


FAECAL SHEDDING OF ARCOBACTER SPECIES IN BELGIAN PIGS

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Summary: The prevalence of Arcobacter was determined in porcine faecal samples collected at slaughterhouse and two unrelated finishing barns (A and B) using the previously developed Arcobacter isolation procedure. In 43.9% of the slaughterhouse samples tested (n=82) arcobacters were detected, and identified as A. butzleri and A. cryaerophilus. Two pigs shedded both species simultaneously. On farm A (n=98), arcobacters were isolated from 16.3% of the samples and identified as A. cryaerophilus and A. skirrowii. In samples (n=118) collected at farm B, arcobacters were detected in 45.1% of the samples. A. butzleri was the most frequently occurring species. Co-infections were found in 11 animals. Arcobacters were detected in clinically healthy pigs at contamination levels up to 10^3 cfu/g faeces.

Keywords: Porcine faeces, Arcobacter prevalence, Slaughterhouse, Farm level, Belgium.

Introduction: The genus Arcobacter includes bacteria formerly known as aerotolerant campylobacters. They are Gram-negative non-spore-forming rods with a single polar flagellum and differ from the closely related campylobacters in their ability to grow aerobically from 15 up to 42 °C. Within the genus Arcobacter, four species are presently recognized: Arcobacter nitrofigilis, a nitrogen-fixing plant associated species (McClung et al., 1983) and the animal and human related species Arcobacter butzleri, Arcobacter cryaerophilus and Arcobacter skirrowii. Arcobacters are frequently present on foods of animal origin, including pork (Collins et al., 1996). Contamination probably occurs by faecal contamination during slaughter. Foods of animal origin are considered as a main source of Arcobacter infection in humans and therefore, arcobacters are established as an emerging foodborne pathogen (Wesley, 1996). In pigs, arcobacters are associated with reproductive problems and are found in stomachs of pigs with gastric ulcers. Moreover, arcobacters can be isolated from faeces of clinically healthy animals. The aim of the present study was to determine the prevalence and contamination level of Arcobacter in Belgian pigs at slaughter age and during raising.
Materials and Methods: Porcine faecal samples were rectally collected at the slaughterhouse (n=78) and at two unrelated finishing farms (n1=98; n2=118). On farm B, samples were also collected from available water sources (n=7) and from the sole on the farmers boots (n=1). One g faeces per sample was transferred into a stomacher bag. Next, nine ml Arcobacter Selective Isolation Broth supplemented with 50 ml/l lysed defibrinated horse blood was added (Van Driessche et al., 2003). The mixtures were homogenized with a stomacher blender and 100 ml of each homogenate was brought onto Arcobacter Selective Isolation Agar (ASIA) plates by the spiral plating method (Van Driessche et al., 2003). The remaining homogenates were incubated for 48 h at 28°C. Following incubation, 50 ml of the enrichment was streaked onto ASIA plates. Plates were incubated for 24 to 72 h at 28°C and checked every 24 h for bacterial growth. All colonies were counted, picked and subcultured onto blood agar plates. Bacterial growth was harvested and identified at species level by a multiplex-PCR assay (Houf et al, 2000).

Results: From the 82 slaughterhouse samples, A. butzleri was isolated from 29 and A. cryaerophilus from seven samples after enrichment. Twenty-three of the 35 pigs were also positive by direct isolation, 18 of which with A. butzleri and three with A. cryaerophilus. Two pigs had a co-infection with both species. From the collected samples at farm A, six of the 98 had a bacterial load of more than 10² arcobacters/g faeces. Arcobacters were isolated from five animals by the enrichment procedure. A. cryaerophilus was isolated from 14 pigs. Two animals shedded A. cryaerophilus and A. skirrowii simultaneously. From the samples (n=118) collected at farm B, arcobacters were isolated from 20 pigs at levels of 10² to 10³ cfu/g faeces. Additionally, 29 animals tested positive after enrichment. A. butzleri was isolated from 32 pigs, A. cryaerophilus from 2 animals and A. skirrowii was found in 4 animals. Furthermore, 11 pigs had a co-infection with more than one species. From the 7 water samples, arcobacters were isolated from five samples using enrichment. A. butzleri was found in two samples, A. cryaerophilus in one and A. butzleri and A. cryaerophilus were present simultaneously in two samples. From the sole on the farmers boots, A. cryaerophilus was isolated by direct isolation and A. butzleri by enrichment.

