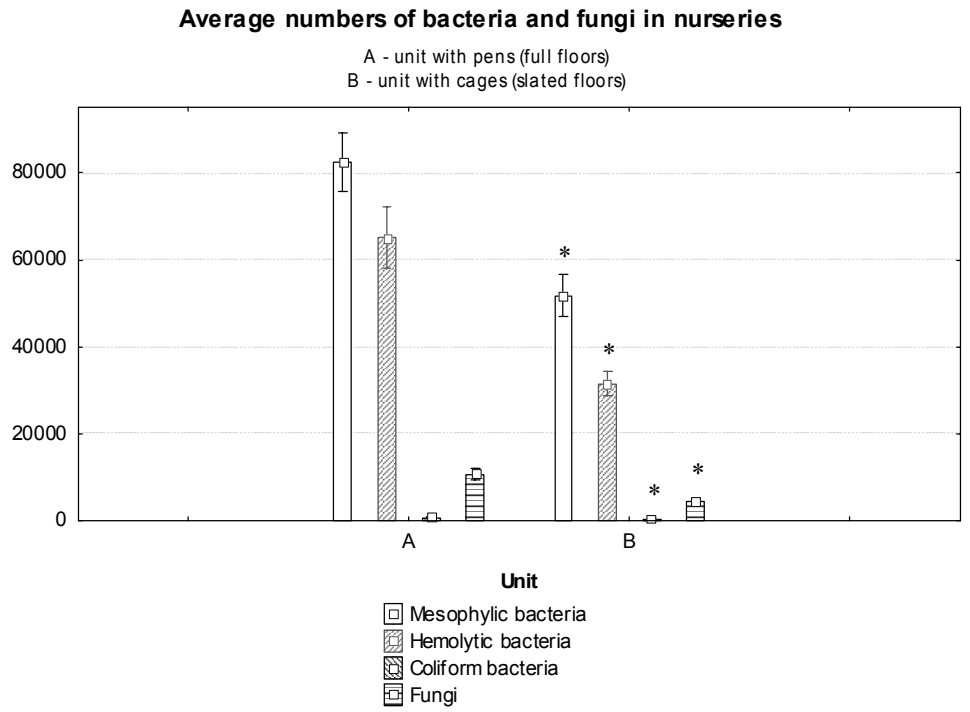
RESULTS

Average numbers of bacteria and fungi in two different nurseries during the entire trial period is presented in Table 1 and Graph 1.

Table 1. Average numbers of bacteria and fungi in nurseries during the trial

Microbes	Trial period					
	Nursery A			Nursery B		
	Mean	±	SD	Mean	±	SD
Mesophylic bacteria	82360,00	±	6742,315	51742,22*	±	4807,924
Hemolytic bacteria	65104,44	±	7050,595	31442,22*	±	2777,711
Coliform bacteria	746,00	±	134,171	422,22*	±	67,044
Fungi	10678,22	±	1336,499	4517,78*	±	630,760

* Statistically significant lover value (significance level p<0, 01) relative to value recorded in the other facility



Graph 1. Average numbers of bacteria and fungi in nurseries during the trial.

* Statistically significant lover value (significance level p<0, 01) relative to value recorded in the other facility

Average temperature in both facilities ranged from 25°C ± 1°C in the first 14 days to 21°C ± 1°C in the rest of the piglet production cycle. Average relative humidity in both facilities was within optimal values from 65–70%, airflow speed was 0,2 m/s, and ammonia concentration was 10 ppm.

DISCUSSION

Breeding of weaned piglets can be conducted the classic way on full floors with bedding or in cages, during which both housing types can have a different effect on hygienic air quality in the nursery. Well-known stable microorganisms such as gram-positive and negative bacteria along with environmental saprophytes like fungi define hygienic air quality (Kiekhaefer et al., 1995). Although overall numbers of mesophylic bacteria represent the basis of hygienic air quality, we selected a greater range of selective growth medium, as to acquire a more detailed insight into microbiologic air composition in both types of nurseries. According to the obtained results a significantly higher number of individual microbes are observed in nursery A in relation to nursery B. In so doing, the number of hemolytic bacteria during the production cycle varied

proportionally with the number of mesophylic bacteria, and the number of coliform bacteria was substantially lower than other microbes, which could be attributed to their weak survival capability in the air (Zucker and Müller, 2002). As potential endotoxin carriers, the gram negative bacteria represent a very important group of microbes that can negatively affect animal health so it is recommended that their number does not exceed 10^3 CFU/m^3 air (Clark et al., 1983), which is in agreement with our investigation. The greatest difference in results between the two facilities was in total number of fungi, which was 57, 70% higher in nursery A. The increase in fungi and other microbes in nursery A needs to be addressed through the use of bedding, which was identified as a cause in similar investigations in the fattening unit (Bækbo, 1998). However, total microbe numbers in both units did not exceed 10^4 CFU/m^3, which certainly represent optimal values in pig production (Donham, 1989). Having in mind other microclimatic parameters that were within reference values in both housing systems and the losses that were within acceptable 4% it can be concluded that the environment was beneficial to animal health (Fišer, 1970).

CONCLUSION

Total number of microbes in the nursery air is closely related to the housing system. The use of bedding in nurseries can be the cause of an increase in microbe numbers in relation to housing systems without bedding. However, this number does not have to exceed values that may influence an increase in piglet losses, considering that primary microclimatic parameters and floor space per piglet are within optimal limits**.**

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