A rapid, sensitive enrichment PCR to detect Salmonella and ETEC infections in pigs

Davies, H¹, Dodd, C.E.R¹, Tötemeyer, S², Wiseman, J¹, Mellits, K.H.¹∗

School of Biosciences¹ and School of Veterinary Medicine and Science², University of Nottingham, Leicestershire, UK.

∗corresponding author: Ken.Mellits@nottingham.ac.uk

Abstract

Salmonella and Escherichia coli infections, particularly enterotoxigenic E. coli (ETEC), are a problem in piglet production. In addition, Salmonella is a major concern in the pork industry as a carrier state can be induced post infection allowing the pathogen to spread across the pig herd, onto many carcasses at slaughter and into the human food chain. Detection methods for these pathogens are currently highly laborious, with Salmonella detection taking over 5 days to give a verified positive result. Identification of ETEC isolates involves detecting the presence of toxin or fimbriae (or their genes by PCR), particularly F4, the most common fimbriae in piglet ETEC infection. Alternative methods such as real time PCR are unable to detect low levels of infection directly from the sample. Enrichment PCR assays have been successfully implemented for the detection of pathogens in foodstuffs, however, faecal material often is inhibitory to PCR based methods.

The enrichment PCR assay presented here overcomes these problems and allows the rapid detection of Salmonella and ETEC from piglet faeces. Faecal samples are pre-enriched in buffered peptone water and DNA is extracted, followed by a multiplex PCR. This shortens the detection time for the presence of these organisms to 30 h. The multiplex PCR uses primers for detection of both the invasion gene (invA) in Salmonella required for enteric infection, and the F4 fimbriae of ETEC. Spiked faecal samples have shown a detection limit of <10 cells of either pathogen per 1g faeces. Moreover, pathogens at low levels have been detected on farm. This assay will facilitate early detection of enteric infections, and subsequently enable monitoring of the pathogen status of the pigs until all low level carriage has been eliminated. This has strong potential to control pathogen spread within pig herds, and thus the human food chain.

Introduction

Piglets undergo a growth check at weaning as a result of diet change, social stresses and increased pathogen susceptibility as a consequence substantial losses occur during this time (Lalles et al., 2007). The foremost bacterial pathogens at weaning are Escherichia coli and Salmonella, both of which cause serious enteric infections that result in dehydration, profuse diarrhoea and sometimes death (Lalles et al., 2007). Often pathogens can exist as co-infections, resulting in increased infection severity (Melin et al., 2004). During infection Salmonella penetrates the intestinal barrier, causes necrotising enterocolitis and is spread system wide (Letellier et al., 2000). This results in a carrier state being induced where Salmonella can be carried, and therefore excreted, by the animal for up to 28 weeks (Wood and Rose, 1992). In addition, enterotoxigenic E.coli (ETEC) causes significant financial losses in the pork industry due to infections in young pigs. ETEC infection is induced by a heat labile or heat stable toxin switching on electrolyte secretion into the gut lumen (Lalles et al., 2007). Fimbriae are required for adherence of ETEC to the gut epithelium and for toxin delivery (Lalles et al., 2007). The toxin and fimbriae types present in infection vary, however, research suggests the heat labile toxin and F4 are the most predominant factors in post-weaning piglets (Osek, 1999). As these pathogens can be transferred to the carcass at slaughter, there is a large amount of emphasis placed on the "farm to fork" strategy to control zoonotic transmissions into meat.

Conventional methods for identification of these pathogens include isolation of a strain with subsequent biochemical, serological or gene detection tests. E.coli isolates are selected from diagnostic media whereas Salmonella requires a three stage enrichment process with confirmatory tests, taking over 5 days.
Both of these “gold standard” methods are laborious and time consuming, and involve screening many negative results and for ETEC, exhibit limited sensitivity.

