
Prevalence and Genetic Heterogeneity of *Coxiella burnetii* Strains from Reservoir Goat Placentas: Implications for Human Q Fever Risk

Decha Pangjai¹, Ratana Tacharoenmuang¹, Sittiporn Parnmen¹, Maskiet Boonyaretha¹, Nattapon Nukhunthod¹, Dararat Bangdee¹, Chonlada Meesub¹, Kanjana Sanongboon¹, Sumalee Boonmar², Kamchai Kidsin³, and Archawin Rojanawiwat⁴

¹National Institute of Health, Department of Medical Sciences, Nonthaburi 11000, Thailand

²Akkhraratchakumari Veterinary College, Walailak University, Nakhon Si Thammarat 80161, Thailand

³Animal Health Section, The Eight Regional Livestock Development, Surat Thani 84000, Thailand

⁴Bureau of Cosmetics and Hazardous Substances, Department of Medical Sciences, Nonthaburi 11000, Thailand

ABSTRACT *Coxiella burnetii* is an obligate intracellular Gram-negative bacterium that causes Q fever in humans and coxiellosis in animals. Goats are important reservoirs of *C. burnetii*, particularly through heavily contaminated placental tissues, yet the epidemiology and genetic diversity of this pathogen in Thailand remain insufficiently characterized. This study investigated the molecular prevalence and genetic heterogeneity of *C. burnetii* in goat placentas collected from 26 farms across 10 provinces in northern, central, western, and southern Thailand in 2022. DNA was extracted from 1,404 placental samples and screened by real-time PCR targeting the *IS1111* gene. Representative positive samples were further characterized by multispacer sequence typing (MST) and phylogenetic analysis based on concatenated sequences from 10 loci. Overall, *C. burnetii* DNA was detected in 27.64% (388/1,404) of samples. Phylogenetic and MST analyses demonstrated marked genetic heterogeneity among Thai strains and revealed three novel genotypes, designated MST94, MST95 and MST96, which were closely related to

MST85, MST27, MST28, MST31, MST55, and MST77. These findings indicate that *C. burnetii* strains detected in goat placentas in Thailand belong to a broader transregional zoonotic lineage maintained within a ruminant–tick–human transmission cycle similar to that described in Eurasia and Europe.

Keywords: *Coxiella burnetii*, Genotyping, Multispacer sequence typing, Goat placenta, Thailand

Corresponding author E-mail: decha.p@dmsc.mail.go.th

Received: 6 May 2026

Revised: 3 July 2026

Accepted: 8 July 2026



Introduction

Coxiella burnetii is an obligate intracellular Gram-negative bacterium that causes Q fever in humans and coxiellosis in animals.⁽¹⁾ The organism is widely distributed worldwide and can infect a broad range of hosts, with domestic ruminants (cattle, sheep, and goats) serving as the primary reservoirs.^(1,2) *C. burnetii* is recognized as an emerging infectious pathogen by international organizations such as WHO/FAO/OIE and EFSA/ECDC⁽³⁾ and is classified as a category B potential bioterrorism agent by the Centers for Disease Control and Prevention (CDC), USA.⁽⁴⁾ Polymerase chain reaction (PCR) has become the preferred method for screening large numbers and diverse types of biological samples, thereby reducing reliance on bacterial culture and isolation. The remarkable environmental persistence of the organism, its transmission via inhalation, and its extremely low infectious dose necessitate handling *C. burnetii* in biosafety level 3 laboratories.⁽⁵⁻⁷⁾ A variety of molecular approaches have been developed to genotype and characterize *C. burnetii* strains. Currently, the three principal discriminatory genotyping methods include multiple-locus variable-number tandem repeat analysis (MLVA), multispacer sequence typing (MST), and single nucleotide polymorphism (SNP) genotyping. PCR-based methods such as MLVA and MST are widely applied in epidemiological investigations.⁽⁸⁾ MST targets housekeeping genes, which are less susceptible to selective pressure and exhibit greater genetic stability than MLVA.⁽⁹⁻¹¹⁾ Numerous studies have reported MST genotyping of *C. burnetii* isolated from human, animal,

and environmental sources, contributing to a global database that enables interlaboratory comparison and reproducibility.⁽¹²⁾ Additionally, MST has therefore been described as a “geotyping” method, as many genotypes display broad geographical distribution. Differences in pathogenicity and virulence have been observed among distinct genogroups.⁽¹³⁾ However, the current MST scheme remains incomplete and requires further expansion to achieve a comprehensive representation of global genetic diversity.⁽¹⁴⁾ SNP genotyping has also been proposed as an alternative approach, identifying polymorphisms within the same spacer regions used in MST.⁽¹⁰⁾ This method allows assignment of sequence types compatible with MST without requiring sequencing or bacterial isolation.⁽¹⁵⁾ In contrast, MST can be more complex to interpret and may require highly purified DNA derived from cultured isolates. More recently, whole-genome sequencing has emerged as a potential approach for revealing the substantial genetic diversity of *C. burnetii*. These technologies have identified geographically structured populations, host-associated patterns, and novel genotypes that are highly relevant to outbreak investigation and transmission dynamics.⁽¹⁶⁻¹⁸⁾ Despite these advances, the molecular epidemiology of *C. burnetii* in Thailand remains poorly characterized and underreported, largely because of limited diagnostic capacity and laboratory resources.

In animals, *C. burnetii* infection is frequently subclinical but may lead to reproductive disorders, including abortion, stillbirth, and weak offspring, particularly in

goats with extensive placental colonization. Infected ruminants can shed large amounts of bacteria in the absence of clinical signs, facilitating silent transmission within herds and environmental persistence.⁽¹⁹⁾ During parturition or abortion, extremely high bacterial loads present in placental tissues, birth fluids, and vaginal secretions can generate infectious aerosols, which represent the primary route of human infection.⁽²⁰⁾ Consequently, transmission of *C. burnetii* to humans is most commonly associated with small ruminants, particularly goats, which play a key epidemiological role and have been implicated in numerous outbreaks linked to goat farms.^(21,22) In humans, infection is often asymptomatic; however, when symptoms occur, they may include headache, flu-like illness, chills, pneumonia, fatigue, weight loss, nausea, and myalgia. More severe complications can develop, including pericarditis, myocarditis, endocarditis, hepatitis, vascular infections, prosthetic joint arthritis, osteoarticular infections, and lymphadenitis.^(23,24) The pathogen is highly infectious, with an estimated infectious dose of a single bacterium sufficient to cause infection in 50% of exposed individuals, highlighting the risk even at very low exposure levels.⁽²⁵⁾

