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Cryptosporidium and Giardia in Danish organic pig farms: seasonal and age-related variation in prevalence, infection intensity and species/genotypes

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Highlights

- High Cryptosporidium and Giardia prevalence in organic pigs throughout the year
- Piglets predominantly hosted C. suis, while older pigs mainly hosted C. scrofarum
• The intensity of infection was >6 x higher for *C. suis* compared to *C. scrofarum*
• *Crypto/Giardia* infected pigs excreted fewer oocysts compared to mono-infected pigs
• Public health risk of *Cryptosporidium/Giardia* in Danish organic pigs seems negligible

**Abstract**

Although pigs are commonly infected with *Cryptosporidium* spp. and *Giardia duodenalis*, including potentially zoonotic species or genotypes, little is known about age-related infection levels, seasonal differences and genetic variation in naturally infected pigs raised in organic management systems. Therefore, the current study was conducted to assess seasonal and age-related variations in prevalence and infection intensity of *Cryptosporidium* and *Giardia*, evaluate zoonotic potential and uncover correlations between species/genotypes, infection intensity and faecal consistency. Shedding of oocysts and cysts (oo-oysts) was monitored at quarterly intervals (September 2011 to June 2012) in piglets (n=152), starter pigs (n=234), fatteners (n=230) and sows (n=240) from three organic farms in Denmark. (Oo-oysts) were quantified by immunofluorescence microscopy; and 56/75 subsamples from *Cryptosporidium* infected pigs were successfully analysed by PCR amplification and partial sequencing of the small subunit (SSU) 18S rRNA and hsp70 genes, while 13/67 *Giardia* subsamples were successfully analysed by amplification and partial sequencing of the 18S rRNA and the gdh genes. Altogether, *Cryptosporidium* or *Giardia* infections were observed in 40.9% (350/856) and 14.0% (120/856) of the pigs, respectively, including 8.2% (70/856) infected with both parasites. Prevalence, intensity of infections and presence of *Cryptosporidium* species varied significantly between age-groups; 53.3% piglets, 72.2% starter pigs, 40.4% fatteners and 2.9% sows were infected with *Cryptosporidium*, whereas 2.0% piglets, 27.4% starter pigs, 17.8% fatteners and 5.0% sows were infected with *Giardia*. The overall prevalence was stable throughout the year, except for dual-infections that were more prevalent in September and
December (p<0.05). The infection intensity was age-related for both parasites, and dual-infected pigs tended to excrete lower levels of oocysts compared to pigs harbouring only *Cryptosporidium*. Likewise, pigs infected with *C. scrofarum* excreted fewer oocysts (mean CPG: 54,848±194,508 CI: 9085–118,781) compared to pigs infected with *C. suis* (mean OPG: 351,035±351,035 CI: 67,953–634,117). No correlation between faecal consistency and (oo-)cyst excretion levels was observed.

Of the successfully genotyped isolates, 38/56 (67.9%) were *C. scrofarum* and 18/56 (32.1%) were *C. suis*, while the livestock specific *G. duodenalis* Assemblage E was detected in 11/13 (84.6%) isolates and the potentially zoonotic Assemblage A was identified in 2/13 (15.4%) isolates. Piglets exclusively hosted *C. suis*, with one exception, while starter pigs and fatteners predominantly hosted *C. scrofarum*. As organic pigs are partly reared outdoors, environmental contamination with *Cryptosporidium* and *Giardia* is inevitable. Nevertheless, the present data indicate that the potential public health risk associated with both of these parasites in Danish organic pig production seems to be negligible.

**Keywords:** *Cryptosporidium; Giardia duodenalis; organic pigs; prevalence; molecular typing.*
1. Introduction

Protozoan parasites belonging to the genera *Cryptosporidium* and *Giardia* are prevalent in a variety of animal species, including cattle, pigs and humans (Current and Garcia, 1991; Maddox-Hyttel et al., 2006). Both parasites can cause severe symptoms, primarily diarrhoea, e.g. in young calves and humans. In addition, giardiasis is known to induce chronic malnutrition and growth retardation with subsequent risk of impaired cognitive function in humans (Berkman et al., 2002). Moreover, post-giardiasis complications such as fatigue and abdominal symptoms years after infection have been observed (Morch et al., 2009, 2013; Naess et al., 2012). Natural porcine infections with either of the parasites are typically asymptomatic (Quilez et al., 1996; Maddox-Hyttel et al., 2006; Kváč et al., 2009a; Nemejc et al., 2013; Zhang et al., 2013), whilst watery diarrhoea, anorexia and increased mortality have been described in piglets experimentally infected with *C. parvum* (Tzipori et al., 1982; Enemark et al., 2003).

