JOURNAL OF CLINICAL MICROBIOLOGY, May 2003, p. 1869–1874
0095-1137/03/$08.00+0   DOI: 10.1128/JCM.41.5.1869–1874.2003

Vol. 41, No. 5

Evaluation of *Coxiella burnetii* Antibiotic Susceptibilities by Real-Time PCR Assay

Robert E. Brennan and James E. Samuel*

*Department of Medical Microbiology and Immunology, Texas A&M University System
Health Science Center, College Station, Texas*

Coxiella burnetii is an obligate intracellular bacterium. The inability to cultivate this organism on axenic medium has made calculation of infectious units challenging and prevents the use of conventional antibiotic susceptibility assays. A rapid and reliable real-time PCR assay was developed to quantify *C. burnetii* cells from J774.16 mouse macrophage cells and was applied to antibiotic susceptibility testing of *C. burnetii* Nine Mile, phase I. For calculation of bacterial replication, real-time PCR performed equally as well as immunofluorescent-antibody (IFA) assay when J774.16 cells were infected with 10-fold serial dilutions of *C. burnetii* and was significantly ($P < 0.05$) more repeatable than IFA when 2-fold dilutions were used. Newly infected murine macrophage-like J774.16 cells were treated with 8 μg of chloramphenicol per ml, 4 μg of tetracycline per ml, 4 μg of rifampin per ml, 4 μg of ampicillin per ml, or 1 μg of ciprofloxacin per ml. After 6 days of treatment, tetracycline, rifampin, and ampicillin significantly ($P < 0.01$) inhibited the replication of *C. burnetii*, while chloramphenicol and ciprofloxacin did not. In general, these results are consistent with those from prior reports on the efficacy of these antibiotics against *C. burnetii* Nine Mile, phase I, and indicate that a real-time PCR-based assay is an appropriate alternative to the present methodology for evaluation of the antibiotic susceptibilities of *C. burnetii*.

Coxiella burnetii, the etiologic agent of Q fever, is an obligate intracellular bacterium. *C. burnetii* is widely distributed in nature and infects a variety of mammals, birds, reptiles, fish, and ticks (19). In humans, infection is usually the result of inhalation of contaminated aerosols associated with infected sheep, goats, and, to a lesser extent, cattle. The prevalence of *C. burnetii* infections has been difficult to determine, in part, due to the lack of surveillance. One recent retrospective study indicated that seropositivity rates in Japan were greater than 20% in at-risk individuals (7). Q fever may manifest as either an acute or chronic illness (13). Acute disease commonly presents as a self-limiting influenza-like illness accompanied by fever and severe headaches, and the prognosis is usually favorable (16). Recovery from acute infections usually occurs within 1 to 2 weeks and can be accelerated with antibiotics such as tetracyclines. However, diagnosis of acute infections often occurs too late for tetracyclines to be effective, and misdiagnoses can lead to inappropriate treatment or a lack of treatment altogether (10, 24). Chronic disease can be life threatening and most often presents as endocarditis or hepatitis (13). Even with antimicrobial intervention, mortality rates have been reported to be as high as 24% (2). The most effective treatment of chronic Q fever includes a combination of doxycycline and chloroquine administered for at least 18 months (13). In cases of tetracycline intolerance or contraindication, alternative and often less effective antibiotics are used (13). The pursuit of new and more effective treatments for Q fever remains an area of active research. Two recent studies based on in vitro

sensitivities indicated that certain macrolides and trovafloxacin were good potential candidates for the treatment of Q fever (5, 6).