Q fever in Thailand. Several serological and molecular studies have documented the presence and epidemiology of *C. burnetii* in Thailand. Evidence of infection has been reported since 1966 in both humans and domestic animals (goats, sheep, and cattle), initially identified using the complement fixation test.^(26,27) Between 2002 and 2005, acute Q fever cases were detected among patients presenting with acute febrile illness using the indirect

fluorescent antibody test (IFA).^(28,29) In 2012, two fatal cases of *C. burnetii* endocarditis in northeastern Thailand were confirmed through various methodologies, ranging from serology, PCR, and immunohistochemistry.⁽³⁰⁾ In 2013, subsequent investigations expanded to animal reservoirs through PCR-based surveillance of placental tissues from healthy ruminants in areas associated with reported human cases.⁽³¹⁾ Furthermore, serological studies conducted in the same year using ELISA reported animal- and herd-level antibody prevalence of *C. burnetii* in dairy cattle in Chiang Mai.⁽³²⁾ Further nationwide assessments were reported in 2017, describing the seroprevalence of *C. burnetii* among ruminants and occupationally exposed individuals during 2012–2013 using ELISA, IFA, and PCR.⁽³³⁾ In 2018, combined serological and molecular analyses, including SNP genotyping, characterized *C. burnetii* strains in ruminants from northern and northeastern Thailand, identifying sequence types ST20 and ST18/25 in buffalo and goat placentas.⁽³⁴⁾ Regional surveys conducted between 2013 and 2015 in the upper northern and central regions of Thailand reported individual seroprevalence in goats ranging from 3.5% to 12.8%, based on IFA testing.⁽³⁵⁾ In 2021, additional serological evidence was reported in water buffalo (*Bubalus bubalis*) in Phatthalung Province using IFA.⁽³⁶⁾ More recently, studies conducted during 2021–2023 reported substantially higher seroprevalence in goats, with individual- and herd-level rates of 22.39% and 58.42%, respectively, determined using commercial ELISA in central and western Thailand.⁽³⁷⁾ In 2024, investigations of meat

goat herds in northeastern Thailand identified prevalence and associated risk factors using both serological and molecular approaches. Notably, herd owners' knowledge of coxiellosis transmission was identified as a protective factor against infection at the herd level.⁽³⁸⁾ In Thailand, serological evidence indicates that approximately 4% of goats are positive for *C. burnetii* antibodies, while up to 12.6% of occupationally exposed individuals demonstrate seropositivity, highlighting a notable risk of zoonotic transmission.⁽³³⁾ Similarly, *Brucella* spp. seropositivity has been documented in goats and goat herds, with human outbreaks associated with direct contact with parturient animals and the consumption of raw goat products. A high proportion of individuals involved in outbreak settings have been shown to possess antibodies against *B. melitensis*, underscoring close livestock exposure as a major risk factor for infection.⁽³⁹⁾

Despite these findings, genomic and molecular data on *C. burnetii* in Thailand remain limited. Characterizing circulating strains in reproductive tissues, particularly placentas, is therefore essential to improve understanding of local epidemiology and to better assess zoonotic risk. In this study, we investigated the prevalence and genetic heterogeneity of *C. burnetii* in goat placentas collected from farms in Thailand. Molecular detection combined with MST was employed to identify circulating strains and compare them with globally reported lineages. The findings

provide critical baseline data and offer insights into the evolution, host adaptation, and epidemiology of *C. burnetii* in Thailand.

Materials and Methods

Study Population

Goat placental samples were collected in 2022 from four regions of Thailand: northern (Chiang Mai and Phrae provinces), central (Nonthaburi and Chai Nat provinces), western (Kanchanaburi and Ratchaburi provinces), and southern (Krabi, Surat Thani, Chumphon, and Phatthalung provinces) (Figure 1). A total of 26 goat farms across these regions were included in the study. These areas were selected because of their high density of ruminant populations, particularly goats.

Pregnant goats at the late gestation stage were recruited on a voluntary basis. For each collected placental sample and its corresponding animal, data were recorded, including owner information, geographic location, age, production purpose, and farm type. In addition, reproductive history was obtained using a standardized one-page data collection form, including parity number, history of abortion, stillbirth, weak offspring, and gross placental characteristics. Then, placental samples were collected immediately after parturition and stored at -20°C until DNA extraction. Genomic DNA was extracted from all samples using the DNeasy® Blood and Tissue Kit (QIAGEN, Hilden, Germany) according to the manufacturer's instructions.

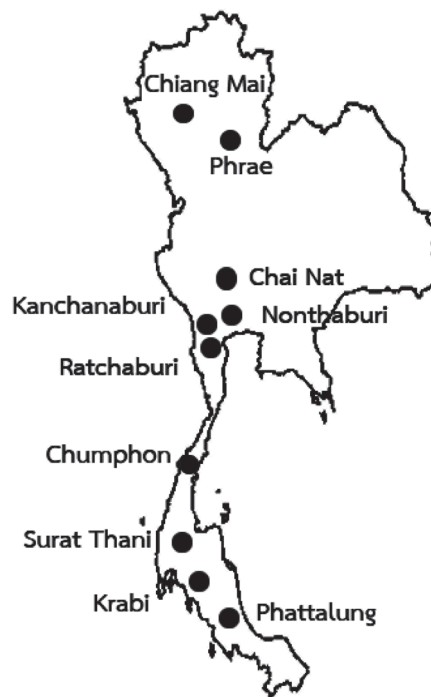


Figure 1 Geographical locations of *C. burnetii* infection, showing the regions and provinces included in the study in Thailand.

Detection of *C. burnetii* by real-time PCR

Extracted DNA from each sample was screened for *C. burnetii* using a real-time PCR assay targeting the *IS1111* gene, employing primers and a TaqMan probe⁽⁴⁰⁾ with in-house optimization. Each 20 μ L reaction mixture contained 0.1 μ M of forward primer (5'-CAT CACATTGCCGCGTTTAC-3'), 0.1 μ M of reverse primer (5'-GGTTGGTCCCTCGA CAACAT-3'), and 0.2 μ M of TaqMan probe (FAM-AATCCCCAACAACACCTCCT TATTCCCAC-BHQ1), together with 10 μ L of 2 $\times$ PerfeCTa[®] Multiplex qPCR Supermix (Quantabio, USA), 1 μ L of DNA template, and nuclease-free water to the final volume. Amplification was performed on a Bio-Rad Real-time PCR system (Bio-Rad, USA) with an initial denaturation at 95°C for 5 min, followed by 45 cycles of denaturation at 95°C for 5 s and annealing/extension at 60°C

for 25 s. Each run included a positive control consisting of purified *C. burnetii* DNA and a no-template negative control to verify assay performance and monitor potential contamination.

Multispacer sequence typing (MST) and phylogenetic analysis

Each PCR was performed using a GeneAmp PCR System 9700 (Applied Biosystems, USA). A total of 40 μ L reaction mixture comprised 14 μ L of nuclease-free water, 20 μ L GoTaq[®] Green Master Mix, 400 μ M of dATP, dGTP, dCTP and dTTP, and 3 mM MgCl₂ (Promega, USA), 2 μ L each of forward and reverse of 200 nM primers (Table 1) and 2 μ L of DNA template. Amplification was conducted under the following conditions: initial denaturation at 95°C for 10 min, followed by 37 cycles of denaturation at 95°C, for 30 s, annealing

at 57°C for 30 s, and extension at 72°C for 1 min.⁽⁹⁾ A 5 µL aliquot of each PCR product was analyzed by electrophoresis on 1.5% agarose gels containing ethidium bromide and visualized under UV illumination. The PCR products were purified using the QIAquick PCR purification kit (Qiagen, Denmark), and subjected to DNA sequencing with the BigDye Terminator Cycle Sequencing Ready Reaction kit (Applied Biosystems, USA) and a Genetic Analyzer (Model 3130x1; Applied Biosystems, USA). Each fragment of sequence data was verified using GeneMapper™ Software 5 (Applied Biosystems, USA), and confirmed fragments were assembled in Sequencher 4.10.1 (Gene Codes Corporation, MI, USA), resulting in consensus sequences. Spacer sequence alignments were performed using Geneious Pro

