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GENETIC DIVERSITY AND PREVENTION OF *CAMPYLOBACTER* SPP. IN BROILER BREEDERS
AND BROILERS

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A Dissertation Submitted in Partial Fulfillment of the Requirements
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เนื้อสัตว์ปีกที่มีการปนเปื้อนนับเป็นสาเหตุสำคัญของโรคแคมไพโลแบคทีเรียในมนุษย์ การศึกษาเกี่ยวกับเรื่องนี้ในประเทศไทยมีเพียงจำนวนน้อย ดังนั้นวัตถุประสงค์ของการศึกษานี้ประกอบด้วย 1) เพื่อระบุหาความสัมพันธ์ของเชื้อ *แคมไพโลแบคเตอร์* ที่แยกได้จากไก่พันธุ์เนื้อ โรงฟัก ไก่เนื้อ และสิ่งแวดล้อมในโรงเรือนเหล่านั้น 2) เพื่อประเมินระดับการดื้อยาต้านจุลชีพของเชื้อ *แคมไพโลแบคเตอร์* 3) เพื่อประเมินประสิทธิภาพการป้องกันเชื้อของ competitive exclusion ภายหลังจากการให้เชื้อพิษทับบของ *แคมไพโลแบคเตอร์* เจจูไน ในไก่เนื้อ เพื่อให้บรรลุวัตถุประสงค์ดังกล่าว การศึกษานี้จึงประกอบด้วย 2 ส่วนย่อย ได้แก่ 1) เก็บตัวอย่างจากฟาร์มไก่พันธุ์ จำนวน 5 ฟาร์ม โรงฟัก จำนวน 2 โรง และฟาร์มไก่เนื้อ จำนวน 5 ฟาร์ม จำนวนไอโซเลตของเชื้อ *C. jejuni* และ *C. coli* ที่แยกได้จากกระบวนการผลิตไก่เนื้อ 2 ช่วงโซ่อุปทาน เท่ากับ 36 และ 94 ไอโซเลตตามลำดับ นำมาทดสอบหาความไวรับต่อยาต้านจุลชีพด้วยวิธี two-fold agar dilution เชื้อ *แคมไพโลแบคเตอร์* ส่วนใหญ่มีรูปแบบการดื้อต่อยาหลายชนิด และดื้อต่อยาเอนโรฟลอกซาซิน ในสัดส่วน *C. jejuni* เท่ากับ 100% และ *C. coli* เท่ากับ 98.9% สุ่มเลือกเชื้อ *C. jejuni* และ *C. coli* อย่างละ 24 ไอโซเลต เพื่อวิเคราะห์หาการกลายพันธุ์ที่ quinolone resistance determining region (QRDR) ของยีน *gyrA* ด้วยวิธีการวิเคราะห์ลำดับนิวคลีโอไทด์ พบว่าทุกไอโซเลตสามารถตรวจพบการเปลี่ยนแปลงที่ตำแหน่ง Thr-86-Ile (ACA-ATA สำหรับ *C. jejuni* หรือ ACT-ATT สำหรับ *C. coli*) การศึกษานี้พบว่าการติดเชื้อ *แคมไพโลแบคเตอร์* เกิดจากการติดเชื้อแบบ horizontal เป็นหลัก ดังที่เห็นได้จากเมื่อนำเชื้อ *แคมไพโลแบคเตอร์* ทุกไอโซเลตมาจำแนกด้วยเทคนิค *flaA*-RFLP สามารถแยกกลุ่มของเชื้อได้เป็น 10 กลุ่มที่แตกต่างกัน 2) เก็บตัวอย่างมูลไก่จากไก่พื้นบ้านและไก่ที่เลี้ยงแบบชีวภาพจากฟาร์มที่ไม่มีประวัติการใช้ยาต้านจุลชีพ จำนวน 60 ตัวอย่าง นำมาจำแนกหา competitive exclusion (CE) โดยตรวจพบเชื้อ *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium* แล้วจึงนำไปทดสอบความไวรับต่อยาต้านจุลชีพ เพื่อป้องกันการส่งผ่านการดื้อยาตามคำแนะนำของ EFSA และทดสอบการทนกรดและน้ำดีในห้องปฏิบัติการ พบว่า *Lactobacillus acidophilus* 1/4, *Bacillus subtilis* 206/1 and *Enterococcus faecium* 122 มีประสิทธิภาพสูงในการทนกรดและน้ำดี จึงถูกคัดเลือกมาใช้เป็น CE เพื่อป้องกันแบคทีเรียที่อายุ 1-3 วัน ภายหลังจากการให้เชื้อพิษทับบด้วย *C. jejuni* แก่ไก่เนื้อที่อายุ 14 วัน พบว่าจำนวนเชื้อ *C. jejuni* และอัตราการแลกเนื้อที่อายุ 41 วันไม่พบความแตกต่างอย่างมีนัยสำคัญทางสถิติ โดยสรุปแล้ว การศึกษานี้ชี้ให้เห็นถึงอุปสรรคที่เพิ่มขึ้นอย่างรวดเร็วของการดื้อยาต้านจุลชีพหลายชนิด ซึ่งเป็นสิ่งที่น่ากังวล ดังนั้นการใช้ยาต้านจุลชีพที่ฟาร์ม ควรใช้อย่างรอบคอบและมีการตรวจเฝ้าระวังการดื้อยา เพื่อช่วยลดความเสี่ยงทางด้านสาธารณสุข

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Contaminated poultry meat is regarded as the main source of human campylobacteriosis. In Thailand, there is only a few publications studied in poultry farms, so the aims of this study were 1) to identify the relationship of *Campylobacter* isolates among broiler breeders, broilers and their environments, 2) to examine antimicrobial resistance profiles of *Campylobacter* spp., and 3) to examine the protection of competitive exclusion after challenging *Campylobacter jejuni* in broilers. To complete the objectives, there were 2 parts in this study. First, five commercial breeder flocks, 2 hatcheries, and 5 broiler flocks were sampled. Thirty-six *C. jejuni* and 94 *C. coli* isolates collected through two broiler production chains were tested by two-fold agar dilution for their susceptibility to antimicrobial agents. Most *Campylobacter* isolates were multidrug resistance (MDR) (*C. jejuni*: 100%; *C. coli*: 98.9%), and exhibited high resistance to enrofloxacin (*C. jejuni*: 100%; *C. coli*: 98.9%). A selected subset of 24 *C. jejuni* and 24 *C. coli* were characterized for their mutations in the quinolone resistance determining region (QRDR) of the *gyrA* gene by nucleotide sequence analysis. The Thr-86-Ile substitution (ACA-ATA in *C. jejuni* or ACT-ATT in *C. coli*) was found in all isolates. Horizontal transmission was the major route of *Campylobacter* transmission in this study, as all *Campylobacter* isolates were typed and ten distinct clusters were recognized by *flaA*-RFLP typing. Second, competitive exclusion (CE) were identified from 60 adult chicken feces of native chickens and organic layers raised under non-antimicrobial usage farms. *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium* were identified and tested their antimicrobial susceptibilities for preventing transmissible antimicrobial resistance, as recommended by EFSA. Furthermore, those isolates were *in vitro* tested for acid and bile tolerances. *Lactobacillus acidophilus* 1/4, *Bacillus subtilis* 206/1 and *Enterococcus faecium* 122 demonstrated their powerful *in vitro* activities and were, therefore, used as CE during oral gavage of 1-day-old broilers for 3 days consecutively. After *C. jejuni* challenges at 14 days in broilers, the treatment groups had no significant differences in *C. jejuni* re-isolations or feed conversion ratio at 41 days. In conclusions, the emergence of MDR and high resistance rates to several antimicrobials are major concerns identified in this study. The prudent use of these agents and active surveillance of resistance at the farm level are essential steps to reduce the public health risks identified in this work.

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LIST OF ABBREVIATIONS

°C	degree Celcius
C.	<i>Campylobacter</i>
CBA	Columbia blood agar
CFU	colony forming unit
CLSI	Clinical and Laboratory Standards Institute
<i>flaA</i>	<i>flagellin A gene</i>
<i>gyrA</i>	gyrase A gene
mCCDA	modified Charcoal Cefoperazone Deoxycholate Agar
MIC(s)	Minimum Inhibitory Concentration(s)
ml	milliliter
PCR	polymerase chain reaction
RFLP	restriction fragment length polymorphism
μl	microlitre
spp.	species

CHAPTER I

INTRODUCTION

Campylobacter has considered to be a major cause of foodborne bacterial gastro-infectious disease in both developed and developing countries for several years (Jay-Russell et al., 2012; Sahin et al., 2012). The pathogen causes mild to severe symptoms including bloody diarrhea (Blaser et al., 1979). Invasive infections infrequently result in reactive arthritis, meningitis, pneumonia and a severe form of Guillain-Barré syndrome involving neuromuscular paralysis of the extremities (Blaser et al., 1986).

The organism is a cytochrome oxidase positive, microaerophilic, curved gram-negative rod, 0.2 to 0.8 μm wide and 0.5 to 5 μm long exhibiting cockscrew motility. Cells in old cultures may form coccoid bodies which are considered degenerative forms rather than a dormant stages of the organism. There are currently 29 recognized species and 4 subspecies of *Campylobacter* (Takamiya et al., 2011). The human pathogenic species of *Campylobacter* comprise 4 species including *C. jejuni*, *C. coli*, *C. lari* and *C. upsaliensis* which are often referred as the thermophilic *Campylobacter* species. The term thermotolerant means that those *Campylobacter* species are capable of growing at 41-43°C. The species most frequently associated with human campylobacteriosis is *C. jejuni* with only 10% due to *C. coli* and less than 1% from *C. lari* (Nachamkin et al., 1998). Even though campylobacteriosis is generally self-limiting,

incapacity may last a few weeks and up to 10% of reported cases may require medical treatment (Arcila-Londono and Lewis, 2012). More serious systemic infections are well demonstrated and occur most commonly in the immunocompromised person. In addition, an association of campylobacteriosis with post-infectious neuropathies such as Guillain-Barre syndrome has been identified; however, neurological consequences of infection are rare, they might be extremely serious (Arcila-Londono and Lewis, 2012).

Campylobacter jejuni and *C. coli* live in the avian gut as commensal bacteria. These organisms are not only be isolated from domestic chickens, but they are also recovered from all other domestic poultry including turkeys, ducks, quails and pigeons, as well as from wild birds and even ostriches (Yogasundram et al., 1989; Borck and Pedersen, 2005). Only in the ostrich this colonization is associated with clinical disease (Verwoerd, 2000). The different pathogenesis of *Campylobacter* in human and poultry is not clearly understood.

There are many risk pathways for human exposure to *Campylobacter*. *Campylobacter* spp. are found widespread in the environment and in farmed animals (Evans and Wegener, 2003). Despite the fact that multiple sources of *Campylobacter* have been recognized with different importance in relation to human illness, the handling and consumption of undercooked poultry is an important source of human campylobacteriosis (Ridley et al., 2011; Thakur et al., 2013). *Campylobacter* contamination of broiler carcasses during slaughter is primarily due to cross-contamination during the feather removal and evisceration process (Hue et al., 2010).

Formerly, *Campylobacter* was normally susceptible to various antimicrobials, but recent reports showed that *Campylobacter* isolates derived from animals and humans increased resistance to several antibiotics including fluoroquinolones, macrolides and tetracyclines (Price et al., 2005; Han et al., 2007). Based on laboratory diagnosis and farm studied, treatment of infected chickens with fluoroquinolones resulted in fluoroquinolones-resistant *Campylobacter* mutants passing through human eating contaminated meat (Padungtod et al., 2006). In Thailand, there is also an increasing trend of multiple antimicrobial resistances in both animal and human origins which the cause might be an inappropriate use of antimicrobial drugs in animals (Boonmar et al., 2005; Padungtod and Kaneene, 2005).

The aims of this study had three reasons. First, the relationship of *Campylobacter* isolates among broiler breeders, broilers and their environments was identified. Second, antimicrobial resistance profiles of *Campylobacter* spp. were updated. Third, the protection of competitive exclusion after challenging *Campylobacter jejuni* in broilers was demonstrated.

Objectives of Study

1. To identify the relationship of *Campylobacter* isolates among broiler breeders, broilers and their environments.
2. To examine antimicrobial resistance profile of *Campylobacter* spp.

3. To examine the protection of competitive exclusion after challenging *Campylobacter jejuni* in broilers.

Keywords (Thai): การดื้อยาต้านจุลชีพ, ไก่เนื้อ, ไก่พันธุ์เนื้อ, แคมไพโลแบคเตอร์, คอมเพทิทีฟ
เอ็กคลูชัน, ความหลากหลายทางพันธุกรรม

Keywords (English): antimicrobial resistance, broiler, broiler breeder, *Campylobacter* spp., competitive exclusion, genetic diversity

Research questions

1. Is there any relationship of *Campylobacter* isolates among broiler breeders, broilers and their environments?
2. What is the MIC value of *Campylobacter* spp. isolated from broiler breeders and broilers?
3. Can competitive exclusion reduce numbers of *Campylobacter jejuni* infection?

CHAPTER II

LITERATURE REVIEW

2.1 Taxonomy and characteristics of *Campylobacter* spp.

The genus *Campylobacter* belongs to the *Epsilon-proteobacteria*, in the family *Campylobacteraceae* (Vandamme et al., 1991), which includes the genera *Campylobacter*, *Arcobacter*, *Dehalospirillum* and *Sulfurospirillum*. Available genomes of the genus *Campylobacter* currently comprises 29 species and 4 subspecies (Takamiya et al., 2011). *Campylobacter* is a spiral rod shape with one or two flagella at the pole and is motile. *Campylobacter* grows at optimum temperature of 42°C, with a range between 30.5°C and 45°C, optimum growth at 10% carbon dioxide, 5-6% oxygen and 85% nitrogen (Blaser et al., 1986). *Campylobacter* cells in old cultures may form coccoid bodies which are considered as degenerative forms (Hazeleger et al., 1995). Biochemical characteristics of several species generally require fumarate with formate or hydrogen for a microaerobic growth. This genus can reduce nitrate to nitrite. Tyrosine, casein, gelatin and starch are not hydrolyzed. There is no lipase or lecithinase activity but oxidase activity is presented in every species except *C. gracilis*. Most enteropathogenic *Campylobacters* are catalase-positive. *Campylobacter* is generally sensitive to oxygen, desiccation, osmotic stress, low pH and high temperature (>60°C) (Park, 2002).

2.2 Incubation period, clinical signs and pathological lesions

Although chickens can be easily infected with *Campylobacter* naturally or experimentally, they normally do not show clinical illness and *Campylobacter*-associated diarrhea in poultry is quite not happened. Colonization could experimentally occur as early as one day after inoculation (Knudsen et al., 2006). Incubation period is between 1 and 3 days (Sanyal et al., 1984; Welkos, 1984).

Campylobacter is rarely detected in birds that are younger than 2-3 weeks of age. The reasons may be related to multiple factors including the presence of maternally-derived antibodies (Sahin et al., 2003) or environmental or host-related factors differences. Once a flock is infected, *Campylobacter* spreads thoroughly within the flock causing colonization of most of birds within a few days (Evans and Sayers, 2000).

The members of thermophilic *Campylobacter*, primarily *C. jejuni* and *C. coli*, are frequently isolated from avian species, especially domestic poultry including chickens, turkeys, ducks and geese (Sahin et al., 2002). *C. jejuni* and *C. coli* well adapt to the avian host and habit in the intestinal tract of birds. Even though poultry have extensive colonization, *Campylobacter* infections produce little or no clinical diseases in them (Corry and Atabay, 2001). On the other hand, there was a published report indicating that infectious hepatitis associated with *C. coli* and *C. jejuni* in ostriches caused a high morbidity and mortality (Stephens et al., 1998). There was an experiment inoculated with a high dose of *C. jejuni* to 3 days old chickens resulting diarrhea within

72 hours which lasted for 10 days, weight losses as well as a mortality of 32% (Ruiz-Palacios et al., 1981). In experimentally infected chicks, gross pathological lesions associated with *Campylobacter* infection were minimal and mainly found only in the gastrointestinal tract. Blood and mucus in the small intestinal tract and petechial hemorrhages in the gizzard mucosa of chicks can be seen sometimes (Welkos, 1984).

2.3 Isolation and identification of *Campylobacter* spp.

Thermophilic *Campylobacter* are fastidious and slow-growing requiring a microaerobic atmosphere (containing 5% O₂, 10% CO₂ and 85% N₂) and showing optimal growth at 42°C. Culture-based isolation and detection methods can be divided into 2 groups including passive filtration and using selective media. Firstly, passive filtration is a method developed by Steele and McDermott (Steele and McDermott, 1984). According to the characteristic of the organism, *Campylobacter* has a cockscrew shape that can pass through 0.45 or 0.65 µm filter paper onto a Columbia blood agar (CBA). CBA, an enriched non-selective medium, is created for the isolation, quantitation and partial identification of a variety of microorganism. Passive filtration is very useful for the isolation of antimicrobial-sensitive *Campylobacter* spp. This method does not use expensive media, so it may be useful for laboratories with limited resources. CBA is also suitable for use in antibiotic differential disk examination and spot biochemical testing (ISO10272-1, 2006). Secondly, selective media is widely used for the recovery of *Campylobacter* spp. because the use of selective media for *Campylobacter*

isolation showed higher prevalence than using the filtration method (Bolton and Robertson, 1982). Many selective media can be used for isolation of *Campylobacter* spp. There are 2 types of selective media for *Campylobacter* isolation including charcoal-based solid media and blood-containing solid media. The examples of charcoal-based solid media composed of modified charcoal-cefoperazone-deoxycholate agar (mCCDA), which is the recommend medium, Karmali agar and CAT agar (cefoperazone, amphotericin and teicoplanin) (Corry et al., 1995). The latter medium was developed for facilitating growth of *C. upsaliensis* (Aspinall et al., 1993). The examples of blood-containing solid media composed of Preston, Skirrow, Butzler and Campy-cefex agar which are considered alternative choices (Skirrow, 1977; Bolton and Robertson, 1982). The major characteristics of *C. jejuni* and *C. coli* are shown in Table 1.

Formerly, hippurate hydrolysis could be used to differentiate of *C. jejuni* and *C. coli* because the hippuricase gene was only found in *C. jejuni* (Rautelin et al., 1999). Even though some *C. jejuni* isolates are hippuricase-negative, they are unable to differentiate *C. coli* from hippuricase-negative *C. jejuni* by using purely biochemical tests (Fields and Swerdlow, 1999).

