



# Comparative of conventional dot blot hybridization and CARD dot blot hybridization for *Salmonella* detection in pork

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## Abstract

Dot blot hybridization assay was evaluated with Sal3 probe for rapid detection of *Salmonella* from pork samples. The Sal 3 probe (-5'OH) specificity with dot-blot hybridization found a DNA positive result of all salmonella serovars (*S. typhimurium*, *S. enteritidis*, *S. vichow*): while, there was negative result from 9 DNA samples of the negative control group. The conventional dot-blot hybridization methods (method A: System probe labeled DIG at 5'-OH labeling DIG hybrids/ anti DIG-AP, detection with NBT/BCIP and method B: System probe labeled with biotin at 5'-OH labeling biotin hybrids/ streptavidin-HRP, detection with DAB) were compared with an application of catalyzed reporter deposition (CARD) to dot blot platform (method C: System probe labeled with biotin at 5'-OH labeling biotin hybrids /1°streptavidin-HRP /2°streptavidin-HRP,+ system tyramide signal amplification (TSA), detection with DAB). The sensitivity of dot-blot hybridization methods for systems A, B and C were found C system has a high sensitivity for dot-blot hybridization method. The results were obtained at the lowest concentrations of  $3 \times 10^4$  cfu / ml using a 2-day examination period. So, the separation processing of pathogens from meat samples is therefore essential. It is recommend that the use of appropriate DNA extraction kits or methods is critical for successful and valid CARD dot blot hybridization posed a challenge for salmonella detection on pork samples.

**Keywords:** Dot-blot hybridization method, *salmonella* spp., pork

**Article history:** Received 31 May 2021, Revised 15 July 2021, Accepted 15 July 2021

## 1. Introduction

The prevalence of salmonellosis incidence in people of industrialized countries is often implicated severe serotypes such as *S. enteritidis*, *S. typhimurium* and salmonella 1,4, (5), 12. : i: - [1 – 4]. The salmonella can be adaptive in animal foods and can be transmitted to infectious agents. There is a wide range of living environments both in humans and in pigs [5]. Pork is one of the main animal products that transmit salmonella to the population in EU and USA [1], [2], [6 – 8]. In Thailand, the prevalence of salmonella in swine reported a swine carcass (27.1%), water (36.7%), workers (19.5%) and slaughterhouses (10.7%) respectively [9]. The bacteria culture is gold standard method of bacteria detection in food, which is both a time-consuming conventional culture method and labor-intensive [10]. Molecular methods used to detect organisms are reliable and rapid than traditional meth-

ods, involving culture methods or microscopy. Several researchers have developed new screening methods for alternative methods of detecting and enumerating pathogens in food within 1 day including enzyme-linked immunosorbent assay (ELISA), PCR, biosensor and nucleic hybridization technique such as fluorescence *in situ* hybridization (FISH) [11 – 16]. Recently, FISH method was developed to detect the genetic material of salmonella in pig meat. It was found that salmonella could be detected  $3 \times 10^4$  cfu/ml of salmonella cells within 1 day, When comparing to accuracy salmonella results between FISH method and bacteria culture (ISO 6579) from pork in the slaughterhouse, both results were accuracy consistent at moderate level (Kappa Statistics = 0.46) [17]. However, these two methods are not feasible in most clinical laboratories in developing countries. Currently, strategies based on dot blot hybridization and an application using the catalyzed reporter deposition (CARD) to dot blot platform (CARD-dot blot hybridization) with rRNA-targeted oligonucleotide probes. CARD

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is a method developed to increase the signal strength of reporter molecules. CARD utilizes the property of peroxidase to catalyze the deposition of tyramide conjugates at the site of enzyme reaction [18]. It may be another alternative method that requires improved approaches to enable specific and sensitivity screening to salmonella and can be conducted using common equipment biotechnology laboratories. Therefore, we developed a dot blot platform and combined with the signal amplification method, CARD to rapidly assess for detection of salmonella in pork. Lastly, we evaluated its efficiency when compared to conventional dot blot hybridization analysis.

## 2. Material and Method

### 2.1 Reference strains, culture and DNA extraction

All bacteria isolates were further clinical isolates identified and characterized from genus to species by the Kamphaengsaen Veterinary Diagnostic Center, Faculty of Veterinary Medicine, Kasetsart University, Thailand. *Salmonella enteritidis*, *Salmonella Typhimurium* and *Salmonella Virchow* were grow as a reference strain and campylobacter spp., *Corynebacterium* spp., *Escherichia coli*., *Klebsiella* spp., *Pseudomonas* spp., staphylococcus aureus., *Aeromonas hydrophila* and *Enterobacter aerogenes* were grown as a negative control. The reference strain of *Salmonella* spp., and negative bacteria were streaked into MAC agar plates for over-night culture at 37°C for activating bacteria. 1 – 2 colony of each bacterial were picked and inoculated each into a 5 ml nutrient broth and grew overnight at 37°C with Orbital Shaker (BIOSAN, LATVIA) before harvesting cell at logarithmic phase to obtain cells with high ribosome content for DNA extract. Genomic DNA extraction of all isolates was performed using commercially available the E.Z.N.A. Bacterial DNA Kit (Omega Bio-Tek, Norcross, GA, USA) according to the manufacturer's instructions and the concentrations of genomic DNA samples were measured using a Nano-Drop ND-2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, United States) and the concentration was adjusted to 100 µg/ml for test specificity of Sal3 probe determined by dot-blot hybridization.