5.4.3 (<http://www.geneious.com/>). Reference sequences from 65 groups were retrieved from the MST database (https://ifr48.timone.univ-mrs.fr/mst/coxiella_burnetii/spacers.html) and combined with sequences, obtained in this study for phylogenetic analysis. Phylogenetic analysis was inferred using the maximum likelihood (ML) method implemented in RAxML 7.2.6 using the GTRGAMMA model with 25 rate parameter categories,⁽⁴¹⁾ with assessed node support using 1,000 bootstrap replicates. Phylogenetic trees were illustrated using FigTree 1.3.1 (<http://tree.bio.ed.ac.uk>), and allele profiles were compared with reference sequences available in the MST database, which is available on the website (https://ifr48.timone.univ-mrs.fr/mst/coxiella_burnetii/groups.html).

Table 1 Primers used for PCR amplification and sequencing of *C. burnetii* gene spacers.⁽⁹⁾

Spacer name	ORF	Nucleotide Sequence (5'–3')	Amplified Fragment length (bp)
Co×2	Hypothetical protein	Co×20766 CAACCCTGAATACCCAAGGA	397
	Hypothetical protein	Co×21004 GAAGCTTCTGATAGGCGGGA	
Co×5	Sulfatase domain protein	Co×77554 CAGGAGCAAGCTTGAATGCG	395
	Entericidin putative	Co×77808 TGGTATGACAACCCGTCATG	
Co×18	Ribonuclease H	Co×283060 CGCAGACGAATTAGCCAATC	557
	DNA polymerase III, epsilon subunit	Co×283490 TTCGATGATCCGATGGCCTT	
Co×20	Hypothetical protein	Co×365301 GATATTTATCAGCGTCAAAGCAA	631
	Hypothetical protein	Co×365803 TCTATTATTGCAATGCAAGTGG	
Co×22	Hypothetical protein	Co×378718 GGGAATAAGAGAGTTAGCTCA	383
	Amino acid permease family protein	Co×378965 CGCAAATTTTCGGCACAGACC	
Co×37	Hypothetical protein	Co×657471 GGCTTGTCTGGTGTAAGTGT	463
	Hypothetical protein	Co×657794 ATTCCGGGACCTTCGTTAAC	

Table 1 Primers used for PCR amplification and sequencing of *C. burnetii* gene spacers.⁽⁹⁾
(Continue)

Spacer name	ORF	Nucleotide Sequence (5'–3')*	Amplified Fragment length (bp)
Co×51	Replicative DNA helicase, intein-containing	Co×824598 TAACGCCCCGAGAGCTCAGAA	674
	Conserved hypothetical protein– Uridine kinase	Co×825124 GCGAGAACCGAATTGCTATC	
Co×56	OmpA-like transmembrane domain protein	Co×886418 CCAAGCTCTCTGTGCCCAAT	479
	Conserved hypothetical protein	Co×886784 ATGCGCCAGAAACGCATAGG	
Co×57	Rhodanese-like domain protein	Co×892828 TGGAAATGGAAGGCGGATTC	617
	Hypothetical protein	Co×893316 GGTGGAAGGCGTAAGCCTTT	
Co×61	Dioxygenase, putative	Co×956825 GAAGATAGAGCGGCAAGGAT	611
	Hypothetical protein	Co×957249 GGGATTTCAACTTCCGATAGA	

Statistical analysis

Pearson's chi-square test or Fisher's exact test was applied in the bivariate analyses through bivariate odds ratios (ORs), along with their 95% confidence intervals, which were estimated using binary logistic regression analysis to assess the magnitude of association between study factors and *C. burnetii* infection in goats in Thailand. For multiple comparisons in the post hoc analysis, *p*-values were adjusted using the Bonferroni correction.

Ethical approval

The research procedures in this study were reviewed and approved by the Department of Medical Sciences, under animal protocol number 64-037 on 31 January 2021, granted by the Institutional Animal Care and Use Committee (DMSc IACUC), for the use of animals.

Results

The overall prevalence of *C. burnetii* infection in goat placentas by PCR was 27.64% (388/1,404). At the provincial level, the highest prevalence was observed in Nonthaburi at 61.58% (125/203). This was followed by Ratchaburi at 49.26% (167/339), Krabi at 29.51% (36/122), and Kanchanaburi at 22.92% (33/144). Lower prevalence was recorded in Chiang Mai at 7.50% (6/80), Chai Nat at 6.50% (8/123), Surat Thani at 5.19% (8/154), and Phrae at 4.35% (5/155). No positive samples were detected in Chumphon (0/35) or Phatthalung (0/89) (Table 2). At the regional level, the western region had the highest molecular prevalence at 41.41% (200/483), followed by the central region at 40.80% (133/326), and the southern region at 11.00% (44/400). In contrast, the northern region demonstrated the lowest prevalence at 5.64% (11/195) (Table 3).

Table 2 Molecular prevalence of *C. burnetii* in goat placental samples classified by the selective regions and provinces.

Region	Province	No. of samples tested	No. of positive qPCR	Prevalence (%)
Central	Nonthaburi	203	125	61.58
	Chai Nat	123	8	6.50
Northern	Chiang Mai	80	6	7.50
	Phrae	115	5	4.35
Western	Ratchaburi	339	167	49.26
	Kanchanaburi	144	33	22.92
Southern	Krabi	122	36	29.51
	Surat Thani	154	8	5.19
	Chumphon	35	0	0.00
	Phatthalung	89	0	0.00
Total		1,404	388	27.64

Table 3 Association of demographic characteristics with *C. burnetii* infection among goats in Thailand.

Risk Factor	Category	Prev. (%)	OR	95% CI	p-value
Region	Western	200/483 (41.41)	ref		
	Central	133/326 (40.80)	0.98	0.73–1.30	0.863 ^a
	Southern	44/400 (11.00)	0.17	0.12–0.25	< 0.001 ^a
	Northern	11/195 (5.64)	0.08	0.04–0.16	< 0.001 ^a
Age	< 6 years	385/1378 (27.94)	ref		
	≥ 6 years	3/26 (11.54)	0.34	0.10–1.13	0.064 ^a
Breed	Cross-breed	83/644 (12.89)	ref		
	Pure-breed	298/730 (40.82)	4.66	3.55–6.13	< 0.001 ^a
	Native breed	7/30 (23.33)	2.06	0.85–4.94	0.103 ^b
Production type	Meat goat	97/822 (11.80)	ref		
	Dairy goat	291/582 (50.00)	7.47	5.72–9.76	< 0.001 ^a
Parity	1–3	335/1078 (31.08)	ref		
	≥ 4	53/326 (16.26)	0.43	0.31–0.59	< 0.001 ^a
Farming condition	Type A (free roaming)	8/123 (6.50)	ref		
	Type B (semi-free roaming)	41/266 (15.41)	2.62	1.19–5.77	0.014 ^a
	Type C (indoor)	334/776 (43.04)	10.86	5.23–22.55	< 0.001 ^a
Presence of other livestock	No	286/922 (31.02)	ref		
	Yes	102/482 (21.16)	0.60	0.46–0.77	< 0.001 ^a
Introduction of new goats within 6 months	No	383/1164 (32.90)	ref		
	Yes	0/125 (no prev.)	0.01 ^c	0.00–0.13 ^c	< 0.001 ^b

Note: Prevalence (Prev.), odds ratio (OR), confidence interval (CI), ^a = Pearson's chi-square test, ^b = Fisher's exact test and ^c = Haldane–Anscombe correction.