Table 1: Characteristics of *C. jejuni* and *C. coli* (ISO 10272-1, 2006)

Characteristic	<i>C. jejuni</i>	<i>C. coli</i>
Morphology	small curved bacilli	
Motility	corkscrew motility	
Microaerobic growth at 25 C	-	
Aerobic growth at 41.5 C	-	
Oxidase	+	
Catalase	+	+
Nalidixic acid	R/S*	R/S
Cephalothin	R	R
Hydrolysis of hippurate	+/-	-
Indoxyl acetate	+	+

*R = resistant, S= sensitive

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Polymerase chain reaction (PCR) was also recognized as a method for culture confirmation or for direct detection of *Campylobacter* from environmental or poultry samples. PCR primers can be designed for genus detection or differentiation of species or strains (Wang et al., 2002). There are a variety of PCR assays targeting genus or species-specific sequences developed to detect and identify *Campylobacter* from poultry feces and environmental samples (Waegel and Nachamkin, 1996; Chuma et al., 1997; Wang et al., 2002).

2.4 Public Health Significance

Campylobacter has now emerged as an important bacterial agent of foodborne gastroenteritis worldwide (Zenner and Gillespie, 2011). In 2007, the Foodborne Diseases Active Surveillance Network reported 5,818 *Campylobacter*'s cases per 100,000 enteric cases (FoodNet, 2007). Regarding Thai human campylobacteriosis, Thailand do not have national surveillance programs for this pathogen, so incidence values in terms of number of cases for a population do not exist (Coker et al., 2002). Most estimates of incidence in developing countries are from laboratory surveillance of pathogens responsible for diarrhea (Coker et al., 2002). Echeverria et al. (1989) reported that isolation rate from diarrhea specimens from <5-year-old children in Thailand was about 13%. Most of *Campylobacter*-related illnesses in humans are sporadic and characterized by self-limiting watery and/or bloody diarrhea, abdominal cramp and possible fever. Severe conditions may occur in immunocompromised patients requiring an effective antibiotic treatment (Mead et al., 1999). In addition, it can be associated with Guillain-Barré syndrome (GBS), a post-infection autoimmune disease characterized by acute and progressive neuromuscular paralysis (Nachamkin et al., 1998). Human campylobacteriosis generally presents 3-5 days of acute watery or bloody diarrhea, usually with severe abdominal pain. Most cases of infection are due to *C. jejuni*, with only 10% due to *C. coli* and less than 1% from *C. lari* (Nachamkin et al., 1998).

A high prevalence of *Campylobacter* has been detected both in the intestinal tract of poultry at a farm level and in poultry carcasses at the processing plants.

Consequently, poultry products at retail are often contaminated by *Campylobacter* (Jeffrey et al., 2001). A significant risk factor for human campylobacteriosis is a handling or eating undercooked poultry meat (Friedman et al., 2004).

2.5 Prevalence

Many types of poultry such as broilers, layers, turkeys, ducks, fowl, quails and ostriches can become colonized with *Campylobacter* (Sahin et al., 2002). The numbers of *Campylobacter* positive poultry flocks are commonly high (Sahin et al., 2002). The proportion of *C. jejuni* was higher than *C. coli*, but it was vary by regions, seasons and the production types (conventional, free-range and organic farms) (Heuer et al., 2001). Focusing on broiler breeder, there were 30-90% prevalence rate (Colles et al., 2011; Perez-Boto et al., 2012). From the prevalence studies conducted in Europe and the United States reported *Campylobacter* positive in broiler flocks ranging from 50-97% (Heuer et al., 2001; Bouwknecht et al., 2004; Barrios et al., 2006). From the data collected in Thailand, Chansiripornchai and Sasipreeyajan (2009) found that the prevalence of *C. jejuni* was between 55 and 80% (average at 65%) from samples of seven broiler flocks. Likewise, the prevalence of *Campylobacter* in chickens at the farm, slaughterhouse and market in northern Thailand were 64, 38 and 47%, respectively (Padungtod and Kaneene, 2005). Interestingly, several longitudinal studies indicated that broilers were not detected *Campylobacter* at day-old chicks, but intensively

reared flocks became detectably positive normally at 2 to 3 weeks of age (Berndtson et al., 1996; Evans and Sayers, 2000).

2.6 Mode of transmission of *Campylobacter* in poultry

2.6.1 Horizontal transmission

According to farm-based studies, horizontal transmission from the environment to poultry houses is the most usual mode of *Campylobacter* transmission on poultry farms (Sahin et al., 2002). Key sources of infection come from mainly through fecal contact old litter, other farm animals, domestic pets, wildlife species, house flies, insects and farm personnel via their boots (Sahin et al., 2002). Poultry feed does not play an important role in the spread of *Campylobacter* because it is very sensitive to oxygen and temperature (Humphrey et al., 1993). *Campylobacters* are not able to grow outside an animal host and either die or enter a viable but non-culturable (VBNC) state (Buswell et al., 1998). However, they can be isolated from fecal contaminated environmental sources, such as soil and surface water (Sahin et al., 2002). The presence of *Campylobacters* is the result from recent fecal contamination, because they are unable to multiply outside of host animals (Jones, 2001).

2.6.2 Vertical transmission

Although there were some reports showing that vertical transmission of *Campylobacter* can be occurred, this finding was still unclear (Doyle, 1984; Petersen et al., 2001). Some studies showed that *C. jejuni* had been isolated from the reproductive tract of healthy hens (Camarda et al., 2000; Buhr et al., 2002) and from semen of commercial broiler breeder roosters (Cox et al., 2002), but another side of this argument had several reasons also. Firstly, although breeders were infected with *Campylobacter*, young broiler chickens hatched from their eggs frequently lack of *Campylobacter* before 2 or 3 weeks of age (Bull et al., 2006). Secondly, the infected strains found in broiler flocks were usually different from their breeder flocks (Chuma et al., 1997). Finally, isolation of *Campylobacter* from eggs has been rarely found, and no studies have reported isolation of live *Campylobacter* cells from hatcheries or young chickens (Hiatt et al., 2002).

2.7 Molecular techniques for genetic characterization of *Campylobacter*

Epidemiological investigations are important to discover the source of broiler house contamination and the mechanisms by which *Campylobacter* spp. spreads between the chickens in order to develop appropriate strategies for reducing the risk of this foodborne zoonosis. To know the epidemiological relationship between bacteria, molecular genotyping is the best way to explore and establish them because the reported genetic instability in *Campylobacter* spp. limited their molecular

epidemiological interpretation (Dingle et al., 2008). Nowadays, several genotyping methods were developed to demonstrate genetic diversity of *Campylobacter* spp. such as multilocus enzyme electrophoresis (MLEE), repetitive element sequence-based PCR (rep-PCR), amplified fragment length polymorphism (AFLP), PCR-restriction fragment length polymorphism analysis of the *flaA* gene (*flaA*-RFLP), sequencing of the short variable region of the *flaA* gene (*flaA*-SVR sequencing), pulse-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) (Charununtakorn et al., 2015; Duffy et al., 2015). These techniques have both advantages and disadvantages. For example, MLST, a technique of typing by sequencing seven house-keeping genes, is considered the gold standard, but typing of large strain sets can be costly and time consuming. Recently, a study found that *flaA*-RFLP is a suitable preliminary typing method due to the ease of operation, equipment availability and cost (O'Reilly et al., 2006).

2.7.1 Flagellin gene typing

The characteristic motility of *Campylobacter* spp. is due to the fact that they have a single unsheathed polar flagellum at one end or both ends of the cell (Lastovica et al., 2014). The flagellar filaments are composed of repeats of a flagellin subunit which is encoded by a *fla* gene (Lastovica et al., 2014). *C. jejuni* and *C. coli* have two flagellin genes, designated *flaA* and *flaB* (Lastovica et al., 2014). Each gene is approximately 1.7 kb and is separated by an intergenic space region of 170 bp

(Nachamkin et al., 1993). These genes encode repeats of flagellin subunits that form the flagellum found on one or both ends of *Campylobacter* cells. The 5' and 3' regions of each gene are highly conserved, with considerable sequence variation in the region in between (Nachamkin et al., 1993). The achievable genotyping methods for *Campylobacter* spp. is *flaA*-RFLP due to the fact that it is a simple and reliable method with a good discriminatory power (Petersen and Newell, 2001). In addition, *flaA*-RFLP was the best method associated with epidemiology in the Walkerton outbreak in 2000 (Clark et al., 2005). The concept of *flaA*-RFLP is to amplify *flaA* gene which has highly conserved with considerable sequence variation followed by restriction fragment length polymorphism to exhibit the variability within an amplicon.

2.8 Antimicrobial resistance in *Campylobacter* spp.

C. jejuni and *C. coli* are increasingly resistant to antimicrobials which have become a major concern for public health because antimicrobials used in poultry production may lead to the rise of antimicrobial-resistant bacteria in humans (Smith et al., 2002). Although *Campylobacter* infections in humans are mild, self-limiting and usually resolve without antimicrobial therapy, antimicrobial treatment is required for some severe, prolonged infections or for infections in immunocompromised patients (Gibreel and Taylor, 2006). Macrolides are considered the drugs of choice, but fluoroquinolones (FQs) are also frequently used because of their broad spectrum of activity against enteric pathogens (Engberg et al., 2001). This pathogenic organism is

increasingly resistant to antimicrobials used in humans. In addition, FQ-resistant *Campylobacter* spp. was rapidly emerged among poultry flocks (Hein et al., 2003) and antimicrobial-resistant *Campylobacter* were increasingly found in developing countries using unrestricted antibiotics for humans and animals. Increasingly, antimicrobial use in food animal production is a global concern as antimicrobial-resistant zoonotic pathogens can develop at the farm level and lead to human exposure and infection via various pathways, including meat and poultry products (Quinn et al., 2007). Importantly, the use of FQs such as enrofloxacin in poultry production might lead to an increasing of FQ-resistant *Campylobacter* populations (Gupta et al., 2004). In 2002, a United States FDA quantitative risk assessment estimated that fluoroquinolone use in chickens and turkeys caused >10,000 human infection with FQ-resistant *Campylobacter* in people seeking medical care and subsequent antimicrobial treatment (USFDA, 2000). In 2005, FQs were banned from poultry production in U.S., but the proportion of FQ-resistant *Campylobacter* isolates following this withdrawal was not statistically different to that before withdrawal (Price et al., 2007). From chicken samples, there were some reports found high proportions of *Campylobacter* resistant to nalidixic acid and ciprofloxacin in Thailand (Padungtod et al., 2003; Padungtod et al., 2006). Sukhapesna et al. (2005) also reported that they the proportions of *C. jejuni* isolated from retail markets in Nakhon Pathom province which was resistant to tetracycline, sulfamethoxazole, nalidixic acid and norfloxacin,

respectively and nearly 97% of the isolates were multiple resistance to more than 4 antimicrobial agents tested.

2.9 Fluoroquinolones resistance mechanism in *Campylobacter* spp.

FQs belong to a family of broad-spectrum synthetic antimicrobial agents. The FQs are used for the treatment of gastrointestinal tract infection of both animal and human diseases (Van Bambeke et al., 2005; Martinez et al., 2006). Generally, the FQs target two important microbial enzymes, DNA gyrase and DNA topoisomerase IV (Smith and Fratamico, 2010). In *Campylobacter*, the resistance to FQs is mainly mediated by point mutations in the quinolone resistance-determining region (QRDR) of DNA gyrase A (*gyrA*) (Payot et al., 2006). No mutations in DNA gyrase B (*gyrB*) have been associated with FQ resistance in *Campylobacter* (Pidcock et al., 2003). Although the genes encoding topoisomerase IV (*parC/parE*) are involved in FQ resistance in gram-negative bacteria, these genes are absent in *Campylobacter* meaning that *parC/parE* mutations are not implicated in *Campylobacter* resistance to FQ antimicrobials (Pidcock et al., 2003; Payot et al., 2006). Several studies have shown that mutations in the quinolone resistance determining region (QRDR) of the *gyrA* gene of *Campylobacter* confers high-level resistance to FQs, with the mutation at position threonine-86-isoleucine (ACA - ATA in *C. jejuni* or ACT - ATT in *C. coli*) being most common (Zirnstien et al., 1999; Zirnstien et al., 2000). Mismatch amplification mutation assay by PCR (MAMA-PCR) is a rapid method applied to detect the Thr-86-Ile mutation (Zirnstien et al., 1999; Zirnstien

et al., 2000). Mismatch primers were created to fully complement to the template strand except for one nucleotide at the 3' end. These primers are used to detect the mutants. Thus, wild types and mutants can be differentiated by this technique. In addition, a list of amino acid substitutions conferring resistance to FQs is given in Table 2 (Smith and Fratamico, 2010).

Table 2: Amino acid substitutions in the QRDR of gyrase A
conferring resistance to FQs

Gyrase subunit	Amino acid substitution
	Ala-70-Ser
	Thr-86-Ile
A	Thr-86-Ala
	Asp-90-Tyr
	Asp-90-Asn
	Gly-119-Ser

*Ala, alanine; Ser, serine; Thr, threonine; Ile, isoleucine; Asp, aspartic acid; Tyr, tyrosine;
Asn, asparagine; Gly, glycine

2.10 Intervention strategies

It is widely recognized that the handling and consumption of undercooked chickens is a major source of human campylobacteriosis, so many researchers have

tried to reduce its population at the farm level. One of the most challenging tasks is to control the flock colonization by *Campylobacter* because poultry houses can be contaminated by *Campylobacter* in many different ways from various environmental sources. Nowadays, there is no single protocol to completely control *Campylobacter* infections on poultry farms. For controlling *Campylobacter*, on-farm control strategies can be divided into two approaches: (1) biosecurity-based interventions, and (2) non-biosecurity based measures such as vaccination and competitive exclusion.

2.10.1 Biosecurity

There are many reports found a correlation between decreased *Campylobacter* infection in broiler flocks and the use of strict biosecurity measures and hygienic practices on farms (Humphrey et al., 1993; Berndtson et al., 1996; Evans and Sayers, 2000). Most of these studies showed that the use of strict biosecurity measures could either reduce the level or delayed the onset time of *Campylobacter* colonization, but they were not totally successful in preventing introduction of *Campylobacter* into broiler flocks (Humphrey et al., 1993; Berndtson et al., 1996; van de Giessen et al., 1998). Considering on-farm biosecurity measures, they showed different results in controlling of *Campylobacter* in Europe. In northern European countries such as Norway, Sweden, and Finland, these measures are successful in reducing *Campylobacter* incidence in broilers. On the other hand, they have met limited success in UK, the Netherlands and Denmark (EFSA, 2011).

2.10.2 Vaccination

Nowadays, there are no commercial vaccines available for controlling *Campylobacter* in poultry (de Zoete et al., 2007). It is a critical challenge for developing effective vaccines of *Campylobacter* conferring broad-spectrum protection because the commensal nature of this organism in poultry and the antigenic diversity among different *Campylobacter* strains. Formerly, Some researchers developed *Campylobacter* vaccines using different methods such as killed whole cells, live-attenuated vaccines, flagellin-based subunit vaccines, genetically engineered live vectors expressing *Campylobacter*-specific antigens, and chitosan-encapsulated DNA vaccine which most of them demonstrated some protection in chickens (Wyszynska et al., 2004; de Zoete et al., 2007; Lin, 2009; Buckley et al., 2010). However, more attempts are needed to develop vaccines that induce protective immune responses and can be done on poultry farm in a practical.

2.10.3 Competitive exclusion

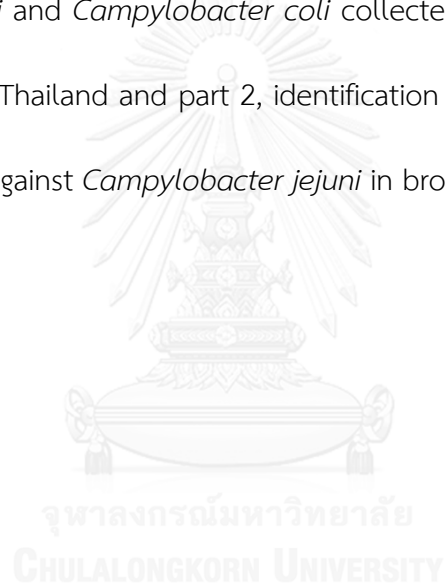
Competitive exclusion (CE) was first discovered by Nurmi and Rantala (1973). The definition of CE is the oral administration of non-pathogenic intestinal bacteria which can establish and colonize the intestinal tract and maintain or increase the natural flora to prevent or decline colonization of pathogenic organisms (Nurmi and Rantala, 1973; Vanbelle et al., 1990). The CE cultures can be categorized into 2 groups: defined and undefined cultures. The defined CE cultures are microbial isolates

identified and characterized for their properties such as antimicrobial sensitivity and acid and bile tolerance, while the latter are incompletely characterized (Zhang et al., 2007). Ideally, CE should use defined cultures instead of crude intestinal mucus suspension. Importantly, CE or probiotics used in poultry should not have antimicrobial resistance phenotypes because they can increase the risk of transferrable drug resistant genes to other gut bacteria (Schwarz et al., 2001). For defined CE cultures, *Lactobacillus* spp. *Bacillus* spp. and *Enterococcus faecium* are focused for studying on their CE properties against pathogenic bacteria (Morishita et al., 1997; Thomrongsuwannakij et al., 2016). The treatment of broilers with pure cultures of *Lactobacillus acidophilus* and *Streptococcus faecium* from day 1 to day 3 demonstrated a 70% reduction in the frequency of *C. jejuni* shedding in colonized chickens (Morishita et al., 1997). A recent report has shown that *Enterococcus faecalis* MB 5259 showed an *in vitro* inhibitory effect to *C. jejuni* MB 4185, but there was no inhibition in the *in vivo* experiment (Robyn et al., 2013) leading to raise a question to find the appropriate non-pathogenic bacteria that can reduce *Campylobacter* colonization in chickens in the future. Nevertheless, the effect of defined CE on *Campylobacter* was variable and inconsistent (Schoeni and Wong, 1994; Mead et al., 1996).

CHAPTER III

Materials and Methods

The experiment was divided into 2 parts, including part 1, antimicrobial resistance, the characterization of *gyrA* mutation, and genetic diversity by *flaA*-RFLP of *Campylobacter jejuni* and *Campylobacter coli* collected through commercial broiler production chains in Thailand and part 2, identification of competitive exclusion and its ability to protect against *Campylobacter jejuni* in broilers (Figure 1).