Both parasites can be transmitted directly through contact with infected individuals or indirectly by consumption of faeces contaminated food or water (Meinhardt et al., 1996; Fayer, 2004).Livestock, in particular cattle, has been implicated as a major source of surface water contamination with *Cryptosporidium* and *Giardia* (oo-)cysts (Bodley-Tickell et al., 2002; Thurston-Enriquez et al., 2005). Moreover, *Cryptosporidium* contamination of water sources through surface run-off from faeces deposited on agricultural land has repeatedly been documented (Tate et al., 2000; Davies et al., 2004; Thurston-Enriquez et al., 2005). In addition, Petersen et al. (2012) demonstrated that *C. parvum* oocysts present in pig slurry applied to soil can leach and potentially contaminate groundwater. Cryptosporidiosis and giardiasis are widespread and debilitating diseases in calves, and cattle often host the zoonotic *C. parvum* and to a lesser degree also *G. duodenalis* Assemblage A. Thus, cattle have frequently been the
subject of Cryptosporidium and Giardia surveys (Appelbee et al., 2003; Maddox-Hytte et al., 2006; Silverlås et al., 2013). The opposite applies for pigs, where cryptosporidiosis and giardiasis generally have been disregarded. Additionally, pigs are mostly reported to host C. suis and C. scrofarum (Ryan et al., 2003; Langkjaer et al., 2007; Yin J.H. et al., 2013; Nemejc et al., 2013; Nguyen et al., 2013; Zhang et al., 2013), that are considered relatively host specific; and G. duodenalis Assemblage E (Langkjaer et al., 2007; Armson et al., 2009; Sprong et al., 2009), which is restricted to livestock. Recently, the awareness of porcine infections with these protozoan parasites has, nevertheless, increased worldwide. This has led to occasional observations of the zoonotic C. parvum and G. duodenalis Assemblage A in pigs (Xiao et al., 2006; Leoni et al., 2006; Langkjaer et al., 2007; Armson et al., 2009 Kváč et al., 2009b), as well as C. andersoni (Hsu et al., 2008), C. muris (Zintl et al., 2007), C. tyzzeri (Budu-Amoako et al., 2012), G. duodenalis Assemblage C, D, E and F (Langkjaer et al., 2007; Armson et al., 2009; Minetti et al., 2014), all of which have been documented sporadically in humans (Leoni et al., 2006; Sprong et al., 2009; Raskova et al., 2013). However, none of these studies provided a comprehensive description of seasonal and age-related differences in prevalence or genetic variation of Cryptosporidium and Giardia in outdoor reared pigs. Detailed knowledge of potential zoonotic transmission is furthermore hampered because only few studies in pigs have characterised specimens by sequence analysis of molecular markers (Spong et al., 2009).

As pigs have the capability to excrete extremely high numbers of oocysts and cysts per gram of faeces (OPG and CPG) (Fayer et al., 2006; Maddox-Hytte et al., 2006), fertilisation of agricultural land with slurry or faecal deposition directly on the ground from infected free-range pigs can eventually be a source of human waterborne cryptosporidiosis and giardiasis. Organic pigs, contrary to conventionally reared pigs, have access to outdoor areas throughout most of their lives. Therefore, this study was conducted to: 1) assess seasonal- and age-related
variations in prevalence and infection intensity of *Cryptosporidium* and *Giardia* in organic pig farms, 2) to evaluate the zoonotic potential of these infections through DNA sequence analyses, and 3) to uncover any correlation between species/genotypes hosted by the pigs, infection intensity and faecal consistency in the pigs.

2. Material and methods

2.1 Study farms

Three commercial Danish organic pig farms with laboratory confirmed *Cryptosporidium* and *Giardia* infections were selected for the study based on the owner’s willingness to participate. The farms were visited at quarterly intervals from September 2011 to June 2012. In all farms, piglets were born outdoor on farrowing pastures and weaned at seven to nine weeks of age. The farrowing pastures were subdivided into smaller paddocks, with one to five sows separated by a single electrical wire; in practice, allowing the piglets free access to the entire area. Post-weaning, the starter pigs were housed indoor in concrete pens with access to a partially roofed outdoor area. Moreover, all weaned pigs were provided with straw bedding up to 25 cm deep.

On farm 1, weaned pigs from several sows were randomly allocated into pens accommodating 20–25 pigs. At 35 kg (= 15 weeks of age) the group was split in two, and half of the pigs were relocated to a new pen. The stable was partly roofed with no clear distinction between indoor and outdoor areas. Bedding was deepest underneath the roofed part of the stable and gradually decreased towards the open part where the floor was partially slat ted. On farm 2 and 3, starter pigs and fatteners were kept in separate, fully roofed units with separate outdoor runs and separate feeding areas.
2.2 Sample collection

Individual faecal samples were collected rectally at quarterly intervals from September 2011 to June 2012. At each visit, we aimed at taking 20 samples from sows (10 pregnant and 10 lactating), fatteners (80–100 kg) and starter pigs (20–30 kg corresponding to 9–14 weeks of age), respectively. In addition, samples were collected immediately after defecation from 9–19 suckling piglets (≤7 weeks) in the farrowing paddocks. The samples were transported on ice to the laboratory and stored at 5°C until processing.