The risk of *C. burnetii* infection was significantly higher in Ratchaburi and Nonthaburi than in Kanchanaburi (both $p < 0.001$). In contrast, significantly lower risks were observed in Chai Nat, Phrae, and Surat Thani than in Kanchanaburi (all $p < 0.001$). Chiang Mai also had a lower risk than Kanchanaburi ($p = 0.004$). At the regional level, the northern and southern regions had significantly lower risks of infection than the western region (both $p < 0.001$).

Moreover, the associations between demographic characteristics and *C. burnetii* infection in goats in Thailand are presented in Table 3. Goats aged < 6 years had a significantly higher risk of infection than those aged ≥ 6 years (all p -values < 0.001). Pure-bred goats, including Anglo-Nubian, Boer, and Saanen, had a higher risk of infection than cross-bred goats (a mix of Anglo-Nubian and Boer; all p -values < 0.001). Dairy goats also showed a higher risk of infection than meat goats (all p -values < 0.001). Goats with 1st–3rd parity had a higher risk than those with $\geq 4^{\text{th}}$ parity (all p -values < 0.001). In addition, goats reared under Type C (indoor) farming conditions had a significantly higher risk of infection than those under Type A (free-roaming) conditions (all p -values < 0.001).

The absence of other livestock on the farm was associated with a higher risk of *C. burnetii* infection than the presence of other livestock (all p -values < 0.001). Introduction of new goats to the farm within 6 months was also associated with a higher risk of infection than in farms without newly introduced goats (all p -values < 0.001).

Genotyping by MST and phylogenetic analysis based on concatenated sequences

from 10 loci of *C. burnetii* from four provinces identified novel genotypes among the examined strains (Figure 2). Phylogenetic analysis demonstrated that *Coxiella* DNA, isolated from goat placentas from Kanchanaburi (TH-KRI-16), Nonthaburi (TH-NBI-3), Phrae (TH-PRE-80), and Ratchaburi (TH-RBR-114), formed a monophyletic group distinct from previously described *C. burnetii* sequence types. The MST profiles of these strains differed from publicly available reference strains and from one another. The strains from Kanchanaburi (TH-KRI-16) and Nonthaburi (TH-NBI-3) were assigned to MST94, whereas the strains from Phrae (TH-PRE-80) and Ratchaburi (TH-RBR-114) were assigned to MST95 and MST96, respectively (Table 3).

These findings indicate that multiple novel *C. burnetii* sequence types are circulating in Thailand. Sequence data for the *Cox2*, *Cox5*, *Cox18*, *Cox20*, *Cox22*, *Cox37*, *Cox51*, *Cox56*, *Cox57*, and *Cox61* genes in this study were submitted to GenBank (<https://www.ncbi.nlm.nih.gov/WebSub/>), with the corresponding accession numbers shown in Tables 4 and 5. Most of the *C. burnetii* sequence type data in humans have been reported in European, African, and Central Asian countries; in particular, France has reported the presence of various groups of MST in humans, including MST1, MST2, MST3, MST4, MST5, MST6, MST9, MST11, MST12, MST13, MST16, MST18, MST20, MST32, MST33, MST42, and MST49 (Table 5). (https://ifr48.timone.univ-mrs.fr/mst/coxiella_burnetii/strains.html)

The phylogenetic tree based on multispacer sequence typing shows that the Thai genotypes MST94, MST95, and MST96

cluster within the same clade as the previously reported MST66, MST67, MST68, MST69, and MST70, all of which were detected in goat

placentas. This Thai placental clade is closely related to MST27, MST28, MST31, MST55, and MST85 (Figure 2).

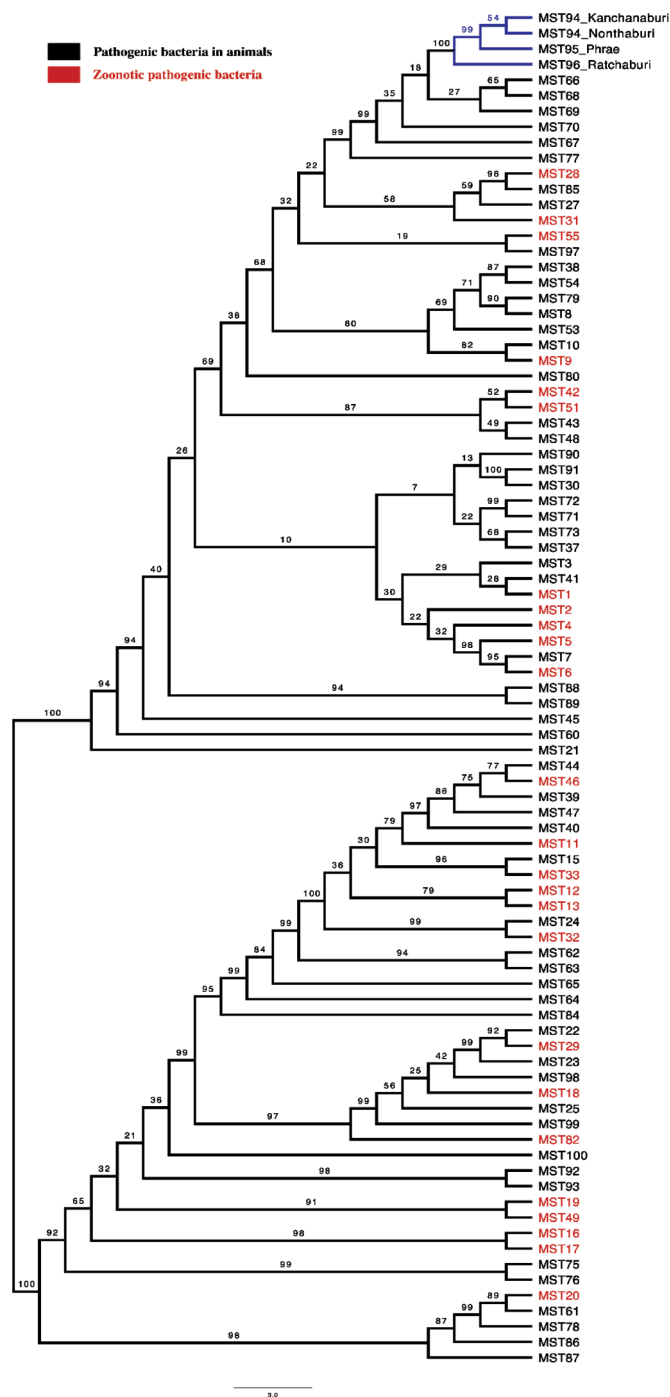


Figure 2 Phylogenetic analysis using the Maximum Likelihood (ML) method with the IQ-TREE program (<http://www.iqtree.org/>), applying the General Time-Reversible (GTR) model with a gamma distribution. Clade support was then assessed using bootstrap analysis with 1,000 replicates to evaluate statistical confidence and construct the phylogenetic tree. Clades with bootstrap (BS) values greater than 70% were considered strongly supported. The phylogenetic tree was visualized using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Table 4 GenBank accession numbers of *C. burnetii* sequences identified from goats placental samples in Thailand, 2022.