### 2.2 Oligonucleotide probe

A specific oligonucleotide probe for dot-blot hybridization was used Sal3 primer (5'-AATCACTTCACCTACGTG-3'), specific to target the 23S rRNA for *Salmonella* spp. [16], [19 – 23]. The Sal3 probe were all synthesized and labelled with digoxigenin in (Sal3-digoxigenin) and the biotin (Sal3-Biotin) at the 5' end (Asia Pacific. Integrated DNA Technologies, Singapore).

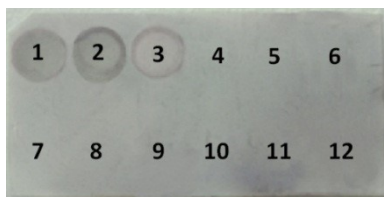
### 2.3 Evaluation of the specificity of Sal3 probe by dot blot analysis

The specificity of the Sal 3 probe was tested by hybridization with dot-blot hybridization assay. For this study, Sal3 probe was tested against *Salmonella* DNA 3 serovars and 9 negative controls.

The pellet DNA of each bacterium was diluted to a concentration of 100 µg/ml, DNA boiling for 5 minutes at 100°C and placing on ice for 10 minutes. Four µl volumes of DNA sample were dotted on nitrocellulose membrane and dried at 80°C for 2 hr in hot air oven. Dot-blot hybridization in this study followed with the procedure of [24]. Nitrocellulose membrane were sealed in a polypropylene bag with, per cm<sup>2</sup>, 1 ml of a prehybridization mixture containing 20xSSC (3M NaCl, 0.3M Na-Citrate), 50x Denhardt's solution, yeast tRNA, 1M Na<sub>2</sub>HPO<sub>4</sub>·7H<sub>2</sub>O, 10% Dextran sulfate) that were incubated at 37°C for 2 hr in water bath. After that prehybridization mixture was removed and replaced with mixed probe/hybridization buffer solution (4 µl: 500 µl). The membranes were incubated in water bath at 37°C overnight and membrane was carefully washed away with consecutive washes in wash buffer 1 (1xSSC, 0.1%SDS, pH 7) at 37°C for 5 minutes, wash buffer 2 (0.1xSSC, 0.2%SDS, pH 7) at 37°C for 5 minutes and in wash buffer 3 (0.5x SSC, pH 7) at 37°C for 1 hr. After that blocking reagent with skim milk (5% in 1xTris-buffered saline, TBS) was added and applied to the membrane for 1 hr at room temperature and wash membrane with 1xTBS, pH 7 for 5 minutes at room temperature. In detection step, the membranes were incubated at room temperature for 1 hr with anti-digoxigenin Fab fragments conjugated to alkaline phosphatase (diluted 1:100 in 3% BSA, Roche Diagnostics, German) and washed three times with 1xTBS, each time for 5 minutes. Alkaline phosphatase substrate NBT/BCIP (nitro-blue tetrazolium and 5-bromo-4-chloro-3'-indolylphosphate, Thermo-scientific) was added to membrane. The development of a dark blue positive reaction was allowed to proceed for 20 minutes at room temperature and membrane was washed for 5 minutes with 1xTBS buffer, air dried and stored in a polypropylene bag.

### 2.4 Analytical sensitivity of the methods

The sensitivity of conventional dot-blot hybridization methods (method A: System probe labeled DIG at 5'-OH labeling DIG hybrids/ anti DIG-AP, detection with NBT/BCIP and method B: System probe labeled with biotin at 5'-OH labeling biotin hybrids / streptavidin-HRP, detection with DAB), were compared with an application of catalyzed reporter deposition (CARD) to dot blot platform (method C: System probe labeled with biotin at 5'-OH labeling biotin hybrids/ 1°streptavidin-HRP/2°streptavidin-HRP, + system tyramide signal amplification (TSA), detection with DAB).