2.3 Faecal examination

Faecal consistency was assessed on a scale from one to five (1: normal; 2: soft, 3: liquid; 4: watery; 5: watery with blood and/or intestinal tissue). Giardia cysts and Cryptosporidium oocysts ((oo-)cysts) were isolated and enumerated as previously described by Maddox-Hytte et al. (2006). Briefly, 1 g faeces was suspended by vortexing in 3.5 mL 0.01% Tween 20 and filtered through multilayered 20-thread gauze (a 5 cm × 5 cm piece placed in a 10 mL syringe and held in place by a piece of wire). Another 3.5 mL 0.01% Tween 20 was added and the fluid pressed through the gauze with the syringe piston. The filtrate was under layered with 3.5 mL flotation fluid (saturated saline with glucose (50 g in 100 mL) diluted 1:1 with MQ water (final specific gravity = 1.13 g mL⁻¹) and centrifuged at 53 × g for 3 min. The supernatant was transferred to a clean tube and washed three times using MQ water and subsequently centrifuged at 1540 × g for 10 min to obtain a final sample volume of 2 mL. For each sample, a 10 μL subsample was placed in a well on a 3-well Teflon printed diagnostic slide (Immuno-Cell Int., Belgium) with 10 μL MQ water already added to the well. The slide was air-dried overnight, fixed with acetone and left to dry for 5 min before adding 25 μL of anti-Giardia/ and anti-Cryptosporidium fluorescein isothiocyanate (FITC)-labelled antibody mix (Crypto/Giardia-CEL IF, Cellabs, Australia) according to the manufacturer’s instructions. The (oo-)cysts were
quantified by epifluorescence microscopy at 200× or 400× magnification and expressed as oocysts or cysts per g (OPG, CPG). The theoretical detection limit was 200 (oo-)cyst per gram of faeces corresponding to (oo-)cysts counted in 10 μL of an initial 2 mL of processed suspension.

2.4 Molecular and phylogenetic analyses

Purified (oo-)cysts were stored at 5°C for approximately one year prior to DNA extraction using a QIAamp® DNA Stool Mini Kit (QIAGEN GmnH, Hilden, Germany) according to the manufacturer’s directions, except that the lysis temperature was increased to 95°C, and the DNA was eluted with only 100 μl Buffer AE, and subsequently stored at -20°C.

When possible, samples from the two pigs containing the highest OPG and CPG were selected for molecular and phylogenetic analyses from each farm, age-group and season. Furthermore, all samples from pigs with CPG≥1000 were selected (n=32). Thus, for some groups at particular time points, faeces from more than two animals were included in the molecular analyses.

Partial nucleotide sequences of the Cryptosporidium isolates were obtained by polymerase chain reaction (PCR) and subsequent sequencing of the small subunit ribosomal RNA gene (18S SSU rDNA locus) and the heat shock protein (hsp) 70 gene, whereas molecular typing of G. duodenalis was performed by PCR and partial sequencing of the 18S rRNA and the glutamate dehydrogenase (gdh) genes (Langkjaer et al., 2007).

PCR products were purified either directly from the PCR reaction, or following electrophoresis and extraction of specific DNA fragments from the agarose gel using the High Pure PCR Product Purification Kit (Roche Diagnostics GmbH, Mannheim, Germany). The purified PCR products were sequenced in both directions on an ABI 3130-4 Genetic Analyzer (Applied Biosystems, Europe BV, Danish branch in Nærum, DK) using Big Dye1 Terminator V3.1 cycle sequencing kit (Applied Biosystems). Alignment of selected representative fragments
each species and each molecular marker) and reference sequences from GenBank were made
with Clustal W using the software MEGA6 (Tamura et al., 2013). Phylogenetic relationships
were determined by neighbour joining analyses using 1000 bootstrap replicates, and the
evolutionary distances were computed using the Jukes-Cantor method. In addition, the
average evolutionary divergence over sequence pairs was determined for each of the gene
fragments to estimate the number of nucleotide substitutions per site from averaging over all
sequence pairs within each species (Tamura et al., 2013).

2.5 Statistical analyses

Mono-infection with Cryptosporidium or Giardia and dual infection with both parasites were
binary response variables, and differences between age-groups, farms and sampling seasons
were evaluated using a logistic regression model allowing findings from the same farm to be
correlated. The model was estimated using restricted pseudo-likelihood estimation (SAS
Glimmix procedure).

The OPG were In (x) transformed, while CPG were square root transformed to ensure a
normally distributed interval dependent variable. The differences in OPG means between
mono/dual infected pigs and age-groups were analysed by linear regression to test whether
the mean number of (oo-)cysts excreted per pig differed by age-group, mono/dual infection or
if there was any interaction between these. The normality assumption was validated by
quantile-quantile plots and Shapiro–Wilk test, and variance homogeneity was validated by
residual plot. Thereafter, the non-significant effects were removed by stepwise backward
model reduction on a 5% significance level. The final model for excreted oocysts (OPG)
included farm number, season and age-group as fixed factors. The differences in CPG were
square root transformed and analysed using a generalized linear regression model assuming a
gamma error distribution and an inverse link function. The distributional assumptions were validated by inspecting the residual distribution. One extreme CPG value was omitted from the analysis. All mean data ± standard deviation (S.D.) are stated as arithmetic means calculated from the raw non-transformed data. All statistical analyses were done in SAS, version 9.3 (SAS institute Inc., Cary, NC).

