

Adzitey et al. 2013 : 3 (1) 87-93

# GENOTYPING OF SALMONELLA STRAINS ISOLATED FROM DUCKS AND THEIR ENVIRONMENTS IN PENANG, MALAYSIA USING REPETITIVE EXTRAGENIC PALINDROMIC (REP)

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ARTICLE INFO	ABSTRACT
Received 17. 1. 2013 Revised 29. 7. 2013 Accepted 29. 7. 2013 Published 1. 8. 2013 Regular article	Salmonella are important foodborne pathogens of worldwide concern. The objective of this study was to determine the genetic diversity of 107 Salmonella strains isolated from ducks, their rearing and processing environments in Penang, Malaysia using repetitive extragenic palindromic-polymerase chain reaction (REP-PCR). REP-PCR of the Salmonella strains produced DNA bands of different sizes for differentiation purposes. The DNA band sizes ranged from 105-7692 bp for <i>S</i> . Typhimurium, 116-7033 bp for <i>S</i> . Hadar, 127-7399 bp for <i>S</i> . Enteritidis, 140-7497 bp for <i>S</i> . Braenderup and 123-5857 bp for <i>S</i> . Albany. Cluster analysis at a coefficient of 0.85 grouped the Salmonella strains into various clusters and singletons. <i>S</i> . Typhimurium were grouped into 4 clusters and 26 singletons at a discriminatory index ( <i>D</i> -value) of 0.98, <i>S</i> . Hadar were grouped into 3 clusters and 13 singletons at a <i>D</i> -value of 0.914, <i>S</i> . Enteritidis were grouped into 3 clusters and 9 singletons at a <i>D</i> -value of 0.971, <i>S</i> . Braenderup were grouped into 2 clusters and 11 singletons at a <i>D</i> -value of 0.981, and <i>S</i> . Albany were grouped into 3 clusters and 7 singletons at a <i>D</i> -value of 0.978. With the exception of <i>S</i> . Hadar strains which were grouped into two major groups (genotypes) by REP-PCR, the rest were grouped into three major genotypes. REP-PCR successfully typed all the Salmonella strains and proved to be a useful typing tool for determining the genetic diversity of the duck Salmonella strains. Determining the genetic diversity among Salmonella strains, other foodborne pathogens and their sources of isolation is important to trace their primary or potential sources and the sources of human infection.

Keywords: Ducks, genetic diversity, REP-PCR, Salmonella strains

## INTRODUCTION

Salmonellae are important foodborne pathogens in both developed and developing countries. Salmonellae are involved in a number of foodborne disease outbreaks which have resulted into human illnesses, hospitalizations or deaths. **CDC (2010)** reported a total of 190 illnesses in the United State of America due to the outbreak of *Salmonella* Heidelberg which was linked to the consumption of contaminated kosher broiled chicken livers. Among all foodborne bacterial infections in the United State of America, salmonellae have been estimated as the second largest cause of human illnesses and first in hospitalization and human deaths (**Scallan et al., 2011**). In the United Kingdom, 9,685 cases of human salmonella infections were reported in 2010 (**Defra, 2010**). In most developing countries, data on salmonella infections or outbreaks is unavailable due the lack of effective monitoring and reporting systems of foodborne infections.

Effective monitoring and reporting systems of foodborne pathogens will depend largely on effective surveillance studies, effective methods of isolating foodborne pathogens and/or effective characterization or typing of foodborne pathogens (Adzitey and Corry, 2011; Adzitey and Nurul, 2011; Frederick and Huda, 2011; Adzitey et al., 2012a). Typing of foodborne pathogens have be achieved using molecular methods like pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), random amplified polymorphic deoxyribonucleic acid (RAPD), enterobacterial repetitive intergenic consensus (ERIC), repetitive extragenic palindromic (REP), ribotying and many more (Versalovic et al., 1991; Jersek et al., 1999; Bennasar et al., 2000; Adzitey et al., 2012a; Adzitey et al., 2013a, b). These typing methods are used to analyze foodborne pathogens isolated from various sources and by comparing the DNA bands of these pathogens, the genetic relatedness or diversity can be established. Comparing the DNA bands of foodborne pathogens can also lead to establishing the source of human infection and/or major source of contamination.

Duck production is an important agricultural business in Malaysia. FAO statistics in 2009 indicated that Malaysia is the third world producer of duck meats (FAO, 2009). Current agricultural policies in Malaysia also continue to encourage duck farmers to increase their production for local consumption and export purposes

(Adzitey et al., 2012b). Important foodborne pathogens like *Campylobacter* species, *Salmonella* species, *Listeria* species and *Escherichia coli* have been isolated from ducks in Malaysia (Adzitey et al., 2011a, b; Adzitey et al., 2012b, c, d, e; Adzitey et al., 2013a). Contact with ducklings or the consumption of duck eggs, meats or products contaminated with salmonellae have been associated with salmonellosis, hospitalization and/or death of affected persons (Merritt and Herlihy, 2003; Noble et al., 2012). Therefore, determining the genetic relatedness or diversity among duck foodborne pathogens and their environments is essential to give an idea about the distribution of these foodborne pathogens in various samples and their possible roles in human infections.

Thus this study was carried out to determine the genetic relatedness of *Salmonella* strains isolated from ducks and their environmental sources in Penang, Malaysia.

### MATERIAL AND METHODS

#### Salmonella strains

A total of 107 Salmonella strains isolated from ducks, their rearing and processing environments were used in this study (Adzitey et al., 2012b). The Salmonella strains were made up of 37, 26, 15, 15 and 14 of S. Typhimirium, S. Hadar, S. Enteritidis, S. Braenderup, and S. Albany, respectively. They were isolated from duck faeces (n=36), intestines (n=25), cloaca swabs (n=14), soils (n=11), wash water (n=8), pond water (n=3), carcass rinses (n=3), drinking water (n=2), floor swabs (n=2), transport crate swabs (n=2), feed (n=1) and table swab (n=1).

#### Extraction of deoxyribonucleic acid (DNA)

A single colony of pure *Salmonella* was inoculated into 10 ml Trypticase Soy Broth and incubated at a temperature of 37 °C overnight. One ml of the overnight culture was centrifuged for 2 min at 14,000 x g. Pelleted bacterial cells were subjected to DNA extraction using Wizard® Genomic DNA Purification Kit by

following the manufacturer's instructions (**Anonymous, 2011**). Briefly, bacterial cells were lysed in 600  $\mu$ l nuclei lysis solution (for 5 min at 80 °C) and in 3  $\mu$ l RNase solution (for 30 min at 37 °C). The protein was precipitated in 200  $\mu$ l of protein precipitate solution, incubated on ice for 5 min and centrifuged for 5 min at 14,000 x g. DNA precipitation was achieved by transferring the supernatants into 600  $\mu$ l isopropanol (centrifuged for 3 min at 14,000 x g) and into 600  $\mu$ l 70% ethanol (centrifuged for 3 min at 14,000 x g). The ethanol was aspirated and the pellet air-dried for 10-15 min at room temperature. Finally, DNA pellets were rehydrated in 100  $\mu$ l rehydration solution for 1 h at 65 °C and the concentration adjusted to 100 ng/ $\mu$ l for further use.