**Figure 1:** Determination of specificity of Sal3 probe by dot blot hybridization. DNA of Salmonella (1 = *S. enteritidis*, 2 = *S. typhimurium* and 3 = *S. paratyphimurim*). DNA of negative bacteria (4 = *Actinomyces* spp., 5 = *Campylobacter jejuni*, 6 = *Corynebacterium* spp., 7 = *Escherichia coli*, 8 = *Klebsiella* spp., 9 = *Pseudomonas* spp., 10 = *Staphylococcus aureus*, 11 = *Streptococcus agalactiae* and 12 = *Streptococcus suis*)

Method A: DNA extracted from *S. enteritidis* of each tenfold dilution sequence was tested for the sensitivity of dot blot hybridization, using a Sal 3 probe (labeled DIG at 5'-OH) and detection step according to step 2.3

Method B: DNA extracted from *S. enteritidis* of each tenfold dilution sequence was tested for the sensitivity of dot blot hybridization, by following per under step 2.3 using a Sal 3 probe (biotin at 5'-OH labeling) and detection step. 3 – 4 drops of the diluted Primary Streptavidin-HRP solution (GenPoint™, DAKO) were applied to cover the membrane and incubate at room temperature for 30 minutes. Membranes were rinsed in TBST wash buffer and placed in three fresh TBST wash buffer baths for 5 minutes each to remove residual primary streptavidin-HRP solution. 3 – 4 drops of diluted DAB chromogen were applied to cover the membrane and incubated at room temperature for 5 minutes, which contrasted well with the brown DAB signals and stopped the chromogen reaction by immersing membrane in water for 1 minute, air dried and storing in a polypropylene bag.

Method C: DNA extracted from *S. enteritidis* of each tenfold dilution sequence was tested for the sensitivity of dot blot hybridization, by following per under step 2.3 using a Sal 3 probe (biotin at 5'-OH labeling) and detection was performed using the Dako GenPoint™, 3 – 4 drops of the diluted Primary Streptavidin-HRP solution were applied to cover the membrane and incubated at room temperature for 15 minutes. Membranes were rinsed in TBST wash buffer and placed in three fresh TBST wash buffer baths for 5 minutes each to remove the residual primary streptavidin-HRP solution. Catalyzed signal amplification method (CARD) for biotinylated probes. Briefly, 3 – 4 drops of biotinyl tyramide were applied to cover the membrane and incubated at room temperature for 15 minutes. Membranes were rinsed in TBST wash buffer and placed in three fresh TBST wash buffer baths for 5 minutes each to remove residual biotinyl tyramide solution. 3 – 4 drops of secondary streptavidin-HRP solution were applied to cover the specimen and incubated at room temperature for 15 minutes. Membranes were rinsed in TBST wash buffer and placed in three fresh TBST wash buffer baths for 5 minutes each to remove residual secondary

Streptavidin-HRP solution. After that, 3 – 4 drops of diluted DAB chromogen were applied to cover the membrane and incubated at room temperature for 5 minutes, which contrasted well with the brown DAB signals and stopped the chromogen reaction by immersing membrane in water for 1 minute, air drying and storing in a polypropylene bag.

#### 2.4.1 Evaluation of detection limit of dot blot hybridization of three systems (A, B and C) in pure culture

*S. enteritidis* was the culture in 5 ml of tryptic soy broth (TSB), incubate at 37°C for 18 – 24 hr., at a concentration of McFarland turbidity standard of 1 (Grantbio, U.K.), which was approximately  $3 \times 10^8$  cfu/ml. Suspended cultures were diluted serially in 10-fold steps. Each serials dilution of bacteria sample were performed as DNA was extracted described previously and measurement of DNA concentration (Nanodrop, Thermoscientific) as described above to determine the sensitivity of all three different detection methods of dot blot hybridization, according to 2.3. One of the systems was chosen to detect the lowest amount of salmonella to continue for the next steps (2.4.2).

#### 2.4.2 Sensitivity of dot-blot hybridization in spiked pork

Hygienic pork obtained from the supermarket was confirmed as without contamination of external microorganisms (Charoen Pokphand Foods PCL (CP Foods), Thailand). Pork meat spiked with different concentrations of *S. enteritidis* that made tenfold dilution according to step 2.4.1. One milliliter of each serial dilutions of *S. enteritidis* was spiked on 25 g of pork meat that was added to 25 ml BPW with 0.1% Tween 80 solution and homogenized with a stomacher (BagMixer®400W) at high speed for 90 s. The 25 ml of bacteria cells were collected by filtration through 33-µm pore-size nylon screen mesh (diameter, 25 mm) into centrifuge tubes 50 ml, and then centrifuged at 7,000 rpm for 20 minutes. The BPW solution of each serial dilution was poured and dissolved the microbial sludge with 2 ml PBS and vortex at high speed for 5 minutes. So, one milliliter of each samples was centrifuged at 8,000 rpm for 10 minutes and cell pellet was extracted DNA as previously described for exam-

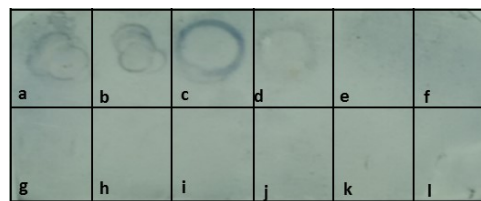
ining the sensitivity of the CARD-dot blot hybridization [17].