One of the challenges investigators face when determining *C. burnetii* antibiotic sensitivities is calculating bacterial numbers. In many intracellular bacterial infection models, infectious units can be measured by plating lysates on semisolid media for CFU determination or performing an agar overlay for PFU determination. However, *C. burnetii* has yet to be cultivated on axenic medium, and a plaquing system (23) has been difficult to adapt to most laboratories. Thus, the inability to cultivate this bacterium on axenic medium prevents the use of conventional assays to test antibiotic susceptibilities. Therefore, three different systems have been used to evaluate the antibiotic susceptibilities of *C. burnetii*, including an animal model (8), an embryonated egg model (9), and several cell culture models (26). These methods are time-consuming and difficult to use for testing of multiple antibiotics with multiple clinical isolates. In order to overcome this limitation, a shell vial assay was developed that used immunofluorescent-antibody (IFA) assay to determine the bacteriostatic and bactericidal activities of antibiotics (17). The disadvantages of this technique are that it is labor-intensive and results must be determined by blinded scoring because of the subjectivity of the test. Therefore, techniques based at the molecular level have the potential to be more efficient methods for determination of the antimicrobial susceptibilities of *C. burnetii*.

In this report, we describe the application of a SYBR Green I dye-based real-time PCR assay to antibiotic susceptibility testing of *C. burnetii*. This assay provides a rapid and sensitive method for determination of *C. burnetii* antibiotic sensitivities and eliminates the subjectivity associated with other methods.

* Corresponding author. Mailing address: Department of Medical Microbiology and Immunology, Texas A&M University System Health Science, Center College Station, TX 77843-1114. Phone: (979) 862-1684. Fax: (979) 845-3479. E-mail: jsamuel@tamu.edu.
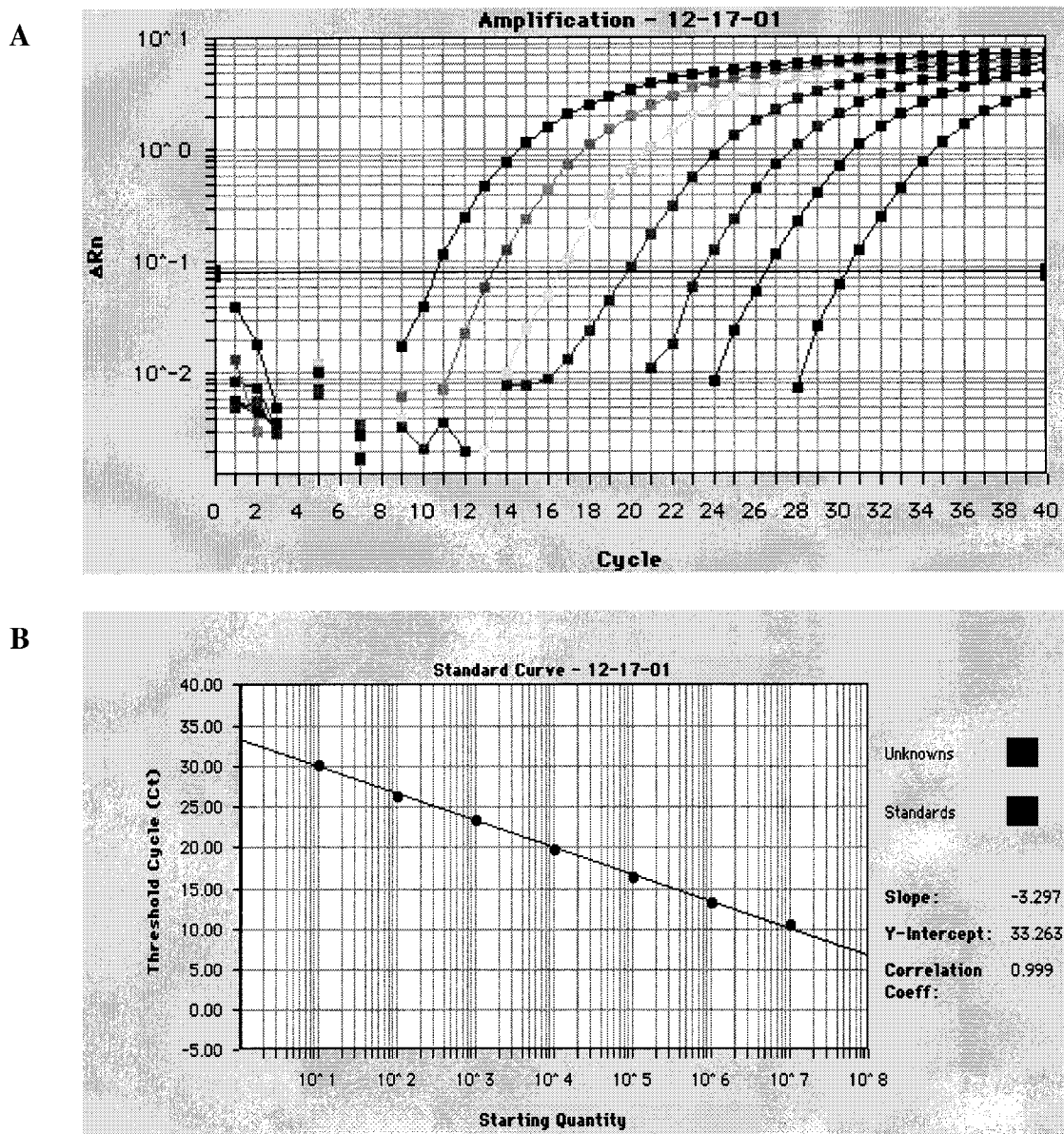
FIG. 1. Establishment of the standard curve for *C. burnetii* quantification. (A) Amplification plots of *C. burnetii* standards. Genome concentrations are (from left to right) 10^7, 10^6, 10^5, 10^4, 10^3, 10^2, and 10^1. For each dilution the normalized fluorescence signal (ΔRn) is plotted against the PCR cycle number. (B) Standard curve generated from the C_t values of the amplification plots with ABI Sequence Detection software. This curve represents the standard curve only; no unknowns are represented in this graph.