#### **REP** analysis of Salmonella strains

Extracted DNA was subjected to a modified REP-PCR described by **Versalovic** *et al.* (1991) and Jersek *et al.* (1999). The (18-mer) primer REP1R-I (5'-IIIICGICGICATCIGGC-3') and REP2-I (5'-ICGICTTATCIGGCCTAC-3) was used for the REP-PCR. REP-PCR was carried out in a 25  $\mu$ l volume containing 12.5  $\mu$ l GoTaq mastermix (M5132, Promega, USA), 7  $\mu$ l nuclease free water, 2  $\mu$ l 25 mM MgCl<sub>2</sub>, 2.5  $\mu$ l template DNA and 0.5  $\mu$ l of each primer (2  $\mu$ M concentration). Amplification was done with the following temperature cycle: 1 cycle at 95 °C for 2 min; followed by 35 cycles at 90 °C for 30 s, 52 °C for 1 min and 65 °C for 8 min; and 1 cycle at 65 °C for 16 min. The amplification was performed using Biometra® TProfessional thermocycler, Germany. Amplicons (10  $\mu$ l) were stained with EZ-Vision® One DNA Dye (2  $\mu$ l), loaded on a 1.5% agarose gel and electrophoresed at 90 V for 1h 30 min. VC 1 kb and 100 bp DNA ladders (Vivantis, USA) were used as the molecular weight marker and the amplicons were visualized under UV transilluminator gel imaging system (Bio-Rad Gel Imaging System, USA).

#### Cluster analysis and calculation of discriminatory index

Cluster analysis and calculation of discriminatory index were done individually for the various *Salmonella* strains. DNA band sizes were determined using the detect band button of the NTSYSpc Version 2.2 programme. Band sizes were then scored as presence of DNA band (a score '1') and absence of DNA band (a score '0'). These scores were entered in NTedit to obtain a data matrix and then inserted in NTSYSpc Version 2.2 computer software for the construction of dendogram based on simple matching coefficient and UPGMA (Unweighted Pair-Group Arithmetic Average Clustering) cluster analysis to determine the genetic relatedness of the *Salmonella* strains. Clustering was defined at a coefficient of 0.85 and *Salmonella* strains not belonging to any particular cluster were referred to as singletons (single isolates). The discriminatory index (*Dvalue*) was calculated according to **Hunter and Gaston (1988**).

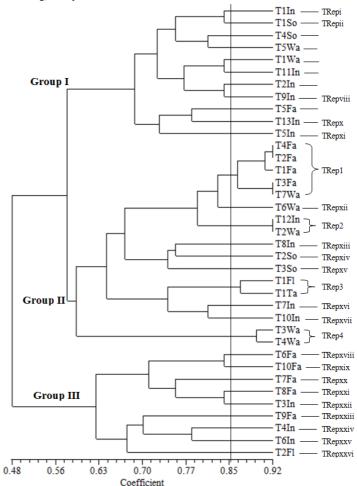
#### **RESULTS AND DISCUSSION**

Repetitive extragenic palindromic-polymerase chain reaction (REP-PCR) analysis of the 107 Salmonella strains isolated from ducks, their rearing and processing environments in Penang, Malaysia between 2009 to 2010 produced DNA bands/fingerprints of different sizes for differentiation among the strains of Salmonella and their sources of isolation. The DNA band sizes of S. Typhimurium ranged from 105-7692 bp, S. Hadar ranged from 116-7033bp, S. Enteritidis ranged from 127-7399 bp, S. Braenderup ranged from 140-7497 bp and that of S. Albany ranged from 123-5857 bp. Dendograms were constructed separately for the various Salmonella serovars thus S. Typhimurium (Figure 1a), S. Hadar (Figure 1b), S. Enteritidis (Figure 1c), S. Braenderup (Figure 1d), and S. Albany (Figure 1e). Clustering at a coefficient of 0.85 and the calculation of discriminatory index based on the number of clusters and singletons categorized the 37 S. Typhimirium into 4 clusters and 26 singletons at a D-value of 0.980, the 26 S. Hadar into 3 clusters and 13 singletons at a D-value of 0.914, the 15 S. Enteritidis into 3 clusters and 9 singletons at a D-value of 0.971, the 15 S. Braenderup into 2 clusters and 11 singletons at a D-value of 0.981, and the 14 S. Albany into 3 clusters and 7 singletons at a D-value of 0.978. Hunter and Gaston (1988) reported that if the *D*-value of a typing result is greater than 0.900, the typing result is desirable and can be interpreted with confidence. This study showed that the discriminatory indexes of the various Salmonella serovars at a coefficient of 0.85 were all greater than 0.900.

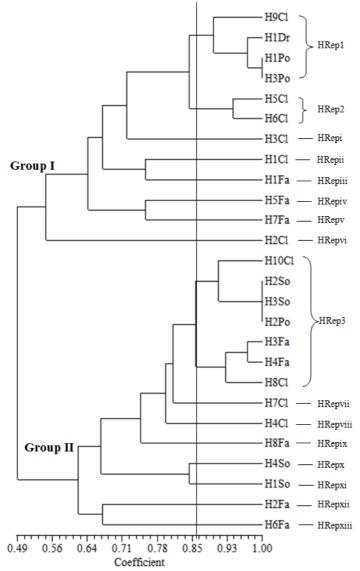
Clusters consisted of 2 or more *Salmonella* strains, for example, *S*. Typhimurium cluster 1 (TRep1), *S*. Hadar cluster 1 (HRep1), *S*. Enteritidis cluster 1 (ERep1), *S*. Braenderup cluster 1 (BRep1), *S*. Albany cluster 1 (ARep1) and so on (Figures 1a to 1e). *Salmonella* strains in the same cluster are clonal and genetically closely related. *Salmonella* serovars in the same cluster but isolated from different sources suggest possible cross contamination. Examples of such clusters are *S*. Typhimurium cluster 2 (TRep2) which consists of one isolate each isolated from duck intestines and wash water sample (Figure 1a), *S*. Hadar cluster 3 (HRep3) which consists of two isolates each isolated from duck cloaca, duck faces and soil sample, and one pond water sample (Figure 1b), and *S*. Braenderup cluster 2 (BRep2) which consists of one isolate each isolated from duck intestines and wash water sample (Figure 1b), and *S*. Braenderup cluster 2 (BRep2) which consists of one isolate each isolated from duck intestines and wash water sample (Figure 1d). *Salmonella* strains isolated from cloaca, wash water, soil and pond water might have taken their origin from duck

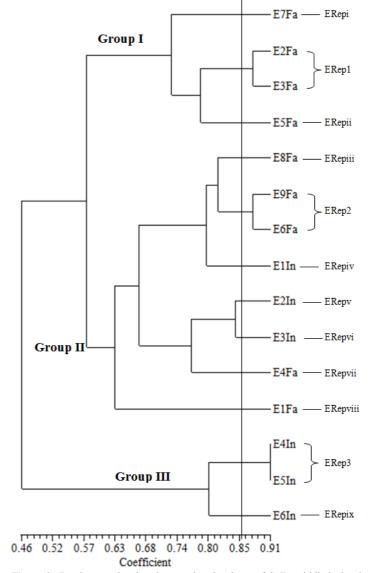
intestines and faeces. This is because duck intestines and faeces are known as primary sources of *Salmonella* species rather than cloaca, wash water, pond water and wash water samples (**Defra**, **2010**; **Adzitey** *et al.*, **2012**; **Adams and Moss**, **2008**; **EFSA**, **2012**). Singletons (single isolates) include *S*. Typhimurium singleton i (TRepi), *S*. Hadar singleton i (HRepi), *S*. Enteritidis singleton i (ERepi), *S*. Braenderup singleton i (BRepi), *S*. Albany singleton i (ARepi) and so on (Figures 1a to 1e). Singleton strains are genetically heterogeneous to other *Salmonella* strains.