### 3. Results and Discussion

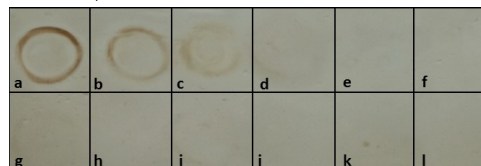
#### 3.1 Evaluation of specificity of Sal3 probe by dot blot analysis

The results of the specificity of the Sal 3 probe was tested by dot blot hybridization. The Sal 3 probe was found to be 100% specific for *S. enteritidis*, *S. typhimurium* and *S. Virchow*. (Fig.1), and can be directly determined by observing the Sal3 hybridized probes. The existence of purple dots at salmonella DNA dots at the locations was spotted. But, no cross-hybridization was observed with 9 strains of negative control. It showed that Sal 3 primer labeled with digoxigenin at the end of 5'OH was specific to all 3 *salmonella typhimurium*, *salmonella Virchow*, *salmonella enteritidis*, which are serovars important for causing gastrointestinal poisoning in Thai people [25], [26].

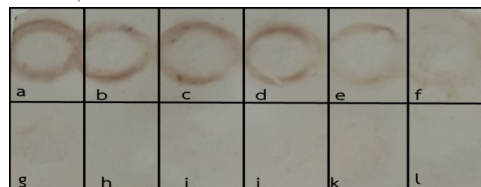
In this study, we have developed a dot blot hybridization assay for the detection of *Salmonella* using Sal3 oligonucleotide probe (5,-ATCACTCACC TACGTG-3.). The DNA target was hybridized with the membrane immobilized probe and the hybridization was detected by chemiluminescence. 23S rRNA gene of *Salmonella* from 3 different serovars of *Salmonella* hybridized with the probes was found, whereas those of species of *Actinomyces* spp, *Campylobacter jejuni*, *Corynebacterium* spp, *Escherichia coli*, *Klebsiella* spp, *Pseudomonas* spp, *Staphylococcus aureus*, *Streptococcus agalactiae*, and *Streptococcus suis* failed to hybridize. The specific probe binding in this study indicated hybridized Sal3 probe of 100% all salmonella strains. No cross-reaction to other strains of the Enterobacteriaceae family was observed (Fig.1). Nordentoft [19] has been published, that Sal3 oligonucleotide probes designed from the base sequence of the 23S rRNA gene (rDNA), salmonella-specific. The rRNA region has databases from domain or other higher taxa down to a species and rRNA was a routine region used for species identification. Moreover, species-specific probes designed from these genes can be applied for the analysis of any community. They can be detected using whole cell methods in which the cell remains intact and thus also the morphology, or using cell free methods in which total nucleic acids were extracted and probes were applied directly to the nucleic acid target [27 – 29]. A previous study showed that a Sal3 probe has been used for the detection of salmonella in food, wastewater [19], [20], [30 – 32]. The sequence of Sal3 probes was complementary with the helix 63 regions of 23S rRNA gene of salmonella [19]. The region was a highly conserved region of salmonella DNA among different species [33], [34].



**1. A-DIG:** System probe labeled DIG at 5'-OH labeling / anti DIG-AP, detection with NBT/BCIP



**2. B-BIOTIN:** System probe labeled with biotin at 5'-OH labeling / streptavidin-HRP, detection with DAB.



**3. C-CARD:** System probe labeled with biotin at 5'-OH labeling / 1°streptavidin-HRP/ 2°streptavidin-HRP, +system tyramide signal amplification (TSA), detection with DAB

**Figure 2:** Comparative dot blot analysis determining the sensitivity of three methods for the visualization of dilution factors of salmonella DNA with enhanced haptens signal as chromogen: Dilution factor of *Salmonella* cell was DNA extraction: a= Initial concentration  $\sim 10^8$  cfu/ml, b = -1, c = -2, d = -3, e = -4, f = -5, g = -6, h = -7, i = -8, j = *Escherichia coli*, k = *Aeromonas hydrophila*, and l = *Enterobacter aerogenes* (negative control)

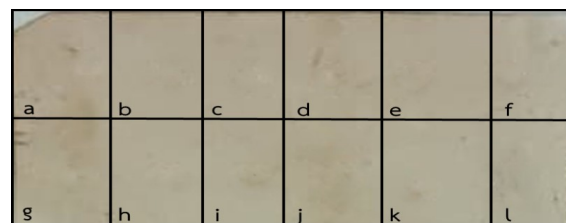
#### 3.2 Evaluation of detection limit of dot blot hybridization of three methods (A, B and C) in pure culture

To determine the lower limit of dot blot hybridization assay, ten-fold serially diluted ( $10^0 - 10^8$ ); then, we tested the 3 methods of detection by dot blot hybridization assay established in this study for simultaneous detection of *Salmonella* spp. As a consequence of conventional dot blot hybridization assay such as method A: System probe was labeled DIG at 5'-OH labeling DIG hybrids/ anti DIG-AP, detection with NBT/BCIP and method B: System probe was labeled with biotin at 5'-OH labeling biotin hybrids /streptavidin-HRP, detection with DAB), the detection limit in pure culture of *S. enteritidis* was determined to be  $10^6$  cfu/ml (DNA concentration  $22.40 \mu\text{g}/\mu\text{l}$ ; expected cell concentration =  $< 3 \times 10^3 - 10^4$  cfu/ml). However, method C: System probe was labeled with biotin at 5'-OH labeling biotin hybrids /1°streptavidin-HRP /2°streptavidin-HRP, + system tyramide signal amplification (TSA), detection with DAB), the detection limit in pure culture of *S. enteritidis* was determined to be  $10^4$  cfu/ml (DNA concentration  $9.41 \mu\text{g}/\mu\text{l}$ ; expected cell concentration =  $< 3$  cfu/ml), as shown in (Fig. 2; Table 1).