MATERIALS AND METHODS

Oligonucleotide primers. Primers FAF216 (5′-GCACTATTTTTAGCCGG AACCTT-3′) and RAF290 (5′-TTGAGGAGAAAAACTGGATTGAGA-3′), which amplify a 74-bp fragment of the *C. burnetii com1* gene (GenBank accession no. AF318146), which is highly conserved among 21 *C. burnetii* strains (27), were selected by using Primer Express software (PE Applied Biosystems, Foster City, Calif.). The primers were synthesized by the Gene Technologies Laboratory at Texas A&M University, College Station.

Preparation of standard curve. To construct a standard curve, total genomic DNA was purified from *C. burnetii* Nine Mile, phase I (RSA 493), which is considered the representative strain for acute infections (10, 18). The DNA concentration was measured spectrophotometrically and converted to genome copy numbers by using the molecular weight of DNA. Briefly, the weight of one *C. burnetii* genome copy (in grams) was calculated by multiplying the size of the *C. burnetii* genome ($\sim 2.1 \times 10^6$ bp) by the average mass of a DNA base pair (615

Da) (20) and then multiplying this number by the weight of 1 atomic mass unit (1.67×10^{-24} g) (22). This number was then divided into the concentration of the total genomic DNA to determine how many genome copies were in each microliter of the genomic DNA. Tenfold serial dilutions ranging from 10^7 to 10^1 genome copies were then made.

