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Comparative evaluation of Real-Time and Insulated Isothermal PCR for detection of *Mycoplasma gallisepticum*

ABSTRACT

Mycoplasma gallisepticum is a common cause of chronic respiratory disease in commercial poultry, affecting both egg and meat production. The infection is often complicated by secondary bacterial and viral pathogens, adding complexity to the diagnosis. Administration of antibiotics to mitigate clinical disease outcomes and reduce production losses poses threats of increased antimicrobial resistance. PCR-based diagnostic techniques are of paramount significance for early and sensitive detection of *M. gallisepticum*, in-time management for disease therapeutics. So far, a number of molecular techniques have been devised for quick, efficient and cost-effective detection, including insulated isothermal PCR (iiPCR). The current study was performed to validate iiPCR in comparison with real-time PCR (qPCR) and conventional PCR (con-PCR). Analytical sensitivity was evaluated by preparing 10-fold diluted concentrations of *M. gallisepticum* F (live vaccine), and three field isolates in *M. gallisepticum* broth (10^0 – 10^7 CFU/ml). Diagnostic performance of iiPCR was assessed using 95 field samples. The analytical and diagnostic performance of the assays was evaluated and compared with the gold standard that is qPCR. In the present study, the detection limit of iiPCR was found to be comparable with that of qPCR. Statistical analysis and comparison of reliability of different PCR-based techniques for detection of *M. gallisepticum* provided almost perfect agreement between all techniques. It was found that iiPCR can be a good, efficient and relatively cost-effective alternative to qPCR. It can be employed for initial detection of infectious organisms, leading to effective management strategies.

INTRODUCTION

Among the many challenges encountered by mankind, food security and infectious diseases stand as some of its most formidable existential threats. One health is a unifying approach prioritizing human, animal and environmental health by mitigating threats at the interface of these sectors. Poultry in Pakistan have experienced various outbreaks that directly or indirectly affects human health and food safety. White meat is an affordable source of protein, rich in nutrients such as essential vitamins and minerals, while offering fewer calories and less cholesterol as compared to red meat (Jaturasitha *et al.*, 2008). Owing to the per capita consumption of white meat, poultry industry demands high production levels, disease management and quality assurance. However, in developing countries, poultry industries faces big challenges to guarantee the health and hygiene of flocks.



Respiratory diseases in poultry poses a serious health concern due to its high prevalence, substantial mortality and morbidity, expensive treatment, and adverse impacts on bird performance. Furthermore, some of these infections have zoonotic potential and exhibit major risk to public health. Major bacterial pathogens include *Escherichia coli*, *Staphylococcus*, *Pasteurella multocida*, and *Mycoplasma gallisepticum* (Yehia *et al.*, 2023).

The genus *Mycoplasma* is comprised of species and subspecies with genome sizes ranging from 500kb to 1500kb. Mycoplasmas have developed various genetic systems, encoding variable surface proteins as mechanisms of immune evasion. *M. gallisepticum* is a cell wall deficient bacterium enclosed in triple layered plasma membrane. It exhibits independent replication, but lacks biosynthetic pathways (Razin, 1998; Halium *et al.*, 2019; Lui *et al.*, 2024). The genome of *M. gallisepticum* strain R_{low} is 996kb in size with 742 coding DNA sequences (CDSs), showing 91% coding density. Strain A5969 possess 1076.9kb genome, with 766 CDS (Papazisi *et al.*, 2003; Leigh & Evans, 2024).

M. gallisepticum infections in poultry cause high morbidity when complicated by secondary pathogens. In the absence of secondary infections, *M. gallisepticum* infections can be mild or asymptomatic and may be overlooked. In addition, when the organisms remain located in the upper respiratory tract of birds, initial signs of respiratory infections cannot be differentiated from other bacterial and viral respiratory infections (Farooq *et al.*, 2020). Detection of *M. gallisepticum* is most successful during the acute phase, when a high number of organisms are present in the trachea (Gaunson *et al.*, 2006). Early detection of *M. gallisepticum* infections and differentiation from other respiratory pathogens could aid in designing and implementing therapeutic or preventive approaches to maintain disease-free flocks. Losses attributed to mycoplasmosis, mainly *M. gallisepticum* infections, are due to decreases in egg production and egg quality, poor hatchability (high rate of embryonic mortality and culling of day-old birds), poor feed efficiency, increase in mortality and carcass condemnations, as well as medication costs (OIE, 2019). In an infected farm, infection can be transmitted horizontally via respiratory droplets, and vertical transmission can occur in breeding flocks from infected parental flocks (Levisohn & Kleven, 2000; Bradbury, 2005; Nascimento

et al., 2005; Machado *et al.*, 2017). To reduce *M. gallisepticum* outbreaks and to maintain biosecurity, routine monitoring of poultry farms is recommended (Umar *et al.*, 2017).