Spacer	GenBank acc no. of identified <i>C. burnetii</i>			
	TH-KRI-16	TH-NBI-3	TH-PRE-80	TH-RBR-114
<i>Co</i> ×2	PX619166	PX619167	PX619168	PX619169
<i>Co</i> ×5	PX672292	PX672293	PX672294	PX672295
<i>Co</i> ×18	PX672296	PX672297	PX672298	PX672299
<i>Co</i> ×20	PX672300	PX672301	PX672302	PX672303
<i>Co</i> ×22	PX672304	PX672305	PX672306	PX672307
<i>Co</i> ×37	PX672308	PX672309	PX672310	PX672311
<i>Co</i> ×51	PX672312	PX672313	PX672314	PX672315
<i>Co</i> ×56	PX672316	PX672317	PX672318	PX672319
<i>Co</i> ×57	PX672320	PX672321	PX672322	PX672323
<i>Co</i> ×61	PX672324	PX672325	PX672326	PX672327

Table 5 Alleles of 10 spacers which allow the definition of the different *C. burnetii* sequence. Comparison of the reference sequence types from humans and goats worldwide with the novel genotypes described in the present study.

Geographic	MST group	Co×2	Co×5	Co×18	Co×20	Co×22	Co×37	Co×51	Co×56	Co×57	Co×61
Human											
France	1	5	6	3	4	6	5	8	1	5	6
France, Russia and Kyrgyzstan	2	5	6	3	5	6	5	8	1	5	6
France	3	5	6	3	4	6	7	8	1	5	6
France, Spain and Portugal	4	5	6	3	2	6	5	8	1	5	6
France and Tunisia	5	4	6	3	5	6	2	8	2	5	6
France	6	4	3	3	5	6	5	8	2	5	6
France	9	1	4	2	5	1	5	2	3	4	6
France and Belgium	11	6	5	1	6	5	4	5	4	3	2
France, Switzerland, and Senegal	12	3	5	1	6	5	4	5	4	3	2
France and Portugal	13	3	5	1	6	5	4	5	5	3	2

Table 5 Alleles of 10 spacers which allow the definition of the different *C. burnetii* sequence. Comparison of the reference sequence types from humans and goats worldwide with the novel genotypes described in the present study. (Continue)

Geographic	MST group	Co×2	Co×5	Co×18	Co×20	Co×22	Co×37	Co×51	Co×56	Co×57	Co×61
Poland, Central Africa, Romania, France, Italy and USA	16	3	8	5	3	4	1	6	7	6	5
French Guiana	17	3	8	5	7	4	1	10	8	6	7
Romania, France, Slovakia, Romania, Greece, Italy and Italy	18	3	8	1	6	3	4	7	9	6	3
Senegal	19	3	7	7	8	5	4	11	7	6	5
USA and France	20	3	2	6	1	5	4	4	10	6	5
Kazakhstan	28	8	4	9	5	7	5	2	3	4	6
Italy	29	3	8	1	6	3	8	7	1	6	3
Uzbekistan	31	9	4	9	5	8	5	2	3	4	6
Germany, France and Austria	32	3	5	1	6	5	4	5	12	3	2
Netherlands, France and Reunion	33	7	5	1	6	5	9	9	4	3	2
France and USA	42	5	4	1	5	8	5	2	3	4	6
France	46	7	5	2	4	5	9	9	4	3	2
France	49	3	7	2	6	5	4	11	7	6	5
Saudi Arabia	51	5	4	1	5	8	5	2	3	4	2
United Kingdom	55	5	4	9	5	8	5	2	3	4	6
Iran	82	3	8	1	6	3	4	10	9	6	3
Iran	83	12	11								
Goat											
Spain and USA	8	5	4	2	5	1	5	3	3	4	4
Spain	13	3	5	1	6	5	4	5	5	3	2
Spain and Germany	18	3	8	1	6	3	4	7	9	6	3
Namibia	30	5	6	10	5	6	5	8	13	9	6
Austria	32	3	5	1	6	5	4	5	12	3	2
France	53	5	4	2	5	1	7	3	3	4	6
Liban	58	4	8	2							
Iran	62	3	8	1	6	5	4	5	4	6	11

Table 5 Alleles of 10 spacers which allow the definition of the different *C. burnetii* sequence. Comparison of the reference sequence types from humans and goats worldwide with the novel genotypes described in the present study. (Continue)

Geographic	MST group	Co×2	Co×5	Co×18	Co×20	Co×22	Co×37	Co×51	Co×56	Co×57	Co×61
Thailand	66	5	4	9	5	8	13	15	16	11	6
Thailand	67	5	4	9	5	9	11	14	15	11	6
Thailand	68	5	4	9	5	8	11	15	16	11	6
Thailand	69	5	4	9	5	8	12	14	16	11	6
Thailand	70	5	4	9	5	10	11	14	16	11	6
Brazil	74	3	2	5			10		10		5
Thailand	94 ^a	5	16	16	14	8	11	19	16	18	17
Thailand	95 ^b	5	16	16	14	8	11	20	25	19	18
Thailand	96 ^c	5	17	17	14	8	16	21	16	20	19

Note: ^a = Kanchanaburi no. TH-KRI-16, ^b = Phrae no. TH-PRE-80 and ^c = Ratchaburi no. TH-RBR-114

Discussion

The present study revealed that 27.64% of the goats sampled in Thailand harboured *C. burnetii* in placental tissues. *C. burnetii* has previously been reported in goat milk and placental samples, with a prevalence of 100% (2/2) and sequence types of MST18/25.⁽¹¹⁾ Data retrieved from the MST database (https://ifr48.timone.univ-mrs.fr/mst/coxiella_burnetii/strains.html) indicated a wide distribution of sequence types in goats across different countries. Specifically, MST8 has been identified in goat placentas from Spain and the USA, whereas MST13 and MST18 have been reported in Spain, with MST18 also identified in Germany. In addition, MST30, MST32, and MST53 have been identified in goat placentas from Namibia, Austria, and France, respectively. Regarding MST58, it has also been reported in goat milk in Liban, while MST62 has been identified in aborted goat fetuses and goat milk

in Iran. In Thailand, a previous study assigned a goat placenta sample no. L34 from Lopburi province to MST66, whereas goat samples no. C1 from Chai Nat, no. N130 from Nonthaburi, no. K2 from Kanchanaburi, and no. R180 from Ratchaburi provinces corresponded to MST67, MST68, MST69, and MST70, respectively. In contrast, MST74 has been reported in cattle, goats, and sheep in Brazil (Table 5).