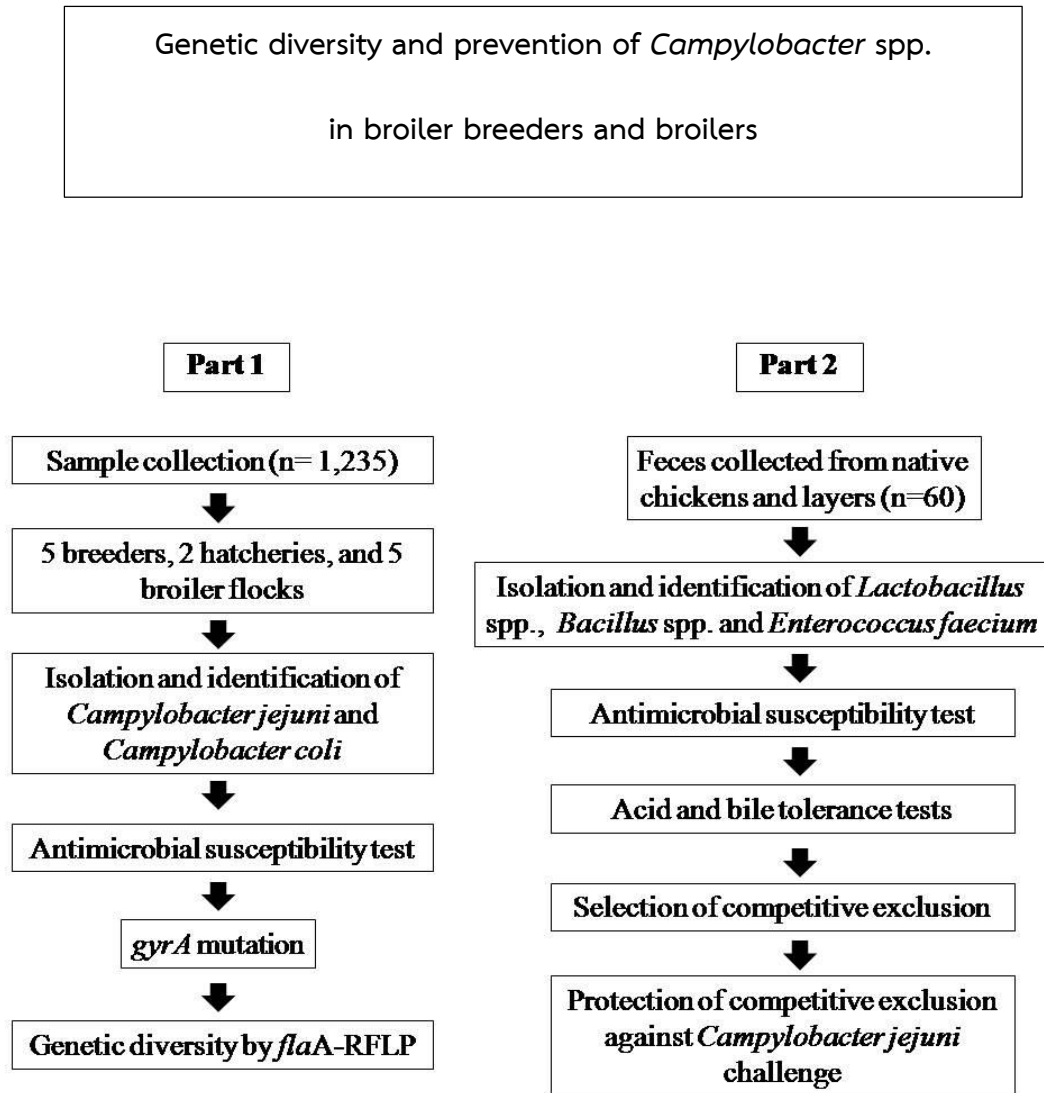


Figure 1: The flow chart of experiments

3.1 Antimicrobial resistance, the characterization of *gyrA* mutation, and genetic diversity by *flaA*-RFLP of *Campylobacter jejuni* and *Campylobacter coli* collected through commercial broiler production chains in Thailand

3.1.1 Farm description

During the period between September 2014 and February 2015, two chicken production chains from one integrated chicken company located in Lopburi province, a central area of Thailand were chronologically sampled from broiler breeder farms, hatcheries, and the broiler farms. This province has intensive poultry production facilities and other companies are also facilitated in the same province. Five commercial breeder flocks (breeder 1, 2, 3, 4, and 5), 2 hatcheries (hatchery A and B), and 5 broiler flocks (broiler 1, 2, 3, 4, and 5) were sampled in this study (Figure 2). Cobb chickens were raised in all flocks except that breeder flock 4 and broiler flock 4 were Hubbard chickens. The number of birds in each of breeder and broiler flocks was approximately 8,000 and 18,000 birds, respectively. Breeder flocks 1 and 2 were located on the same farm while breeder flocks 3, 4, and 5 were on another farm. Likewise, broiler flocks 1 and 2 were raised on the same farm while broiler flocks 3, 4, and 5 were raised on another farm. Fertile eggs from breeder flocks 1 and 2 were sent to hatchery A, while breeder flocks 3, 4, and 5 supplied eggs to hatchery B (Figure 2). All farms were located within a radius of around 50 km (Figure 3). Birds were raised under standard, controlled environment sheds that used evaporative cooling systems.

The “all in-all out” by flock system was used on all broiler farms. Hence, one-day-old birds were placed in one day for each broiler flock, grown in the same house and all birds were sent to the processing plant on the same day. Broilers from flocks 1 and 2 were reared until 35 days of age whereas broilers from flock number 3, 4, and 5 were reared until 43 days of age. This difference reflected market demands during the time of the study. The houses were cleaned and disinfected, and litter was totally removed after each production cycle. All cleaned houses always have a 21-day-downtime period before starting a new production cycle. No other livestock is raised on these farms. All visitors must sign their names, and their vehicles must be disinfected before entering the farms.

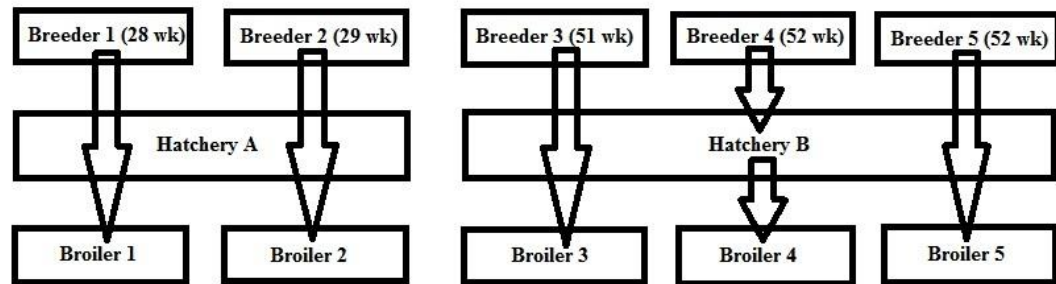


Figure 2: Diagram of sample collection from breeder flocks, hatcheries, and broiler flocks.

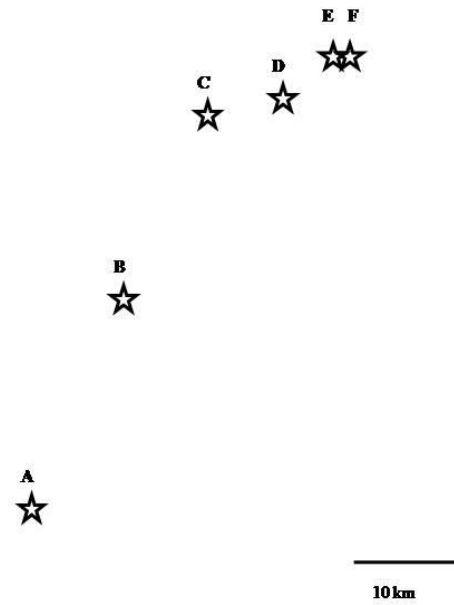


Figure 3: Geographic location of sampling sites in Lopburi province. A = broiler flocks 3, 4, and 5, B= breeder flocks 3, 4, and 5, C= breeder flocks 1 and 2, D= broiler flocks 1 and 2, E = hatchery A and F= hatchery B.

3.1.2 Sample collection

In total, 1,235 samples were collected from the breeder and broiler farms and the hatcheries (Table 3). *Campylobacter* colonization of both breeder and broiler flocks was determined from cloacal swabs and environmental samples (e.g., pan feeders, footwear, darkling beetles, flies, feed and water). The eggs from the breeder flocks were followed to hatcheries. At the hatcheries, early embryonic deaths were investigated. Samples from the egg tray, egg shells, hatcher and water were investigated as well. Boot swabs, house equipment, and environmental samples (pan feeders, footwear) from the cleaned broiler houses were obtained before the chicks arrived. One-day-old broilers were sampled by cloacal swabbing. After that, cloacal swabs, boot swabs and environmental samples (e.g., pan feeders, footwear, darkling beetles, flies, feed and water) were taken at days 14 and 28 for all farms and at day 35 (broiler flock 1 and 2) or day 43 (broiler flock 3, 4 and 5). The number and type of samples taken in this study are shown in Tables 3 and 4, respectively. All samples were kept on ice and transported to the laboratory, where they were then processed for bacterial isolation within 6 hr from the time of collection.

Table 3: Number of samples collected in this study

	Number of samples from each flock				
	Flock 1	Flock 2	Flock 3	Flock 4	Flock 5
Breeder flock					
- Cloacal swabs	30	30	30	30	30
- Boot swabs	4	4	4	4	4
- House equipment and environmental samples (e.g., pan feeders, footwear, beetles, flies, feed, and water)	19	19	19	19	19
Hatchery					
- Equipment and environmental samples (e.g., egg tray, egg shell, hatcher and water)	8	8	8	8	8
- Early embryonic deaths	5	5	5	5	5
Broiler flock					
<u>Before rearing period</u>					
- Boot swabs	4	4	4	4	4
- House equipment and environmental samples (e.g., pan feeders, footwear)	9	9	9	9	9
<u>During rearing period</u>					
- Cloacal swabs					
Day 1	20	20	20	20	20
Day 14	20	20	20	20	20
Day 28	20	20	20	20	20
Day 35	20	20	-	-	-
Day 43	-	-	20	20	20
- Boot swabs	16	16	16	16	16
- House equipment and environmental samples (e.g., pan feeders, footwear, beetles, files, feed and water)	72	72	72	72	72
<u>Total</u>	247	247	247	247	247

Table 4: Sample collection procedures used in this study

Type of sample	Sample collection procedures
Farm samples	
Cloacal swab	Moistened cotton swab was inserted into cloaca and then put into Cary-Blair transport medium
Animal feed	Approximately 500 grams of animal feed were collected from silo and 3 areas of pan feeder (front, middle and back of the house).
Boot swab	The man whose footwear covered by boot swabs walked inside or around the house. After that, they were kept in sterile plastic bags.
Pan feeder	Pan feeder was sampled using a moistened cotton swab. Three pan feeders from front, middle and last areas of the house were grouped into 1 sample.
Water	
- Nipple water	Nipple water was collected from 3 areas of the house including front, middle and back of the house. Each sterile bottle contained around 500 ml of water.
-Water inlet	Water from the main water inlet to each house was collected (approximately 500 ml) in a sterile glass bottle.
Beetle	Approximately 10 g of beetles were collected from litter in the house and kept in a sterile plastic bag.
Flies	Approximately 10 g of flies were collected from each house and kept in a sterile plastic bag.
Footwear	Footwear used inside or outside the house were sampled
Hatchery samples	
Hatcher	The hatcher walls were swabbed by moistened gauze swab on 3 inner sides and the swab kept in a sterile plastic bag.
Egg shell	Approximately 25 g of egg shell were collected from each egg tray. Three egg trays were sampled per flock.
Early embryonic death	Five samples of early embryonic death were collected from each flock. Their ceca were cut using a sterile technique in the laboratory.
Water	Approximately 500 ml of water used for egg's incubator, hatcher, and general use in the hatchery was sampled and kept in a sterile glass bottle.

3.1.3 *Campylobacter* isolation and identification

Campylobacter isolation was performed as described in ISO 10272-1 (ISO10272-1, 2006). All samples were inoculated into Bolton broth (OXOID, Basingstoke, Hampshire, England) with a ratio 1:10 (v/v) of sample: enrichment medium. The inoculated broths were incubated at 37°C for 4-6 hr, and then at 41.5°C for 40-48 hr under microaerobic conditions (5% O₂, 10% CO₂, and 85% N₂) using a gas pack jar system (Mitsubishi Chemicals, Tokyo, Japan). One loopful (1 µl) of enrichment broths was streaked onto modified charcoal cefoperazone deoxycholate agar (mCCDA) and incubated in a microaerobic atmosphere at 41.5°C for 40-48 hr. Suspected *Campylobacter*-like colonies were subcultured onto Columbia blood agar (CBA) (OXOID, Basingstoke, Hampshire, England) and incubated in a microaerobic atmosphere 41.5°C for 24-48 hr. Genomic DNA was extracted from fresh cultures by using a Presto™ mini gDNA bacterial kit (Geneaid Biotech, Taiwan) following the manufacturer's instructions. Presumptive *Campylobacter* colonies were confirmed by multiplex PCR as previously described (Wang et al., 2002). Sets of primers for *Campylobacter* identification were shown in Table 5. The 25 µl of PCR mixture contained 2.5 µl of 10x PCR buffer; 1 µl of 10 mM deoxynucleoside triphosphate; 1 µl of 10 µM primers 23S, *C. jejuni*, and *C. coli*; 2.5 µl (100 ng) of DNA template; and 0.2 µl of a 5 U/ µl *Taq* DNA Polymerase (Roche Diagnostics, GmbH, Germany). Two reference strains, *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559, were used as positive controls. PCR mixtures were amplified in a thermal cycler (Life express, BIOER®). The PCR cycles included an initial

denaturation step at 95°C for 6 min followed by 30 cycles of denaturation at 95°C for 0.5 min, amplification at 59°C for 0.5 min and extension at 72°C for 0.5 min, ending with a final extension at 72°C for 7 min. PCR products were examined on 1% agarose gel in 1xTris-borate-EDTA (TBE) buffer at 80 V for 30 min. All gels were stained with ethidium bromide and visualized by ultraviolet transilluminator (E-BOX VX2, Vilber-Lourmat®). Confirmed isolates were stored in tryptone soya broth (TSB) (OXOID, Basingstoke, Hampshire, England) with 15% glycerol at -80°C for further study.

Table 5: Sets of primers for *Campylobacter* identification (Wang et al., 2002)

Primer	Sequence (5'-3')	size (bp)	Target gene
23SF	TAT ACC GGT AAG GAG TGC TGG AG	650	<i>Campylobacter</i>
23SR	ATC AAT TAA CCT TCG AGC ACC G		23S rRNA
CJF	ACT TCT TTA TTG CTT GCT GC	323	<i>C. jejuni hipO</i>
CJR	GCC ACA ACA AGT AAA GAA GC		
CCF	GTA AAA CCA AAG CTT ATC GTG	126	<i>C. coli glyA</i>
CCR	TCC AGC AAT GTG TGC AAT G		

3.1.4 Antimicrobial susceptibility test

Minimum inhibitory concentrations (MICs) tests were done using Muller Hinton agar (MHA) supplemented with 5% defibrinated sheep blood and a two-fold agar dilution technique (CLSI, 2013). Briefly, the *Campylobacter* isolates were grown on MHA supplemented with 5% defibrinated sheep blood (Difco®, MD, USA) at 42°C overnight under microaerobic condition. Single colonies were picked and transferred to 0.85% normal saline. The turbidity of bacterial suspension was adjusted to 0.5 McFarland (~ 10⁸ CFU/ml). The suspension was then decimally diluted to 10⁷ CFU/ml in normal saline and inoculated onto MHA supplemented with 5% defibrinated sheep blood containing appropriate concentrations of antimicrobials using multipoint inoculators (~ 10⁴ CFU/ml). After incubation at 42°C for 24 hr under microaerobic condition, the MIC value, the lowest concentration of an antimicrobial agent that completely inhibits visible growth of bacteria, was recorded. The control organisms for antimicrobial susceptibility determination were *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559. The nine antimicrobials used and the breakpoints for determining resistance were as follows: amoxicillin (AMX, 32 µg/ml), bacitracin (BAC, 8 µg/ml), colistin (COL, 8 µg/ml), doxycycline (DOX, 8µg/ml), enrofloxacin (ENR, 4 µg/ml), erythromycin (ERY, 32 µg/ml), gentamicin (GEN, 16 µg/ml), tetracycline (TET, 16 µg/ml) and trimethoprim-sulfamethoxazole (SXT, 4/76 µg/ml). Susceptibility categorization for DOX, ERY, GEN, and TET were based on the Clinical and Laboratory Standards Institute (CLSI) guidelines for *C. jejuni* and *C. coli* (CLSI, 2013). For ENR, the breakpoint for

ciprofloxacin was used according to CLSI guidelines for *C. jejuni* and *C. coli* (CLSI, 2013). For AMX and SXT, the interpretation criteria were the CLSI recommendations for enteric bacteria in the family *Enterobacteriaceae* (CLSI, 2013) since there are no available specific breakpoints for *Campylobacter* spp. for these drugs. For BAC and COL breakpoints, the breakpoints recommended by CLSI for other non-*Enterobacteriaceae* isolates was used for the same reason (CLSI, 2011). All antimicrobials were obtained from Sigma-Aldrich (St Louis, MO).

3.1.5 Detection of mutation(s) in the quinolone resistance determining region (QRDR) of the *gyrA* and mismatch amplification mutation assay by PCR (MAMA-PCR) detecting the Thr-86-Ile mutations

A total of 24 *C. jejuni* and 24 *C. coli* isolates, which were resistant to enrofloxacin, were subjected to nucleotide sequence analysis of the QRDR of the *gyrA* gene using the forward and reverse primers as previously described (Zirnstein et al., 1999; Zirnstein et al., 2000). The QRDRs of the *gyrA* genes of the *Campylobacter* isolates were amplified by PCR. PCR primers used in this protocol were shown in Table 6. The 50 μl of PCR mixture contained 5 μl of 10x PCR buffer; 2 μl of 10 mM deoxynucleoside triphosphate; 2.5 μl of 10 μM of forward and reverse primers; 5 μl (100 ng) of DNA template; and 0.4 μl of a 5 U/ μl *Taq* DNA Polymerase (Roche Diagnostics, GmbH, Germany). PCR mixtures were amplified in a thermal cycler (Life

express, BIOER®). The PCR cycles included an initial denaturation step at 94°C for 3 min followed by 30 cycles of denaturation at 94°C for 1 min, amplification at 50°C for 1 min and extension at 72°C for 1 min, ending with a final extension at 72°C for 5 min. *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559 served as control strains and were also sequenced. Five microliters of each PCR mixture were loaded onto agarose gels and stained with ethidium bromide for analysis after electrophoresis. The remaining *gyrA* PCR products were purified using the GenepHlow™ gel/pcr kit (Geneaid Biotech, Taiwan) and were submitted for nucleotide sequencing at First Base Laboratories (Seri Kembangan, Selangor, Malaysia). The DNA sequences obtained were compared and aligned with that of *C. jejuni* UA580 (Genbank accession number L04566). In addition, all 50 isolates were examined, as previously described (Zirnstein et al., 1999; Zirnstein et al., 2000), by a MAMA-PCR for the single point mutation (Thr-86-Ile) in the QRDR of the *gyrA* gene. This mutation is known to be a cause of high-level resistance to fluoroquinolones (Zirnstein et al., 1999). The MAMA-PCR protocols (25 µl each) were the same as above except the PCR cycling conditions were as follows: an initial denaturation step at 94°C for 3 min followed by 30 cycles of denaturation at 94°C for 0.5 min, amplification at 50°C for 0.5 min and extension at 72°C for 0.3 min. Primers used in this protocol were shown in Table 7. PCR products were examined on 1% agarose gel in 1xTris-borate-EDTA (TBE) buffer at 80 V for 30 min. All gels were stained with ethidium bromide and visualized by ultraviolet transilluminator (E-BOX VX2, Vilber-Lourmat®).