The main approaches to diagnose avian mycoplasma infections are based on isolation of organisms, detection of immune response, and molecular detection of the organism's nucleic acid by polymerase chain reaction (PCR) (Raviv & Kleven, 2009). Some studies comparing the sensitivity and specificity of different diagnostic tests - including serum plate agglutination (SPA), Haemagglutination inhibition (HI), polymerase chain reaction (PCR) and real time PCR - have been published, indicating the significance of different diagnostic tests when undertaking field diagnosis (Hanif & Najeeb, 2007; Rauf *et al.*, 2013; Asif *et al.*, 2015; Haque *et al.*, 2015). Studies from Bangladesh and Egypt also reported bacterial isolation and molecular detection (Basit *et al.*, 2021; Qorra *et al.*, 2023). In addition, gene-targeted sequence analysis is now being used to discriminate the field and vaccinal strains of *M. gallisepticum* (Muhammad *et al.*, 2021; Qorra *et al.*, 2023).

For detection of four different avian mycoplasma, a real time Taq-man PCR assay was developed. The species-specific assay was targeted against the 16S-23S intergenic spacer region of *M. synoviae* and *M. meleagridis*, the upstream region to the 16S rDNA of *M. iowea*, and the conserved region of the *mgc2* gene of *M. gallisepticum* (Raviv & Kleven, 2009). Multiplex real time PCR assay offers concurrent detection of 2 or more pathogens at the same time. The assay has been used for simultaneous detection of *M. gallisepticum* and *M. synoviae* by Fraga *et al.* (2013) to detect mycoplasma infection among Brazilian commercial poultry. A similar study from Idowu *et al.* (2024) reported detection of *M. gallisepticum* and *M. synoviae* when targeting 16S rRNA and *vlhA* by qPCR followed by sequence analysis.

The World Organization for Animal Health (OIE) recommends isolation, serology and polymerase chain reaction (PCR) for the diagnosis of *M. gallisepticum* infections in poultry. PCR provided a sensitive and rapid method of *M. gallisepticum* detection, since culturing the organism requires specialized media reagents and is time consuming (Nascimento *et al.*, 1991; Kleven, 2008). Isolation of *M. gallisepticum* may also be compromised in case of complicated infections



due to the presence of competing microorganisms, overgrowth of non-pathogenic mycoplasma spp., and low infectious dose of the organisms under investigation (Ley, 2008; Kleven, 2008). Real-time PCR proved to be more sensitive, with a higher detection limit than conventional PCR (con PCR). However, it needs a specialized laboratory setup and trained manpower to conduct the test. To facilitate in-time and rapid detection of *M. gallisepticum*, a sensitive, specific, and user friendly molecular diagnostic assay is in order. In developing countries, poultry farmers would benefit from early and cheap detection of pathogens, so that economic losses due to disease outbreaks, medication costs, and production losses could be minimized by adopting appropriate and timely measures.

The use of insulated isothermal PCR (iiPCR) for detection of various human and animal pathogens has been reported in different previous studies. The assay is based on the Rayleigh-Bernard convention (Krishnan *et al.*, 2002), which operates on the principle of heat transfer due to movement of fluids. The POCKIT™ Nucleic Acid analyzer by (POCKIT™; GeneReach, Taichung, Taiwan) claimed to provide a rapid and sensitive procedure for the diagnosis of different pathogens (Tsai *et al.*, 2012). The application of iiPCR using POCKIT™ Nucleic Acid analyzer could provide sensitive and rapid detection of *M. gallisepticum* for poultry in Pakistan. For this purpose, the analytical and diagnostic performance criteria of iiPCR (POCKIT Central Nucleic Acid Analyzer and POCKIT Micro Plus Nucleic Acid Analyzer) was evaluated, and a comparison between different PCR-based diagnostic techniques was made. The aim of the present study was to validate the use of iiPCR as a reliable technique for the detection of *M. gallisepticum* from field samples and to compare con-PCR, real time PCR, and iiPCR for the detection of *M. gallisepticum*.