From Figures 1a to 1e, the various Salmonella serovars could also be grouped generally into three major groups (genotypes) except for S. Hadar strains which were grouped into 2 major groups. This is expected since the Salmonella strains were isolated from the same animal species, similar environment and geographical area. Furthermore, each of this major group consists of Salmonella strains isolated from different sources and places (Table 1-3). For example, S. Typhimurium group I consists of Salmonella strains isolated from soil (farm 1), wash water (processor 1, processor 3), intestines (processor 1, processor 2) and faeces (farm 1) (Table 1), S. Hadar group I consist of Salmonella strains isolated from drinking water (farm 4), pond water (farm 4), cloacal (farm 3, farm 4) and faeces (farm 3, farm 4) (Table 2), S. Braenderup group 1 consist of Salmonella strains isolated from cloacal (farm 1), intestines (processor 1), wash water (processor 1) and faeces (farm 1) (Table 3), and other major groups (Tables 1 to 3). The afore-mentioned examples strongly suggest that Salmonella strains of similar genotypes were distributed within ducks and their environmental samples in Penang, Malaysia between 2009 to 2010.



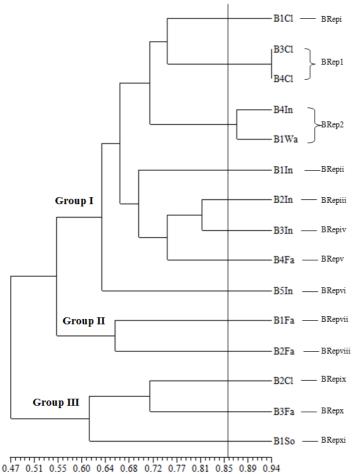
**Figure 1a** Dendogram showing the genetic relatedness of *S*. Typhimirium isolated from ducks and their environmental sources performed by REP-PCR. TRep1-TRep4 = *S*. Typhimirium cluster 1-4 by REP; TRepi-TRepxvi = *S*. Typhimirium singleton i-xxvi by REP; T = S. Typhimirium; 1-13 = strain number; In = intestines; Fa = faeces; Wa = wash water; So = soil; Fl = floor swab; and Ta = table swab.





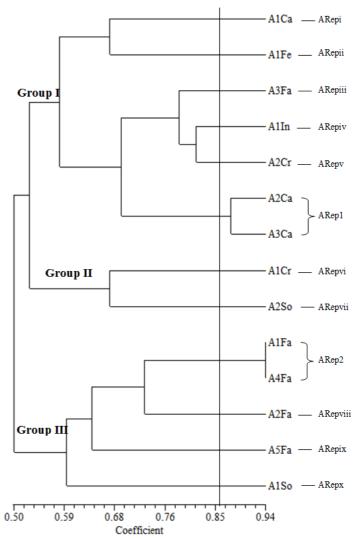
**Figure 2b** Dendogram showing the genetic relatedness of *S*. Hadar isolated from ducks and their environmental sources performed by REP-PCR. HRep1-HRep3 = *S*. Hadar cluster 1-3 by REP; HRepi-HRepxiii = *S*. Hadar singleton i-xiii by REP; H = *S*. Hadar; 1-10 = strain number; Cl = cloaca swab; Po = pond water; So = soil; Fa = faeces; and Dr = drinking water.

**Figure 3c** Dendogram showing the genetic relatedness of *S*. Enteritidis isolated from ducks and their environmental sources performed by REP-PCR. ERep1-ERep3 = *S*. Enteritidis cluster 1-3 by REP; ERepi-ERepix = *S*. Enteritidis singleton i-ix by REP; E = S. Enteritidis; 1-9 = strain number; Fa = faeces; and In = intestines.



Coefficient

**Figure 4d** Dendogram showing the genetic relatedness of *S*. Braenderup isolated from ducks and their environmental sources performed by REP-PCR. BRep1-BRep2 = *S*. Braenderup cluster 1-2 by REP; BRepi-BRepxi = *S*. Braenderup singleton i-xi by REP; B = *S*. Braenderup; 1-5 = strain number; Cl = cloaca swab; So = soil; In = intestines; Fa = faeces; and Wa = wash water



**Figure 5e** Dendogram showing the genetic relatedness of *S*. Albany isolated from ducks and their environmental sources performed by REP-PCR. ARep1-ARep2 = *S*. Albany cluster 1-2 by REP; ARepi-ARepx = *S*. Albany singleton i-x by REP; A = S. Albany; 1-5 = strain number; Ca = carcass rinse; So = soil; Cr=crate swab; Cl = cloaca swab; Fe = feed; In = intestines; and Fa = faeces.

REP depends on repetitive DNA elements present in salmonellae which are amplified during PCR process and when electrophoresed produce DNA bands of different sizes and numbers. The differences in band sizes and numbers are used/analyzed to determine the genetic relatedness or diversity among different salmonellae or foodborne pathogens. **Kerouanton** et al. (1996) used REP-PCR to differentiate 32 S. Dublin strains isolated from cattle and reported that, REP-PCR grouped the 32 S. Dublin strains into one type. **Bennasar** et al. (2000) also used REP to determine the genetic diversity of S. Enteritidis, S. Typhimurium and S. Virchow strains. They reported that these three serovars gave reproducible and distinguishable profiles using REP, ERIC or ITS, and the conserved patterns in each serovar allowed for easy differentiation from other serovars of Salmonella. Albufera et al. (2009) showed that REP-PCR analysis of Salmonella isolates from human and food sources generated different profiles for isolates of the same serogroup for differentiation purposes. This present study also revealed that REP-PCR could discriminate between Salmonella strains of the same serogroup.

## Table 1 Major groups of S. Typhimurium according to REP-PCR analysis

No.	Strain	Source of isolation	Strain code	Place of isolation	
1	S. Typhimurium	Wash water	T7Wa	Processor 1	Group II
2	S. Typhimurium	Faeces	T1Fa	Farm 1	Group II
3	S. Typhimurium	Faeces	T2Fa	Farm 1	Group II
4	S. Typhimurium	Faeces	T3Fa	Farm 1	Group II
5	S. Typhimurium	Faeces	T4Fa	Farm 1	Group II
6	S. Typhimurium	Intestines	T12In	Processor 2	Group II