PCR assay conditions. Real-time PCR was performed with an ABI Prism 7700 sequence detector (PE Applied Biosystems) according to the empirical design of the manufacturer. Briefly, template DNA was added to a reaction mixture containing 0.3 μM each primer, 12.5 μl of 2× SYBR Green I PCR Master Mix (PE Applied Biosystems), and 8 μl of distilled H_2O in a final volume of 25 μl. All reactions were carried out in 96-well plates. After initial activation of AmpliTaq Gold DNA polymerase at 95°C for 10 min, 40 PCR cycles of 95°C for 15 s and 60°C for 1 min were performed. Cycle threshold (C_t) values were determined by using cycles 3 to 9 as the baseline. Assay specificity was confirmed by subjecting the PCR products to agarose gel electrophoresis and SYBR Green I melting
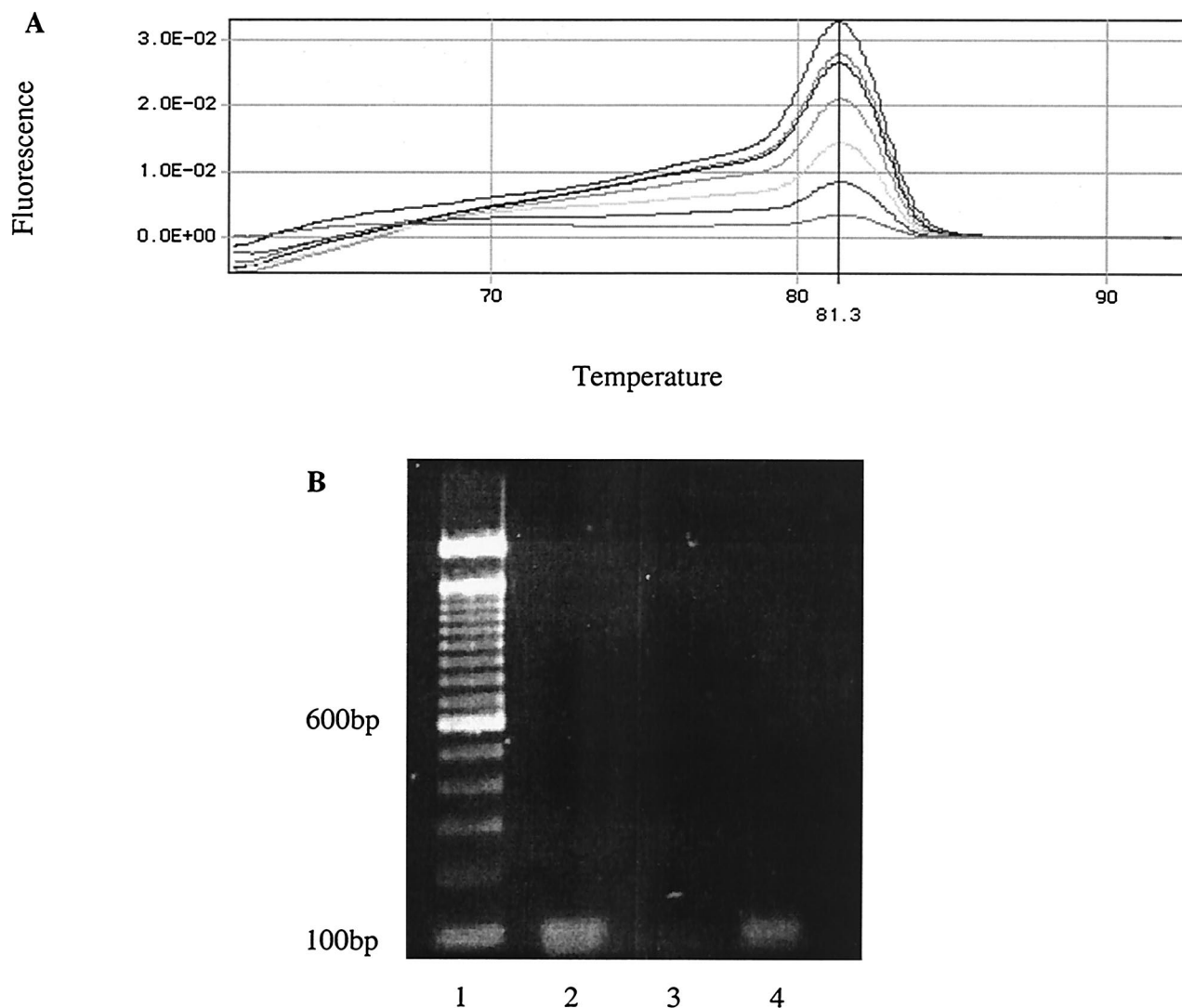
FIG. 2. Determination of PCR specificity. (A) Melting curve analysis performed with ABI Dissociation Curve software revealed that the *com1*-specific primer pair amplified a single predominant product with a melting temperature of 81.3°C. (B) Agarose gel electrophoresis of the amplified product with ethidium bromide staining shows the presence of a single band, confirming the specificity of the PCR assay. Lane 1, 100-bp molecular mass marker; lane 2, amplified product from a *C. burnetii* DNA standard dilution of 10^7; lane 3, blank; lane 4, amplified product from a 1:200 dilution of the *C. burnetii* inoculum.

curve analysis by using three separate holds of 95°C for 15 s, 60°C for 20 s, and 95°C for 15 s, with a ramp time of 19 min and 59 s from the second to the third holding temperatures.