Table 6: Set of primers for QRDRs of the *gyrA* genes of *Campylobacter* spp.

(Zirnstein et al., 1999; Zirnstein et al., 2000)

Primer	Sequence (5'-3')	Purpose	size (bp)
GZgyrA5	ATT TTT AGC AAA GAT TCT GAT	<i>C. jejuni gyrA</i> forward primer	673
GZgyrA6	CCA TAA ATT ATT CCA CCT GT	<i>C. jejuni gyrA</i> reverse primer	
GZgyrACcoli3F	TAT GAG CGT TAT TAT CGG TC	<i>C. coli gyrA</i> forward primer	505
GZgyrACcoli4R	GTC CAT CTA CAA GCT CGT TA	<i>C. coli gyrA</i> reverse primer	

Table 7: Set of primers detecting Thr-86-Ile mutation of the *gyrA* genes of *Campylobacter* spp. (Zirnstein et al., 1999; Zirnstein et al., 2000)

Primer	Sequence (5'-3')	Purpose	size (bp)
CampyMAMAgryA1	TTT TTA GCA AAG ATT CTG AT	<i>C. jejuni</i> Thr-86-Ile (ACA-ATA) mutation detection forward primer	265
CampyMAMAgryA5	CAA AGC ATC ATA AAC TGC AA	<i>C. jejuni</i> Thr-86-Ile (ACA-ATA) mutation detection reverse primer	
GZgyrACcoli3F	TAT GAG CGT TAT TAT CGG TC	<i>C. coli</i> Thr-86-Ile (ACT-ATT) mutation detection forward primer	192
CampyMAMAgryA8	TAA GGC ATC GTA AAC AGC CA	<i>C. coli</i> Thr-86-Ile (ACT-ATT) mutation detection reverse primer	

3.1.6 *flaA*-RFLP Typing

flaA-RFLP typing was conducted by following the procedure of Nachamkin et al. (Nachamkin et al., 1993). For *flaA* amplification (Table 8), the 50 µl of PCR mixture contained 5 µl of 10x PCR buffer; 2 µl of 10 mM deoxynucleoside triphosphate; 2.5 µl of 10 µM of forward and reverse primers; 5 µl (100 ng) of DNA template; and 0.4 µl of a 5 U/ µl *Taq* DNA Polymerase (Roche Diagnostics, GmbH, Germany). Two reference strains, *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559, were used as positive controls. PCR mixtures were amplified in a thermal cycler (Life express, BIOER®). The PCR cycles included an initial denaturation step at 94°C for 1 min followed by 35 cycles of denaturation at 92°C for 0.5 min, amplification at 55°C for 1.5 min and extension at 72°C for 2.5 min, ending with a final extension at 72°C for 5 min. Ten microlitres of PCR product were brought to examine on 1% agarose gel in 1xTris-borate-EDTA (TBE) buffer at 80 V for 30 min. All gels were stained with ethidium bromide and visualized by ultraviolet transilluminator. For RFLP analysis, each PCR product was prepared a reaction mix containing 3.0 µl H₂O, 1.5 µl 10x H buffer (New England Biolabs, Massachusetts, USA), 0.5 µl *DdeI* (10 units/µl) (New England Biolabs, Massachusetts, USA) and added 10 µl PCR product. All reactions were incubated at 37°C for 3 hours. The whole reaction was run in 2% DNA grade agarose (Progen) gel in 1xTris-borate-EDTA (TBE) buffer at 70 V for 100 min. All gels were stained with ethidium bromide and visualized by ultraviolet transilluminator (E-BOX VX2, Vilber-Lourmat®). TIFF image

files were imported into Bionumerics 6.5 (Applied MathsSint-Martens-Latem, Belgium). The similarity matrix was computed using Dice similarity coefficient and clustering by the Unweighted Paired Group Method with Arithmetic Mean Values (UPGMA). Band position tolerance and the optimization coefficient were both set to 2%. Clusters were defined at the 72% similarity level using Bionumerics.

Table 8: A set of primers for *flaA* gene amplification (Nachamkin et al., 1993)

Primer	Sequence (5'-3')	size (bp)	Target gene
flaA-F	GGA TTT CGT ATT AAC ACA AAT GGT GC	1700	<i>flaA</i>
flaA-R	CTG TAG TAA TCT TAA AAC ATT TTG		

3.2 Identification of competitive exclusion and its ability to protect against *Campylobacter jejuni* in broilers

3.2.1 Sample collections from native chickens and layers

Four native chicken farms and 1 commercial layer farm in the Central area of Thailand which age of birds were in a range of 30-40 weeks for native chicken farms and 90 weeks for the commercial layer farm were selected based on their non-use antimicrobial history. The native chicken farms had no record of *Campylobacter* spp. prevalence while the commercial layer farm had 35% of *Campylobacter jejuni* prevalence. Feces were collected from 10, 10, 10, 10 and 20 birds at each farm, respectively. Fecal samples were kept at 4°C and transported to the laboratory where they were then processed for bacterial isolation within 24 hr.

3.2.2 Isolation of *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium*

Isolation of *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium* was performed following ISO 15214, ISO 7932 and European Community Project SMT4 CT98-2235 standards, respectively (ISO-7932, 1993; ISO-15214, 1998; European_commission, 2003). Briefly, a single 1 g from each fecal sample was dissolved in 9 ml of 0.85% normal saline. Using 1 loopful, the samples were streaked onto selective agar including de Mans Rogosa and Sharpe (MRS) agar, Manitol Egg Yolk

Polymyxin-B agar and SF-streptococcus agar for *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus* spp., respectively. The inoculated plates were incubated at 37°C for 24-48 hr. Suspected colonies were primarily identified by Gram staining and biochemical tests. All bacterial isolates were kept as 15% glycerol stock at -80°C

3.2.3 Identification of genus and species

Oligonucleotide primers used in this study are listed in Table 9. DNA template was extracted by heating method (Kwon et al., 2004). In brief, single colonies of each strain on an agar plate were suspended in distilled water and heated at 100°C for 10 min. They were then centrifuged at 12,000 rpm for 5 min. The supernatants were collected for use as the DNA template of polymerase chain reactions (PCRs). Multiplex PCR assay was done to verify genus and species of *Lactobacillus* and *Enterococcus faecium* (Ke et al., 1999; Dubernet et al., 2002; Jackson et al., 2004; Kwon et al., 2004). Amplified ribosomal DNA restriction analysis (ARDRA) was demonstrated for *Bacillus* identification (Wu et al., 2006). All PCRs were performed using KAPA® master mix (KapaBiosystems, Wilmington, USA) as described in the manufacturer's instructions. Reference strains obtained from the Thailand Institute of Scientific and Technological Research (TISTR) were as follows: *L. acidophilus* TISTR 1034, *L. casei* subsp. *rhamnosus* TISTR 108, *L. plantarum* TISTR 1265, *L. delbrueckii* subsp. *bulgaricus* TISTR 892, *B.*

subtilis TISTR 1460, *B. licheniformis* TISTR 1109, *E. faecium* TISTR 2058 and *E. faecalis* TISTR 379.

Table 9: Oligonucleotide primers used in this study

Primers	Sequence (5'-3')	PCR type	PCR products (bp)	References
<i>Lactobacillus</i>				
R16-1	CTT GTA CAC ACC GCC CGT CA	Genus-specificity	250	(Dubernet et al., 2002)
LbLMA1-rev	CTC AAA ACT AAA CAA AGT TTC			
IDL03R	CCA CCT TCC TCC GGT TTG TCA	All <i>lactobacillus</i>	-	(Kwon et al., 2004)
IDL04F	AGG GTG AAG TCG TAA CAA GTA GCC	All <i>lactobacillus</i>	-	(Kwon et al., 2004)
IDL11F	TGG TCG GCA GAG TAA CTG TTG TCG	<i>L. casei</i> group	727	(Kwon et al., 2004)
IDL22R	AAC TAT CGC TTA CGC TAC CAC TTT GC	<i>L. acidophilus</i>	606	(Kwon et al., 2004)
IDL31F	CTG TGC TAC ACC TAG AGA TAG GTG G	<i>L. delbrueckii</i>	184	(Kwon et al., 2004)
IDL42R	ATT TCA AGT TGA GTC TCT CTC TC	<i>L. gasseri</i>	272	(Kwon et al., 2004)
IDL52F	ACC TGA TTG ACG ATG GAT CAC CAG T	<i>L. reuteri</i>	1105	(Kwon et al., 2004)
IDL62R	CTA GTG GTA ACA GTT GAT TAA AAC TGC	<i>L. plantarum</i>	428	(Kwon et al., 2004)
IDL73R	GCC AAC AAG CTA TGT GTT CGC TTG C	<i>L. rhamnosus</i>	448	(Kwon et al., 2004)
<i>Bacillus</i>				
B-K1F	TCA CCA AGG CRA CGA TGC G	All <i>Bacillus</i>	1,114	(Wu et al., 2006)
B-K1R	CGT ATT CAC CGC GGC ATG			
<i>Enterococcus</i>				
Ent1	TAC TGA CAA ACC ATT CAT GAT G	Genus-specificity	112	(Ke et al., 1999)
Ent2	AAC TTC GTC ACC AAC GCG AAC			
FM1	GAA AAA ACA ATA GAA GAA TTA T	<i>E. faecium</i>	215	(Jackson et al., 2004)
FM2	TGC TTT TTT GAA TTC TTC TTT A			

3.2.4 Antimicrobial susceptibility test

Antimicrobial susceptibilities to ampicillin, vancomycin, gentamicin, kanamycin, streptomycin, erythromycin, clindamycin, tetracycline, chloramphenicol and tylosin were evaluated by determining the minimum inhibitory concentrations (MICs). According to Clinical and Laboratory Standards Institute guidelines (CLSI) (CLSI, 2013), MICs were done in Muller Hinton agar (MHA) using a two-fold agar dilution technique which is almost the same as mentioned in 3.1.4 except that the bacterial isolates were grown in MHA at 37°C overnight and the MIC value was recorded after incubation at 37°C for 18-24 hr. The choice of antimicrobials and breakpoints for clarifying *Lactobacillus*, *Bacillus* and *Enterococcus faecium* as resistant were suggested by the European Food Safety Authority (EFSA) (EFSA, 2012). *Escherichia coli* ATCC 25922 was used as a control organism. All antimicrobials were bought from Sigma-Aldrich (St Louis, MO).

3.2.5 Acid and Bile tolerance tests

Acid and bile tolerance tests were performed to strains that qualified the acceptable range of MIC values according to the protocols of Hyronimus et al. (2000) with some modifications. For the acid tolerance test, the stock bacteria kept at -80°C were grown in MRS broth at 37°C for 24 hr; they were then pipetted into another MRS broth with pH value adjusted to 2.5 using 5M HCl (Merck) and sampled for counting

colony numbers at 0 and 3 h of incubation time onto MRS agar by a pour plate technique. Survival rates were calculated by using the below formula. Like the bile tolerance test, it has a similar protocol with the acid test, but it was changed from MRS broth (pH 2.5) to oxgall bile 0.3% (Difco) (Gilliland et al., 1984). Counting colony numbers for bile tolerance test were conducted at 0 and 24 hours of incubation time.

$$\text{Survival rates (\%)} = \frac{\log N}{\log N_0} \times 100$$

where log N equals the log number of the presenting colony at the end of the test

and log N₀ equals the log number of presenting colony at the start of the test.

3.2.6 *Campylobacter jejuni* challenges

Two hundred and ten 1-day-old non-vaccinated female Cobb broilers from a commercial hatchery were divided into ten groups. As shown in Table 10, groups 1-7 were orally gavaged with 0.5 ml of the top-three qualified CE bacteria that passed MICs and acid and bile tolerance criteria as a single, double or triple strain at 1-3 days of age. Group 8 was gavaged by a commercial product (AVIPROB™, Diasham Resources, Singapore) at 1-3 days of age. Group 9 and 10 served as positive control and negative control groups, respectively. At 11 days of age, the feces of all broilers were collected

to produce cultures to confirm *Campylobacter* spp. free status before challenges. All *Campylobacter*-negative broilers except the negative control group were orally inoculated with Thai field strain number CU11 of *Campylobacter jejuni* with an approximate concentration at 10^6 CFU/ml, 1 ml/each at 14 days. Fifteen fecal samples of each group were collected to count *Campylobacter* colonies at 17, 21, 28 and 35 days of age, respectively. At 41 days of age, all broilers were euthanized and ceca were collected to count *Campylobacter* colonies. All broilers were weighed at 1, 14 and 41 days to calculate their feed conversion ratio (FCR) and body weight. Birds were provided feed and water *ad lib* and raised under an ethical approval for animal experimentation approved by Chulalongkorn University Animal Care and Use Committee no. 13310021.

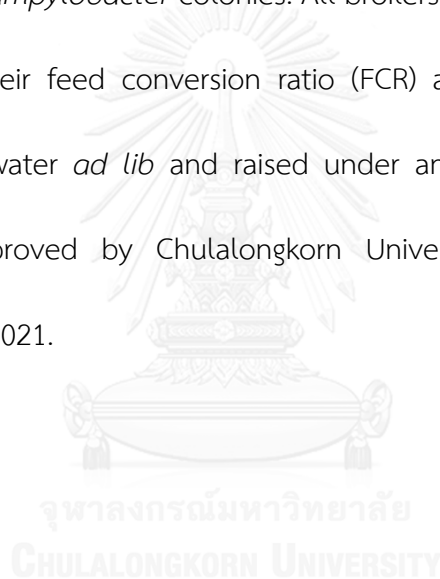


Table 10: CE application programs in broilers during 1-3 days of age

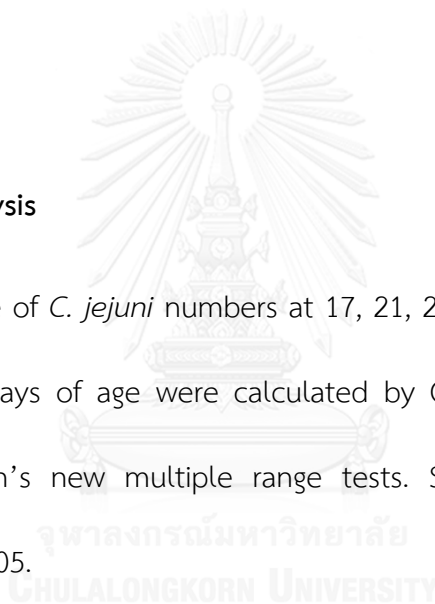
Group	Selected CE or products	Total Conc.		Challenge
		(CFU/ml)	<i>C.jejuni</i> at 14 days	
1	<i>Lactobacillus acidophilus</i> 1/4	2×10^8	+	
2	<i>Bacillus subtilis</i> 206/1	2×10^8	+	
3	<i>Enterococcus faecium</i> 122	2×10^8	+	
4	<i>Lactobacillus acidophilus</i> 1/4 + <i>Bacillus subtilis</i> 206/1	4×10^8	+	
5	<i>Lactobacillus acidophilus</i> 1/4 + <i>Enterococcus faecium</i> 122	4×10^8	+	
6	<i>Bacillus subtilis</i> 206/1 + <i>Enterococcus faecium</i> 122	4×10^8	+	
7	<i>Lactobacillus acidophilus</i> 1/4 + <i>Bacillus subtilis</i> 206/1+ <i>Enterococcus faecium</i> 122	6×10^8	+	
8	Commercial product (AVIPROB™)	2×10^8	+	
9	positive control	0.85% NSS	+	
10	negative control	0.85% NSS	-	

3.2.7 *Campylobacter* isolation, identification and enumeration

One gram fecal samples were added to 9 ml of 0.85% normal saline. The suspension was decimally diluted, and 0.1 ml of each diluted suspension was spread onto mCCDA in duplicate for *Campylobacter* enumeration. The inoculated plates were incubated at 42°C for 48-72 hr under microaerobic conditions using a gas pack jar system. Presumptive *Campylobacter* colonies were confirmed by multiplex PCR as mentioned in 3.1.3.

3.2.8 Statistical analysis

The difference of *C. jejuni* numbers at 17, 21, 28, 35 and 41 days of age and body weight at 41 days of age were calculated by One-way Analysis of Variance (ANOVA) and Duncan's new multiple range tests. Significance was tested at a probability level of 0.05.



CHAPTER IV

RESULTS

4.1 Antimicrobial resistance, the characterization of *gyrA* mutation, and genetic diversity by *flaA*-RFLP of *Campylobacter jejuni* and *Campylobacter coli* collected through commercial broiler production chains in Thailand

4.1.1 Prevalence of *Campylobacter* from 5 chicken production flocks

Overall of 1,235 samples, 130 samples were positive for *Campylobacter* spp. (10.5%) which was composed of 36 (2.9%) *C. jejuni* and 94 (7.6%) *C. coli* isolates. In this study, *Campylobacter* isolates were categorized into 2 groups -*Campylobacter* isolated from chicken-related samples and those isolated from environmental samples. In breeder flocks, the prevalence of *Campylobacter* spp. was between 53.3% and 86.7% (Figure 4). Birds from breeder flock 2 showed the highest prevalence of *Campylobacter* spp. at 86.7%. *C. coli* were isolated from environmental samples (e.g. boot swabs inside and outside the houses, darkling beetles and pan feeder) of all breeder flocks at a range between 4.3% and 13% whereas *C. jejuni* was only isolated from boot swabs of breeder flock 1 at 8.7% prevalence. No *Campylobacter* was detected in either hatchery, with the samples being from early embryonic deaths and

the environment. In broiler flocks, *Campylobacter* spp. was not detected until 35 days of age. Only *C. coli* was recovered from broiler flock 1 and 2 at 12.5% and 2.5% prevalence, respectively. Broiler flocks 3, 4, and 5 were *Campylobacter* negative throughout this study. *Campylobacter* spp. was not isolated from environmental samples taken in any broiler flock.