7S. TyphimurianWash waterT2WaProcessor 3Group II8S. TyphimurianTable swabT1TaProcessor 4Group II9S. TyphimurianFloor swabT1FIProcessor 1Group II10S. TyphimurianWash waterT4WaProcessor 1Group II11S. TyphimurianMash waterT4WaProcessor 1Group II12S. TyphimurianIntestinesT1InProcessor 1Group II13S. TyphimurianSoilT1SoFarm 1Group II14S. TyphimurianSoilT4SoParcesor 1Group II15S. TyphimurianWash waterT1WaProcessor 1Group II16S. TyphimurianMash waterT1WaProcessor 1Group II17S. TyphimurianIntestinesT2InProcessor 1Group II18S. TyphimurianIntestinesT9InProcessor 1Group II20S. TyphimurianIntestinesT5InProcessor 1Group II21S. TyphimurianIntestinesT5InProcessor 1Group II22S. TyphimurianIntestinesT5InProcessor 1Group II23S. TyphimurianIntestinesT5InProcessor 1Group II24S. TyphimurianIntestinesT6WaProcessor 1Group II25S. TyphimurianIntestinesT1MaProcessor 1Group II26S. TyphimurianI						
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135. TyphimuriumSoilTISoFam 1Group I14S. TyphimuriumSoilT4SoFam 1Group I15S. TyphimuriumWash waterTSWaProcessor 1Group I16S. TyphimuriumWash waterTIWaProcessor 3Group I17S. TyphimuriumIntestinesT11hnProcessor 1Group I18S. TyphimuriumIntestinesT2lnProcessor 1Group I19S. TyphimuriumIntestinesT9lnProcessor 1Group I20S. TyphimuriumIntestinesT9lnProcessor 1Group I21S. TyphimuriumIntestinesT5FaFarm 1Group I22S. TyphimuriumIntestinesT5InProcessor 1Group I23S. TyphimuriumIntestinesT8InProcessor 1Group II24S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumIntestinesT10hProcessor 1Group II26S. TyphimuriumIntestinesT10hProcessor 1Group II27S. TyphimuriumIntestinesT10hProcessor 1Group II28S. TyphimuriumIntestinesT10hProcessor 1Group II29S. TyphimuriumIntestinesT10hProcessor 1Group II29S. TyphimuriumIntestinesT10hProcessor 1Group III29S. TyphimuriumIntestines <t< td=""><th>11</th><td>S. Typhimurium</td><td>Wash water</td><td>T4Wa</td><td>Processor 1</td><td>Group II</td></t<>	11	S. Typhimurium	Wash water	T4Wa	Processor 1	Group II
14S. TyphimuriumSoilT4SoFarm 1Group 115S. TyphimuriumWash waterT5WaProcessor 1Group 116S. TyphimuriumIntestinesT111nProcessor 3Group 117S. TyphimuriumIntestinesT21nProcessor 1Group 118S. TyphimuriumIntestinesT21nProcessor 1Group 119S. TyphimuriumIntestinesT91nProcessor 1Group 120S. TyphimuriumIntestinesT13nProcessor 2Group 121S. TyphimuriumIntestinesT5FaFarm 1Group 122S. TyphimuriumIntestinesT5InProcessor 1Group 123S. TyphimuriumIntestinesT5InProcessor 1Group 1124S. TyphimuriumIntestinesT8InProcessor 1Group 1125S. TyphimuriumIntestinesT8InProcessor 1Group 1126S. TyphimuriumIntestinesT10nProcessor 1Group 1127S. TyphimuriumIntestinesT10nProcessor 1Group 1128S. TyphimuriumFacesT0FaFarm 1Group 1129S. TyphimuriumFacesT10FaFarm 1Group 1129S. TyphimuriumFacesT10FaFarm 1Group 1131S. TyphimuriumFacesT7FaFarm 1Group 1131S. TyphimuriumFacesT31nProcessor 1 <th>12</th> <td>S. Typhimurium</td> <td>Intestines</td> <td>T1In</td> <td>Processor 1</td> <td>Group I</td>	12	S. Typhimurium	Intestines	T1In	Processor 1	Group I
14J. TyphimuriumWash waterTSWaProcessor 1Group 115S. TyphimuriumWash waterTIWaProcessor 3Group 116S. TyphimuriumIntestinesT11InProcessor 1Group 117S. TyphimuriumIntestinesT2InProcessor 1Group 118S. TyphimuriumIntestinesT9InProcessor 1Group 119S. TyphimuriumIntestinesT9InProcessor 1Group 120S. TyphimuriumIntestinesT5FaFarm 1Group 121S. TyphimuriumIntestinesT5InProcessor 2Group 122S. TyphimuriumIntestinesT5InProcessor 1Group 1123S. TyphimuriumIntestinesT8InProcessor 1Group 1124S. TyphimuriumSoilT2SoFarm 1Group 1125S. TyphimuriumIntestinesT7InProcessor 1Group 1126S. TyphimuriumIntestinesT10InProcessor 1Group 1127S. TyphimuriumFacesT6FaFarm 1Group 1130S. TyphimuriumFacesT10FaFarm 1Group 1131S. TyphimuriumFacesT7FaFarm 1Group 1133S. TyphimuriumFacesT9FaFarm 1Group 1133S. TyphimuriumFacesT9FaFarm 1Group 1133S. TyphimuriumIntestinesT3InProcessor 1 <td< td=""><th>13</th><td>S. Typhimurium</td><td>Soil</td><td>T1So</td><td>Farm 1</td><td>Group I</td></td<>	13	S. Typhimurium	Soil	T1So	Farm 1	Group I
1517NumberNumberTiWaProcessor 3Group 116S. TyphinuriumIntestinesT11InProcessor 1Group 117S. TyphinuriumIntestinesT2InProcessor 1Group 118S. TyphinuriumIntestinesT9InProcessor 1Group 119S. TyphinuriumIntestinesT9InProcessor 1Group 120S. TyphinuriumIntestinesT13InProcessor 1Group 121S. TyphinuriumIntestinesT5InProcessor 1Group 1122S. TyphinuriumIntestinesT5InProcessor 1Group 1123S. TyphinuriumIntestinesT8InProcessor 1Group 1124S. TyphinuriumIntestinesT8InProcessor 1Group 1125S. TyphinuriumSoilT2SoFarm 1Group 1126S. TyphinuriumIntestinesT10nProcessor 1Group 1127S. TyphinuriumIntestinesT10nProcessor 1Group 1128S. TyphinuriumFaccesT0FaFarm 1Group 1130S. TyphinuriumFaccesT0FaFarm 1Group 1131S. TyphinuriumFaccesT3FaFarm 1Group 1133S. TyphinuriumFaccesT9FaFarm 1Group 1133S. TyphinuriumIntestinesT3InProcessor 1Group 1133S. TyphinuriumIntestinesT3In	14	S. Typhimurium	Soil	T4So	Farm 1	Group I
1017S. TyphimuriumIntestinesT11InProcessor 1Group I18S. TyphimuriumIntestinesT2lnProcessor 1Group I19S. TyphimuriumIntestinesT9lnProcessor 1Group I20S. TyphimuriumFaccesT5FaFarm 1Group I21S. TyphimuriumIntestinesT13InProcessor 2Group I22S. TyphimuriumIntestinesT5InProcessor 1Group I23S. TyphimuriumIntestinesT8InProcessor 1Group II24S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT10InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaccesT6FaFarm 1Group II29S. TyphimuriumFaccesT10InProcessor 1Group II30S. TyphimuriumFaccesT10FaFarm 1Group II31S. TyphimuriumFaccesT8FaFarm 1Group III31S. TyphimuriumFaccesT10FaFarm 1Group III33S. TyphimuriumFaccesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1 </td <th>15</th> <td>S. Typhimurium</td> <td>Wash water</td> <td>T5Wa</td> <td>Processor 1</td> <td>Group I</td>	15	S. Typhimurium	Wash water	T5Wa	Processor 1	Group I
111.1	16	S. Typhimurium	Wash water	T1Wa	Processor 3	Group I
161718195. TyphimuriumIntestinesT9InProcessor IGroup I20S. TyphimuriumFaecesT5FaFarm 1Group I21S. TyphimuriumIntestinesT13InProcessor 2Group I22S. TyphimuriumIntestinesT5InProcessor 1Group I23S. TyphimuriumIntestinesT6WaProcessor 1Group II24S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT10InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT0FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III33S. TyphimuriumFaecesT9FaFarm 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumIntestinesT3InProcessor 1Group III35S. TyphimuriumIntestinesT3InProcessor 1Group III36S. TyphimuriumIntestines<	17	S. Typhimurium	Intestines	T11In	Processor 1	Group I