Extraction of *C. burnetii* DNA from infected tissue culture cells. *C. burnetii* DNA was extracted from murine macrophage-like J774.16 cells by resuspending cell pellets in 200 µl of lysis buffer (6.25 ml of 2 M Tris [pH 7.5], 1 ml of 0.5 M EDTA, 50 mg of glucose, and 200 mg of lysozyme brought to a final volume of 50 ml with distilled H$_2$O) plus 10 µl of 20 mg of proteinase K per ml for 4 h at 60°C. Following this treatment, 21 µl of 10% sodium dodecyl sulfate was added, and the mixture was incubated for 1 h at room temperature. DNA was recovered by using the High Pure PCR template preparation kit (Roche Molecular Biochemicals, Indianapolis, Ind.).

Comparison of real-time PCR to IFA. J774.16 mouse macrophages were plated at a concentration of 10^5 cells/ml in 24-well tissue culture plates (Becton Dickinson, Franklin Lakes, N.J.) with or without coverslips and incubated for 4 h at 37°C in 5% CO$_2$ for attachment. The cells were then inoculated with either 10- or 2-fold serial dilutions of *C. burnetii* Nine Mile, phase I (RSA 493), and incubated overnight at 37°C in 5% CO$_2$. Samples for real-time PCR were prepared as described above.

Immunofluorescence antibody staining (IFA) was performed on samples plated into wells containing coverslips. The wells were washed three times with warm Dulbecco modified Eagle medium with L-glutamine and supplemented with 10% fetal bovine serum (DMEM; Fisher Scientific, Houston, Tex.), fixed with 2% paraformaldehyde–100% methanol–1% toluene, and washed once with phosphate-buffered saline (PBS). Five hundred microliters of rabbit anti-*C. burnetii* Nine Mile antiserum diluted 1:300 in PBS–2% normal goat serum was added, and the mixture was incubated at room temperature for 1 h, followed by three 5-min washes in PBS. Five hundred microliters of Alexa Fluor 488 goat anti-rabbit immunoglobulin G (heavy and light chains; Molecular Probes, Eugene, Oreg.) diluted 1:300 in PBS–2% normal goat serum was added, and the mixture was incubated at room temperature for 1 h. Coverslips were washed three times for 5 min each time in PBS, mounted on slides, and examined by fluorescence microscopy. The IFA result was expressed as an infection index, which is the product of the mean number of bacteria per infected cell and the percentage of infected cells multiplied by 100 (3).

Antibiotic susceptibility testing. J774.16 mouse macrophages were plated at a concentration of 10^5 cells/ml in 24-well tissue culture plates and incubated for 4 h at 37°C in 5% CO$_2$ to allow attachment. The medium was removed, and the monolayers were inoculated with *C. burnetii* Nine Mile, phase I (RSA 493), diluted 1:500 in DMEM, and incubated overnight. Infected cells were washed

TABLE 1. Summary of eight different PCR runs performed
on eight separate dilution series

Concn (no. of copies/µl)	Mean C_t	SD[a]	CV (%)
10^7	10.68	0.35	3.3
10^6	13.52	0.16	1.2
10^5	17.08	0.21	1.2
10^4	20.82	0.61	2.9
10^3	24.72	1.39	5.6
10^2	28.92	1.63	5.6
10^1	31.61	0.84	2.7

[a] SD, standard deviation of eight replicates.

three times with warm DMEM to remove noninternalized bacteria and were then treated with antibiotics or sham treated. The concentrations of each of the antibiotics used were as follows: chloramphenicol, 8 µg/ml; tetracycline, 4 µg/ml; rifampin, 4 µg/ml; ampicillin, 4 µg/ml; and ciprofloxacin, 1 µg/ml. These concentrations are the lower critical concentrations according to the French Antibiogram Committee (1) and were previously reported to have bacteriostatic effects against *C. burnetii* (17, 21). Fresh medium with antibiotics was added on days 1, 2, 3, 4, 5, and 6 postinoculation. Sham-treated cells received DMEM only and served as a reference to create growth curves for treated samples. Samples for real-time PCR were collected on days 1, 2, 4, and 7 postinoculation.