Dot blot hybridization assay is a diagnosis tool of routine use in the diagnosis laboratory. When

**Table 1.** The relationship between serial dilutions and the amount of DNA of *S. enteritidis* extracted from pure culture on dot blot hybridization assays.

Dilution factor	Number of salmonella cell(cfu/ml)	Elute of 30 $\mu$ l of DNA extraction, concentration ( $\mu$ g/ $\mu$ l)	Wavelength (A260/280)	4/ $\mu$ l of DNA concentration were dot on membrane ( $\mu$ g/ $\mu$ l)	Expected cell concentration (cfu/ml)	Observation of Dot blot hybridization assay		
						Method A	Method B	Method C
Initial	$3 \times 10^8$	220.9	1.85	36.81	$\sim 10^4$	+	+	+
-1	$3 \times 10^7$	152.45	1.89	25.4	$\sim 3 \times 10^3 - 10^4$	+	+	+
-2	$3 \times 10^6$	134.45	1.82	22.4	$\sim 3 \times 10^3 - 10^4$	+	+	+
-3	$3 \times 10^5$	82.4	1.84	13.73	< 3	-	-	+
-4	$3 \times 10^4$	56.5	1.88	9.41	< 3	-	-	+
-5	$3 \times 10^3$	21.7	1.71	3.61	< 3	-	-	-
-6	$3 \times 10^2$	19.2	1.72	3.2	< 3	-	-	-
-7	$3 \times 10^1$	13.5	1.51	2.25	< 3	-	-	-
-8	$3 \times 10^0$	14.7	1.6	2.45	< 3	-	-	-

**Figure 3:** The sensitivity of the salmonella DNA detection limits of CARD dot blot hybridization. : Dilution factor of Salmonella cell: a = Initial concentration  $\sim 10^8$  cfu/ml, b =  $10^7$ , c =  $10^6$ , d =  $10^5$ , e =  $10^4$ , f =  $10^3$ , g =  $10^2$ , h =  $10^1$ , i =  $10^0$ , j =  $10^{-1}$ , k = *Escherichia coli*, l = *Enterobacter aerogenes* (negative control)

a pure culture was used, the direct detection methods of digoxigenin probe by antitoxigenin-alkaline phosphatase conjugate (method A) and biotinylated probe by streptavidin- Horseradish peroxidase conjugate (method B) were compared with the CARD detection method (Method C). The third one proved to more sensitive than the conventional detection using homologous 23S rRNA targets of salmonella. The dot blot hybridization assay using the CARD detection method was able to minimum amount of detectable 9.41  $\mu$ g/  $\mu$ l of salmonella DNA corresponding approximately to  $10^4$  genome copies. CARD detection method based on signal amplification by the tyramide reaction is generally considered the most sensitive of the dot blot hybridization methods; on average their sensitivity is 100 times greater than that of conventional dot blot hybridization. Corresponding, previous studies showed that CARD-FISH methods are more sensitive than the conventional FISH methods [35 – 37]. The sensitivity of the different of assays is in the range of  $10^4 - 10^8$  genome copies; therefore, even if slightly higher sensitivity can be reached with different method detection (A, B and C), dot blot hybridization assays can detect the total number of salmonella cells. Consequently, dot blot hybridization methods add a signal amplification step (method C), Using tyramide substrates in sequential horseradish peroxidase reactions that described here could be completed within 2 days and was specific for the detection of salmonellae. However, the sensitivity of the CARD dot blot hybridization that was determined uses different serial diluted salmonella cell concentrations

of DNA extracted from pork samples. The CARD dot blot hybridization was not detection of all DNA range of spike concentrations of salmonella cells. This suggested that the recovery of salmonella rRNA from pork was not as good as from pure cultures.

By this assay, the method C: was possible to detect in the order of  $10^4$  salmonella cell of pure culture in 16 – 18 hr. Therefore, we chose method C to test artificial contamination with *S. enteritidis* on pork meat.

### 3.3 Sensitivity of dot-blot hybridization for salmonella detection on pork spiked

Regarding the sensitivity test for determination of the DNA content from serially diluted salmonella cells in step 2.1 that spiked on pork samples, CARD - Dot blot hybridization by Sal3 probe was not possible to hybridize both with salmonella DNA and negative control of bacterial as shown in fig.3, (Table 2).