The *Cryptosporidium* spp., *C. suis* or *C. scrofarum*, were a binary response variable, and differences between age-groups, farms and sampling seasons were evaluated using a logistic regression model allowing findings from the same farm to be correlated. The model was estimated using restricted pseudo-likelihood estimation (SAS Glimmix procedure).

3. Results

3.1 Prevalence

Faecal samples were collected from 240 sows, 230 fatteners, 234 starter pigs and 152 piglets, yielding a total of 856 samples. Based on microscopical examination, 46.7% (400/856) of the sampled pigs tested positive for *Cryptosporidium*, *Giardia* or both parasites. Of these, 40.9% (350/856) were infected with *Cryptosporidium* and 14.0% (120/856) with *Giardia*. Of the *Cryptosporidium*-positive pigs, 20.0% were dual-infected with *Giardia*, while 58.3% of the *Giardia*-positive pigs were concomitantly infected with *Cryptosporidium*, corresponding to a total of 8.2% (70/856) dual-infected pigs. The theoretical expected prevalence of dual-infections was 5.7% (0.409 × 0.140). Pigs infected with *Giardia* thus had an increased relative risk of being concomitantly infected with *Cryptosporidium* (relative risk= 2.02; CI 1.45–2.83; p<0.0001) and vice versa (relative risk= 1.53; CI 1.28–1.83; p<0.0001).
The prevalence of *Cryptosporidium* infections was significantly age-related both on study level (p=0.0002) and within each farm (p<0.05) (Table 1). Infections were markedly more prevalent in starter pigs (72.2%) compared to any other age-group (p<0.0001) and least prevalent in sows (2.9%). Likewise, the overall prevalence of *Giardia* was significantly age-related (p=0.0017) with higher prevalence in starter pigs (27.4%) and lower prevalence in piglets (2.0%) compared to other age-groups. Yet, the prevalence of *Giardia* mono-infections was similar in starter pigs (7.3%), fatteners (9.6%) and sows (4.6%), whereas no piglets (0.0%) were mono-infected with this parasite (Table 1). In agreement with the overall high prevalences observed in starter pigs, dual-infections were significantly (p<0.0001) more prevalent in this age-group (20.1%) compared to any other age-group.

Generally, the prevalences of both parasites were unaffected by season at study level and within each farm and age-group. Yet, fatteners and starter pigs tended to have more *Giardia* infections during autumn and winter, and dual-infections were more prevalent in September and December (p<0.05).

### 3.2 Oocyst and cyst excretion levels

In general, regardless of age, farm, season and species, *Cryptosporidium* were excreted at considerably higher levels compared to *Giardia*. The intensity of infection ranged 200–10,551,200 OPG with a mean of 99,062 ± 35,151 OPG and median of 2100 OPG for *Cryptosporidium* infected pigs, and 200–21,400 CPG with a mean of 1,285 ± 261 CPG and median of 400 CPG for *Giardia* infected pigs. In addition, the excretion levels of *Cryptosporidium* were markedly lower for dual-infected pigs (all ages) compared to mono-infected pigs (all ages) (mean ± S.E., and median, dual-infected: 11,157 ± 3,776 OPG and 1,600 OPG; mono-infected: 121,038 ± 43,846 OPG and 2200 OPG), although not statistically
significant (p>0.05). Moreover, only 1.4% of the dual-infected pigs (all ages) excreted $10^4$–$10^5$ OPG while the corresponding number was 8.6% for Cryptosporidium mono-infected pigs (all ages), and with one exception (a dual-infected piglet), excretion levels $>10^5$ OPG were only observed in Cryptosporidium mono-infected piglets. Moreover, only three of 152 (4.3%) piglets were dual infected, while 78 out of 152 (51.3%) were mono-infected with Cryptosporidium.

At all four sampling seasons, some pigs did not excrete detectable numbers of (oo-)cysts, while others excreted extreme quantities. The average excretion levels for each age-group are presented in Figure 1, demonstrating an age-related excretion pattern, where the infection intensity decreased with increasing age. Piglets excreted, on average, 1,177 times more OPG and 8 times more CPG than sows. Infection intensity was independent of season and farm.

Mean oocyst excretion for C. suis infected pigs was 351,035 OPG (range: 2.4 x $10^3$ - 1.6 x $10^6$; S.D. 351,035; 95% CI: 67953–634117) while pigs infected with C. scrofarum excreted 54,848 OPG (range: 0.6 x $10^3$ - 1.2 x $10^6$; S.D. 194,508; 95% CI: -9085–118781). The average excretion levels of C. suis and C. scrofarum are presented for each age-group in Table 2. Scouring animals (faecal scores $\geq$ 3) were not detected among the sampled animals and infection intensity was unrelated to faeces consistency (p>0.05).