191711720S. TyphimuriumFacesTSFaFarm 1Group 121S. TyphimuriumIntestinesT13InProcessor 2Group 122S. TyphimuriumIntestinesT5InProcessor 1Group 123S. TyphimuriumWash waterT6WaProcessor 1Group 1124S. TyphimuriumIntestinesT8InProcessor 1Group 1125S. TyphimuriumSoilT2SoFarm 1Group 1126S. TyphimuriumSoilT3SoFarm 1Group 1127S. TyphimuriumIntestinesT7InProcessor 1Group 1128S. TyphimuriumIntestinesT10InProcessor 1Group 1129S. TyphimuriumFacesT6FaFarm 1Group 11130S. TyphimuriumFacesT10FaFarm 1Group 11131S. TyphimuriumFacesT3FaFarm 1Group 11133S. TyphimuriumFacesT9FaFarm 1Group 11134S. TyphimuriumIntestinesT3InProcessor 1Group 11134S. TyphimuriumIntestinesT4InProcessor 1Group 11136S. TyphimuriumIntestinesT4InProcessor 1Group 11136S. TyphimuriumIntestinesT4InProcessor 1Group 11136S. TyphimuriumIntestinesT4InProcessor 1Group 11136S. Typhimurium	18	S. Typhimurium	Intestines	T2In	Processor 1	Group I
20S. TyphimuriumIntestinesT13 InProcessor 2Group 121S. TyphimuriumIntestinesT5 InProcessor 1Group 122S. TyphimuriumIntestinesT6 WaProcessor 1Group 123S. TyphimuriumWash waterT6 WaProcessor 1Group II24S. TyphimuriumIntestinesT8 InProcessor 1Group II25S. TyphimuriumSoilT2 SoFarm 1Group II26S. TyphimuriumSoilT3 SoFarm 1Group II27S. TyphimuriumIntestinesT7 InProcessor 1Group II28S. TyphimuriumIntestinesT10 InProcessor 1Group II29S. TyphimuriumFaecesT6 FaFarm 1Group III30S. TyphimuriumFaecesT10 FaFarm 1Group III31S. TyphimuriumFaecesT7 FaFarm 1Group III32S. TyphimuriumFaecesT8 FaFarm 1Group III33S. TyphimuriumIntestinesT3 InProcessor 1Group III34S. TyphimuriumIntestinesT4 InProcessor 1Group III35S. TyphimuriumIntestinesT6 InProcessor 1Group III36S. TyphimuriumIntestinesT6 InProcessor 1Group III36S. TyphimuriumIntestinesT4 InProcessor 1Group III36S. TyphimuriumIntestines<	19	S. Typhimurium	Intestines	T9In	Processor 1	Group I
211122S. TyphimuriumIntestinesT5InProcessor 1Group I23S. TyphimuriumMash waterT6WaProcessor 1Group II24S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT7InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT3InProcessor 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumIntestinesT4InProcessor 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III37S. TyphimuriumIntestinesT4InProcessor 1Group III36S. T	20	S. Typhimurium	Faeces	T5Fa	Farm 1	Group I
2211123S. TyphimuriumWash waterT6WaProcessor 1Group II24S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT7InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III31S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumIntestinesT4HnProcessor 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT4InProcessor 1Group III37S. TyphimuriumIntestinesT4InProcessor 1Group III36<	21	S. Typhimurium	Intestines	T13In	Processor 2	Group I
2511124S. TyphimuriumIntestinesT8InProcessor 1Group II25S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT7InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumFaecesT9FaFarm 1Group III34S. TyphimuriumIntestinesT4InProcessor 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III	22	S. Typhimurium	Intestines	T5In	Processor 1	Group I
24125S. TyphimuriumSoilT2SoFarm 1Group II26S. TyphimuriumSoilT3SoFarm 1Group II27S. TyphimuriumIntestinesT7InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumFaecesT9FaFarm 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III37S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III	23	S. Typhimurium	Wash water	T6Wa	Processor 1	Group II
251SoilT3SoFarm 1Group II26S. TyphimuriumIntestinesT7InProcessor 1Group II27S. TyphimuriumIntestinesT10InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaccesT6FaFarm 1Group III30S. TyphimuriumFaccesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III37S. TyphimuriumIntestinesT6InProcessor 1Group III38S. TyphimuriumIntestinesT6InProcessor 1Group III39S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6In	24	S. Typhimurium	Intestines	T8In	Processor 1	Group II
26127S. TyphimuriumIntestinesT7InProcessor 1Group II28S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III	25	S. Typhimurium	Soil	T2So	Farm 1	Group II
21128S. TyphimuriumIntestinesT10InProcessor 1Group II29S. TyphimuriumFaecesT6FaFarm 1Group III30S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III	26	S. Typhimurium	Soil	T3So	Farm 1	Group II
23 <i>AAFacesTGFarm</i> 1 <i>GG</i> <th>27</th> <td>S. Typhimurium</td> <td>Intestines</td> <td>T7In</td> <td>Processor 1</td> <td>Group II</td>	27	S. Typhimurium	Intestines	T7In	Processor 1	Group II
2911111130S. TyphimuriumFaecesT10FaFarm 1Group III31S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III37S. TyphimuriumFaecesT2EIProcessor 4Group III	28	S. Typhimurium	Intestines	T10In	Processor 1	Group II
3031S. TyphimuriumFaecesT7FaFarm 1Group III32S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumFleer surphT2FIProcessor 4Group III	29	S. Typhimurium	Faeces	T6Fa	Farm 1	Group III
31313131313132S. TyphimuriumFaecesT8FaFarm 1Group III33S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumFloer suchT2FIProcessor 4Group III	30	S. Typhimurium	Faeces	T10Fa	Farm 1	Group III
3233S. TyphimuriumIntestinesT3InProcessor 1Group III34S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumFlace suchT2FIProcessor 4Group III	31	S. Typhimurium	Faeces	T7Fa	Farm 1	Group III
33S. TyphimuriumFaecesT9FaFarm 1Group III35S. TyphimuriumIntestinesT4InProcessor 1Group III36S. TyphimuriumIntestinesT6InProcessor 1Group III36S. TyphimuriumFloor suchT2FIProcessor 4Group III	32	S. Typhimurium	Faeces	T8Fa	Farm 1	Group III
34343735S. TyphimuriumIntestinesT4In36S. TyphimuriumIntestinesT6InS. TyphimuriumFloor suchT2FlS. TyphimuriumFloor suchT2Fl	33	S. Typhimurium	Intestines	T3In	Processor 1	Group III
35     36     S. Typhimurium     Intestines     T6In     Processor 1     Group III       36     S. Typhimurium     Electromythyperative     T2El     Processor 4     Croup III	34	S. Typhimurium	Faeces	T9Fa	Farm 1	Group III
S. Turkimumium Electrowich T2El Drocoscer 4 Crown III	35	S. Typhimurium	Intestines	T4In	Processor 1	Group III
37 S. Typhimurium Floor swab T2Fl Processor 4 Group III	36	S. Typhimurium	Intestines	T6In	Processor 1	Group III
	37	S. Typhimurium	Floor swab	T2Fl	Processor 4	Group III