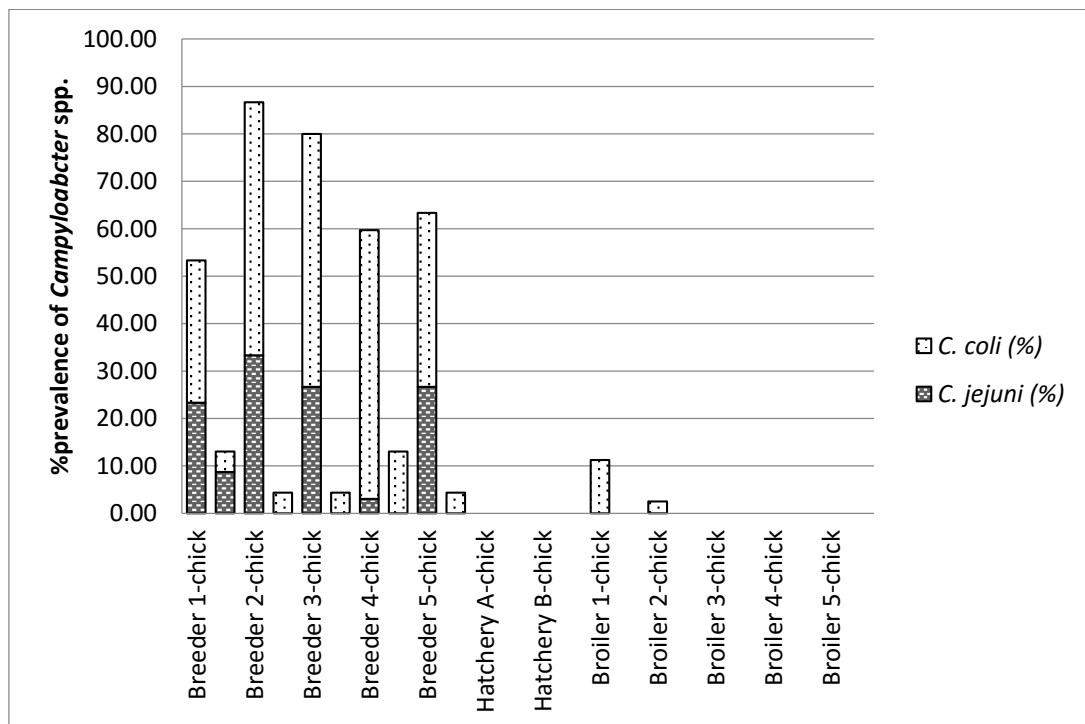


Figure 4: Prevalence percentage of *C. jejuni* and *C. coli* isolated from chicken-related samples and environmental samples.

4.1.2 Phenotypic antimicrobial resistance

According to CLSI protocols (CLSI, 2013), *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559 was used as control organisms and all MIC values were within the MIC quality control ranges in all batches. Overall, Thai *Campylobacter* isolates were commonly resistant to various classes of antimicrobial agents except erythromycin and gentamicin. Sixty-six percent of *C. jejuni* isolates and 97.9% of *C. coli* isolates were multidrug resistance (MDR), defined as being resistant to three or more antimicrobial classes. As well, all *C. jejuni* and *C. coli* isolates were resistant to amoxicillin and bacitracin (Figure 5). Moreover, a high frequency resistance was shown against enrofloxacin (100%), colistin (66.7%), tetracycline (55.6%), doxycycline (50%), and trimethoprim-sulfamethoxazole (36.1%) for *C. jejuni*. For *C. coli*, there was a high level of resistance to enrofloxacin (98.9%), tetracycline (97.9%), trimethoprim-sulfamethoxazole (81.9%), and doxycycline (79.8%). However, only 16% of *C. coli* isolates were resistant to colistin. All Thai *Campylobacter* isolates were susceptible to erythromycin and gentamicin. The most resistance patterns found in this study were AMX-BAC-COL-ENR for *C. jejuni* and AMX-BAC-DOX-ENR-TET-SXT for *C. coli* as shown in Table 11.

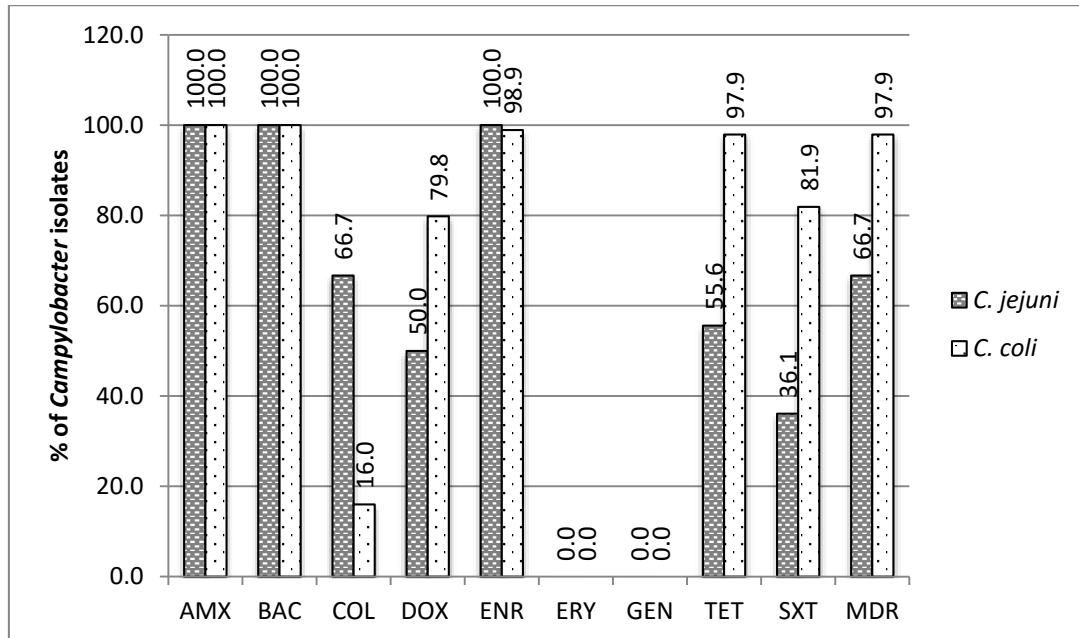


Figure 5: Frequency of resistance to 9 antimicrobial agents in *C. jejuni* (n = 36) and *C. coli* (n = 94). AMX, amoxicillin; BAC, bacitracin; COL, colistin; DOX, doxycycline; ENR, enrofloxacin; ERY, erythromycin; GEN, gentamicin; TET, tetracycline; SXT, trimethoprim-sulfamethoxazole; MDR, multidrug resistance.

Table 11: Antimicrobial resistance pattern of *C. jejuni* (n = 36) and *C. coli* (n = 94).

species	Antimicrobial resistance pattern ^a	No. of isolates (%)
<i>C.jejuni</i>	AMX-BAC-COL-ENR	9 (25.0)
	AMX-BAC-COL-DOX-ENR-TET	5 (13.9)
	AMX-BAC-DOX-ENR-TET-SXT	5 (13.9)
	AMX-BAC-COL-DOX-ENR-TET-SXT	5 (13.9)
<i>C. coli</i>	AMX-BAC-ENR-TET	5 (5.3)
	AMX-BAC-DOX-ENR-TET	9 (9.6)
	AMX-BAC-ENR-TET-SXT	10 (10.6)
	AMX-BAC-DOX-ENR-TET-SXT	55 (58.5)
	AMX-BAC-COL-DOX-ENR-TET-SXT	11 (11.7)

^aOnly the antimicrobial resistance patterns represented by at least five isolates are shown. AMX, amoxicillin; BAC, bacitracin; COL, colistin; DOX, doxycycline; ENR, enrofloxacin; TET, tetracycline; SXT, trimethoprim-sulfamethoxazole;

4.1.3 Genetic characterization of *gyrA* mutation and MAMA-PCR

The DNA sequences of the *gyrA* gene of *C. jejuni* ATCC 33560, the 24 Thai *C. jejuni* isolates, *C. coli* ATCC 33559 and the 24 Thai *C. coli* isolates were submitted to Genbank and run in numerical order from KX982317 to KX982366. The MIC values for enrofloxacin of the selected 48 Thai *Campylobacter* isolates ranged between 4 and 16 µg/ml. All enrofloxacin resistant *C. jejuni* isolates had Thr-86-Ile non-synonymous mutation (ACA-ATA). In addition, some isolates had additional non-synonymous mutations such as Arg-6-Ser (AGC-AGG), Gln-7-Lys (AAA-CAA), Ser-22-Gly (AGT-GGT), Asn-203-Ser (AAT-AGT) and Ala-206-Val (GCA-GTA). In contrast, only the Thr-86-Ile non-synonymous mutation (ACT-ATT) was found in the 24 selected *C. coli* isolates (Table 12). In addition, all selected Thai *Campylobacter* isolates were positive to MAMA-PCR detecting *gyrA* mutation at a position of Thr-86-Ile.

Table 12: The *gyrA* mutations and the MIC for enrofloxacin of the selected *Campylobacter* isolates and the two control

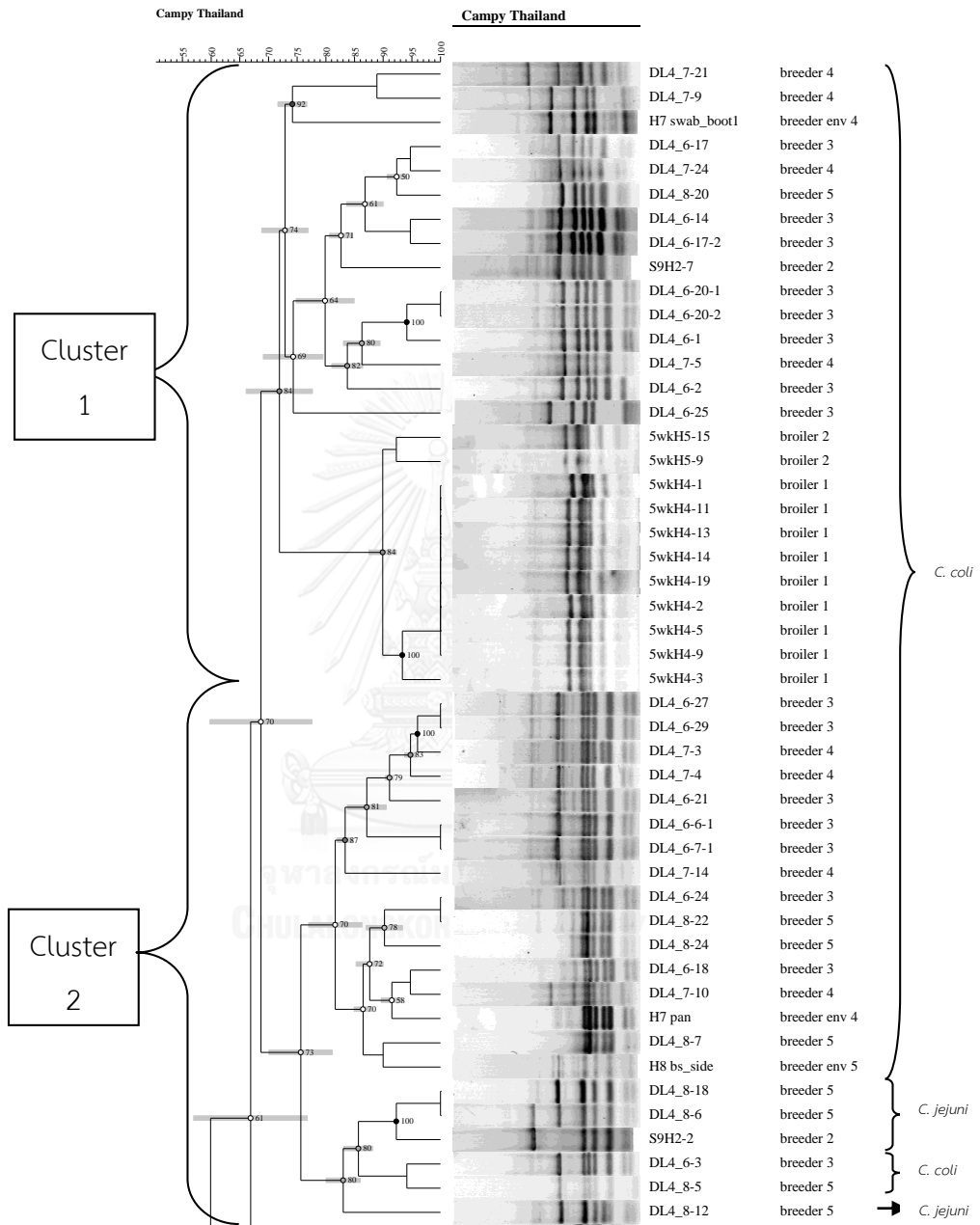
Enrofloxacin		Nucleic acid codons and corresponding amino acid of <i>Campylobacter</i> QRDR of <i>gyrA</i> ^b												
Pattern ^a	n	MIC range (µg/ml)	Amino acid		Amino acid		Amino acid		Amino acid		Amino acid		Amino acid	
			Codon	acid	Codon	acid	Codon	acid	Codon	acid	Codon	acid	Codon	acid
<i>C. jejuni</i>														
ATCC 33560-Enr ^S	1	0.125	AGG	Arg-6	CAA	Gln-7	AGT	Ser-22	ACA	Thr-86	AAT	Asn-203	GCA	Ala-206
UA 580-Cip ^{S/d}	1	<0.5	-C	Ser-6	A--	Lys-7	---	-	---	-	---	-	---	-
Enr ^R -1	3	4-16	-C	Ser-6	A--	Lys-7	G--	Gly-22	-T-	Ile-86	-G-	Ser-203	---	-
Enr ^R -2	3	8-16	---	-	---	-	G--	Gly-22	-T-	Ile-86	-G-	Ser-203	-T-	Val-206
Enr ^R -3	17	4-16	---	-	---	-	G--	Gly-22	-T-	Ile-86	-G-	Ser-203	---	-
Enr ^R -4	1	8	---	-	---	-	---	-	-T-	Ile-86	---	-	---	-
<i>C. coli</i>														
ATCC 33559-Enr ^S	1	0.25	n/a ^c	n/a	n/a	n/a	n/a	n/a	ACT	Thr-86	n/a	n/a	n/a	n/a
Enr ^R -1	24	2-16	n/a	n/a	n/a	n/a	n/a	n/a	-T-	Ile-86	n/a	n/a	n/a	n/a

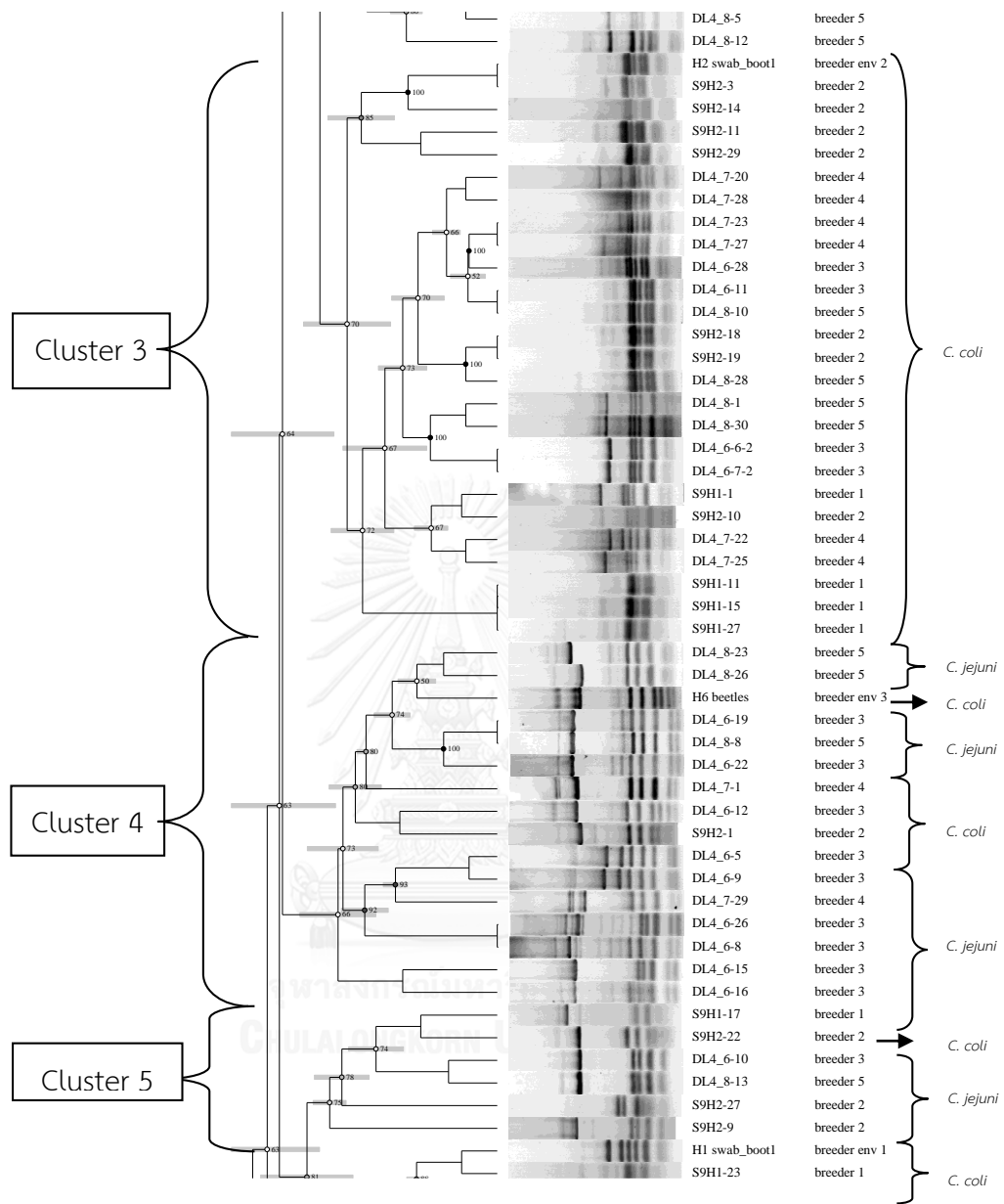
^aEnr^S, enrofloxacin susceptible (MIC ≤ 0.25 µg/ml); Enr^R, enrofloxacin resistant (MIC ≥ 2 µg/ml); Cip^S, ciprofloxacin susceptible (MIC ≤ 1 µg/ml)

^b-, no change compared to enrofloxacin-susceptible isolates, ^cn/a, not available due to no amplified based at that position, ^d*C. jejuni* UA 580

4.1.4 Genotypic diversity by *flaA*-RFLP

All of the 130 *Campylobacter* isolates (36 *C. jejuni* and 94 *C. coli*) were genotyped by *flaA*-RFLP. Ten distinct genotypic clusters were obtained at 72% similarity (Figure 6). Breeder flocks 1 and 2 were co-located on the same farm while breeder flocks 3 to 5 were co-located on another farm. Broiler flocks 1 and 2 were co-located on another farm (Fig. 2). Cluster 1-5 contained *Campylobacter* isolated from a variety of breeder flocks, whereas cluster 6, 7, and 9 contained isolates from breeder flocks 1 and 2 and cluster 8 contained isolates from breeder flocks 3, 4, and 5. In addition, cluster 10 was composed of a unique of isolates from breeder flock 2. For environmental samples from breeder flocks, cluster 1-4 contained isolates from environment of those breeder flocks. For broiler samples, these isolates were genotyped in cluster 1 only which also contained isolates from breeder flock 2, 3, 4, and 5. The largest clusters were clusters 1 and 3 which contained 26 strains of *C. coli* each. Thai *C. jejuni* and *C. coli* isolates cannot be separately genotyped as a different cluster by *flaA*-RFLP as seen in cluster 2, 4, 5, and 6.