3.2 Molecular characterization of Cryptosporidium and Giardia

Of the 350 Cryptosporidium positive samples, we attempted to analyse 75 samples by partial sequencing of the 18S rDNA locus and the hsp70 gene; 55 samples from Cryptosporidium mono-infected pigs and 20 samples from dual-infected pigs. Of these, 40 samples from mono-infected pigs and 16 from dual-infected pigs were successfully sequenced revealing 38 (67.9%) C. scrofarum and 18 (30.9%) C. suis. Of the 16 successfully sequenced samples from dual-
infected pigs, 14 were \textit{C. scrofarum} and two were \textit{C. suis}. Seasonal- and age-related prevalences of \textit{Cryptosporidium} species on the three farms are presented in Table 3.

The \textit{Cryptosporidium} species infecting the pigs was determined by age. Piglets hosted exclusively \textit{C. suis} (except for one piglet infected with \textit{C. scrofarum}), while starter pigs and fatteners were infected with \textit{C. suis} as well as \textit{C. scrofarum}; the latter species occurring most frequently. Species distribution appeared unaffected by season or farms. The sows excreted few oocysts (below 1,000 OPG), and no typing results could be obtained from this age-group. Both \textit{C. suis} and \textit{C. scrofarum} were detected on all three farms during all seasons.

For those \textit{Cryptosporidium} isolates where typing results were obtained with both molecular markers (n=35), the results were consistent. Phylogenetic analyses of the \textit{Cryptosporidium} 18S rDNA (Fig. 2) and \textit{hsp70} gene sequences (Fig. 3) were largely consistent, and the sequences were 95-100\% identical to those previously published for porcine isolates of \textit{C. suis} and \textit{C. scrofarum} from GenBank. Estimates of the number of base substitutions per site from averaging over all sequence pairs within each group involved 44 18S rDNA nucleotide sequences (13 \textit{C. suis}, 31 \textit{C. scrofarum}) with a total of 476 base pairs in the final dataset, and 47 \textit{hsp70} sequences (13 \textit{C. suis}, 34 \textit{C. scrofarum}) with a total of 354 base pairs in the final datasets. Rates of nucleotide substitutions were generally higher in the \textit{hsp70} sequences compared to 18S rDNA sequences, but while \textit{hsp70} sequences of \textit{C. suis} (0.046) were more variable relative to \textit{C. scrofarum} (0.020) the opposite was the case for 18S rDNA sequences (\textit{C. suis}: 0.001; \textit{C. scrofarum}: 0.004). Selected representative sequences (B14, B26, B35, B37) from the present study have been uploaded to GenBank under the Accession numbers: KT223028–29 and KT716819–20.
Of the 120 Giardia positive samples, we attempted to analyse 67 by partial sequencing of the 18S rDNA locus and the gdh gene; 31 samples from Giardia mono-infected pigs and 36 samples from dual-infected pigs. None of the dual-infected pigs were successfully sequenced, while genotypes were successfully obtained from 13 of the mono-infected isolates, revealing 11 (84.6%) G. duodenalis Assemblage E and two (15.4%) Assemblage A. Assemblage E was detected in samples from all seasons and was found in pigs from all three farms, whereas Assemblage A was only detected in pigs from farm 2 and 3 in June and September, respectively (Table 4). Giardia species distribution was only analysed to calculate the relative risk of a co-infection with both parasites, while too few data were obtained from the screening to do logistic regression.

4. Discussion

4.1 Prevalence

Cryptosporidium and Giardia infected pigs were identified on all three farms, at all seasons and from pigs of all ages. Nevertheless, young age was strongly associated with prevalence and intensity of infections, particularly for Cryptosporidium, which had very high prevalence rates in piglets and starter pig whereas Giardia infections were more prevalent only in starter pigs compared to any other age-group. The prevalences of both parasites were unaffected by season, while the prevalence of dual-infections peaked in September and December. In accordance with previous studies in pigs, sheep and cattle (Maddox-Hytte et al., 2006; Santín et al., 2007; Siwila and Mwape, 2012; Budu-Amoako et al., 2012), Cryptosporidium infections were approximately three times more prevalent than Giardia infections. Moreover, the dual-infections constituted a substantial part of the infections: 20.0% of the Cryptosporidium and 58.3% of the Giardia positive pigs. Hence, pigs infected with one parasite appeared more likely
to be simultaneously infected with the other. Most previous studies of *Cryptosporidium* infection in pigs did not include *Giardia*, and in the few studies that did, dual-infected animals were not reported (Budu-Amoako *et al*., 2012; Farzan *et al*., 2011). However, studies in cattle, sheep and horses identified *Cryptosporidium/Giardia* dual-infected young animals by PCR or immunofluorescence assay with prevalences ranging 7–26% (Xiao *et al*., 1993; Xiao and Herd, 1994 Castro-Hermida *et al*., 2006; Hamnes *et al*., 2006; Sweeny *et al*., 2011). None of these studies compared the intensity of the infections, while others have reported cryptosporidiosis to be a risk factor for giardiasis in children and vice versa (e.g. Wang *et al*., 2013). The relatively high prevalence of dual-infections reported here as well as in other livestock, indicates that dual-infections are fairly common. This may be the result of identical infection routes and infectivity of the two parasite species, rather than one being a risk factor for the other. Yet, solid data, e.g. experimental infection studies, to support this hypothesis is lacking.