MATERIALS AND METHODS

The study was conducted in the Microbiology Laboratory of Allama Iqbal Open University (AIU), Islamabad, National Reference Laboratory for poultry Disease (NRLPD) (ISO/IEC 17025-2017) National Agriculture Research Centre, Pakistan and Averroes Laboratories (ISO 9001-2015), Islamabad, Pakistan.

Tracheal swabs received from *M. gallisepticum*-infected farms were processed according to established

laboratory protocols for detection and isolation of infectious agents.

Initially, each sample was subjected to PCR using the 16S rRNA primer (OIE 2019), followed by isolation of *M. gallisepticum* on *Mycoplasma gallisepticum* agar (Farooq *et al.*, 2020). Using selected laboratory isolates of *M. gallisepticum*, the analytical performance of iiPCR was evaluated. The diagnostic performance of the assay was assessed by comparing molecular detection of clinical samples already tested by con-PCR at NRLPD with real-time PCR and iiPCR.

Real-time / Quantitative Polymerase chain reaction (Q-PCR)

To evaluate the analytical and diagnostic performance of iiPCR, real-time PCR (qPCR) was performed as a standard assay. *M. gallisepticum* F (live vaccine) strain was used as a positive standard along with three laboratory isolates including Pak MG1 (ARL-1963) (Farooq *et al.*, 2021; Farooq *et al.*, 2024), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668). The laboratory isolates of *M. gallisepticum* included in the study were characterized on the basis of the gene-targeted sequence analysis described by Farooq (2021). Each sample was optimised at the concentration range of 100–107 CFU/ml by using 10-fold dilutions of *M. gallisepticum* broth. DNA extraction was done by using Invitrogen-Pure Link™ Genomic DNA Kit-K182002. In addition, 95 clinical samples already tested by con-PCR were subjected to qPCR. Reactions with a threshold cycle (Ct) number value 35 or fewer were considered positive.

qPCR reaction was performed using Invitrogen Super Script™ One step QRT-PCR kit, following the manufacturer's protocol. The qPCR was performed in a thermal-cycler (ABI 7500 Real time PCR Plus) using the temperature parameters mentioned by the manufacturer.

Validation of Insulated Isothermal Polymerase Chain Reaction (iiPCR)

For validation of iiPCR, POCKIT Central Nucleic Acid Analyzer and POCKIT Micro Plus Nucleic Acid Analyzer (both with automatic nucleic acid extraction procedures) were appraised for the detection of *M. gallisepticum*. The analytical performance criteria of the assay comprising analytical sensitivity (ASe) and



analytical specificity (ASp) were estimated. Diagnostic performance of assay was evaluated by comparison with *M. gallisepticum* qPCR using clinical samples.

Insulated Isothermal PCR (iiPCR) using Micro Plus Nucleic Acid Analyzer (Field deployable POCKIT™ device)

Test samples were transferred to the lysis buffer vial. Vials with lysis buffer and sample were capped and mixed by vigorous shaking for 30 times. Drop-n-Go cassette provided with the kit was unscrewed to load the sample. A single sample was loaded to each cassette. 60 µl of sample (pre-treated with lysis buffer) was transferred to the sample well with the help of a V-dropper. Fibre disc was gently pressed, and the sample was incubated for 5-10 secs. Two drops of wash buffer were added to the sample well and incubated for 10 mins to air dry the fibre disc. The fibre disc was transferred from sample well to elution buffer vial and mixed 30 times. Nucleic acid extract of sample was used to reconstitute the premix tube. The constituted premix was transferred to the respective R-tube, which was then capped tightly. R-tubes for each sample were placed in the POCKIT™ device and the "RUN" button was pressed. The Micro Plus Nucleic Acid Analyzer was run on a default program set by the manufacturer, with a total run time of 45 min.

Insulated Isothermal PCR (iiPCR) using POCKIT Central Nucleic Acid Analyzer

For each sample, 1 transfer cartridge and 1 extraction cartridge were prepared. The transfer cartridge was labelled with the sample ID, and premix vial was added to the well no. 3 of the respective cartridge. The extraction cartridge was labelled with sample ID, and 200µl sample was added to the first well of cartridge. Both cartridges were loaded to the POCKIT Central Nucleic Acid Analyzer, and the program was initiated. The sequence information of the iiPCR primers and probes and the components of the assay were proprietary to GeneReach Taiwan.