In our phylogenetic analysis, all Thai *C. burnetii* genotypes identified in goat placentas (MST66, MST67, MST68, MST69, MST70, MST94, MST95, and MST96) clustered within a single monophyletic clade. This clade showed close relatedness to MST85, which was originally detected in ticks in China,⁽⁴²⁾ to MST27 and MST28 reported from ewe placenta, cow milk, Hyalomma ticks and human blood in Kazakhstan, to MST31 and MST55 described from human blood and a human heart valve in Uzbekistan and the

United Kingdom(https://ifr48.timone.univ-mrs.fr/mst/coxiella_burnetii/strains.html) and to MST77 recently identified in ticks in Korea.⁽⁴³⁾ The tight clustering of Thai placental genotypes with these tick- and ruminant-associated MSTs, as well as with MSTs linked to human Q fever and endocarditis, indicates that the strains circulating in goats in Thailand are part of a wider Eurasian zoonotic lineage maintained by ticks and small ruminants, rather than a distinct local population. The repeated association of this lineage with reproductive tissues and milk in small ruminants suggests that parturition and lactation are key points for environmental contamination and human exposure, as documented in outbreaks in other regions. The close relationship to MST31 and MST55, which have caused bacteremia and endocarditis in humans, further raises concern that Thai strains may have comparable pathogenic potential, particularly among occupationally exposed groups such as farmers, veterinarians, and abattoir workers. Taken together, these findings highlight the need to integrate Q fever into national surveillance and control programs focusing on goat herds and tick vectors, and to increase clinical awareness of Q fever and Q fever endocarditis in Thailand.

To date, no studies have specifically examined the association between *C. burnetii* infection in goats and factors such as parity, farming conditions, the presence of other livestock species on the farm, or the introduction of new goats within the previous 6 months. In the present study, goats with 1st–3rd parity show a significantly higher prevalence

of *C. burnetii* infection than those with higher parity.⁽⁴⁴⁾ This finding suggests that goats of lower parity could cause a greater risk of infection. In addition, Type C farming conditions (indoor housing) were associated with a higher risk of *C. burnetii* infection than Type A conditions (free-roaming management).⁽⁴⁵⁾ Goat farms without other livestock species also had a higher risk of infection than farms where goats were co-housed with other livestock species.^(46,47)

Introduction of new goats to the farm within the previous 6 months was also associated with a higher risk of *C. burnetii* infection than in farms without newly introduced goats.⁽⁴⁸⁾ In addition, the Co×5, Co×18, Co×20, Co×22, Co×37, Co×51, Co×56, Co×57, and Co×61 spacer loci have been suggested as the most appropriate markers for discriminating *C. burnetii* strains in Thailand. The studies have proposed that phylogenetic analysis based on concatenated sequences of the Co×2, Co×5, Co×18, Co×20, Co×22, Co×37, Co×51, Co×56, Co×57, and Co×61 loci can separate *C. burnetii* into distinct clusters and may therefore be useful for strain characterization at the species level. Accordingly, phylogenetic analysis in this study was performed to further characterize the genetic relationships among four goat-derived strains from Kanchanaburi, Nonthaburi, Phrae, and Ratchaburi. The Kanchanaburi and Nonthaburi strains shared identical genetic characteristics, while all four goat strains were clearly separated from previously reported *C. burnetii* strains in the phylogenetic tree. Their MST profiles also

differed from publicly available reference strains. These findings suggest that goat populations in Thailand harbour novel strains of *C. burnetii*. Comprehensive surveillance and further characterization of isolates are needed to determine the distribution of distinct sequence types in goats and humans in Thailand.

Conclusion

This study provides new molecular epidemiological and genetic characterization data on *C. burnetii* in Thailand based on MST analysis. The findings demonstrate the prevalence of *C. burnetii* infection in goat placentas and identify three novel genotypes in four provinces: Kanchanaburi, Nonthaburi, Phrae, and Ratchaburi. To further characterize strains within the same MST group, MST analysis should be complemented by MLVA.⁽⁴⁹⁾ In conclusion, Thai *C. burnetii* genotypes from goat placentas form a single clade that is closely related to MST85, MST27, MST28, MST31, MST55, and MST77 detected in ticks, ruminant reproductive tissues, milk and human Q fever cases across China, Kazakhstan, Korea, Uzbekistan and the United Kingdom. This genetic relatedness suggests that Thailand is part of a broader transregional network of *C. burnetii* circulation involving ticks, small ruminants and humans, with important implications for veterinary and human public health.

Declaration of the Use of Artificial Intelligence

No artificial intelligence was used.

Acknowledgements

The present study was financially supported by the project “Prevalence and genetic study of important bacterial zoonotic diseases in Thailand: Q fever, Rickettsiosis, Bartonellosis, Brucellosis, Leptospirosis, and Melioidosis (Project code: DGHP-BAC-ZOO-NOSIS, 2022–2024),” Thailand MOPH–United States CDC Collaboration, National Institute of Health, Department of Medical Sciences, Ministry of Public Health, Thailand. We would like to express our sincere gratitude to Dr. Pongpun Sawatwong, Division of Global Health Protection, Thailand MOPH–U.S. CDC Collaboration, Thailand, for his invaluable support and guidance throughout this study.

References

1. Ullah Q, Jamil T, Saqib M, Iqbal M, Neubauer H. Q fever—a neglected zoonosis. *Microorganisms* 2022; 10(8): 1530. (17 pages).
2. Angelakis E, Raoult D. Q fever. *Vet Microbiol* 2010; 140(3–4): 297–309.
3. Bielawska-Drózd A, Cieřlik P, Mirski T, Gawęł J, Michalski A, Niemcewicz M, et al. Prevalence of *Coxiella burnetii* in environmental samples collected from cattle farms in Eastern and Central Poland (2011–2012). *Vet Microbiol* 2014; 174(3–4): 600–6.
4. Rotz LD, Khan AS, Lillibridge SR, Ostroff SM, Hughes JM. Public health assessment of potential biological terrorism agents. *Emerg Infect Dis.* 2002; 8(2): 225–30.
5. Sidi-Boumedine K, Adam G, Angen Ø, Aspán A, Bossers A, Roest HIJ, et al. Whole genome PCR scanning (WGPS) of *Coxiella burnetii* strains from ruminants. *Microbes Infect* 2015; 17(11–12): 772–5.