Weaning of piglets may have triggered the high prevalence in starter pigs observed in this study and elsewhere, since weaning is associated with significant social, environmental and nutritional changes resulting in dramatic alterations of gut structure, microbiology and function (Montagne *et al*., 2007). However, two studies in Vietnam demonstrated that the prevalence of *Cryptosporidium* in pre-weaned pigs (< 1 month) was significantly higher than in post-weaned pigs (1–2 month) (Nguyen *et al*., 2012, 2013). This discrepancy, compared to our study where the highest prevalences were detected post weaning, was probably related to differences in weaning age, and diagnostic methods. Pigs in our study were weaned at 7–9 weeks of age, i.e. approximately one month later than pigs in the Vietnamese study. Further, the Vietnamese study used the Modified Ziehl-Neelsen technique, a method known to have low sensitivity. Thus, post weaning samples with low intensity might have remained undetected.
Pigs raised on straw bedding have previously been shown to be more commonly infected with *Cryptosporidium* than pigs raised on slatted floors (Nemejc et al., 2013). Yet, the prevalences of *Cryptosporidium* (72.2%) and *Giardia* (27.4%) in starter pigs in the present study, where the pigs had access to straw bedding, were similar to those described in an earlier Danish study of conventional pig farms, where the animals were raised on slatted floor (Maddox-Hyttele et al., 2006). The *Cryptosporidium* prevalences in our study were, however, considerably higher than the prevalence of 33–48% for starter pigs reported elsewhere (Budu-Amoako et al., 2012; Yui et al., 2014). It should be noted though, that prevalence of *Cryptosporidium* in piglets (53.3%) prior to weaning was noticeably higher than formerly described both in Denmark (Maddox-Hyttele et al., 2006) and abroad (Budu-Amoako et al., 2012; Yui et al., 2014). Outdoor rearing and late weaning as practiced in organic pig production probably contributed to these differences. In Danish organic pig production, suckling piglets have unrestricted access to large pasture areas with accumulation of manure and contact with several sows (Serup, 2010). This is in contrast to conventional pig production where lactating sows and their piglets are housed in individual, indoor pens with slatted floors (Nielsen & Norgaard, 2010). Our results are in agreement with a study of pigs in Western Australia where *Cryptosporidium* was found to be more prevalent in outdoor pig herds (17.2%) than in indoor herds (0.5%) (Ryan et al., 2003). Additionally, stress related to changing weather conditions may have contributed to the high prevalence and infection levels observed in our study of outdoor reared animals. Due to the cross-sectional study design with repeated sampling in each farm, but without repeated sampling of individual pigs, we were unable to demonstrate if the high prevalence in piglets was caused by inability to clear the infection or due to repeated re-infection. In contrast, hardly any piglets had detectable *Giardia* infections, whereas the parasite was relatively prevalent among starter pigs and fatteners.
As cold and humid conditions, occurring during winter, are known to favour (oo-)cyst survival (Robertson et al., 1992; Olson et al., 1999), prevalence was expected to vary in outdoor raised pigs due to seasonality. However, the prevalence of Cryptosporidium was relatively constant during this one-year study, demonstrating a continuous infection pressure and environmental contamination throughout the year; supported by the presence of susceptible piglets due to farrowing at all seasons. Giardia cysts are more sensitive than Cryptosporidium oocysts to adverse environmental conditions (Olson et al., 1999), which might account for the fluctuation of Giardia prevalence observed in starter pigs and fatteners between sampling seasons in the present study.