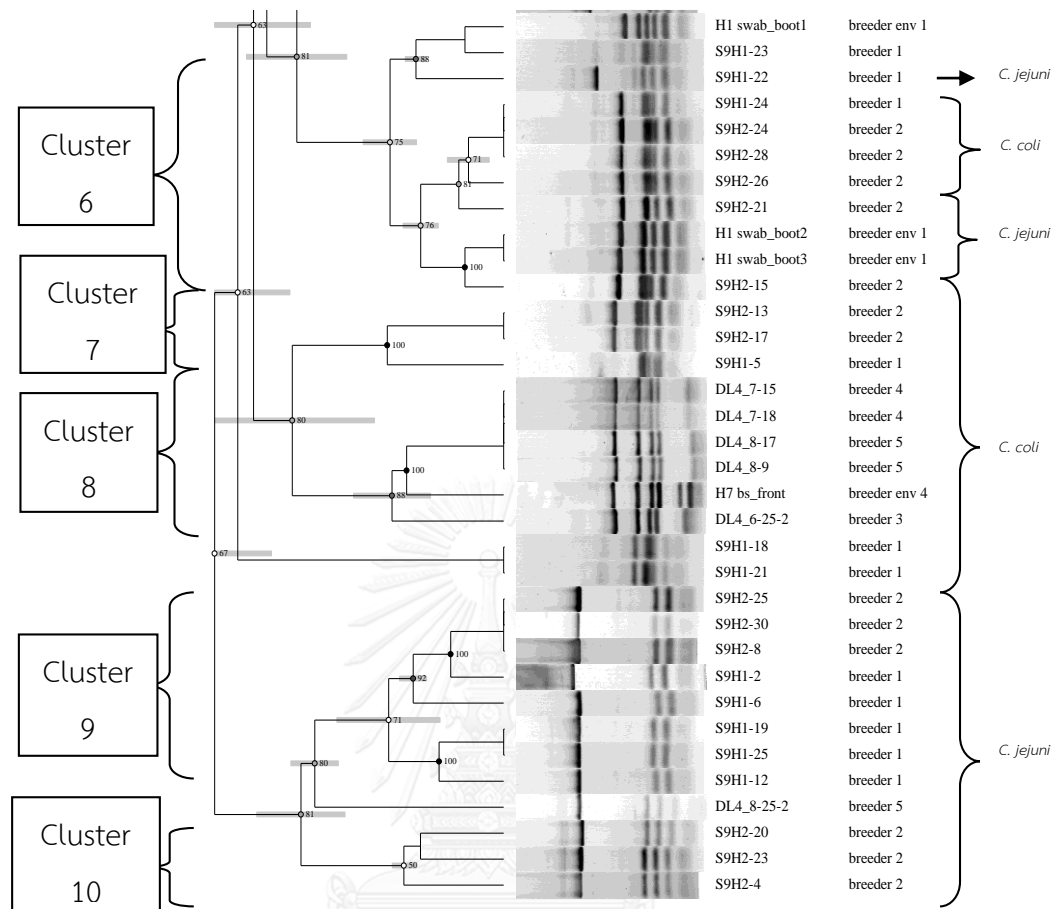


Figure 6: Phylogenetic analysis representing *flaA*-RFLP of *C. jejuni* and *C. coli* isolated from breeders and broilers in Thailand at the 72% cut-off genetic similarity. The similarity matrix was computed using Dice similarity coefficient and clustering by the Unweighted Paired Group Method with Arithmetic Mean Values (UPGMA). Band position tolerance and the optimization coefficient were both set to 2% using Bionumerics.

4.2 Identification of competitive exclusion and its ability to protect against *Campylobacter jejuni* in broilers

4.2.1 Antimicrobial resistance phenotypes

The numbers of all isolates, totally 346 strains, identified as *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium* equaled 195, 93 and 58 strains, respectively. All strains were tested for antimicrobial susceptibility. The frequencies of antimicrobial resistance and their MIC ranges are shown in Table 13. Those strains which had lowered or equaled cut-off MIC values proposed by EFSA totaled 51 strains, which included 27, 15 and 9 strains of *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium*, respectively. Most qualified strains had quite low MIC data compared to the breakpoints in each recommended antimicrobial agent.

Table 13: MIC data of *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium*

Strain (n)	MIC range (µg/ml)										
	AMP (^a)	CHP	CLI	ERY	GEN	KAN	STR	TET	TYL	VAN	
<i>Lactobacillus</i> spp. (27)	0.125-1 (4)	0.5-2 (8)	<0.125-0.5 (2)	<0.125-0.5 (1)	0.5-4 (32)	1-8 (64)	1-8 (64)	0.5-2 (32)	n.r. ^b	0.25-1 (2)	
<i>Bacillus</i> spp. (15)	n.r.	<1-4 (8)	0.5-2 (4)	<0.5-2 (4)	0.25-1 (4)	<0.5-4 (8)	<2-4 (8)	0.5-2 (8)	n.r.	0.5-2 (4)	
<i>E. faecium</i> (9)	0.5-2 (2)	<1-4 (16)	0.5-2 (4)	<0.5-2 (4)	4-16 (32)	64-256 (1024)	32-64 (128)	0.5-2 (4)	0.5-1 (4)	0.5-4 (4)	

n= number of isolates in each row, ^amicrobiological cut-off values (µg/ml) is indicated in brackets, AMP, ampicillin;

CHP, chloramphenicol; CLI, clindamycin; ERY, erythromycin; GEN, gentamicin; KAN, kanamycin; STR, streptomycin;

TET, tetracycline; TYL, tylosin; VAN, vancomycin., ^bn.r. = not required

4.2.2 Survival rate of acid and bile tolerance tests

A total of 27 *Lactobacillus*, 15 *Bacillus* and 9 *Enterococcus faecium* were tested for acid and bile tolerance. Survival rate of those strains are summarized in Table 14. For acid tolerance, 3 *Bacillus* strains had the highest survival rates, with a range 100-110% more than *Lactobacillus* spp. and *Enterococcus faecium*. All strains had a wide range in survival rates for the bile tolerance test. *Enterococcus faecium* showed a quite low ability to tolerate bile acid compared to *Lactobacillus* spp. and *Bacillus* spp. According to the results of MIC values as well as acid and bile tolerance, the best performance of *Lactobacillus* spp., *Bacillus* spp. and *Enterococcus faecium* were selected, and their species level was identified using the PCR method. The top performance of selected CE was *Lactobacillus acidophilus* 1/4, *Bacillus subtilis* 206/1 and *Enterococcus faecium* 122 which had 96.85, 101.47 and 99.39% survival rates of acid tolerance and 113.93, 130.97 and 90.10% survival rates of bile tolerance, respectively. These CE were preferred to use for the challenge experiment in broilers.

Table 14: Number of bacteria in each level of percent of survival rate of acid and bile tolerance tests

Genus	Strains	Survival rates (%)		Strains	Survival rates (%)	
		acid tolerance	bile tolerance		acid tolerance	bile tolerance
<i>Lactobacillus</i> spp.	L 22/2	98.74	95.95	L 58/3	93.19	90.28
	L 31/3	97.13	86.03	L 44/4	93.04	95.25
	L 1/4	96.85	113.93	L 44/1	91.41	101.61
	L 31/4	96.78	95.87	L 28/1	91.4	96.28
	L 48/1	95.96	89.87	L 27/2	91.16	98.74
	L 23/1	95.41	88.48	L 27/1	90.87	92.78
	L 1/3	94.6	94.45	L 49/4	90.46	86.22
	L 40/1	94.27	95.31	L 55/4	90.38	99.36
	L 10/2	93.98	102.08	L 38/1	90.02	92.82
	L 8/1	93.82	87.12	L 19/2	89.69	105.69
	L 5/3	93.58	93.91	L 8/2	88.11	88.54
	L 35/2	93.58	101.56	L 17/1	84.37	89.36
	L 50/1	93.39	88.25	L 19/1	82.27	78.55
	L 14/4	93.36	98.15			
<i>Bacillus</i> spp.	B 201/1	101.57	94.72	B 205/2	92.19	89.34
	B 206/1	101.47	130.97	B 227/2	92.15	102.57
	B 214/2	100.77	93.9	B 220/1	91.43	123.13
	B 230/1	97.3	118.16	B 206/2	90.04	91.3
	B 235/1	95.77	99.18	B 224/1	89.23	103.32
	B 239/1	95.67	102.75	B 230/2	86.16	96.47
	B 204/1	94.36	103.21	B 210/1	84.99	99.27
	B 217/2	93.54	100.87			
<i>Enterococcus</i> <i>faecium</i>	E 122	99.39	90.1	E 172	88.61	75.07
	E 135	98.45	75.06	E 144	88.34	61.09
	E 110	95.36	71.66	E 107	86.74	82.63
	E 130	92.25	82.58	E 118	77.03	78.07
	E 114	91.69	76.72			

4.2.3 *C. jejuni* challenged against CE application

At 11 days of age, all birds tested negative for *Campylobacter* spp. At 14 days of age, the birds in all groups except for the negative control group were challenged with Thai field strain number CU11 of *C. jejuni*. At 17, 21, 28 and 35 days of age, fecal samples of 15 birds were collected for *C. jejuni* counting; at 41 days of age, the cecal content of all broilers was counted for *C. jejuni* colonies. No statistically significant difference in the *C. jejuni* numbers from both fecal and cecal samples was observed between the positive control and treatment groups (Table 15). FCR was recorded at 14 and 41 days and body weight was calculated at 41 days. At 41 days of age, the body weight of broilers in group 8 given a commercial CE was significantly higher than that of broilers in group 1, 2 and 10 given *Lactobacillus acidophilus* 1/4, *Bacillus subtilis* 206/1 and negative control, respectively.

Table 15: Average number of *C. jejuni*, FCR and body weight

Group	Average number of <i>C. jejuni</i> (log CFU/g) (mean±SD)							FCR at 14		FCR at 41		Body weight at 41 days
	17 days	21 days	28 days	35 days	41 days	days	days	days	days			
1	5.80 ± 0.86	6.17 ± 0.64	6.18 ± 0.88	6.24 ± 0.55	6.48 ± 0.99	1.14	1.82	1.84	1.82	1843.50±348.96 ^a		
2	5.94 ± 0.89	6.23 ± 0.66	6.38 ± 0.51	6.53 ± 0.71	6.75 ± 1.00	1.19	1.77	1.84	1.84	1856.32±323.86 ^a		
3	6.29 ± 0.81	6.39 ± 0.73	6.39 ± 0.59	6.09 ± 0.64	6.97 ± 1.03	1.16	1.82	1.77	1.77	1937.25±240.43 ^{ab}		
4	6.43 ± 0.63	6.53 ± 0.41	6.31 ± 0.67	5.59 ± 0.45	6.01 ± 0.89	1.13	1.82	1.82	1.82	1894.75±204.07 ^{ab}		
5	6.53 ± 0.59	6.50 ± 0.57	6.56 ± 0.53	6.10 ± 0.80	6.15 ± 1.19	1.17	1.74	1.74	1.74	1935.00±217.64 ^{ab}		
6	6.22 ± 0.61	6.46 ± 0.94	6.26 ± 0.71	5.54 ± 0.37	6.02 ± 0.89	1.15	1.78	1.78	1.78	1896.90±137.67 ^{ab}		
7	5.92 ± 0.47	6.55 ± 0.62	5.81 ± 0.47	5.82 ± 0.64	5.81 ± 0.65	1.14	1.68	1.68	1.68	1992.62±106.79 ^{ab}		
8	6.78 ± 0.45	6.93 ± 0.76	6.74 ± 0.40	6.20 ± 1.02	6.52 ± 0.90	1.15	1.72	1.72	1.72	2061.94±149.02 ^b		
9	6.46 ± 0.52	6.86 ± 0.40	6.74 ± 0.82	6.79 ± 0.49	6.74 ± 1.03	1.14	1.72	1.72	1.72	1991.05±178.60 ^{ab}		
10	n.d.	n.d.	n.d.	n.d.	n.d.	1.18	1.79	1.79	1.79	1820.52±307.63 ^a		

n.d: not detected (detection limit = 2 log CFU/g), ^{a,b}The different superscript in each column means statistically significant difference ($p < 0.05$), Broilers in all groups received

different CE application program during 1-3 days of age. Gr. 1: *Lactobacillus acidophilus* 1/4 2×10^8 CFU/ml, Gr. 2: *Bacillus subtilis* 206/1 2×10^8 CFU/ml, Gr. 3: *Enterococcus*

faecium 122 2×10^8 CFU/ml, Gr. 4: *Lactobacillus acidophilus* 1/4 + *Bacillus subtilis* 206/1 4×10^8 CFU/ml, Gr. 5: *Lactobacillus acidophilus* 1/4 + *Enterococcus faecium* 122 4×10^8

CFU/ml, Gr. 6: *Bacillus subtilis* 206/1 + *Enterococcus faecium* 122 4×10^8 CFU/ml, Gr. 7: *Lactobacillus acidophilus* 1/4 + *Bacillus subtilis* 206/1 + *Enterococcus faecium* 122 4×10^8

CFU/ml, Gr. 8: Commercial product (AVIPROB[™]) 2×10^8 CFU/ml, Gr. 9: positive control, Gr. 10: negative control

CHAPTER V

DISCUSSIONS

5.1 Antimicrobial resistance, the characterization of *gyrA* mutation, and genetic diversity by *flaA*-RFLP of *Campylobacter jejuni* and *Campylobacter coli* collected through commercial broiler production chains in Thailand

This study was conducted to investigate the prevalence, antimicrobial resistance pattern and genetic diversity of *C. jejuni* and *C. coli* isolates through broiler production chains in Thailand. Furthermore, the presence of mutations in the QRDR of the *gyrA* was assessed also. Although, antimicrobial agents are not used to treat *Campylobacter* spp. infection in chickens, the antimicrobial agents used in the current study were selected to represent several classes, including those commonly used on chicken farms in Thailand for prevention or treatment of other pathogens.

The major *Campylobacter* found in this study was *C. coli* (94/130, 72.31%). While most studies report a predominance of *C. jejuni* when examining broiler chicken feces (Giacomelli et al., 2014; Prachantasena et al., 2016), there are reports of a predominance of *C. coli* in some studies. For example, a previous study in Thailand that reported 51.5% of the isolates from chicken feces were *C. coli* (Padungtod et al., 2006). As well, a study conducted in China (Ma et al., 2014) found that 56% of the isolates from broiler ceca were *C. coli*. It should be noted that the majority of

Campylobacter isolates in this study came from breeder samples and that *C. coli* has been demonstrated as the predominant species in breeders in a previous study (O'Mahony et al., 2011). Another reason that might explain this was a difference of energy sources between *C. jejuni* and *C. coli*. Although the principal energy sources for *C. jejuni* are amino acids, citric acid cycle intermediates and short chain fatty acids, *C. jejuni* is unable to metabolise propionic acid while *C. coli* is able to metabolise this carbon source (Wagley et al., 2014). The presence of propanoate-CoA ligase and 2-methyl-synthase genes were demonstrated in *C. coli* and their absence in *C. jejuni* (Wagley et al., 2014). Levels of propionate have been reported to be high in the gastrointestinal tract of chickens and their litters (Chi et al., 2005). Competition for nutrients in the gut is violent, so the ability to use a potentially toxic metabolic waste product as an energy source may confer *C. coli* with a selective advantage when it colonises in the chicken gastrointestinal tract (Wagley et al., 2014).

The proportion of *Campylobacter* strains resistant to antimicrobial agents, particularly FQs has rapidly surged in many countries worldwide and is a major public health concern (Engberg et al., 2001; O'Mahony et al., 2011). Contaminated poultry meat products are considered as the major source of human campylobacteriosis, meaning that resistant *Campylobacter* strains can be transmitted through the food chain (Quinn et al., 2007). For this reason, updates on the AMR profiles, using both phenotypic and genotypic susceptibility testing methods, of *Campylobacter* strains

from chicken are important to help prevent the risk of the transfer resistant *Campylobacter* to humans. Most isolates in the current study were resistant to the various antimicrobial agents tested except erythromycin and gentamicin. Macrolides are considered the drugs of choice for the treatment of severe human campylobacteriosis (Luangtongkum et al., 2009). In the present study, all *Campylobacter* isolates were sensitive to erythromycin, a similar result to previous studies conducted in Thailand that showed a low percentage of erythromycin resistance at 0.69% and 5.8%, respectively (Padungtod et al., 2006; Charununtakorn et al., 2015). In contrast, 11.1% of *C. jejuni* and 87.5% of *C. coli* isolated from broilers in Italy were resistant to erythromycin (Giacomelli et al., 2014). Likewise, 18.8% of *C. jejuni* and 92% of *C. coli* isolated from broilers in China were resistant to erythromycin (Ma et al., 2014).