Table 2 Major groups of S. Hadar and S. Albany according to REP-PCR and	lysis
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No.	Strain	Source of isolation	Strain code	Place of isolation	
1	S. Hadar	Drinking water	H1Dr	Farm 4	Group I
2	S. Hadar	Pond water	H1Po	Farm 4	Group I
3	S. Hadar	Pond water	НЗРо	Farm 4	Group I
4	S. Hadar	Cloacal swab	H9C1	Farm 4	Group I
5	S. Hadar	Cloacal swab	H5Cl	Farm 4	Group I
6	S. Hadar	Cloacal swab	H6Cl	Farm 4	Group I
7	S. Hadar	Faeces	H3Fa	Farm 4	Group II
8	S. Hadar	Faeces	H4Fa	Farm 4	Group II
9	S. Hadar	Soil	H2So	Farm 4	Group II
10	S. Hadar	Soil	H3So	Farm 4	Group II
11	S. Hadar	Pond water	H2Po	Farm 4	Group II
12	S. Hadar	Cloacal swab	H8C1	Farm 4	Group II
13	S. Hadar	Cloacal swab	H10Cl	Farm 4	Group II

14S. HadarClocal svabH3C1Farm 4Group 115S. HadarClocal svabH1C1Farm 3Group 116S. HadarFacesH1FaFarm 3Group 117S. HadarFacesH5FaFarm 4Group 118S. HadarFacesH7FaFarm 4Group 119S. HadarClocal svabH7C1Farm 4Group 120S. HadarClocal svabH7C1Farm 4Group 1121S. HadarClocal svabH4C1Farm 4Group 1122S. HadarSoliH4SoFarm 4Group 1123S. HadarSoliH4SoFarm 4Group 1124S. HadarSoliH1SoFarm 4Group 1125S. HadarSoliH4SoFarm 4Group 1126S. HadarSoliH1SoFarm 4Group 1127S. AlbanyFacesH2FaFarm 3Group 1128S. HadarSoliH1SoFarm 4Group 1129S. AlbanyCarcas rinseA2CaProcessor 4Group 113S. AlbanyFacesA1FaFarm 2Group 114S. AlbanyGacesA1FaFarm 2Group 115S. AlbanyGaces rinseA1GaProcessor 4Group 115S. AlbanyGacesA3FaFarm 2Group 116S. AlbanyGacesA2FaParm 2<						
16S. HadarFacesH.FaFarm 3Group 117S. HadarFacesHSFaFarm 4Group 118S. HadarCloacal swabH2C1Farm 4Group 119S. HadarCloacal swabH2C1Farm 3Group 120S. HadarCloacal swabH2C1Farm 4Group 121S. HadarCloacal swabH4C1Farm 4Group 122S. HadarCloacal swabH4C1Farm 4Group 123S. HadarSoilH4SoFarm 4Group 1124S. HadarSoilH1SoFarm 4Group 1125S. HadarSoilH1SoFarm 4Group 1126S. HadarSoilH1SoFarm 3Group 1126S. HadarGroup 1Group 1Group 1Group 1126S. HadarGroup 1Group 1Group 1Group 126S. HadarGroup 1Group 1Group 1Group 127S. AlbanyGaces rinseA2CaProcessor 4Group 13S. AlbanyFacesA1FaFarm 2Group 14S. AlbanyFacesA1FaFarm 4Group 15S. AlbanyFacesA1FaFarm 2Group 16S. AlbanyFacesA1FaFarm 2Group 17S. AlbanyFacesA3FaFarm 2Group 18S. AlbanyFacesA3FaFarm 2 <th>14</th> <th>S. Hadar</th> <th>Cloacal swab</th> <th>H3Cl</th> <th>Farm 4</th> <th>Group I</th>	14	S. Hadar	Cloacal swab	H3Cl	Farm 4	Group I
10S. HadarFacesHSFaFarm 4Group 113S. HadarFacesH7FaFarm 4Group 119S. HadarCloacal swabH2C1Farm 3Group 120S. HadarCloacal swabH7C1Farm 4Group 121S. HadarCloacal swabH4C1Farm 4Group 122S. HadarCloacal swabH4C1Farm 4Group 123S. HadarSoilH4SoFarm 4Group 124S. HadarSoilH1SoFarm 4Group 1125S. HadarSoilH1SoFarm 4Group 1126S. HadarFacesH2FaFarm 3Group 1126S. HadarFacesH6FaFarm 4Group 1127S. AlbaryCarcas rinseA2CaProcessor 4Group 113S. AlbanyGaces rinseA1FaFarm 2Group 114S. AlbanyFacesA1FaFarm 2Group 115S. AlbanyFacesA1FaFarm 2Group 114S. AlbanyFacesA1FaFarm 2Group 115S. AlbanyFacesA1FaFarm 4Group 116S. AlbanyFacesA1FaFarm 2Group 117S. AlbanyFacesA1FaFarm 2Group 116S. AlbanyFacesA5FaFarm 4Group 117S. AlbanyIntestinesA1InProcessor 4 </th <th>15</th> <th>S. Hadar</th> <th>Cloacal swab</th> <th>H1Cl</th> <th>Farm 3</th> <th>Group I</th>	15	S. Hadar	Cloacal swab	H1Cl	Farm 3	Group I
18S. HadarFacesH7FaFarm 4Group 119S. HadarCloacal swabH2C1Farm 3Group 120S. HadarCloacal swabH7C1Farm 4Group 1121S. HadarCloacal swabH4C1Farm 4Group 1122S. HadarCloacal swabH4C1Farm 4Group 1123S. HadarSoilH4SoFarm 4Group 1124S. HadarSoilH1SoFarm 4Group 1125S. HadarFacesH2FaFarm 3Group 1126S. HadarFacesH6FaFarm 4Group 112S. AlbanyCarcass rinseA2CaProcessor 4Group 113S. AlbanyCarcass rinseA1FaFarm 2Group 114S. AlbanyFacesA1FaFarm 2Group 115S. AlbanyFacesA1FaFarm 2Group 115S. AlbanyFacesA1FaFarm 2Group 116S. AlbanyFacesA3FaFarm 2Group 117S. AlbanyFacesA3FaFarm 2Group 118S. AlbanyIntestinesA1InProcessor 4Group 119S. AlbanyCarca swabA2CrProcessor 4Group 1110S. AlbanyGroup 1A2SoFarm 2Group 1111S. AlbanySoilA2SoFarm 2Group 1112S. AlbanyFaces <td< th=""><th>16</th><th>S. Hadar</th><th>Faeces</th><th>H1Fa</th><th>Farm 3</th><th>Group I</th></td<>	16	S. Hadar	Faeces	H1Fa	Farm 3	Group I
19S. HadarCloacal swabH2C1Farm 3Group 1120S. HadarCloacal swabH7C1Farm 4Group 1121S. HadarCloacal swabH4C1Farm 4Group 1122S. HadarFaccesH8FaFarm 4Group 1123S. HadarSoilH4SoFarm 4Group 1124S. HadarSoilH1SoFarm 4Group 1125S. HadarFaccesH2FaFarm 3Group 1126S. HadarFaccesH6FaFarm 4Group 112S. AlbanyCarcass rinseA2CaProcessor 4Group 113S. AlbanyCarcass rinseA1FaFarm 2Group 114S. AlbanyFaccesA1FaFarm 2Group 115S. AlbanyFaccesA1FaFarm 2Group 116S. AlbanyFaccesA1FaFarm 2Group 115S. AlbanyFaccesA1FaFarm 2Group 116S. AlbanyFaccesA3FaFarm 2Group 117S. AlbanyFaccesA3FaFarm 2Group 118S. AlbanyIntestinesA1InProcessor 4Group 119S. AlbanyCrate swabA2CrProcessor 4Group 1110S. AlbanyCrate swabA2CaProcessor 4Group 1111S. AlbanySoilA2SoFarm 2Group 1112S. AlbanyS	17	S. Hadar	Faeces	H5Fa	Farm 4	Group I
195. HadarCloacal swabH7C1FarnFarnGroup II20S. HadarCloacal swabH4C1Farn 4Group II21S. HadarEacesH8FaFarn 4Group II22S. HadarSoilH4SoFarn 4Group II23S. HadarSoilH4SoFarn 4Group II24S. HadarSoilH1SoFarn 4Group II25S. HadarFacesH2FaFarn 3Group II26S. HadarFacesA2CaProcessor 4Group II2S. AlbaryCarcass rinseA2CaProcessor 4Group II2S. AlbaryCarcass rinseA3CaProcessor 4Group II3S. AlbaryFacesA4FaFarn 2Group III4S. AlbaryFacesA1FaFarn 2Group III5S. AlbaryFacesA1FaFarn 2Group III5S. AlbaryFacesA1FaFarn 2Group III6S. AlbaryFacesA3FaFarn 2Group II7S. AlbaryFacesA1FaFarn 2Group II8S. AlbaryIntestinesA1InProcessor 4Group II9S. AlbaryCarta swabA2CrProcessor 4Group II10S. AlbaryCarta swabA2CrProcessor 4Group II11S. AlbarySoilA2SoFarn 2Group II12S. Albary </th <th>18</th> <th>S. Hadar</th> <th>Faeces</th> <th>H7Fa</th> <th>Farm 4</th> <th>Group I</th>	18	S. Hadar	Faeces	H7Fa	Farm 4	Group I
21S. HadarCloacal swabH4ClFarm 4Group II22S. HadarFaecesH8FaFarm 4Group II23S. HadarSoilH4SoFarm 4Group II24S. HadarSoilH1SoFarm 4Group II25S. HadarFaecesH2FaFarm 3Group II26S. HadarFaecesH6FaProcessor 4Group II2S. AlbanyCarcass rinseA2CaProcessor 4Group II2S. AlbanyCarcass rinseA3CaProcessor 4Group II3S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyFaecesA3FaFarm 4Group I6S. AlbanyFaecesA1FaProcessor 4Group II5S. AlbanyFaecesA1FaFarm 2Group III6S. AlbanyFaecesA3FaFarm 4Group I7S. AlbanyFaecesA3FaFarm 4Group I8S. AlbanyIntestinesA1InProcessor 4Group I9S. AlbanyCrate swabA2CrProcessor 4Group II10S. AlbanySoilA2SoFarm 2Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 3Group III13S. AlbanyFaeces </th <th>19</th> <th>S. Hadar</th> <th>Cloacal swab</th> <th>H2Cl</th> <th>Farm 3</th> <th>Group I</th>	19	S. Hadar	Cloacal swab	H2Cl	Farm 3	Group I
21EachFaccesH8FaFarm 4Group II23S. HadarSoilH4SoFarm 4Group II24S. HadarSoilH1SoFarm 4Group II25S. HadarFaecesH2FaFarm 3Group II26S. HadarFaecesH6FaFarm 4Group II1S. AlbanyCarcass rinseA2CaProcessor 4Group II2S. AlbanyCarcass rinseA3CaProcessor 4Group II3S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyFaecesA1FaFarm 2Group III5S. AlbanyFaecesA1FaFarm 2Group III6S. AlbanyFaecesA3FaFarm 4Group II7S. AlbanyFaecesA1FaFarm 2Group III6S. AlbanyFaecesA3FaFarm 2Group II7S. AlbanyIntestinesA1InProcessor 4Group II9S. AlbanyCrate swabA2CrProcessor 4Group II10S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 3Group II13S. AlbanyFaecesA2FaFarm 3Group II14S. AlbanyFaeces	20	S. Hadar	Cloacal swab	H7Cl	Farm 4	Group II