More recently the rapid method of polymerase chain reaction (PCR) has been successfully employed to identify pathogenicity genes of these organisms without requiring isolation of the organism itself. Although successful in food (Ferretti et al., 2001), faecal matter has been more problematic due to the presence of PCR inhibitors and a high background flora (Widjooatmodjo et al., 1992). PCR detection directly from faeces can detect as low as \(10^2\) c.f.u. g\(^{-1}\) of the organism of interest (Kongmuang et al., 1994). However, PCR enrichments for Salmonella in faeces have shown detection limits of \(10^3\) c.f.u. g\(^{-1}\), proving it is a viable alternative to culture (Chiu and Ou, 1996; Mainar-Jaime et al., 2008). E.coli pathogenicity genes are often detected in a multiplex PCR that identifies identification of all types of pathogenic E.coli but still requires strain isolation first with detection directly from faeces rarely considered.

The method presented here aims to provide a rapid, sensitive detection system for Salmonella and F4 positive ETEC to aid surveillance of these pathogens in pig populations. Faeces are enriched for 24 h, DNA extracted and the presence of Salmonella and ETEC is detected in a multiplex PCR using previously published primers to produce a 453 bp and a 753 bp product respectively (Arnold et al., 2004; Do et al., 2005).

Material and Methods

Enrichment Multiplex PCR

One g faecal matter was homogenised into 9 mL buffered peptone water. Faecal suspensions were enriched at 37°C, 24 h before being centrifuged at 600 g for 5 min. Then 1 mL supernatant was centrifuged at 13,000 g 5 min. Pellets were washed in 1 mL TE buffer. DNA was extracted from the pellet using the Nucleospin tissue kit (Macherey Nagel, Germany).

PCR reactions used primers F4F and F4R to amplify a 764 bp PCR product of the F4 fimbriae gene of ETEC (Do et al., 2005) and the improved primers, invA1 and invA2, of Arnold et al. (2004) to generate a 476 bp PCR product of the plasmid encoded Salmonella invasion gene.

PCR products were analysed in 1.5% agarose gels in 1x TAE buffer (40 mM Tris Acetate pH 8, 1 mM EDTA) run at 70 V 1 h. Bands were visualised by staining gels in ethidium bromide 0.5 μg ml\(^{-1}\), then UV illumination and photographing with Biorad software (Biorad, USA).

Spiking of Enrichment PCR

To determine the sensitivity of the enrichment/multiplex PCR, diluted cultures of Salmonella Typhimurium LT2 and ETEC F4 positive isolate Y04124 (VLA, Weymouth) in MRD, were spiked into piglet faeces at concentrations of 1 c.f.u. g\(^{-1}\) to \(10^4\) c.f.u. g\(^{-1}\) to represent different levels of infection. One fraction of faeces was always processed unspiked as a negative control.

Conventional Salmonella method

Hundred μL from enriched broth (outlined above) was inoculated into 9.9 mL Rappaport Vassiliadis broth and further enriched for 24 h at 42°C. Ten μL was streaked onto XLD (37°C, 24 h). Presumptive positive colonies were re-streaked onto BHI agar and confirmed using an oxidase test and serological testing with Poly O A - S antisera (VLA, Weybridge, UK).

Results

Primers to detect the F4 fimbriae gene of ETEC and the invA invasion gene of Salmonella were incorporated successfully into the same PCR reaction by modifying the PCR conditions. A representative gel from reference isolates is shown in Figure 1A, Lane b shows the 476 bp product representative of Salmonella, lane c the 764 bp product of the F4 gene of ETEC and lane d both ETEC and Salmonella as represented by the two bands present.
Salmonella and ETEC cultures were spiked into faeces at different concentrations and the enrichment PCR method used to detect samples after enrichment. When cultures were spiked individually into faeces the method was able to detect the pathogens in all samples, where the lowest level of detection was 2 c.f.u.g⁻¹ for Salmonella and 6 c.f.u.g⁻¹ for ETEC (data not shown). Results for the classical enrichments for the spiked Salmonella were comparable to the PCR as at all three levels of spiking samples were positive for Salmonella. Figure 1B shows detection of both organisms when spiked into faeces in combination at set levels using the enrichment PCR. The PCR was able to detect both organisms at levels of 1 c.f.u. g⁻¹ through to 10² c.f.u. g⁻¹ in both samples (Figure 1B, lanes a-i). The lowest level of detection achieved was 3 c.f.u. g⁻¹ for Salmonella and 2 c.f.u.g⁻¹ for ETEC (lane a). However, the enriched PCR was not always successful. The 764 bp band representing the F4 gene of ETEC was often weak, and in one case absent (lane k). However, the enrichment PCR was better than detection by classical methods for the detection of Salmonella as in the mixed spiked samples classical methods failed to detect the organism spiked at 1 c.f.u.g⁻¹ in the second faeces sample.