Several other methods have been described as specificity and sensitivity of technique detection such as PCR and ELISA for salmonella detection that strongly affected by inhibitory substances which might be present in for example food [38]. For example, fat, glycogen, organic and phenolic compounds and humic acids can cause false-negative results of method detection [39]. The DNA concentration and Purity are important factors for the success of DNA base methods including dot blot hybridization. In generally, the DNA extraction kits are often designed for extracting DNA from pure culture consisting of highly concentrated cells and methods detection that are high sensitivity [40]. When we tested the meat samples diluted

**Table 2.** Serial dilutions of the relationship and the amount of DNA of *S. enteritidis* extracted from pork spike on CARD dot blot hybridization assay.

Dilution factor	Number of salmonella cell (cfu/ml)	Elute of 30 $\mu$ l of DNA extraction, concentration ( $\mu$ g/ $\mu$ l)	Wave length (A260/280)	4/ $\mu$ l of DNA concentration were dot on membrane ( $\mu$ g/ $\mu$ l)	Expected cell concentration (cfu/ml)	Observation of CARD dot blot hybridization
Initial	$3 \times 10^8$	21.7	1.98	2.89	< 3	-
-1	$3 \times 10^7$	18.8	1.82	2.51	< 3	-
-2	$3 \times 10^6$	19.2	1.8	2.56	< 3	-
-3	$3 \times 10^5$	29	1.79	3.87	< 3	-
-4	$3 \times 10^4$	9.5	1.82	1.27	< 3	-
-5	$3 \times 10^3$	14.7	1.82	1.96	< 3	-
-6	$3 \times 10^2$	13.5	1.86	1.80	< 3	-
-7	$3 \times 10^1$	4.5	1.57	0.60	< 3	-
-8	$3 \times 10^0$	5.9	2.81	0.79	< 3	-

with salmonella cell concentrations; it found that low amount of DNA extracted and low purity of DNA extracted (Table 2), which is may be caused by fat tissue from the meat samples (Minced pork with pork fat). The complexities of various food materials and the use of various extraction methods result in different DNA yields [41]. Corresponding to Laube *et al.*, [42] it reported a discrepancy in the yield of DNA extracted from various source of tissues. Fatty tissues produced a lower concentration of DNA compared to kidney, liver, heart and tendon tissues. That may be due, to high debris amounts of fatty tissue in the pork and the difficulties of removing fatty substances during the DNA extraction step. Thus, it is necessary to add steps for pretreated sample appropriate such as fat removal before DNA extraction [43]. In addition, the low DNA recovery in this study may be a loss of DNA during sample processing. This is in accordance with Zhang *et al.*, [44] which reported during samples processing of pathogen detections base on a molecular technique (eg. Filtration, centrifugation, DNA extract). So, this causes underestimated quantification of DNA to be significantly lower. However, detection of CARD dot blot hybridization can detect at a low abundance of salmonella cells in pure culture. But, it's not suitable for pork samples. In future study, we recommend that use of appropriate DNA extraction kits or methods is critical for successful and valid CARD dot blot hybridization which posed a challenge for salmonella detection on pork samples.

## Acknowledgments

This work was supported in part by the National Research Council of Thailand is for funding 2018. We would like to thank the Department of Veterinary Pathology, Faculty of Veterinary Medicine, Kasetsart University, Thailand, Department of Veterinary Public Health, Faculty of Veterinary Medicine, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, Thailand, Kamphaeng Saen Veterinary Diagnosis center, Faculty of Veterinary Medicine, Kamphaeng Saen Campus, Nakhon Pathom. Thailand and Department of Animal Sciences, Faculty of Agriculture and Technology, Phetchaburi Rajabhat University,

Phetchaburi, Thailand for providing technical assistance.