23S. HadarSoilH4SoFarm 4Group II24S. HadarSoilH1SoFarm 4Group II25S. HadarFaecesH2FaFarm 3Group II26S. HadarFaecesH6FaFarm 4Group II26S. AlbanyCarcass rinseA2CaProcessor 4Group II2S. AlbanyCarcass rinseA3CaProcessor 4Group II3S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA1FaFarm 2Group III5S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyFaecesA1FaFarm 2Group III6S. AlbanyFaecesA1FaFarm 2Group II7S. AlbanyFaecesA3FaFarm 4Group II8S. AlbanyFaecesA3FaFarm 2Group II9S. AlbanyIntestinesA1InProcessor 4Group I9S. AlbanyCrate swabA2CrProcessor 4Group I10S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group II13S. AlbanyFaecesA2FaFarm 3Group III14S. AlbanySoilA2SoFarm 2Group III15S. AlbanyFaeces </th <th>21</th> <th>S. Hadar</th> <th>Cloacal swab</th> <th>H4Cl</th> <th>Farm 4</th> <th>Group II</th>	21	S. Hadar	Cloacal swab	H4Cl	Farm 4	Group II
24S. HadarSoilH1SoFarm 4Group II25S. HadarFaccesH2FaFarm 3Group II26S. HadarFaccesH6FaFarm 4Group II1S. AlbanyCarcass rinseA2CaProcessor 4Group I2S. AlbanyCarcass rinseA3CaProcessor 4Group II3S. AlbanyFaccesA1FaFarm 2Group III4S. AlbanyFaccesA1FaFarm 2Group III5S. AlbanyFaccesA1FaFarm 2Group III5S. AlbanyFaccesA1FaFarm 2Group III6S. AlbanyFaccesA1FaFarm 4Group I7S. AlbanyFaccesA2FaFarm 4Group II8S. AlbanyIntestinesA1InProcessor 4Group II9S. AlbanyIntestinesA1InProcessor 4Group II9S. AlbanyCrate swabA2CrProcessor 4Group II10S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaccesA2FaFarm 2Group III13S. AlbanyFaccesA2FaFarm 2Group III14S. AlbanyFaccesA2FaFarm 2Group III15S. AlbanyFaccesA2FaFarm 2Group III16S. Albany </th <th>22</th> <th>S. Hadar</th> <th>Faeces</th> <th>H8Fa</th> <th>Farm 4</th> <th>Group II</th>	22	S. Hadar	Faeces	H8Fa	Farm 4	Group II
25S. HadarFacesH2FaFarm 3Group II26S. HadarFacesH6FaFarm 4Group II1S. AlbanyCarcass rinseA2CaProcessor 4Group I2S. AlbanyCarcass rinseA3CaProcessor 4Group II3S. AlbanyFacesA1FaFarm 2Group III4S. AlbanyFacesA4FaFarm 2Group III5S. AlbanyFacesA1FaFarm 2Group III6S. AlbanyCarcass rinseA1CaProcessor 4Group I7S. AlbanyFeedA1FeFarm 4Group I6S. AlbanyFacesA3FaFarm 2Group I7S. AlbanyIntestinesA1InProcessor 4Group I8S. AlbanyIntestinesA1GaProcessor 4Group I9S. AlbanyCrate swabA2CrProcessor 4Group II10S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFacesA3FaFarm 2Group III13S. AlbanyFacesA3FaFarm 3Group III14S. AlbanyFacesA2FaFarm 3Group III15S. AlbanyFacesA3FaFarm 3Group III16S. AlbanyFacesA3FaFarm 3Group III17S. Albany <th>23</th> <th>S. Hadar</th> <th>Soil</th> <th>H4So</th> <th>Farm 4</th> <th>Group II</th>	23	S. Hadar	Soil	H4So	Farm 4	Group II
26S. HadarFacesH6FaFarm 4Group II1S. AlbanyCarcass rinseA2CaProcessor 4Group 12S. AlbanyCarcass rinseA3CaProcessor 4Group 13S. AlbanyFaceesA1FaFarm 2Group III4S. AlbanyFacesA4FaFarm 2Group 15S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyCarcass rinseA1CaProcessor 4Group 17S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFacesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyIntestinesA1CrProcessor 4Group 110S. AlbanyCrate swabA2CrProcessor 4Group 111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFacesA2FaFarm 2Group III13S. AlbanyFacesA2FaFarm 3Group III14S. AlbanyFacesA2FaFarm 3Group III15S. AlbanyFacesA2FaFarm 3Group III16S. AlbanyFacesA2FaFarm 3Group III17S. AlbanyFacesA2FaFarm 3Group III18S. AlbanyFacesA2FaFarm 3Group III19S. Albany </th <th>24</th> <th>S. Hadar</th> <th>Soil</th> <th>H1So</th> <th>Farm 4</th> <th>Group II</th>	24	S. Hadar	Soil	H1So	Farm 4	Group II
201S. AlbanyCarcass rinseA2CaProcessor 4Group 12S. AlbanyCarcass rinseA3CaProcessor 4Group 13S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFaecesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyIntestinesA1CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group 111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFacesA2FaFarm 2Group II13S. AlbanyFacesA2FaFarm 3Group III14S. AlbanyFacesA2FaFarm 2Group III15S. AlbanyFacesA2FaFarm 3Group III	25	S. Hadar	Faeces	H2Fa	Farm 3	Group II
2S. AlbanyCarcass rinseA3CaProcessor 4Group 13S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFeedA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyIntestinesA1CrProcessor 4Group 110S. AlbanyCrate swabA2CrProcessor 4Group 111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group II13S. AlbanyFaecesA2FaFarm 3Group III	26	S. Hadar	Faeces	H6Fa	Farm 4	Group II
2S. AlbanyCarcass rinseA3CaProcessor 4Group 13S. AlbanyFaecesA1FaFarm 2Group III4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFeedA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyIntestinesA1CrProcessor 4Group 110S. AlbanyCrate swabA2CrProcessor 4Group 111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group II13S. AlbanyFaecesA2FaFarm 3Group III		C Allegan	Correspondings	1200	Drooppor 4	Crown 1
2Normal SolutionSolutionSolutionSolutionSolution3S. AlbanyFacesA1FaFarm 2Group III4S. AlbanyFacesA4FaFarm 2Group III5S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFacesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group 1111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFacesA5FaFarm 3Group III13S. AlbanyFacesA5FaFarm 3Group III	1					-
4S. AlbanyFaecesA4FaFarm 2Group III5S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFaecesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III	2	S. Albany	Carcass rinse	A3Ca	Processor 4	Group 1
4115S. AlbanyCarcass rinseA1CaProcessor 4Group 16S. AlbanyFeedA1FeFarm 4Group 17S. AlbanyFaecesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III	3	S. Albany	Faeces	A1Fa	Farm 2	Group III
5A. HarryFeedA1FeFarm 4Group 17S. AlbanyFaecesA3FaFarm 2Group 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group 1111S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III	4	S. Albany	Faeces	A4Fa	Farm 2	Group III
6Image: Solution of the sector of	5	S. Albany	Carcass rinse	A1Ca	Processor 4	Group 1
No. 1No. 1No. 18S. AlbanyIntestinesA1InProcessor 4Group 19S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III14S. AlbanyFaecesA5FaFarm 3Group III	6	S. Albany	Feed	A1Fe	Farm 4	Group 1
9S. AlbanyCrate swabA2CrProcessor 4Group 110S. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III14S. AlbanyFaecesA5FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III	7	S. Albany	Faeces	A3Fa	Farm 2	Group 1
yX. AlbanyCrate swabA1CrProcessor 4Group II11S. AlbanySoilA2SoFarm 2Group II12S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III13S. AlbanySailA1SaFarm 2Group III	8	S. Albany	Intestines	AlIn	Processor 4	Group 1
101011SoilA2SoFarm 2Group II11S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III13S. AlbanyFaecesA5FaFarm 3Group III	9	S. Albany	Crate swab	A2Cr	Processor 4	Group 1
1112S. AlbanyFaecesA2FaFarm 2Group III13S. AlbanyFaecesA5FaFarm 3Group III13S. AlbanyFaecesA1SaFarm 2Group III	10	S. Albany	Crate swab	A1Cr	Processor 4	Group II
12     Faces     A5Fa     Farm 3     Group III       13     S. Albany     Faces     A1Sa     Farm 2     Group III	11	S. Albany	Soil	A2So	Farm 2	Group II
15 S Albami Soil AlSo Form 2 Group III	12	S. Albany	Faeces	A2Fa	Farm 2	Group III
14S. AlbanySoilA1SoFarm 2Group III	13	S. Albany	Faeces	A5Fa	Farm 3	Group III
	14	S. Albany	Soil	A1So	Farm 2	Group III