6. Sidi-Boumedine K, Duquesne V, Prigent M, Yang E, Joulié A, Thiéry R, et al. Impact of IS1111 insertion on the MLVA genotyping of *Coxiella burnetii*. *Microbes Infect* 2015; 17 (11-12): 789-94.
7. World Organization for Animal Health (WOAH). Chapter 3.1.18. – Q fever. In: Manual of diagnostic tests and vaccines for terrestrial animals, 13th ed. Paris: WOAH; 2024. p. 1-19.
8. Astobiza I, Tilburg JJHC, Piñero A, Hurtado A, García-Pérez AL, Nabuurs-Franssen MH, et al. Genotyping of *Coxiella burnetii* from domestic ruminants in northern Spain. *BMC Vet Res* 2012; 8: 241. (8 pages).
9. Glazunova O, Roux V, Freylikman O, Sekeyova Z, Fournous G, Tyczka J, et al. *Coxiella burnetii* genotyping. *Emerg Infect Dis* 2005; 11(8): 1211-7.
10. Hornstra HM, Priestley RA, Georgia SM, Kachur S, Birdsell DN, Hilsabeck R, et al. Rapid typing of *Coxiella burnetii*. *PLoS One* 2011; 6(11): e26201. (8 pages).
11. Pearson T, Hornstra HM, Hilsabeck R, Gates LT, Olivas SM, Birdsell DM, et al. High prevalence and two dominant host-specific genotypes of *Coxiella burnetii* in U.S. milk. *BMC Microbiol.* 2014; 14: 41. (9 pages).
12. van Belkum A. Tracing isolates of bacterial species by multilocus variable number of tandem repeat analysis (MLVA). *FEMS Immunol Med Microbiol* 2007; 49(1): 22-7.
13. Russell-Lodrigue KE, Andoh M, Poels MW, Shive HR, Weeks BR, Zhang GQ, et al. *Coxiella burnetii* isolates cause genogroup-specific virulence in mouse and guinea pig models of acute Q fever. *Infect Immun* 2009; 77(12): 5640-50.
14. Eldin C, Mélenotte C, Mediannikov O, Ghigo E, Million M, Edouard S, et al. From Q fever to *Coxiella burnetii* infection: a paradigm change. *Clin Microbiol Rev* 2017; 30(1): 115-90.
15. Kersh GJ, Priestley RA, Hepp CM, Kaufman EK, Wiley MR, Frey KG, et al. Genotyping and axenic growth of *Coxiella burnetii* isolates found in the United States environment. *Vector Borne Zoonotic Dis* 2016; 16(9): 588-94.
16. Abou Abdallah R, Million M, Delerce J, Anani H, Diop A, Caputo A, et al. Pangenomic analysis of *Coxiella burnetii* unveils new traits in genome architecture. *Front Microbiol* 2022; 13: 1022356. (18 pages).
17. McLaughlin HP, Cherney B, Hakovirta JR, Priestley RA, Conley A, Carter A, et al. Phylogenetic inference of *Coxiella burnetii* by 16S rRNA gene sequencing. *PLoS One* 2017; 12(12): e0189910. (18 pages).
18. Hemsley CM, Essex-Lopresti A, Norville IH, Titball RW. Correlating genotyping data of *Coxiella burnetii* with genomic groups. *Pathogens* 2021; 10(5): 604. (17 pages).
19. Agerholm JS. *Coxiella burnetii* associated reproductive disorders in domestic animals--a critical review. *Acta Vet Scand* 2013; 55(1): 13. (11 pages).
20. Anderson A, Bijlmer H, Fournier PE, Graves S, Hartzell J, Kersh GJ, et al. Diagnosis and management of Q fever—United States, 2013: recommendations from CDC and the Q Fever Working Group. *MMWR Recomm Rep* 2013; 62(RR-03): 1-30.
21. Van den Brom R, van Engelen E, Roest HIJ, van der Hoek W, Vellema P. *Coxiella burnetii* infections in sheep or goats: an opinionated review. *Vet Microbiol* 2015; 181(1-2): 119-29.
22. Bauer AE, Johnson AJ, Weng HY, Pogranichniy RM, Moore GE. An evaluation of risk factors for infection with *Coxiella burnetii* in domestic goats. *Res Vet Sci* 2017; 114: 181-5.
23. Fournier PE, Marrie TJ, Raoult D. Diagnosis of Q fever. *J Clin Microbiol* 1998; 36(7): 1823-34.
24. Gomes MM, Chaves A, Gouveia A, Santos L. Two rare manifestations of Q fever: splenic

- and hepatic abscesses and cerebral venous thrombosis, with literature review *ma non troppo*. *BMJ Case Rep* 2014; 2014:bcr2013202843. (7 pages).
25. Brooke RJ, Kretzschmar ME, Mutters NT, Teunis PF. Human dose response relation for airborne exposure to *Coxiella burnetii*. *BMC Infect Dis* 2013; 13: 488. (8 pages).
 26. Sangkasuwan V, Pongpradit P. SEATO medical research study on rickettsial diseases in Thailand. In: Annual research progress report. Bangkok, Thailand: US Army–SEATO Medical Research Unit; 1967. p. 499–504.
 27. Sangkasuwan V, Pongpradit P. SEATO medical research study on rickettsial diseases in Thailand. In: Annual research progress report. Bangkok, Thailand: US Army–SEATO Medical Research Unit; 1968. p. 444–448.
 28. Suputtamongkol Y, Rolain JM, Losuwanaruk K, Niwatayakul K, Suttinont C, Chierakul W, et al. Q fever in Thailand. *Emerg Infect Dis* 2003; 9(9): 1186–7.
 29. Greiner AL, Bhengsri S, Million M, Edouard S, Thamthitiwat S, Clarke K, et al. Acute Q fever case detection among acute febrile illness patients, Thailand, 2002–2005. *Am J Trop Med Hyg* 2018; 98(1): 252–7.
 30. Pachirat O, Fournier PE, Pussadhamma B, Taksinachanekij S, Lulitanond V, Baggett HC, et al. The first reported cases of Q fever endocarditis in Thailand. *Infect Dis Rep* 2012; 4(1): e7. (2 pages).
 31. Yingst SL, Opaschaitat P, Kanitpun R, Thammasart S, Ekgatat M, Jirathanawat V, et al. Q fever surveillance in ruminants, Thailand, 2012. *Emerg Infect Dis* 2013; 19(12): 2056–8.
 32. Rodtian P, Nuamjit M, Srijan M, Opaschaitat P, Ekgatat M. Q fever among dairy cattle in Chiang Mai Province, Thailand, 2012: a preliminary study. *OSIR* 2013; 6(4): 8–12.
 33. Doung-Ngern P, Chuxnum T, Pangjai D, Opaschaitat P, Kittiwat N, Rodtian P, et al. Seroprevalence of *Coxiella burnetii* antibodies among ruminants and occupationally exposed people in Thailand, 2012–2013. *Am J Trop Med Hyg* 2017; 96(4): 786–90.
 34. Opaschaitat P, Ramrin L, Yingst SL. Epidemiology of Q fever in ruminants in the north-east and the north region of Thailand, 2012 to 2013. *KKU Vet J* 2018; 28(1): 19–25.
 35. Pangjai D, Wangroongsarb P, Boonmar S, Rukkwamsuk T. Seropositivity rate of *Coxiella burnetii* infection in cattle and goats raised in the upper north and central regions of Thailand during 2013–2015. *J Kasetsart Vet* 2021; 31(2): 79–88.
 36. Kidsin K, Panjai D, Boonmar S. The first report of seroprevalence of Q fever in water buffaloes (*Bubalus bubalis*) in Phatthalung, Thailand. *Vet World* 2021; 14(9): 2574–8.
 37. Ratanapob N, Lertwatcharasarakul P, Jala S, Pangjai D, Vongtongsalee K, Rukkwamsuk T. Seroprevalence of *Coxiella burnetii* in goats from central and western Thailand: implications for zoonotic disease surveillance and control. *Vet Sci* 2025; 12(12): 1173. (9 pages).
 38. Rerkyusuke S, Lerk-U-Suke S, Sukon P, Phuektes P. Prevalence and risk factors of coxiellosis in meat goat herds: an epidemiological investigation in Northeastern Thailand. *Int J Vet Sci Med* 2024; 12(1): 60–70.
 39. Burns RJL, Douangngeun B, Theppangna W, Khounsy S, Mukaka M, Selleck PW, et al. Serosurveillance of coxiellosis (Q fever) and brucellosis in goats in selected provinces of Lao People's Democratic Republic. *PLoS Negl Trop Dis* 2018; 12(4): e0006411. (15 pages).
 40. Jones RM, Twomey DF, Hannon S, Errington J, Pritchard GC, Sawyer J. Detection of *Coxiella burnetii* in placenta and abortion