Analytical performance of iiPCR

Analytical Specificity (ASp) of iiPCR using POCKIT Central Nucleic Acid Analyzer and POCKIT Micro Plus Nucleic Acid Analyzer was assessed by testing

live vaccine of *M. gallisepticum* F strain as reference, laboratory isolates Pak MG1 (ARL-1963), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668), along with reference antigens of other poultry pathogens *M. synoviae* (MS), New Castle disease virus (NDV), Avian influenza virus (AIV H9N2) and *Salmonella pullorum* (SP). The Analytical Sensitivity (ASe) and limit of detection of iiPCR by Micro Plus Nucleic Acid Analyzer and POCKIT Central Nucleic Acid Analyzer were assessed by using a range of 10-fold diluted concentrations in *M. gallisepticum* broth (10^0 – 10^7 CFU/ml) of *M. gallisepticum* F (live vaccine), Pak MG1 (ARL-1963), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668). Each sample/dilution was tested by iiPCR and qPCR, as well as con-PCR in triplicates.

Diagnostic performance of iiPCR

The diagnostic performance of iiPCR to detect *M. gallisepticum* in clinical samples was determined by comparing it with qPCR as reference. In total, 95 clinical samples, randomly selected from con-PCR positive and negative samples, were used in the study. Test samples were used for the detection of *M. gallisepticum* by both qPCR and iiPCR (POCKIT™ Micro Plus Nucleic Acid Analyzer and POCKIT Central Nucleic Acid Analyzer) by following the manufacturer's protocol.

Statistical Analysis

Percentage agreement between different PCR-based techniques was calculated, and statistical analysis was performed to assess reliability using Cohen's kappa (Carossino *et al.*, 2016).

RESULTS

Quantitative PCR of *M. gallisepticum* F strain and three field isolates - i.e. Pak MG1 (ARL-1963), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668) - was carried out (Table 1).

Among the 95 clinical samples subjected to qPCR, 70 were already declared positive and 25 were declared negative by con-PCR. However, qPCR revealed 72 positive and 23 negative samples with Ct ranging from 18-35. Samples showing Ct values greater than 35 were considered negative, which resulted in 23 negative samples.



Table 1 – Comparison of analytical sensitivity of iiPCR with qPCR and conventional PCR

	MG CFU/ml	Micro plus Nucleic acid Analyzer			POCKIT Central Nucleic acid Analyzer			Q-PCR C _t	Con-PCR
<i>M. gallisepticum</i> F strain	1×10 ⁷	+	+	+	+	+	+	18.61	3/3 +ve
	1×10 ⁶	+	+	+	+	+	+	22.30	3/3 +ve
	1×10 ⁵	+	+	+	+	+	+	25.14	3/3 +ve
	1×10 ⁴	+	+	+	+	+	+	27.21	3/3 +ve
	1×10 ³	+	+	+	+	+	+	31.58	2/3 +ve
	1×10 ²	-	-	+	-	+	+	Negative	-ve
	10	-	-	-	-	-	-	Negative	-ve
Pak MG1 (ARL-1963)	1×10 ⁷	+	+	+	+	+	+	19.21	3/3 +ve
	1×10 ⁶	+	+	+	+	+	+	22.14	3/3 +ve
	1×10 ⁵	+	+	+	+	+	+	24.67	3/3 +ve
	1×10 ⁴	+	+	+	+	+	+	26.99	3/3 +ve
	1×10 ³	+	+	+	+	+	+	31.3	1/3 +ve
	1×10 ²	-	+	-	-	+	-	Negative	-ve
	10	-	-	-	-	-	-	Negative	-ve
Pak MG2 (ARL-2020)	1×10 ⁷	+	+	+	+	+	+	19.35	3/3 +ve
	1×10 ⁶	+	+	+	+	+	+	22.49	3/3 +ve
	1×10 ⁵	+	+	+	+	+	+	25.43	3/3 +ve
	1×10 ⁴	+	+	+	+	+	+	27.7	3/3 +ve
	1×10 ³	+	+	+	+	+	+	32.05	1/3 +ve
	1×10 ²	+	-	-	-	+	-	Negative	-ve
	10	-	-	-	-	-	-	Negative	-ve
Pak MG3 (ARL-2668)	1×10 ⁷	+	+	+	+	+	+	19.17	3/3 +ve
	1×10 ⁶	+	+	+	+	+	+	22.19	3/3 +ve
	1×10 ⁵	+	+	+	+	+	+	24.56	3/3 +ve
	1×10 ⁴	+	+	+	+	+	+	28.12	3/3 +ve
	1×10 ³	+	+	+	+	+	+	31.95	2/3 +ve
	1×10 ²	-	+	-	+	+	-	Negative	-ve
	10	-	-	-	-	-	-	Negative	-ve