Remarkably, 66.7% of *C. jejuni* isolates and 97.9% of *C. coli* isolates were classified as MDR. All isolates were susceptible to erythromycin and gentamicin. The absence of resistance to gentamicin was similar to previous studies conducted in Thailand (Chokboonmongkol et al., 2013; Charununtakorn et al., 2015) showing that all tested *C. jejuni* isolates were susceptible to gentamicin. In contrast, 71% of *C. jejuni* isolated from broiler ceca in China were resistant to gentamicin (Ma et al., 2014). Beta-lactam antimicrobial agents such as amoxicillin had been widely used for disease prevention in Thai chicken industry (Chongsuvivatwong and Kitikoon, 2007). In this

study, all *Campylobacter* isolates were resistant to amoxicillin. In addition, *Campylobacter* spp. are intrinsically resistant to bacitracin (Luangtongkum et al., 2009), a polypeptide antimicrobial agent, explaining our finding that all isolates were resistant to bacitracin.

Regarding resistance to tetracyclines, we found that the *C. coli* were more resistant (97.9% for tetracycline and 79.8% for doxycycline) than the *C. jejuni* isolates (55.6% for tetracycline and 50% for doxycycline). This result was in agreement with previous studies conducted in Thailand (Padungtod et al., 2006; Chokboonmongkol et al., 2013; Charununtakorn et al., 2015). Moreover, *Campylobacter* spp. isolated from broiler ceca in China demonstrated 100% tetracycline resistance (Ma et al., 2014). Colistin, also known as polymyxin E, is an important drug in humans, being the drug of last choice if the use of a Beta-lactam, aminoglycoside, or quinolone is ineffective (Livermore, 2002). To our knowledge, no data on colistin resistance in *Campylobacter* isolated from chickens in Thailand have ever been published. In this study, we found higher resistance rate of colistin from *C. jejuni* (66.7%) compared to *C. coli* (16%). A previous study showed a similar result that 67% of all *C. jejuni* subsp. *jejuni* isolates from domestic geese in Turkey were resistant to colistin sulphate (Aydin et al., 2001). Interestingly, there is a recent report on the emergence of a plasmid-mediated colistin resistance mechanism, termed MCR-1, in animals and human beings in China that has caused global concern (Liu et al., 2016). Few data are available on the topic of

Campylobacter resistance to sulphonamides and trimethoprim. Nevertheless, high levels of resistance have been published in poultry isolates in different countries (El-Adawy et al., 2012; Giacomelli et al., 2014), similar to the findings of the current study. In addition, resistance to trimethoprim has been considered intrinsic in *C. jejuni* and *C. coli* (Taylor and Courvalin, 1988).

Resistance to enrofloxacin was present in 100% of *C. jejuni* isolates and 98.9% of *C. coli* isolates in the current study. A previous Thai study (Padungtod et al., 2006) showed a high percentage resistance of ciprofloxacin and nalidixic acid, drugs in the group of FQs, with 87% of *C. coli* and 71.4% of *C. jejuni* isolates being resistant to ciprofloxacin and 89.1% of *C. coli* and 69.6% of *C. jejuni* isolates being resistant to nalidixic acid. According to the antimicrobial usage data from the flocks examined in the current study, enrofloxacin was used to treat breeders, on a case by case only. Despite this restricted use, there was a very high prevalence of enrofloxacin resistance. A previous report (Price et al., 2007) indicated that FQ-resistant *Campylobacter* were isolated from poultry products, even though the on-farm use of FQ drugs had been stopped for a year, indicating that the resistance may persist for long periods.

Campylobacter resistance to FQs is generally associated with a mutation in the QRDR of the *gyrA* gene. The current study found apparently novel *gyrA* mutations including Ser-6-Arg, Gln-7-Lys, Ser-22-Gly, Asn-203-Ser and Ala-206-Val that have, to our best knowledge, not been previously reported in *C. jejuni*. All of these isolates also

had the well known Thr-86-Ile mutation that has already been documented in *C. jejuni* (Zirnstein et al., 1999). The MIC values of enrofloxacin of the isolates with these novel mutations ranged from 4-16 µg/ml. We also identified one isolate that detected that had only Thr-86-Ile amino acid substitution – with that isolate having an MIC of 8 µg/ml MIC for enrofloxacin, Hence, while we found additional mutations, our results confirm that the Thr-86-Ile amino acid substitution is still a key target detecting for genotypic tests for FQ resistance as in a previous report (Jesse et al., 2006). In contrast, the only *gyrA* mutation we found in the *C. coli* isolates was the Thr-86-Ile position, with these isolates having MIC values for enrofloxacin that ranged from 4-16 µg/ml. In the current study, the QRDR of the *gyrA* gene in all strains were compared with *gyrA* gene of *C. jejuni* ATCC 33560 (Genbank no. KX982317) and *C. jejuni* UA580 (Genbank no. L04566). A previous study (McIver et al., 2004) selected *C. jejuni* UA580 as an enrofloxacin-susceptible strain, but we found that the 6th and 7th amino acids of this strain were different from strain ATCC 33560. Hence, *C. jejuni* ATCC 33560, in our view, is a better enrofloxacin-susceptible reference strain. The MAMA-PCR detecting Thr-86-Ile in the QRDR of the *gyrA* gene was positive in all isolates, which correlated with the DNA sequencing of the *gyrA* gene of both *C. jejuni* and *C. coli*. This correlation has been previously reported (Zirnstein et al., 1999; Zirnstein et al., 2000). Therefore, the MAMA-PCR technique, a simple and rapid tool as compared with DNA sequencing, can be used as a screening tool or routine detection of the *gyrA* mutation.

The results of the current study provide several lines of evidence that suggest that vertical transmission is not a major route of transmission for *Campylobacter* transmission in the Thai broiler production chain. Firstly, all breeder flocks were found to be positive for both *C. jejuni* and *C. coli*. In contrast, no broiler flock was positive for *C. jejuni* – the only positive broiler flocks, flocks 1 and 2, yielded *C. coli*. Secondly, *Campylobacter* was not isolated from the hatchery and early embryonic death samples. Thirdly, while broiler flock 1 and the connected breeder flock 1, all yielded *C. coli*, the *flaA*-RFLP showed that the isolates belonged to different clusters – clusters 1 and 3, respectively. Another study conducted in Thailand (Prachantasena et al., 2016) also suggested that vertical transmission might not be the major route of *Campylobacter* transmission in Thai broiler production chain because all breeder flocks were colonized with *Campylobacter* whereas the organism was not recovered from hatchery samples or tray liners of 1-day-old chicks.

Interestingly, *Campylobacter* spp. was not recovered from broiler flocks 3, 4, and 5. As well, broiler flocks 1 and 2 had a very low level *Campylobacter* prevalence. These findings might be due to the fact that the risk of *Campylobacter* infection has a correlation with bird age and the biosecurity level of poultry farms (Evans and Sayers, 2000). Evans and Sayers (2000) reported that 50 out of 100 broiler flocks in Great Britain housed in a sound, well functioning buildings were free of *Campylobacter* infection at 35 days of age and 50% and 32% of flocks sent to slaughterhouse at 28-35 and 36-42

days were *Campylobacter* negative, respectively. After Thailand experienced outbreaks of highly pathogenic avian influenza (HPAI) of the H5N1 subtype during 2004-2005 that had serious consequences on poultry production (Tiensin et al., 2007), high standards of biosecurity are strictly used in integrated poultry farms in Thailand. For example, disinfectant solutions in boot dips are always replaced immediately if there has been an increase of organic matter or the solution has been diluted. As well, all-in-all-out production systems are used on all broiler farms. It is possible that this excellent biosecurity, combined with a short bird life, has reduced the risk of infection with *Campylobacter* greatly. Another reason might be the fact that broiler flocks 3, 4 and 5 were located on a farm which was shut down for around 6 months before this study. Reports of broiler flocks that are negative for *Campylobacter* at first pick up do exist. In a study comparing litter management strategies, Chinivasagam et al. (2016) reported that, in six sequential flocks raised on new bedding, one farm was negative for *Campylobacter* in five flocks while a second farm was negative in three flocks. Another study conducted in Thailand also reported a 0.8% prevalence of *Campylobacter* spp. in a large-scale broiler flock (Prachantasena et al., 2016).

Typing of bacterial isolates from different sources delivers epidemiological information that is crucial for infection control and contributes to risk assessment of *Campylobacter* transmission. For molecular typing methods, *flaA*-RFLP has been described as a stable and highly discriminatory analysis of *Campylobacter* isolates

(Nachamkin et al., 1993; Duffy et al., 2015). One-hundred and thirty *Campylobacter* isolates were analyzed by *flaA*-RFLP. All the isolates were successfully typed by this technique, similar to the previous study (Nachamkin et al., 1993). This finding was different to the result of other researchers who reported that some *Campylobacter* isolates were not typeable because DNA was not amplified (Wittwer et al., 2005; Behringer et al., 2011). Amongst 10 clusters recognized in the current study (Fig. 5), clusters 1, 3, 7, and 8 contained only *C. coli* isolates while clusters 9 and 10 contained only *C. jejuni* isolates. In contrast, both species were present in clusters 2, 4, 5, and 6.

Interestingly, all of samples from broiler flock 1 were grouped into cluster 1 but none of the isolates from the connected breeder flock, flock 1, was present in this cluster. This lack of a connection between the genetic types present in the breeder flock and the connected broiler flock supports the absence of vertical transmission as a major transmission route. In a similar manner, an earlier Thai study found that the genotypes of *Campylobacter*, as identified by flagellin A short variable region sequencing and MLST, in breeders and their offspring were different (O'Reilly et al., 2006). Interestingly, eight of the 9 isolates from broiler flock 1 showed the same genetic pattern, meaning that the infection might come from the same source. Cluster 3 was composed of *C. coli* from all breeder flocks. Importantly, all sampled flocks (broiler and breeder) were located in the same province within a radius of around 50 km. As well, the trucks for feed or bird delivery used the same main road. The high

density of farms and the shared transport avenues might explain the occurrence of cluster 3 across all breeder flocks.



5.2 Identification of competitive exclusion and its ability to protect against *Campylobacter jejuni* in broilers

In this study, *in vitro* for characterizing CE and *in vivo* *C. jejuni* challenges were performed, as CE has been known to prevent pathogenic bacteria in poultry for decades. Nurmi and Rantala (1973) showed how newly hatched chickens treated with intestinal contents from adult chickens have increased resistance to infection by *Salmonella* spp. CE bacteria composed of 2 groups, defined and undefined CE. The defined CE cultures are more acceptable because the microbial isolates are identified and characterized for their properties such as antimicrobial susceptibility and acid and bile tolerance (Zhang et al., 2007). Normally, CE bacteria should be isolated and used in the same hosts because of their host specificity (Fuller, 1975). In this study, samples were collected from feces different from previous studies that used samples isolated from intestinal organs (Garriga et al., 1998; Ehrmann et al., 2002). Although *Lactobacillus acidophilus*, *Bacillus subtilis* and *Enterococcus faecium* are considered Generally Recognize as Safe (GRAS), their antimicrobial susceptibility needed to be clarified. CE bacteria may serve as hosts for antibiotic resistance genes that are probably transferred to commensal and pathogenic bacteria in the gut leading to a concern of antimicrobial resistance in humans. All selected strains were sensitive to several antimicrobials, including some of the many drugs used in poultry farms such as amoxicillin, tylosin and erythromycin, none of which will lead to the spread of

resistant properties against these antimicrobials to bacterial hosts (Schwarz et al., 2001).

CE has to survive passage through the gastrointestinal tracts of broilers. From *in vitro* experiments, *Lactobacillus acidophilus* 1/4, *Bacillus subtilis* 206/1 and *Enterococcus faecium* 122 demonstrated good survival rates after 3 and 24 h incubation time for acid and bile tolerance tests. These results indicate that 3 CE bacteria might be able to survive the transit and reach the broiler ceca environment since a total movement through the broiler gastrointestinal tract takes around 4 to 9 h, depending on the feed and age of the broilers (Sundu, 2009). *Bacillus* spp. was quite more tolerable to acid and bile tests compared *Lactobacillus* and *Enterococcus* spp., because *Bacillus* spp. can produce endospores structured by a complex protein coat under stressful environmental conditions (McPherson et al., 2005).

Timmerman et al. (2004) revealed a mixture of different strains, rather than only one strain, would be successful for use as CE bacteria, but this study's results showed no significant difference of *C. jejuni* numbers between treatment and control groups, which is in agreement with the study of Robyn and colleagues (2013). Although some CE bacteria preparations can decrease the level of colonization in chickens (Mead et al., 1996; Zhang et al., 2007), other studies did not observe the protective effect of CE (Shanker et al., 1988; Stern et al., 2001). The reason why the results were inconsistent remains unclear, but it might reflect the variable nature of the CE agent

and susceptibility of *Campylobacter* strain. In this study, the results showed that these CE cannot be able to compete against *C. jejuni* challenges in broilers which might be the result of pathogenesis of *C. jejuni* that it primarily colonized in the mucosal layer in gastrointestinal tract of chickens (Young et al., 2007). This is different from *C. jejuni* pathogenesis in humans that it can move into the intestinal epithelial layer leading to an inflammation and diarrhea.



CONCLUSIONS AND SUGGESTIONS

Campylobacteriosis is a major bacterial gastroenteric disease in humans. Poultry are considered the main reservoir of *Campylobacter* spp. to human due to the consumption of undercooked poultry meats. Most epidemiological data of *Campylobacter* spp. conducted in developed countries, but this study also provided genetic diversity, antimicrobial resistance, *gyrA* mutation profiles of *Campylobacter* isolated in Thailand. Moreover, CEs were identified to compete with *Campylobacter jejuni* challenges.

In conclusion, the genetic diversity of *Campylobacter* isolated from broiler production chains in Thailand demonstrated the spread of this organism is complex. Horizontal transmission is the major route of infection from bird to bird, meaning that prevention methods have to focus on preventing the first entry of *Campylobacter* into a broiler shed. Both the prevalence of isolates that show MDR and the overall high antimicrobial resistance rates are issues of concern. In particular, the resistance to FQs is a major issue. Programs to ensure prudent use of antimicrobial agents and active surveillance at the farm level are essential to monitor the prevalence, and prevention the spread of, antimicrobial resistant *Campylobacter* in Thai chickens.

CE isolated from fecal samples exhibited non-resistant antibiotic profiles and great survival rates for acid and bile tolerance. Although they could not reduce

significantly *C. jejuni* when compared to positive control broilers, these CE bacteria should be further evaluated as protection against other foodborne bacteria found in broilers such as *Salmonella* and *E. coli* in further studies.



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APPENDIX

จุฬาลงกรณ์มหาวิทยาลัย
CHULALONGKORN UNIVERSITY

Appendix A: Culture Media

1. de Mans Rogosa and Sharpe Agar (MRS Agar) (Difco™, MD, USA)

● Proteose peptone	10.0 g
● Meat extract	8.0 g
● Yeast extract	5.0 g
● Tri-ammonium citrate	2.0 g
● Sodium acetate	0.5 g
● $Mg_2SO_4 \cdot 7H_2O$	0.1 g
● K_2HPO_4	2.0 g
● Glucose	20.0 g
● Tween-80	1.0 g
● Tryptone	5.0 g
● Agar	15.0 g
● Distilled water	1,000 ml

2. Manitol Egg Yolk Polymyxin-B Agar (MYP Agar) (Difco™, MD, USA)

● Beef extract	1.0 g
● Peptone	10.0 g
● D-Mannitol	10.0 g
● NaCl	10.0 g

- Agar 15.0 g
- Phenol Red 0.2% aqueous solution 15.0 ml
- Distilled water 1,000 ml

3. SF-Streptococcus Agar (SF Agar) (Difco™, MD, USA)

- Tryptone 20.0 g
- Dextrose 5.0 g
- K₂PO₄ 4.0 g
- NaCl 5.0 g
- Sodium Azide 0.5 g
- Agar 20.0 g
- Bromocresol purple 0.2% aqueous solution 32 mg
- Distilled water 1,000 ml

4. Muller Hinton Agar (MHA) (Difco™, MD, USA)

- Beef Extract Powder 2.0 g
- Acid Digest of Casein 17.5 g
- Starch 1.5 g
- Agar 17.0 g
- Distilled water 1,000 ml

5. Modified charcoal cefoperazone desoxycholate agar (mCCD agar) (Oxoid™, England)

● Meat extract	10.0 g
● Enzymatic digest of animal tissues	10.0 g
● Sodium chloride	5.0 g
● Charcoal	4.0 g
● Enzymatic digest of casein	3.0 g
● Sodium desoxycholate	1.0 g
● Iron (II) sulfate	0.25 g
● Sodium pyruvate	0.25 g
● Agar	12.0 g
● Distilled water	1,000 ml

Antibiotics

1. Antibiotic solution for mCCD agar 1 litre

● Cefoperazone	0.032 g
● Amphotericin B	0.01 g
● Water	5 ml

Appendix B: Alignment of partial *gyrA* gene of 24 *C. jejuni*, 24 *C. coli* and control strains

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L04566	Met	Glu	Asn	Ile	Phe	Ser	Lys	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	ATG	GAG	AAT	ATT	TTT	AGC	AAA	GAT	TCT	GAT	ATT	GAA	CTT	GTA	GAT	ATA	GAA	AAT	TCT	ATA		
AHRU2014CJ0001	-	-	-	-	-	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AHRU2014DL6008	-	-	-	-	-	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AHRU2014DL6009	-	-	-	-	-	Phe	Ser	Lys	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AHRU2014DL6010	-	-	-	-	-	TTT	AGC	CAA	GAT	TCT	GAT	ATT	GAA	CTT	GTA	GAT	ATA	GAA	AAT	TCT	ATA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AHRU2014DL6015	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AHRU2014DL6019	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL7029	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8006	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8012	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8013	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8018	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8023	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL8100	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS1002	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS1006	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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AHRU2014SS1007	-	-	-	-	-	Ile	Phe	Ser	Lys	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	ATT	TTT	AGC	AAA	GAT	TCT	GAT	ATT	GAA	CTT	GTA	GAT	ATA	GAA	AAT	TCT	ATA			
AHRU2014SS1019	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS1022	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS1025	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS2002	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS2004	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS2008	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS2009	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014SS2021	???	???	???	-	-	Ile	Phe	Ser	Lys	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	ATT	TTT	AGC	AAA	GAT	TCT	GAT	ATT	GAA	CTT	GTA	GAT	ATA	GAA	AAT	TCT	ATA			
AHRU2014SS2027	-	-	-	-	-	Ile	Phe	Arg	Gln	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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L04566	Lys	Ser	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014CJ0001	Lys	Ser	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014DL6008	Lys	Gly	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014DL6009	Lys	Gly	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014DL6010	Lys	Gly	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014DL6015	Lys	Gly	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA

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AHRU2014DL8023	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014DL8100	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1002	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1006	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1007	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1019	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1022	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS1025	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2002	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2004	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2008	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2009	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2021	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
AHRU2014SS2027	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Gln Asn Asp Glu Ala
	70
L04566	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014CJ0001	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
	80

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AHRU2014DL6008	AAA AGT AGA ACA GAT TTT GTC AAA TCA GCC CGT ATA GTG GGT GCT GTT ATA GGT CGT TAT
AHRU2014DL6009	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL6010	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL6015	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL6019	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL7029	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8006	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8012	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8013	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8018	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8023	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014DL8100	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014SS1002	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014SS1006	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014SS1007	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014SS1019	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr
AHRU2014SS1022	Lys Ser Arg Thr Asp Phe Val Lys Ser Ala Arg Ile Val Gly Ala Val Ile Gly Arg Tyr

	His	Pro	His	Gly	Asp	Ile	Ala	Val	Tyr	Asp	Ala	Leu	Val	Arg	Met	Ala	Gln	Asp	Phe	Ser
AHRU2014SS2027	CAT	CCA	CAT	GGA	GAT	ATA	GCA	GTT	TAT	GAT	GCT	TTG	GTT	AGA	ATG	GCT	CAA	GAT	TTT	TCT
	110										120									
L04566	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014CJ0001	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL6008	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL6009	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL6010	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL6015	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL6019	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL7029	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8006	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8012	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8013	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8018	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8023	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014DL8100	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS1002	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala

AHRU2014SS1006	ATG	AGA	TAT	CCA	AGT	ATT	ACA	GGA	CAA	GGC	AAC	TTT	GGA	TCT	ATA	GAT	GGT	GAT	AGC	GCT
AHRU2014SS1007	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS1019	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS1022	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS1025	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2002	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2004	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2008	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2009	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2021	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
AHRU2014SS2027	Met	Arg	Tyr	Pro	Ser	Ile	Thr	Gly	Gln	Gly	Asn	Phe	Gly	Ser	Ile	Asp	Gly	Asp	Ser	Ala
	130										140									
L04566	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Lys	Met	Ser	Lys	Leu	Ser	His	Glu	Leu	Leu	Lys	Asp
AHRU2014CJ0001	GCT	GCG	ATG	CGT	TAT	ACT	GAA	GCA	AAA	ATG	AGT	AAA	CTT	TCT	CAT	GAG	CIT	TTA	AAA	GAT
AHRU2014DL6008	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Lys	Met	Ser	Lys	Leu	Ser	His	Glu	Leu	Leu	Lys	Asp
AHRU2014DL6009	GCT	GCG	ATG	CGT	TAT	ACT	GAA	GCA	AAA	ATG	AGT	AAA	CTT	TCT	CAT	GAG	CIT	TTA	AAA	GAT
	130										140									
AHRU2014DL6009	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Lys	Met	Ser	Lys	Leu	Ser	His	Glu	Leu	Leu	Lys	Asp
	GCT	GCG	ATG	CGT	TAT	ACT	GAA	GCA	AAA	ATG	AGT	AAA	CTT	TCT	CAT	GAG	CIT	TTA	AAA	GAT

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AHRU2014DL8018	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014DL8023	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014DL8100	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS1002	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS1006	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS1007	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS1019	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS1022	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS1025	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS2002	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS2004	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS2008	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS2009	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
AHRU2014SS2021	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
AHRU2014SS2027	Ile Asp Lys Asp Thr Val Asp Phe Val Pro Asn Tyr Asp Gly Ser Glu Ser Glu Pro Asp
	ATA GAT AAA GAT ACG GTC GAT TTT GTT CCA AAT TAT GAT GGT TCA GAA AGT GAA CCT GAT
	170
	180

Alignment Report of 26 C.jejuni 101016.meg ClustalW (Slow/Accurate, Gonnet)
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L04566	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014CJ0001	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL6008	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL6009	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL6010	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL6015	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL6019	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL7029	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL8006	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL8012	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL8013	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL8018	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014DL8023	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL8100	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014SS1002	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1006	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT
AHRU2014SS1007	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
	GTT TTA CCT TCT AGG GTT CCA AAT TTA TTA TTA AAT GGT TCA AGT GGT ATA GCT GTA GGT

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AHRU2014SS1019	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1022	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1025	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2002	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2004	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2008	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2009	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2021	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2027	Val Leu Pro Ser Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly

	190	200
L04566	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014CJ0001	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014DL6008	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014DL6009	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014DL6010	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014DL6015	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	
AHRU2014DL6019	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu	

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AHRU2014DL7029	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8006	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8012	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8013	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8018	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8023	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014DL8100	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1002	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1006	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1007	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1019	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1022	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS1025	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS2002	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS2004	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS2008	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
AHRU2014SS2009	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu

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AHRU2014SS2021	ATG GCG ACA AAC ATC CCA CCT CAT AGT TTA AAT GAG TTG ATA GAT GGA CTT TTA TAT TTG
AHRU2014SS2027	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
	ATG GCG ACA AAC ATC CCA CCT CAT AGT TTA AAT GAG TTG ATA GAT GGA CTT TTA TAT TTG
	210
L04566	Leu Asp Asn Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014CJ0001	CTT GAT AAT AAA GAT GCA AGC CTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL6008	Leu Asp Asn Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014DL6009	CTT GAT AAT AAA GAT GCA AGC CTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL6010	Leu Asp Ser Lys Asp Val Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014DL6015	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL6019	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014DL7029	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL8006	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014DL8012	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL8013	Leu Asp Ser Lys Asp Val Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014DL8018	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014DL8023	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT

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AHRU2014DL8100	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS1002	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS1006	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS1007	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS1019	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS1022	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS1025	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS2002	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS2004	Leu Asp Asn Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS2008	CTT GAT AAT AAA GAT GCA AGC CTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS2009	Leu Asp Ser Lys Asp Val Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
AHRU2014SS2021	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014SS2027	Leu Asp Ser Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
	CTT GAT AGT AAA GAT GCA AGC TTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
	230
L04566	Pro Thr Gly Gly Ile Ile Tyr Gly Lys Lys Gly Ile Ile Glu Ala Tyr Arg Thr Gly Arg
AHRU2014CJ0001	CCA ACA GGT GGA ATA ATT TAT GGT AAA AAA GGT ATT ATA GAA GCT TAT CGC ACA GGG CGT
AHRU2014DL6008	Pro Thr Gly Gly

Alignment Report of 26 C.jejuni 101016.meg ClustalW (Slow/Accurate, Gonnet)
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AHRU2014DL6009	CCA ACA GGT GGA Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL6010	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL6015	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL6019	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL7029	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL8006	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL8012	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014DL8013	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014DL8018	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014DL8023	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014DL8100	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS1002	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014SS1006	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014SS1007	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS1019	Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014SS1022	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS1025	Pro Thr Gly Gly



Alignment Report of 26 C.jejuni 101016.meg ClustalW (Slow/Accurate, Gonnet)
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AHRU2014SS2002	CCA ACA GGT GGA Pro Thr Gly Gly Asn CCA ACA GGT GGA A
AHRU2014SS2004	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS2008	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS2009	Pro Thr Gly Gly CCA ACA GGT GGA
AHRU2014SS2021	Pro Thr Gly CCA ACA GGT GGA
AHRU2014SS2027	Pro Thr Gly Gly CCA ACA GGT GGA

	250	260
L04566	Gly Arg Val Lys Val Arg Ala Lys Thr His Ile Glu Lys Lys Thr Asn Lys Asp Val Ile GGT CGC GTG AAA GTG CGA GCT AAA ACT CAT ATT GAA AAA AAG ACA AAT AAA GAT GTT ATT	
AHRU2014CJ0001		
AHRU2014DL6008		
AHRU2014DL6009		
AHRU2014DL6010		
AHRU2014DL6015		
AHRU2014DL6019		
AHRU2014DL7029		
AHRU2014DL8006		

	10										20									
L04566	Met	Glu	Asn	Ile	Phe	Ser	Lys	Asp	Ser	Asp	Ile	Glu	Leu	Val	Asp	Ile	Glu	Asn	Ser	Ile
U63413	ATG	GAG	AAT	ATT	TTT	AGC	AAA	GAT	TCT	GAT	ATT	GAA	CTT	GTA	GAT	ATA	GAA	AAT	TCT	ATA
AHRU2014CC0001	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6001	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6002	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL6003	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6005	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6011	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AHRU2014DL6014	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6017	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL6024	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL7003	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL7014	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL7024	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014DL7025	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014GL4009	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???



	30										40									
AHRU2014GL5009	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS1001	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS1005	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS1015	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS1021	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2001	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2005	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2010	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2013	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2022	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
AHRU2014SS2026	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???	???
L04566	Lys	Ser	Ser	Tyr	Leu	Asp	Tyr	Ser	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala
U63413	AAA	AGT	AGT	TAT	TTA	GAC	TAT	TCT	ATG	AGT	GTT	ATT	ATA	GGT	CGT	GCT	TTG	CCT	GAC	GCA
AHRU2014CC0001	???	???	???	???	???	???	???	???	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala
AHRU2014DL6001	???	???	???	???	???	???	???	???	ATG	AGC	GTT	ATT	ATC	GGT	CGT	GCA	CTT	CCT	GAT	GCT
AHRU2014DL6002	-	-	-	-	-	-	-	-	Met	Ser	Val	Ile	Ile	Gly	Arg	Ala	Leu	Pro	Asp	Ala

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
21 µy*§i, 2016 14:42

Table with 20 columns of amino acid abbreviations (Ile, Gly, Arg, Ala, Leu, Pro, Asp, Ala) and 20 rows of sequence identifiers (AHRU2014DL6003 to AHRU2014SS2001). Each row contains a sequence of amino acids or gaps, with some rows starting with a start codon (ATG AGC GTT) and a stop codon (ATT ATC GGT).

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
21 µy*§i, 2016 14:42

Table with 20 columns of amino acid abbreviations (Met, Ser, Val, Ile, Ile, Gly, Arg, Ala, Leu, Pro, Asp, Ala) and 7 rows of sequence identifiers (AHRU2014SS2005 to AHRU2014SS2026). Each row contains a sequence of amino acids or gaps, with some rows starting with a start codon (ATG AGC GTT) and a stop codon (ATT ATC GGT).

Table with 20 columns of amino acid abbreviations (Arg, Asp, Gly, Leu, Lys, Pro, Val, His, Arg, Arg, Ile, Leu, Tyr, Ala, Met, Gln, Asn, Asp, Glu, Ala) and 10 rows of sequence identifiers (L04566 to AHRU2014DL6017). Each row contains a sequence of amino acids or gaps, with some rows starting with a start codon (AGA GAT GGT) and a stop codon (TAA AAG CCT). Column indices 50 and 60 are marked at the top.

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
21 µy³§; 2016 14:42

AHRU2014DL6024	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014DL7003	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014DL7014	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014DL7024	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014DL7025	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014GL4009	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014GL5009	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS1001	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS1005	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS1015	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS1021	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2001	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2005	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2010	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2013	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2022	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val
AHRU2014SS2026	Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr Ala Met Asn Asp Leu Gly Val

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
21 µy³§; 2016 14:42

	70														80																										
L04566	Lys	Ser	Arg	Thr	Asp	Phe	Val	Lys	Ser	Ala	Arg	Ile	Val	Gly	Ala	Val	Ile	Gly	Arg	Tyr	Lys	Ser	Ala	Arg	Ile	Val	Gly	Ala	Val	Ile	Gly	Arg	Tyr								
U63413	AAA	AGT	AGA	ACA	GAT	TTT	GTC	AAA	TCA	GCC	CGT	ATA	GTG	GGT	GCT	GTT	ATA	GGT	CGT	TAT	AAA	TCA	GCC	CGT	ATA	GTG	GGT	GCT	GTT	ATA	GGT	CGT	TAT								
AHRU2014CC0001	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AHRU2014DL6001	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL6002	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014DL6003	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL6005	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014DL6011	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL6014	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014DL6017	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL6024	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014DL7003	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL7014	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014DL7024	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	
AHRU2014DL7025	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	GGA	AGT	AGA	AGT	GCA	TAT	AAA	AAA	TCT	GCT	CGT	ATA	GTA	GGG	GAT	GTT	ATC	GGT	AAG	TAT	
AHRU2014GL4009	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	Gly	Ser	Arg	Ser	Ala	Tyr	Lys	Lys	Ser	Ala	Arg	Ile	Val	Gly	Asp	Val	Ile	Gly	Lys	Tyr	

AHRU2014GL5009	GGA AGT AGA AGT GCA TAT AAA AAA TCT GCT CGT ATA GTA GGG GAT GTT ATC GGT AAG TAT
AHRU2014SS1001	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS1005	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS1015	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS1021	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2001	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2005	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2010	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2013	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2022	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr
AHRU2014SS2026	Gly Ser Arg Ser Ala Tyr Lys Lys Ser Ala Arg Ile Val Gly Asp Val Ile Gly Lys Tyr

90 100

L04566	His Pro His Gly Asp Thr Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
U63413	CAC CCA CAT GGC GAT ATC ACA GCA GTT TAT GAT GCT TTG GTT AGA ATG GCT CAA GAT TTT TCT
AHRU2014CC0001	His Pro His Gly Asp Thr Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL6001	CAT CCA CAT GGC GAT ACT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTT TCT

AHRU2014DL6002	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL6003	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014DL6005	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL6011	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014DL6014	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL6017	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014DL6024	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL7003	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014DL7014	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014DL7024	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014DL7025	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014GL4009	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014GL5009	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014S1001	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014SS1005	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT
AHRU2014SS1015	His Pro His Gly Asp Ile Ala Val Tyr Asp Ala Leu Val Arg Met Ala Gln Asp Phe Ser
AHRU2014SS1021	CAT CCA CAT GGC GAT ATT GCT GTT TAC GAT GCC TTA GTA AGA ATG GCA CAA GAT TTC TCT

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
 21 µj*§; 2016 14:42

	ATG	CGT	TAT	CCA	AGT	ATC	GAT	GGA	CAA	GGA	AAC	TTT	GGT	TCT	ATC	GAT	GGT	GAT	GGC	GCT
	130										140									
L04566	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Lys	Met	Ser	Lys	Leu	Ser	His	Glu	Leu	Leu	Lys	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCA	AAA	ATG	AGT	AAA	CTT	TCT	CAT	GAG	CIT	TTA	AAA	GAT
U63413	Ala	Ala	Met																	
	GCT	GCA	ATG	CG																
AHRU2014CC0001	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6001	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6002	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6003	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6005	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6011	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6014	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6017	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL6024	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL7003	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL7014	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL7024	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014DL7025	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustalW (Slow/Accurate, Gonnet)
 21 µj*§; 2016 14:42

AHRU2014GL4009	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014GL5009	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS1001	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS1005	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS1015	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS1021	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2001	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2005	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2010	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2013	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2022	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
AHRU2014SS2026	Ala	Ala	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Met	Thr	Ile	Leu	Ala	Glu	Glu	Leu	Leu	Arg	Asp
	GCT	GCA	ATG	CGT	TAT	ACT	GAA	GCT	AGA	ATG	ACA	ATT	TTA	GCA	GAA	GAG	CIT	TTA	CGC	GAT
	150										160									
L04566	Ile	Asp	Lys	Asp	Thr	Val	Asp	Phe	Val	Pro	Asn	Tyr	Asp	Gly	Ser	Glu	Ser	Glu	Pro	Asp
	ATA	GAT	AAA	GAT	ACG	GTC	GAT	TTT	GTT	CCA	AAT	TAT	GAT	GGT	TCA	GAA	AGC	GAA	CCT	GAT
U63413																				
AHRU2014CC0001	Ile	Asp	Lys	Asp	Thr	Val	Asp	Phe	Val	Pro	Asn	Tyr	Asp	Asp	Ser	Met	Ser	Glu	Pro	Asp
	ATA	GAT	AAA	GAT	ACG	GTA	GAT	TTT	GTT	CCA	AAC	TAC	GAT	GAT	TCT	ATG	AGC	GAG	CCC	GAT
AHRU2014DL6001	Ile	Asp	Lys	Asp	Thr	Val	Asp	Phe	Val	Pro	Asn	Tyr	Asp	Asp	Ser	Met	Ser	Glu	Pro	Asp

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustaW (Slow/Accurate, Gonnet)
21 µy²§; 2016 14:42

AHRU2014DL6017	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL6024	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL7003	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL7014	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL7024	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014DL7025	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014GL4009	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014GL5009	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1001	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1005	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1015	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS1021	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2001	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2005	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2010	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2013	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
AHRU2014SS2022	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly

Alignment Report of 1 C.jejuni+26 C.coli 101016.meg ClustaW (Slow/Accurate, Gonnet)
21 µy²§; 2016 14:42

AHRU2014SS2026	Val Leu Pro Ala Arg Val Pro Asn Leu Leu Leu Asn Gly Ser Ser Gly Ile Ala Val Gly
L04566	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Ile Asp Gly Leu Leu Tyr Leu
U63413	ATG GCG ACA AAC ATC CCA CCT CAT AGT TTA AAT GAG TTG ATA GAT GGA CTT TTA TAT TTG
AHRU2014CC0001	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014DL6001	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014DL6002	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Asp
AHRU2014DL6003	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014DL6005	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014DL6011	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Asp
AHRU2014DL6014	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL6017	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL6024	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL7003	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL7014	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL7024	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014DL7025	Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu

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AHRU2014GL4009 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT G
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014GL5009 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT G
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS1001 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS1005 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS1015 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014SS1021 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT G
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS2001 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS2005 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS2010 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT G
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu
AHRU2014SS2013 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS2022 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly
AHRU2014SS2026 ATG GCG ACA AAT ATT CCT CCG CAT AGT CTT AAC GAG CTT GTA GAT GGA C
Met Ala Thr Asn Ile Pro Pro His Ser Leu Asn Glu Leu Val Asp Gly

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                210                220
L04566 Leu Asp Asn Lys Asp Ala Ser Leu Glu Glu Ile Met Gln Phe Ile Lys Gly Pro Asp Phe
U63413 CTT GAT AAT AAA GAT GCA AGC CTA GAA GAG ATT ATG CAG TTT ATC AAA GGT CCA GAT TTT
AHRU2014CC0001

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VITA

Mr. Thotsapol Thomrongsuwannakij was born on August 14, 1984 in Bangkok, Thailand. He got the degree of Doctor of Veterinary Medicine (1st Class Honors) from the Faculty of Veterinary Science, Chulalongkorn University, Thailand in March 2008. After that, he became a sale representative at Fort Dodge animal health (Thailand). In October 2010, he enrolled as a PhD student in the Department of Veterinary Medicine, Faculty of Veterinary Science, Chulalongkorn University.