## References

- [1] CDC. Outbreaks Involving Salmonella(2018), <https://www.cdc.gov/salmonella/outbreaks.html> (accessed 27 April 2021).
- [2] EFSA (European Food Safety Authority), The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2014, EFSA J.13 (12) 4329 (2015) 191.
- [3] R. S. Hendriksen, A. R. Vieira, S. Karlsmose, D. M. A. Lo Fo Wong, A. B. Jensen, H. C. Wegener, F. M. Aarestrup, Global monitoring of *Salmonella* serovar distribution from the World Health Organization Global foodborne infections network country data bank: Results of quality assured Laboratories from 2001 to 2007, Foodborne Pathogens and Disease 8(8) (2011) 1 – 14.
- [4] Z. Liang, B. Ke, X. Deng, J. Liang, L. Ran, L. Lu, D. He, Q. Huang, C. Ke, Z. Li, H. Yu, J. D. Klena, S. Wu, Serotypes, seasonal trends, and antibiotic resistance of non-typhoidal *Salmonella* from human patients in Guangdong Province, China, 2009 – 2012, BMC Infect. Dis. (2015) 55.
- [5] A. Fàbrega, J. Vila, *Salmonella* enterica serovar typhimurium skills to succeed in the host: virulence and regulation, Clin. Microbiol. Rev. 26 (2013) 308 – 341.
- [6] EFSA, The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2017, EFSA J 16 (2018).
- [7] EFSA, European Food Safety Authority. The European Union summary report on trends and sources of zoonoses, zoonotic agents and foodborne outbreaks in 2016, EFSA J. 15 (2017).
- [8] EFSA. European Food Safety Authority. Guidelines for reporting data on zoonoses, antimicrobial resistance and foodborne outbreaks using the EFSA data models for the data collection framework (DCF) to be used in 2017 for 2016 data, ISSN 2397-8325, (2016).
- [9] S. Angkitittrakul, P. Tangkawattana, D. Sithigon, A. Polpakdee, D. Sithigon. Prevalence and antimicrobial resistance of salmonella isolated from been Khon Kaen municipality, Asia-Pacific Journal of Science and Technology 16 (2) (2011) 1 – 7.
- [10] C. Little, S. Walsh, L. Surman-Lee, K. Pathak, Y. Hall, E. De pinna, E. Threlfall, A. Maund, C. Chan, Salmonella contamination in non-UK produced shell eggs on retail scale in some regions of England, Weekly releases (1997 – 2007) 11 (47) (2006).
- [11] Y. Otomo, K. Abe, K. Odagiri, A. Shiroto, K. Takatori, Y. Hara-Kudo, Detection of *Salmonella* in spent hens and eggs associated with foodborne infections, Avian Diseases 51 (2007) 578 – 583.
- [12] M. Vieira-Pinto, M. Oliveira, J. Aranha, C. Martins, F. Bernardo, Influence of an enrichment step on *Salmonella* sp. detection by fluorescent in situ hybridization on pork samples, Food Control 19 (2008) 286 – 290.