Statistical analysis. Significant differences between methods and between antibiotic treatment groups were assessed by the paired Student t test. The repeatability of each method (i.e., the variability of a method when repeated measures are taken within a single experiment) was estimated by computing the percent coefficient of variation (CV; the ratio between the standard deviation and the mean of the repeated measurements multiplied by 100).

RESULTS

Prior to application of the real-time methodology to antimicrobial sensitivity testing of *C. burnetii*, several steps were taken to validate the assay. First, a BLAST search of the ENTREZ database indicated that oligonucleotide primers FAF216 and RAF290 were specific for *com1*. Tenfold serial dilutions of purified *C. burnetii* genomic DNA were used to construct a standard curve, from 10^7 copies at the start to 10^1 copies. Figure 1A presents typical amplification plots for these standards. A standard curve was then generated from the C_ts of the amplification plots with ABI Sequence Detection software (Fig. 1B). The slope of the standard curve was −3.297, indicating that the efficiency of the PCR was approximately 100%, according to the equation $E = 10^{-1/s} - 1$, where E is the run efficiency and s is the slope of the standard curve (4).

Melting curve analysis revealed that the primer pair amplified a single predominant product with a distinct melting temperature, indicating that fluorescence from misprimed products or primer dimers would not hinder *C. burnetii* quantitation (Fig. 2A). Specificity was confirmed by agarose gel electrophoresis, which demonstrated the presence of a single amplicon of approximately 100 bp (Fig. 2B). The primers designed with Primer Express software were predicted to amplify a 74-bp product. This discrepancy between the predicted size and the size of the band seen in the gel is likely due to a decrease in the mobility of the fragment as a result of bound SYBR Green I dye and the limits of resolution of agarose gel electrophoresis.

The precision of the assay was determined by measuring C_t values for eight replicates of the standards (Table 1). The results represent independent dilution series and different PCR runs. The mean C_t, standard deviation, and percent CV

were calculated for each template concentration. The results showed low variability, with CVs ranging from 1.2 to 5.6%, indicating that the assay was efficiently reproducible.

To further validate the assay, tissue culture cells were inoculated with either 10- or 2-fold dilution series of *C. burnetii*, incubated overnight, and quantified by both IFA and real-time PCR. When 10-fold dilutions from 1:100 to 1:100,000 were used, both IFA and real-time PCR results showed strong linear relationships ($r = 0.99$) (Fig. 3A). The repeatability of each assay was determined by calculating the percent CV at each dilution. The CVs ranged from 7.1 to 33% and from 10.3 to 55% for the real-time PCR and IFA, respectively (Table 2). These results show that the repeatabilities of the real-time PCR and IFA were similar at dilutions of 1:100 and 1:1,000, but as the number of infectious organisms decreased, the CV of IFA was considerably greater. The CVs for the real-time PCR at 1:10,000 and 1:100,000 dilutions of the inoculum were 12.5 and 33%, respectively, whereas for IFA they were 44 and 53%, respectively. At twofold dilutions of the inoculum from 1:200 to 1:1,600, the linearities of both assays were again similar ($r = 0.84$) (Fig. 3B). CVs ranged from 3.6 to 13% and from 8.8 to 26% for the real-time PCR and IFA, respectively (Table 2). Again, as the number of infectious organisms decreased, the repeatability of IFA was not as consistent as that of the real-time PCR assay. The CVs for the real-time PCR at 1:800 and 1:1,600 dilutions of the inoculum were 13 and 3.6%, re-
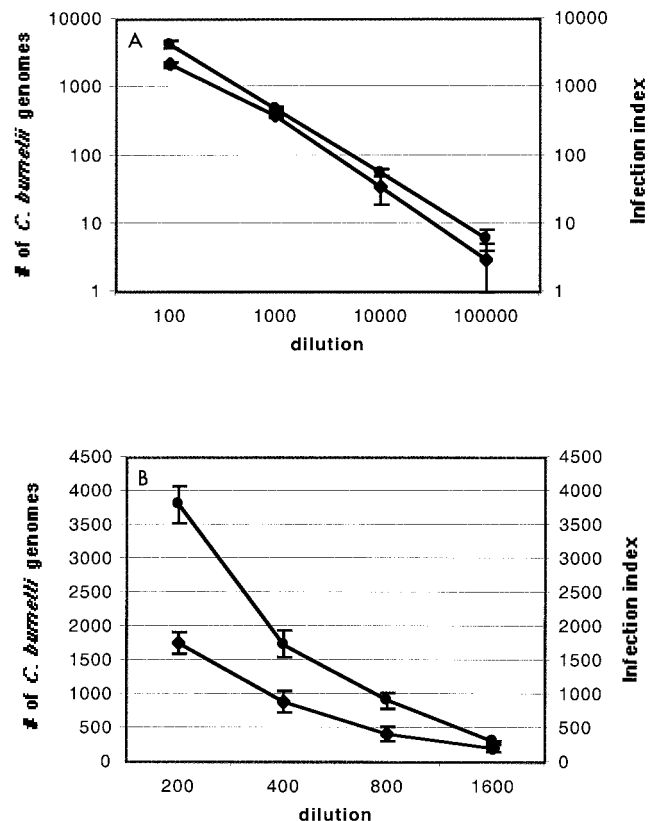