# Table 3 Major groups of S. Braenderup and S. Enteritidis according to REP-PCR analysis

No.	Strain	Source of isolation	Strain code	Place of isolation	
1	S. Braenderup	Cloacal swab	B3Cl	Farm 1	Group I
2	S. Braenderup	Cloacal swab	B4Cl	Farm 1	Group I
3	S. Braenderup	Intestines	B4In	Processor 1	Group I
4	S. Braenderup	Wash water	B1Wa	Processor 1	Group I
5	S. Braenderup	Cloacal swab	B1Cl	Farm 1	Group I
6	S. Braenderup	Intestines	B1In	Processor 1	Group I
7	S. Braenderup	Intestines	B2In	Processor 1	Group I
8	S. Braenderup	Intestines	B3In	Processor 1	Group I
9	S. Braenderup	Faeces	B4Fa	Farm 1	Group I
10	S. Braenderup	Intestines	B5In	Processor 1	Group I
11	S. Braenderup	Faeces	B1Fa	Farm 1	Group II
12	S. Braenderup	Faeces	B2Fa	Farm 1	Group II
13	S. Braenderup	Cloacal swab	B2Cl	Farm 1	Group III
14	S. Braenderup	Faeces	B3Fa	Farm 1	Group III
15	S. Braenderup	Soil	B1So	Farm 1	Group III

1	S. Enteritidis	Faeces	E2Fa	Farm 1	Group I
2	S. Enteritidis	Faeces	E3Fa	Farm 1	Group I
3	S. Enteritidis	Faeces	E6Fa	Farm 1	Group II
4	S. Enteritidis	Faeces	E9Fa	Farm 1	Group II
5	S. Enteritidis	Intestines	E4In	Processor 2	Group III
6	S. Enteritidis	Intestines	E5In	Processor 3	Group III
7	S. Enteritidis	Faeces	E7Fa	Farm 1	Group I
8	S. Enteritidis	Faeces	E5Fa	Farm 1	Group I
9	S. Enteritidis	Faeces	E8Fa	Farm 1	Group II
10	S. Enteritidis	Intestines	E1In	Processor 1	Group II
11	S. Enteritidis	Intestines	E2In	Processor 1	Group II
12	S. Enteritidis	Intestines	E3In	Processor 2	Group II
13	S. Enteritidis	Faeces	E4Fa	Farm 1	Group II
14	S. Enteritidis	Faeces	E1Fa	Farm 1	Group II
15	S. Enteritidis	Intestines	E6In	Processor 1	Group III

#### CONCLUSION

We report for the first time on the use of REP-PCR to determine the genetic relatedness or diversity of salmonellae isolated from ducks and their environmental samples in Malaysia. REP-PCR analysis of the 107 salmonellae resulted in differences and similarities among the strains of salmonellae isolated from the same or different sources. REP-PCR successfully type all the *Salmonella* strains and was a useful tool for determining the genetic relatedness or diversity of the *Salmonella* strains isolated from ducks, their rearing and processing environments.

Acknowledgments: This research was supported by Postgraduate Research Grant Scheme (1001/PTEK1ND/843007) of the Universiti Sains Malaysia.

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