Analytical sensitivity (Ase) of iiPCR for detection of *M. gallisepticum*

Analytical sensitivity (Ase) or limit of detection of iiPCR was established by using concentrations of *M. gallisepticum* F strain, Pak MG1 (ARL-1963), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668) corresponding to CFU ranging from 1×10⁷/ml to 10⁰/ml. Minimum concentration giving 100% positive results by POCKIT Central Nucleic Acid Analyzer and POCKIT Micro Plus Nucleic Acid Analyzer was found to be 1×10³ CFU/ml as represented in Figure 1. Lack of uniformity in test results was found at 1×10² CFU/ml, with a similar trend being recorded by qPCR (Table 1). Comparison of conventional PCR (con-PCR) using 16S rRNA primers (OIE, 2019) and iiPCR in terms of sensitivity revealed

that con-PCR achieved 100% detection with pure culture and at 10⁻¹, 10⁻², and 10⁻³ dilutions. At the 10⁻⁴ dilution, detection dropped to 33.3–66.7%, and no detection was observed at 10⁻⁵ (Table 2).

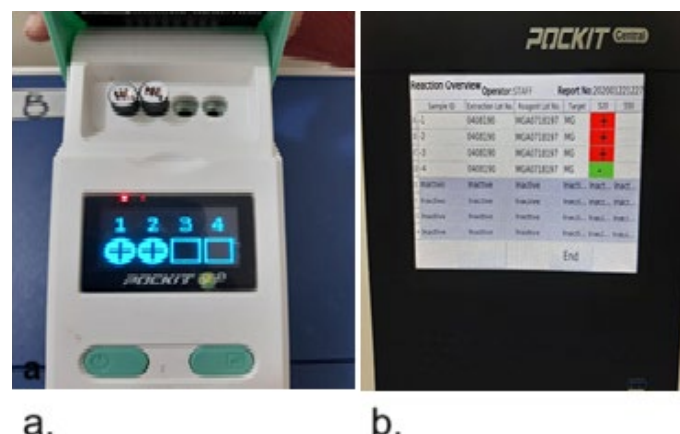


Figure 1 – Presentation of results on a) POCKIT Micro Plus Nucleic Acid Analyzer
b) POCKIT Central Nucleic acid Analyzer

Table 2 – Contingency table for the comparison of qPCR and conventional PCR assay for the detection of *Mycoplasma gallisepticum*

		Q-PCR		
		Positive	Negative	Total
Con PCR	Positive	70	0	70
	Negative	02	23	25
	Total	72	23	95

Analytical specificity (Asp) of iiPCR for detection of *M. gallisepticum*

iiPCR was found to be very specific for detection of *M. gallisepticum*, as no cross reactivity was recorded with other respiratory pathogens on the POCKIT Central Nucleic Acid Analyzer and POCKIT Micro Plus Nucleic Acid Analyzer. Results were negative for *M. synoviae* (MS), New Castle disease virus (NDV), Avian influenza virus (AIV H9N2) and *Salmonella pullorum* (SP), which were used as negative control. On the other hand, *M. gallisepticum* F strain, Pak MG1 (ARL-1963), Pak MG2 (ARL-2020), and Pak MG3 (ARL-2668) were positive for *M. gallisepticum* iiPCR according to both analyzers. Analytical specificity of iiPCR using both analyzers was found to be 100%.

