Introduction
Bioscrubbers are used to reduce odour and noxious gas emissions from animal houses in poultry and pig production. However, the effect of bioscrubbers on emission of organic dust has not been well studied. The aim of this work was to study the influence of a bioscrubber in a duck fattening unit on emission of airborne dust, bacteria, endotoxins and moulds.

Material and Methods
- principle of the bioscrubber

The determined exhaust air washer was a combined bioscrubber and chemowasher. The system consisted of two treatment processes. The air moved to two filter banks. Those filter banks were made of cellulose-combs. Through the filter banks water flows constantly from top to bottom. The water ran into a water basin and was circulated (figure 1).

following parameters were investigated:
- inspirable dust (PGP dust-sampling system)
- endotoxins in the inspirable dust (LAL-Test, QCL-1000, Cambrex)
- concentration of airborne aerobic bacteria
  (impingement, AGI-30; Standard I agar)
- concentration of airborne gram-negative aerobic bacteria
  (impaction, Andersen-sampler; MacConcey 3 agar; Zucker et al., 2000)
- concentration of airborne moulds (Andersen-sampler, DG-18-agar; Schütze, 2001)
- concentration of endotoxins in the washing fluid (LAL-Test, QCL-1000, Cambrex)
- concentration of aerobe gram-negative bacteria in the washing fluid (MacConcey 3 agar)
- species of gram-negative bacteria in air and washing fluid (api 20 NE and api 20 E; bio Mérieux).

Results
- reduction effects

The bioscrubber reduced the concentration of airborne dust, the concentration of endotoxins and the amount of total aerobic bacteria significant (Wilcoxon-test; SPSS). In all cases (n=22) the emissions of dust, endotoxins and total aerobic bacteria were reduced. On average (median) the bioscrubber reduced the emission of dust by the factor 3.0 (min 1.0; max 33.5), the emission of endotoxins by the factor 12.5 (min 1.5; max 66.1) and the emission of total aerobic bacteria by the factor 6.1 (min 1.5; max 314.1).

There was no significant reduction of the emission of airborne gram-negative bacteria and airborne moulds by the washing process. The concentrations of airborne gram-negative aerobic bacteria were reduced in 14 of 22 cases and boosted in 7 cases. In one case the concentration didn’t change. The concentrations of airborne moulds were reduced 16 times and raised in 6 times. In maximum the emission of airborne gram-negative bacteria increased by the factor 14.8. For airborne mould a maximal boost of the emission by the factor 3.8 was detected.

- Composition of airborne gram-negative bacterial flora

The species composition of the airborne gram-negative bacterial flora was different between house exhaust and purified exhaust air. In the house exhaust air we found mainly Enterobacteriaceae (58,3%) in the purified exhaust air mainly Pseudomonadaceae (61,4%) (figure 2).
Discussion and Conclusion

Our results indicate that the bioscrubber investigated in this study, which is mainly used to reduce odour and noxious gas emissions, has also the potential to reduce the emission of dust, total bacteria and endotoxins from animal houses. Further our results indicate that the washing fluid of the bioscrubber, which was recirculated, represented a secondary source for bioaerosol emissions. Due to multiplying of different bacterial species (e.g. *Pseudomonas* spp.) in the washing fluid the composition of the bacterial flora in the purified exhaust air is different to the airborne bacteria flora in the duck house. Therefore techniques that are able to improve the hygienic quality of the washing fluid should be tested (e.g. UV-radiation, ozonation).

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References


Schütze, U. (2001), Sammlung und Differenzierung von luftgetragenen Schimmelpilzen in Tierställen, Dissertat, FU-Berlin

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- Gram-negative bacterial flora in the washing fluid

In the washing fluid always high concentration of gram-negative bacteria were detected. *Pseudomonadaceae* were with 55% the predominating bacteria in the washing fluid, followed by *Vibrionaceae* (13%) and *Enterobacteriaceae* (11%) (Figure 3).

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