- samples from British ruminants using real-time PCR. *Vet Rec* 2010; 165(25): 965-7.
41. Stamatakis A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 2006; 22(21): 2688-90.
42. Xu ZY, Wang FN, Jian R, Xue J, Guo YC, Guo WP. Multiple spacer sequence typing of *Coxiella burnetii* carried by ticks in Gansu, China. *Front Vet Sci* 2024; 11: 1470242. (10 pages).
43. Lee YJ, Chae SJ, Kim B, Shin HS, Kwak SM, Jeong H, et al. First molecular typing of tick-derived *Coxiella burnetii* from wildlife in South Korea: surveillance and genetic characterization. *Transbound Emerg Dis* 2025; 2025: 2533438. (17 pages).
44. Bond KA, Vincent G, Wilks CR, Franklin L, Sutton B, Stenos J, et al. One Health approach to controlling a Q fever outbreak on an Australian goat farm. *Epidemiol Infect* 2016; 144(6): 1129-41.
45. Attia MM, Mahmoud HY, Ali AO, Fereig RM. *Coxiella burnetii* seroprevalence, risk factors, and health hazards in sheep and goats in Upper Egypt. *Ger J Vet Res* 2024; 4(1): 23-31.
46. Bauer BU, Knittler MR, Herms TL, Frangoulidis D, Matthiesen S, Tappe D, et al. Multispecies Q fever outbreak in a mixed dairy goat and cattle farm based on a new bovine-associated genotype of *Coxiella burnetii*. *Vet Sci* 2021; 8(11): 252. (15 pages).
47. Leahy E, Shome R, Deka RP, Sahay S, Grace D, Mazeri S, et al. Risk factors for *Brucella* spp. and *Coxiella burnetii* infection among small ruminant in Eastern India. *Infect Ecol Epidemiol* 2020; 10(1): 1783091. (9 pages).
48. Neare K, Tummeleht L, Lassen B, Viltrop A. *Coxiella burnetii* seroprevalence and associated risk factors in cattle, sheep, and goats in Estonia. *Microorganisms* 2023; 11(4): 819. (12 pages).
49. Di Domenico M, Curini V, De Massis F, Di Provvido A, Scacchia M, Cammà C. *Coxiella burnetii* in Central Italy: novel genotypes are circulating in cattle and goats. *Vector Borne Zoonotic Dis* 2014; 14(10): 710-5.

ความชุกและความหลากหลายทางพันธุกรรมของเชื้อ *Coxiella burnetii* ที่ตรวจพบในรกแพะ: นัยสำคัญต่อความเสี่ยงโรคไข้ควในคน

เดชา แปงใจ¹ รัตนา ตาเจริญเมือง¹ สิทธิพร ปานเม่น¹ มาสเกียรติ บุญยฤทธิ์¹ ณัฐพล นุชนท¹
ดาร์รัตน์ แบ่งดี¹ ชลลดา มีทรัพย์¹ กาญจนา สอนงบุญ¹ สุมาลี บุญมา² กำชัย กิจศิลป์³
และ อาชวินทร์ ไรจนวิวัฒน์⁴

¹สถาบันวิจัยวิทยาศาสตร์สาธารณสุข กรมวิทยาศาสตร์การแพทย์ ถนนพหลโยธิน 11000

²วิทยาลัยสัตวแพทยศาสตร์อัครราชกุมารี มหาวิทยาลัยวลัยลักษณ์ นครศรีธรรมราช 80161

³กลุ่มสุขภาพสัตว์ สำนักงานปศุสัตว์เขต 8 สุราษฎร์ธานี 84000

⁴สำนักเครื่องสำอางและวัตถุอันตราย กรมวิทยาศาสตร์การแพทย์ ถนนพหลโยธิน 11000

บทคัดย่อ *Coxiella burnetii* เป็นแบคทีเรียแกรมลบที่อาศัยอยู่ในเซลล์และก่อให้เกิดโรคไข้ควในคนและโรค coxiellosis ในสัตว์ โดยมีแพะเป็นแหล่งรังโรคสำคัญผ่านทางรกที่ปนเปื้อนเชื้อในปริมาณสูง อย่างไรก็ตามข้อมูลด้านระบาดวิทยาและความหลากหลายทางพันธุกรรมของเชื้อในประเทศไทยยังมีจำกัด การศึกษานี้มีวัตถุประสงค์เพื่อประเมินความชุกเชิงชีวโมเลกุลและลักษณะความหลากหลายทางพันธุกรรมของ *C. burnetii* ในรกแพะในประเทศไทย ตัวอย่างรกแพะจำนวน 1,404 ตัวอย่าง เก็บจากฟาร์ม 26 แห่ง ใน 10 จังหวัด ครอบคลุมพื้นที่ภาคเหนือ ภาคกลาง ภาคตะวันตก และภาคใต้ ในปี พ.ศ. 2565 ทำการสกัดดีเอ็นเอและตรวจหาเชื้อ *IS1111* โดยวิธี real-time PCR จากนั้นคัดเลือกตัวอย่างที่ให้ผลบวกบางส่วนเพื่อนำมาวิเคราะห์ด้วยวิธี multispacer sequence typing (MST) และสร้างแผนภูมิสายวิวัฒนาการจากลำดับนิวคลีโอไทด์แบบต่อรวมของตำแหน่งยีน 10 ตำแหน่ง ผลการตรวจพบดีเอ็นเอของเชื้อ *C. burnetii* ในอัตรา 27.64% (388/1,404) การวิเคราะห์ MST และสายวิวัฒนาการแสดงให้เห็นความหลากหลายทางพันธุกรรมของสายพันธุ์เชื้อในประเทศไทยอย่างชัดเจนและพบจีโนไทป์ใหม่ 3 ชนิด ได้แก่ MST94, MST95 และ MST96 ซึ่งมีความใกล้ชิดกับ MST85, MST27, MST28, MST31, MST55 และ MST77 ผลการศึกษานี้ชี้ให้เห็นว่าสายพันธุ์ *C. burnetii* ที่ตรวจพบในรกแพะของประเทศไทยเป็นส่วนหนึ่งของสายพันธุ์โรคติดต่อระหว่างสัตว์และคนที่แพร่กระจายข้ามภูมิภาค โดยเกี่ยวข้องกับวงจรการแพร่เชื้อแบบสัตว์เคี้ยวเอื้อง-เห็บ-มนุษย์ คล้ายกับที่รายงานในภูมิภาคยูเรเชียและยุโรป

คำสำคัญ: *Coxiella burnetii*, การจำแนกจีโนไทป์, Multispacer sequence typing, รกแพะ, ประเทศไทย