- [13] B. Bisha, Fluorescence in situ hybridization-based detection of *Salmonella* spp. and *Listeria monocytogenes* in complex food matrices. Graduate Theses and Dissertations 10609 (2009).
- [14] D. Liu, Molecular detection of foodborne pathogen, CRC Press, 2009.
- [15] S. Ghazaleh, E. Zeinab, K. Hossein, Efficiency of fluorescence in situ hybridization (FISH) method for the rapid detection of *Salmonella* in minced lamb meat: Method analysis and optimization, *Journal of Microbiological Methods* 175 (2020) 1 – 9.
- [16] O. Adebawale, L. Good, Development of a fixation-free fluorescence in situ hybridization for the detection of *Salmonella* species, *Biology Methods and Protocols* (2020) 1 – 12.
- [17] D. Arlai, S. Chuanchom, T. Sirinarumit, Optimization of cell permeabilization for rapid detection of *Salmonella* in pork by FISH, *Thai J Vet Med.* 2015 45(1) (2012) 91 – 99. (in Thai)
- [18] M. Zerbini, M. Cricca, G. Gentilomi, S. Venturoli, G. Gallinella, M. Musiani, Tyramide signal amplification of biotinylated probe in dot-blot hybridization assay for the detection of parvovirus B19 DNA in serum samples, *Clinica Chimica Acta* 302(1-2) (2000) 79 – 87.
- [19] S. Nordentoft, H. Christensen, H. C. Wegener, Evaluation of a fluorescence-labelled oligonucleotide probe targeting 23S rRNA for in situ detection of *Salmonella* serovars in paraffin-embedded tissue sections and their rapid identification in bacterial smears, *J Clin Microbiol* 35 (1997) 2642 – 2648. (in Thai)
- [20] M. M. Vieira-Pinto, M. Olivera, F. Bernardo, C. Martins, Evaluation of Fluorescent *in situ* hybridization (FISH) as a rapid screening method for detection of salmonella tonsils of slaughtered pig for consumption: a comparison with conventional culture method, *Journal of Food Safety* 25 (2005) 109 – 119.
- [21] B. Örmeci, K. G. Linden, Development of a fluorescence *in situ* hybridization protocol for the identification of microorganisms associated with wastewater particles and flocs. *J. Environ. Sci. and Health, Part A.* 43 (2008) 1484 – 1488.
- [22] C. Almeida, N. F. Azevedo, R. M. Fernandes, C. W. Keevil, M. J. Vieira, Fluorescence *in situ* hybridization method using a peptide nucleic acid probe for identification of *Salmonella* spp. in a broad spectrum of samples, *Appl Environ Microbiol* 76 (2010) 4476 – 4485.
- [23] B. Bottari, G. E. Felis, E. Salvetti, A. Castioni, I. Campedelli, S. Torriani, V. Bernini, M. Gatti, Effective identification of *Lactobacillus casei* group species: genomebased selection of the gene *mutL* as the target of a novel multiplex PCR assay. *Microbiology* 163 (2017) 950 – 960.
- [24] G. H. Keller and M. M. Manak, DNA Probes. In: Stockton Press, New York (1989) 30 – 68
- [25] K. Vaeteewootacharn, S. Sutra, S. Vaeteewootacharn, D. Sithigon, O. Jamjane, C. Chomvarin, C. Hahnvanawong, N. Thongsakulpanich, K. Thaewnon-giew, Salmonellosis and the food chain in Khon Kaen, Northeastern Thailand, *Southeast Asian J Trop Med Public Health* 36(1) (2005) 123 – 129.
- [26] S. Saleh, *Salmonella* Typhi, Paratyphi A, Enteritidis and Typhimurium core proteomes reveal differentially expressed proteins linked to the cell surface and pathogenicity, *PLoS Negl Trop Dis.* 13(5) (2019).
- [27] L. Guillou, M.-J. Chretiennot-Dinet, L. K. Medlin, H. Claustre, S. Loiseaux-de Goer, D. Vulot, *Bolidomonas*, a new genus with two species belonging to new algal class, the Bolidophyceae Heterokonta, *J. Phycol.* 35 (1999) 368 – 381.
- [28] B. Karlsen, C. Cusack, E. Beensen, Microscopic and molecular methods for quantitative phytoplankton analysis. *InIOC Manuals and Guides*, No. 55 UNESCO: Paris, France, 2010.
- [29] Y. Kumar, R. Westram, S. Behrens, B. Fuchs, F. O. Glöckner, R. Amann, H. Meier, W. Ludwig, Graphical representation of ribosomal RNA probe accessibility data using ARB software package. *BMC Bioinform* 6 (2005) 61.
- [30] M. Oliviera, F. Bernardo, Fluorescent *In Situ Hybridization* aplicado à detecção rápida de *Salmonella* de origem alimentar e ambiental, *Rev. Port. Cien. Vet.* 97 (2002) 81 – 85.
- [31] M. Vieira-Pinto, M. Oliveira, F. Bernardo, C. Martins, Rapid detection of *Salmonella* spp. in pork samples using fluorescent in situ hybridization: a comparison with VIDAS (R)-SLM system and ISO 6579 cultural method. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia* 59 (2007) 1388 – 1393.
- [32] B. Örmeci, K. G. Linden, Development of a fluorescence in situ hybridization protocol for the identification of microorganisms associated with wastewater particles and flocs, *J. Environ. Sci. and Health Part A.* 43 (2008) 1484 – 1488.
- [33] N. D. Christensen, R. Kirnbauer, J. T. Schiller, S.-J. Ghim, R. Schlegel, A. B. Jensen, J. W. Kreider, Human papillomavirus types 6 and 11 have antigenically distinct strongly immunogenic conformationally dependent neutralizing epitopes, *Virology* 205 (1994) 329 – 335.
- [34] G. Van Camp, H. Fierens, P. Vandamme, H. Goossens, A. Huyghebaert, R. De Wachter, Identification of enteropathogenic *Campylobacter* species by oligonucleotide probes and polymerase chain reaction based on 16S rRNA genes, *Syst Appl Microbiol* 16 (1993) 30 – 36.
- [35] M. N. Bobrow, T. D. Harris, K. J. Shaughnessy, G. J. Litt, Catalyzed reporter deposition, a novel method of signal amplification: application to immunoassays, *J. Immunol. Methods* 125 (1989) 279 – 285.
- [36] H. Clay, L. Ramakrishnan, Multiplex fluorescent in situ hybridization in zebrafish embryos using tyramide signal amplification, *Zebrafish* 2 (2) (2005) 105 – 111.
- [37] A. U. Zaidi, H. Enomoto, J. Milbrandt, K. A. Roth, Dual fluorescent in situ hybridization and immunohistochemical detection with tyramide signal amplification, *J Histochem Cytochem* 48 (2000) 1369 – 1375
- [38] A. Rohde, J. A. Hammerl, S. Al Dhok, Detection of foodborne bacteria zoonoses by fluorescence in situ hybridization, *Food Control* 69 297 – 305.
- [39] I. G. Wilson, Inhibition and facilitation of nucleic acid amplification, *Appl Environ Microbiol* (1997) 3741 – 3751.
- [40] M. C. Thomas, M. J. Shields, K. R. Hahn, T. W. Janzen, N. Goji, K. K. Amoako, Evaluation of DNA extraction methods for *Bacillus anthracis* spores isolated from spiked food samples, *Journal of Applied Microbiology* 115 (2013) 156 – 162.
- [41] N. Sajali, S. C. Wong, U. K. Hanapi, S. A. B. Jamaluddin, N. A. Tasrip, N. A. Mohd Desa, The challenges of DNA extraction in different assorted food Matrices: A review, *Journal of Food Science* 83(10) (2018) 2409 – 2414.
- [42] I. Laube, J. Zagon, H. Broll, Quantitative determination of commercially relevant species in foods by real-time PCR, *International Journal of Food Science and Technology* 42 (2007) 336 – 341.
- [43] Z. Piskata, E. Pospisilova, G. Borilova, Comparative study of DNA extraction methods from fresh and processed yellowfin tuna muscle tissue. *International Journal of Food, Properties* 20 (1) (2017) 430 – 443.
- [44] Q. Zhang, S. Ishii, Improved simultaneous quantification of multiple waterborne pathogens and fecal indicator bacteria with the use of a sample process control, *Water Research* 137 (2018) 193 – 200.