4.2 Infection intensity

As for the prevalence, the infection intensity of both parasites was age related with the highest Cryptosporidium intensity in piglets, while the highest Giardia intensity appeared in starter pigs. Nonetheless, the dual infected piglets excreted more Giardia cysts than the dual infected starter pigs (Fig. 1). The Cryptosporidium intensities are in accordance with previously reported data (Yui et al., 2014; Jeníková et al., 2011). The lower Cryptosporidium excretion levels in starter pigs compared to piglets (Fig. 1) may have been the result of acquired immunity or parasite factors, as this age-group, in agreement with e.g. Yin et al. (2013), was predominantly infected with a Cryptosporidium species different from that observed in the piglets (Table 3). Nevertheless, excretion levels >10^3 OPG were seen in 68.6% of the infected starter pigs, demonstrating relatively high infection intensities in this age-group despite development of immunity and predominant infection with C. scrofarum. Pigs concomitantly infected with Cryptosporidium and Giardia excreted lower levels of (oo-)cysts compared to mono-infected pigs. Hence, our results may suggest that dual-infections prevent pigs from excreting
extremely high numbers of (oo-)cysts. Yet, the differences were insignificant, probably due to relatively few dual-infected pigs, and large variation in (oo-)cyst excretion within the age-groups. To our knowledge, this is the first study to compare infection intensity of dual- and mono-infected pigs, and, although a few studies have documented prevalence of mono- and dual-infections in cattle and analysed infection intensity, they did not compare the infection intensity between mono- and dual-infected animals (O’Handley et al., 1999; Hamnes et al., 2006). Accordingly, more studies are needed to reveal whether these parasite infections may have antagonistic effects or whether the lower infection intensity observed in dual-infected pigs was mainly caused by Giardia infections occurring later in life compared to Cryptosporidium, and thus the majority of the dual infected pigs are more immunologically mature compared to the young piglets. This study revealed that the intensity of Cryptosporidium infections in pigs was linked to species and age, as C. suis infected pigs excreted above 6 times more oocysts than C. scrofarum infected animals, and piglets exclusively hosted C. suis. This is in agreement with results of Kváč et al. (2009a), who found that pigs infected with C. suis shed statistically higher numbers of oocysts compared with pigs infected with C. scrofarum. Nevertheless, as our study was not specifically designed to analyze species-specific differences in oocyst excretion, firm conclusions regarding variation in reproductive potential of the porcine Cryptosporidium species needs further scrutiny.

Based on scoring of the faecal samples the infections were subclinical over the course of the study and no correlation could be found between faecal consistency and (oo-)cyst excretion levels. A recent Japanese study showed that piglets with signs of diarrhoea shed more Cryptosporidium oocysts than piglets with normal or loose stools (Yui et al., 2014); but the study did not exclude co-infection with other pathogens. In contrast, and in agreement with our findings, most other studies demonstrated a subclinical course of infection (Xiao, 1994;
Quílez et al., 1996; Guselle et al., 2003; Ryan et al., 2003; Vitovec et al., 2006; Suarez-Luengas et al., 2007; Jeníková et al., 2011). This suggests limited clinical importance of Cryptosporidium and Giardia in naturally infected pigs, but does not preclude an impact on productivity. Furthermore, co-infection with other commonly occurring pathogens may result in clinical disease, e.g. rotavirus has previously been demonstrated to enhance pathogenicity leading to severe disease and mortality in pigs with cryptosporidiosis (Enemark et al., 2003).

4.3 Species composition

Cryptosporidium suis, C. scrofarum, G. duodenalis Assemblage E and the zoonotic Assemblage A were identified in the present study. Cryptosporidium scrofarum was the most commonly isolated species on all three farms, and the species predominantly identified in starter pigs and fatteners. In contrast, piglets exclusively hosted C. suis with a single exception. This finding is congruent with results seen in other studies where piglets under the age of four weeks were refractory to C. scrofarum infection (Langkjaer et al., 2007; Johnson et al., 2008; Kváč et al., 2009a; Jeníková et al., 2011; Yin J.H. et al., 2013; Kváč et al., 2014). Likewise, C. suis and C. scrofarum were the most common species in pigs according to studies by others (Xiao et al., 2006; Langkjaer et al., 2007; Zintl et al., 2007; Johnson et al., 2008; Kváč et al., 2009b; Yin J.H. et al., 2013), while infections with species known to be highly zoonotic such as e.g. C. parvum have only occasionally been demonstrated (Budu-Amoako et al., 2012; Kváč et al., 2009; Zintl et al., 2007; Featherstone et al., 2010). Our results may, however, be biased by selection of samples for genotyping only from the two pigs with the highest excretion levels from each farm, age-group and season, rendering them unrepresentative of the entire population. Molecular analyses of samples containing few oocysts might have revealed less host adapted species or other species with lower reproductive capacity.
No typing results were obtained from sows. Low OPG or differences in species and genotypes infecting the sows compared to other age groups may have contributed to this unsuccessful molecular typing. Nevertheless, other studies detected both C. suis and C. scrofarum in sows (Zintl et al., 2007; Budu-Amoako et al., 2012).

We were unable to evaluate any relationship between the presence of G. duodenalis Assemblages and age, as only 13 of 67 Giardia-positive samples were successfully genotyped. The low success rate was probably caused by inadequate storage of the semi-purified cysts, which were stored in MQ water at 5°C for approximately one year prior to DNA extraction and PCR analysis. This was unintended and due to a mistake, and probably resulted in degradation of the DNA (Nechvatal et al., 2008) which could have been prevented by preservation in e.g. ethanol (Wilke and Robertson, 2009) or freezing (Kohli et al., 2008). Nevertheless, the zoonotic Assemblage A was detected in two pigs: a starter pig and a fattener, while the positive isolates containing Assemblage E were obtained from starter pigs, fatteners and sows, from all three farms and at all four seasons.