Diagnostic performance of iiPCR for detection of *M. gallisepticum*

A panel of clinical samples containing positive and negative samples already tested by con-PCR and by qPCR was used to assess the diagnostic performance of



iiPCR using the POKKIT Central Nucleic Acid Analyzer and POKKIT Micro Plus Nucleic Acid Analyzer to detect *M. gallisepticum*. For this purpose, DNA extraction of the designated samples was carried out and qPCR was performed. Out of total 95 tested samples by qPCR, 72 were positive, with Ct ranging from 18-35, and 23 were negative. Results of iiPCR using the POKKIT Central Nucleic Acid Analyzer showed 71 positive and 22 negative sample, with one false positive and one false negative sample (Table 3). The same samples tested by iiPCR Micro Plus Nucleic Acid Analyzer showed 70 positive and 21 negative samples for *M. gallisepticum*, with one false positive and 02 false negative results (Table 4). Statistical analysis revealed almost perfect reliability of both techniques for the detection of *M. gallisepticum* from clinical samples with percentage agreement of 95% -97% (Table 5).

Table 3 – Contingency table for the comparison of qPCR and iiPCR using POKKIT Central Nucleic Acid Analyzer for the detection of *Mycoplasma gallisepticum*

		Q-PCR		
		Positive	Negative	Total
iiPCR (POCKIT Central Analyzer)	Positive	71	01	72
	Negative	01	22	23
	Total	72	23	95

Table 4 – Contingency table for the comparison of qPCR and iiPCR using Micro Plus Nucleic Acid Analyzer for detection of *Mycoplasma gallisepticum*

		Q-PCR		
		Positive	Negative	Total
iiPCR (Micro Plus Analyzer)	Positive	71	01	72
	Negative	01	22	23
	Total	72	23	95

Table 5 – Comparison of reliability of different PCR-based diagnostic techniques for the detection of *Mycoplasma gallisepticum*

Tests in Comparison	Test by Test agreement		
	Percentage of agreement	Kappa	Agreement
Q-PCR Vs Con-PCR	97.89%	0.94	Almost perfect
Q-PCR Vs iiPCR POKKIT Central Analyzer	97.89%	0.94	Almost perfect
Q-PCR Vs Micro Plus Analyzer	95.7%	0.88	Almost perfect

DISCUSSION

Diagnostic assays are validated based on analytical and diagnostic performance after completing their development, optimization and standardization. Modern day isothermal diagnostic techniques including

insulated isothermal polymerase chain reaction PCR (iiPCR) has been demonstrated to be an useful tool for the detection of pathogens. In the present study, iiPCR was assessed for its analytical and diagnostic sensitivity, as well as its specificity for testing for the presence of *M. gallisepticum* causing respiratory infections in birds. Due to production losses and therapeutic burdens, early detection of infectious agents is of the foremost importance to curb transmission across flocks and farms.

PCR has been used for molecular detection and typing of infectious agents in many forms, including random amplification polymorphic DNA (RAPD) analysis or arbitrarily primed-PCR (AP-PCR). For routine diagnosis of *M. gallisepticum*, con-PCR has been the common practice (García *et al.*, 2005; Fraga *et al.*, 2013; Emam *et al.*, 2024). iiPCR was developed based on the principle of convective heat transfer. Heat convection is a phenomenon of heat transfer based on motion of fluid. After initial development of iiPCR based on Rayleigh-Benard convection by Krishnan *et al.* (2002), the technique has undergone several modifications towards user-friendliness for the last couple of decades (Qiu *et al.*, 2019; Song *et al.*, 2022). In its present form, it is now available as an all-in-one version with minimum run time of 45 mins for 4 to 8 samples as a field portable device, i.e. Micro Plus Nucleic Acid Analyzer and the laboratory diagnostic device POKKIT Central Nucleic Acid Analyzer.

In the current study, *M. gallisepticum*-specific iiPCR assay exhibited first-rate analytical sensitivity and specificity. The analytical specificity of the assay was found to be 100%, with no cross reactions observed with the reference antigens of various pathogens. Analytical sensitivity and limit of detection of *M. gallisepticum* iiPCR was found to be 1×10^3 CFU/ml, which is comparable to *M. gallisepticum* qPCR and far better than the con-PCR assay conducted for routine diagnosis.