Discussion: In the present study, the prevalence of Arcobacter in porcine faeces at slaughterhouse level was 43.9%. In a recent study, 10% of the examined faecal samples (n=250) of pigs in a Japanese abbaitoir were found positive for Arcobacter (Kabeya et al., 2003). In our study at farm level, prevalences of 16.3% and 45.1% were obtained. Hume et al. (2001) found on a farrow-to-finish swine facility in Texas 36.3% of sows examined (n=55) positive for the presence of Arcobacter. Difference in prevalence may be caused by the different isolation protocols used, the sampling method, the season, the regional influences, farm management, and animals’ age.

Conclusions: In the present study, arcobacters were detected in clinically healthy Belgian pigs at levels up to 10³ cfu/g faeces. Animals can excrete different Arcobacter species simultaneously.

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References


Introduction: Among domestic animals pigs are highly sensitive to mycobacterial infection. Tuberculous lesions in pigs involve mainly the head and/or the mesenteric lymph nodes (Thorel et al., 1997). Occurrence of tuberculous changes in the lymph nodes at abattoirs leads to confiscations of pork meat and organs or their assessment as conditionally comestible. The main agents causing infection in pigs are the group of mycobacteria referred to as Mycobacterium avium complex (MAC). Serotypes 4-6, 8-11 and 21 belonging to M. a. hominissuis are the most frequently isolated from pigs (Komijn et al., 1999). Epidemiological studies on mycobacterial lymphadenitis indicate that the environment may represent a possible source of infection (Gardner and Hird, 1989). The main environmental sources of mycobacteria comprise beddings, feed, water and peat. The aim of this study was to assess the impact of environmental mycobacteria in relation with finding of gross tuberculoid alterations on head and mesenteric lymph nodes.

Materials and Methods: A total of 2 411 samples from inner and outer stable environment (Table 1) were originated from 50 farms of 29 districts. Bedding materials constituted straw, hay, silage, sawdust and tree bark. Smears made from specimens were examined by direct microscopy according to Ziehl-Neelsen staining. All samples were decontaminated by 1N HCl and 2N NaOH. The resuspended samples were inoculated onto Herrold's, Stonebrink and Sula medium and incubated at 25°C and 37°C, respectively. Growth of mycobacteria was evaluated after one week of incubation and then each two weeks. Isolates of mycobacteria were identified by IS901 and IS1245 PCR, serotyping and biochemical tests.

Results: Results of microscopic and culture examination and identification of isolated mycobacteria from different environmental material is shown in Table 1.

Summary: The purpose of this study was to find source of mycobacterial infections in pig farms. A total of 2 411 environmental samples (bedding materials, water, biofilm from pipelines, peat, etc.) were examined by microscopy and culture. Isolates were identified by serotyping and PCR. Mycobacteria were isolated from 579 (24.0%) samples. 47.0% isolates were Mycobacterium avium subsp. hominissuis isolates (IS901-, IS1245+, serotypes 4, 6, 8, 9), 2.2% isolates were M. a. avium (IS901+, IS1245+, serotype 2) and 50.8% belong to atypical mycobacteria comprising of fifteen species. The frequent isolates were found in peat samples (213/65.1%) in which 81.2% isolates comprised M. a. hominissuis. High amount of mycobacteria were isolated from biofilm (36.4%) and water (29.6%). Alike peat, non-pathogenic species were predominant. The third sources of mycobacteria were bedding materials, mostly sawdust (43.6%). Presence of mycobacteria in the animals’ environment leads to economic losses due to meat condemnation in abattoirs.

Keyword: Mycobacterium avium complex, mycobacteriosis, peat, water, bedding