The phylogenetic analysis showed that Danish isolates grouped together with C. scrofarum and C. suis isolates from GenBank. Yet, intraspecies variations within the hsp70 gene fragments were demonstrated particularly for C. suis where an evolutionary distance of 0.046 was revealed between the isolates. This is considerably higher than observed for C. scrofarum. In comparison, little variation was present within the 18S rDNA fragments, but interestingly, C. scrofarum was more variable than C. suis within this gene locus. In accordance with our results, actin gene variants of C. suis and C. scrofarum were recently described in Japan (Yui et al., 2014). However, few studies have analysed genetic variation within porcine
Cryptosporidium species and further epidemiological studies are needed to fully understand the extent and significance of this variation.

No simultaneous infection with several Cryptosporidium species/genotypes was observed, which corresponds with earlier studies, where only few have reported mixed Cryptosporidium infection (Kváč et al., 2009b). Diagnosis of mixed infections is limited by one species usually predominating. Thus, as most PCR assays only amplify the dominant type (Tanriverdi et al., 2003), other species may remain undetected.

In conclusion, the study of three organic, Danish pig farms including examination of 856 faecal samples collected from different age-groups throughout one year revealed high prevalences of Cryptosporidium and Giardia infections leading to an inevitable risk of environmental contamination. However, the identified Cryptosporidium species were all of the pig-specific species and while the zoonotic G. duodenalis Assemblage A was present, it was rare. Although, sporadic cases of C. suis and C. scrofarum are reported in humans (Xiao et al., 2002; Cama et al., 2003; Bodager et al., 2015), the contribution from organic pigs in this study to the epidemiology of cryptosporidiosis and giardiasis in humans is apparently of minor importance. Accordingly, our findings suggest that the public health risk associated with Cryptosporidium and Giardia originating from organically outdoor reared pigs seems to be negligible in Denmark.
5. Acknowledgements

This research was part of the project Parasites in organic livestock: innovative solutions to new challenges (project no. 3405-10-OP-00137) funded by Green Development and Demonstration Program (GDDP), China Scholarship Council and the Technical University of Denmark. The following people are acknowledged for dedicated technical assistance: Marie Ståhl, Lise-Lotte Christiansen and Boi-Tien Thi Pham.
References


Hsu, B., Wun, H., Hsu, C.L., 2008. Detection and species identification of Cryptosporidium from Taiwan feeding animals. J. Parasitol. 94 (1), 252-256.


Figure captions:

**Figure 1:** Intensity of infection in organic pigs naturally mono-infected with *Cryptosporidium* (n=280) and *Giardia* (n=50), or dual-infected with both parasites (n=70). Mean ± SEM (oo-cysts per gram of faeces (OPG/CPG) per age-group. Based only on data from positive animals and merged across four seasons in a year. Please note the different scales on the Y-axes.

**Figure 2:** Phylogenetic relationships of porcine *Cryptosporidium* isolates inferred by Neighbour Joining analysis of 18S rRNA partial nucleotide sequences (628 base pairs in the final dataset). Percentage bootstrap support from 1,000 replicate samples is indicated at the left of each node. Accession numbers are shown in parentheses. The scale bar indicates 0.02 nucleotide substitution/site.

**Figure 3:** Phylogenetic relationships of porcine *Cryptosporidium* isolates inferred by Neighbour Joining analysis of partial nucleotide sequences of the hsp70 gene (268 base pairs in the final dataset). Percentage bootstrap support from 1,000 replicate samples is indicated at the left of each node. Accession numbers are shown in parentheses. The scale bar indicate 0.02 nucleotide substitution/site.
Table 1: Seasonal- and age-related prevalence of Cryptosporidium and Giardia in mono-infected and dual-infected pigs determined by quantitative immuno-fluorescence microscopy of faecal samples from 856 pigs from three Danish organic pig farms, September 2011–June 2012.

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<th>Fatteners</th>
<th></th>
<th>Sows</th>
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<th>Total number of positive pigs. (%)</th>
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<tr>
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Table 2: Age-related oocyst excretion of *Cryptosporidium* species in pigs from three Danish, organic pig farms, September 2011–June 2012.

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<th>Fatteners (%)</th>
<th>Sows (%)</th>
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<td>C. suis</td>
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<td>1.0 x 10^4 – 9.4 x 10^4</td>
<td>2.4 x 10^3 – 3.2 x 10^3</td>
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Table 3: Seasonal- and age-related prevalence of *Cryptosporidium* species in pigs, based on molecular analyses of 75 *Cryptosporidium* isolates from three Danish, organic pig farms, September 2011–June 2012.

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<th>Starter pigs (%)</th>
<th></th>
<th>Fatteners (%)</th>
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<th>Sows (%)</th>
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Table 4: Seasonal and age-related prevalence of *Giardia duodenalis* Assemblages in pigs, based on molecular analyses of 67 *G. duodenalis* isolates from three Danish, organic pig farms, September 2011–June 2012.

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<th></th>
<th>Piglets</th>
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<th>Fatteners</th>
<th>Sows</th>
<th>Total number of pos. animals (%)</th>
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Fig. 1
Fig. 3