Figure 1.
A Detection of ETEC and Salmonella Typhimurium LT2 in multiplex PCR reaction. Lane a) 100 bp ladder, b) Salmonella Typhimurium LT2, c) ETEC isolate Y04124, d) Salmonella Typhimurium and ETEC isolate Y04124, e) negative control (water).
B Detection of spiked levels of Salmonella Typhimurium LT2 and enterotoxigenic E.coli isolate Y041424 in replicate samples of piglet faeces. Each sample contains equal quantities of spiked Salmonella and ETEC into faeces. Lanes a-d are faeces sample 1, lanes e to i are sample 2. Lane a & e contain 1 c.f.u. g⁻¹ Salmonella and ETEC in faeces; lanes b & f 10 c.f.u. g⁻¹ Salmonella and ETEC in faeces; lanes c & g 10² c.f.u. g⁻¹ Salmonella and ETEC in faeces; lane h 10⁵ c.f.u. g⁻¹ Salmonella and ETEC in faeces; and lanes d & i unspiked faeces. Lane j contained a 100 bp ladder, lane k combined DNA of Salmonella Typhimurium LT2 & ETEC wild type isolate Y041424.

Discussion

Our results show that the multiplex PCR described here is able to detect pathogens in faeces, when present together or separately, and present at <10 c.f.u.g⁻¹. This level is lower than previously reported for detection of Salmonella by combination enrichment PCR (Chiu and Ou, 1996). The low sensitivity threshold is essential for Salmonella detection due to the low level shedding that occurs for several months post-infection (Wood and Rose, 1992). This method sensitivity is similar to typical culture methods but has the advantage taking less than 30 h compared to 5 d for cultured results. We are not able to compare ETEC detection limits with conventional culture methods as identification by PCR or antisera is generally based on a disease isolate, not direct detection from faeces (Osek, 1999). Therefore detection limits are dictated by the dilutions from which the colonies are selected, often exceeding levels of 10⁶ c.f.u. g⁻¹. The
ability to detect low levels of ETEC in faeces is highly advantageous as an indicator of early stages of infection or sub-clinical infections.

The one false negative result for ETEC, (Figure 1B, lane f) may be due to high background levels of E. coli not permitting ETEC to grow to detectable levels. False negative results are a problem when detecting pathogens from faeces, although this effect may be minimised with further optimisation (Arnold et al., 2004). However, results for Salmonella detection by the classical method indicated the multiplex PCR was more sensitive than existing classical and molecular methods for detection of Salmonella from faeces, and also quicker than classical culture. Our results correlate to those previously found where PCR detection of Salmonella was more effective by enrichment PCR than by culture (Chiu and Ou, 1996; Mainar-Jaime et al., 2008).

Conclusions

This enrichment multiplex PCR provides a sensitive detection method for Salmonella and ETEC, with a detection limit of less than 10 cells g⁻¹ faeces for both organisms. This is a very effective method to study sub-clinical infections and also the low level pathogen shedding associated with Salmonella infection. Moreover, detection of Salmonella can be completed within 30 h as compared with the five days required for conventional bacterial culture methods, therefore greatly reducing time and labour. This method is currently being applied to large intervention farm trials to aid our surveillance capacity for these pathogens within the pig, and therefore, the pork industry.

References


*Safe pork 2009 - Québec city, Québec, Canada*