To assess reliability of iiPCR for intended results, a comparative study was conducted with qPCR as a standard molecular method for the detection of *M. gallisepticum*. Using qPCR as the reference standard technique, the diagnostic performance of con-PCR and iiPCR was evaluated and compared. Comparison of reliability of different PCR based diagnostic techniques revealed 97.89% (Cohen's Kappa value, 0.94) agreement between qPCR and con-PCR, as well as between qPCR and iiPCR POKKIT Central Analyser. qPCR and POKKIT Micro Plus Nucleic Acid Analyser



had 95.7% (Cohen's Kappa value, 0.88) agreement, in consistence with previous reports (Carossino *et al.*, 2016). Statistical analysis to assess reliability of iiPCR in comparison to qPCR showed the compatibility of both techniques for use in the diagnosis of *M. gallisepticum*. The samples showing false positive results were processed tissue samples, and since iiPCR assay is based on direct detection from sample, tissue exudates can have been the hinderance for appropriate detection. The current study is consistent with the findings of Kuo *et al.* (2017), who reported 97.8% agreement of iiPCR with real time PCR for detection of *M. synoviae* infection in poultry by using the filed deployable POCKIT™ device for timely detection in a suspected farm. In iiPCR, steady circulation of energy by fluid density gradient leads to sequential development of the denaturation, annealing and extension temperatures carried out in conventional process. The whole process has been described by Chou *et al.*, (2011) in developing capillary convective PCR (CCPCR). Natural convection drives reagents in capillary to circulate through different temperature zones, corresponding to the PCR cycle, leading to the amplification of the target DNA. To overcome the influence of environmental temperature variations, a thermally baffled device has been developed by Chang *et al.*, (2012). The insulated isothermal device (iiPCR) was further used by Tsai *et al.* (2012) to successfully demonstrate the diagnosis of white spot syndrome virus (WSSV). Analysis of amplified products was carried out by agarose gel electrophoresis. Post-amplification processing was then replaced by real time detection, using fluorescent dyes and optical detection system (Tsen *et al.*, 2013).

Insulated isothermal PCR has found wide application in prompt detection of several bacterial and viral pathogens for effective and swift control of infections. The assay was successfully used for detection of *Salmonella* from chicken meat samples employing TaqMan probes and PCR primers targeting *yrfH* gene (Tsen *et al.*, 2013). A field deployable device, POCKIT™ Micro Plus Nucleic Acid Analyzer, has been used for detection of Canine distemper virus (CDV) (Wilkes *et al.*, 2014), Equine influenza Virus (EIV) H3N8 (Balasuriya *et al.*, 2014), equine arteritis virus (having an agreement limit of more than 90% with the standard assays) (Carossino *et al.*, 2016), Foot-and-mouth disease (FMD) and Bluetongue virus in ruminants (Ambagala *et al.*, 2017a Ambagala *et al.*, 2017b), classical swine fever virus (CSFV) (Lung *et al.*,

2016), *M. synoviae* (MS) (Kuo *et al.*, 2017), malaria (Chua *et al.*, 2016), rotavirus (Soltan *et al.*, 2016), Feline leukaemia virus (FeLV) (Wilkes *et al.*, 2018), Dengue virus (DENV) infection and its serotypes (Go *et al.*, 2016; Wang and Gubler 2018; Tsai *et al.*, 2019), Seneca Valley virus (SVV) (Zhang *et al.*, 2019), and *Staphylococcus aureus* from food samples (Yin *et al.*, 2019). The current study further demonstrated the utility of iiPCR for rapid detection of *M. gallisepticum* for the first time, thus paving the way for its integration into national surveillance frameworks to control mycoplasma infections in avian populations.

CONCLUSION

Insulated isothermal PCR (iiPCR) using Micro Plus Nucleic Acid Analyzer and POCKIT Central Nucleic Acid Analyzer showed similar results and both were good alternatives to qPCR for the detection of *M. gallisepticum*. The result showed a high sensitivity of 90.9% and 100% of Micro Plus Nucleic Acid Analyzer and POCKIT Central Nucleic Acid Analyzer when considering qPCR as the gold standard. The detection limit of iiPCR was found to be comparable with qPCR. No non-specific detections were observed.

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AUTHOR CONTRIBUTIONS

Conceptualization, FS and NK; methodology, FS, LS; validation, FS, and KR; formal analysis, FS; investigation, FS,NK,SAA; resources, FS; data curation, FS(2),LS; writing—original draft preparation, FS,NK; writing—review and editing,FS(2) , KR; visualization, LS; supervision, NK, SAA; project administration, SL. All authors have read and agreed to the published version of the manuscript.

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DATA AVAILABILITY STATEMENT

All relevant data is available in manuscript tables.

CONFLICT OF INTEREST

Authors declared no conflict of interests.

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