FIG. 3. Validation of real-time PCR by comparison to IFA. The results are represented as the means and standard errors of three replicates. (A) Tenfold dilution series; (B) twofold dilution series. Circles, real-time PCR data; diamonds, IFA data.

TABLE 2. CVs of 10- and 2-fold dilutions of *C. burnetii* inoculum quantified by real-time PCR and IFA

Dilution	CV (%)	
	Real-time PCR	IFA
10-fold		
1:100	10.7	10.8
1:1,000	7.1	10.3
1:10,000	12.5	44.0
1:100,000	33.0	53.0
2-fold		
1:200	6.0	8.8
1:400	11.0	18.0
1:800	13.0	26.0
1:1,600	3.6	25.0

spectively, whereas for IFA they were 26 and 25%, respectively.

Real-time PCR was used to evaluate the effectiveness of antibiotics previously shown to be bacteriostatic for *C. burnetii* Nine Mile, phase I, by the shell vial assay. Newly infected J774.16 cells were treated for 6 days with 8 μg of chloramphenicol per ml, 4 μg of tetracycline per ml, 4 μg of rifampin per ml, 4 μg of ampicillin per ml, or 1 μg of per ciprofloxacin ml, which are the lower critical bacteriostatic concentrations (1). Total DNA was extracted and antibiotic efficacies were determined. Sham-treated infected cells served as positive controls for *C. burnetii* replication. For each treatment or control

group, J774.16 cell viabilities were greater than 90%. The results of *C. burnetii* antibiotic susceptibility testing are shown in Fig. 4. After 6 days of treatment, tetracycline, rifampin, and ampicillin significantly inhibited the replication of the bacteria ($P < 0.01$) while chloramphenicol and ciprofloxacin did not inhibit replication compared to the results for the sham-treated controls. Of the bacteriostatic antibiotics, rifampin was the most effective, followed by tetracycline and ampicillin.

DISCUSSION

The results of this study demonstrate that a real-time PCR assay can be used for the rapid and reliable determination of *C. burnetii* antimicrobial susceptibilities without the subjectivity associated with microscopic enumeration methodologies. The use of *com1* as a target gene allowed the specific amplification of *C. burnetii* DNA over a 7-log DNA concentration range. The specificity of the assay was confirmed by a search for primer-specific sequences with the BLAST program, melting curve analysis, and agarose gel electrophoresis of the PCR-amplified products. Comparison of the real-time PCR and IFA revealed that the real-time PCR assay was more repeatable. No statistically significant difference ($P > 0.05$) was found between the percent CVs obtained by the real-time PCR assay and those obtained by the IFA method when 10-fold dilutions were used. However, when twofold dilutions were used, the real-time PCR assay did perform significantly better ($P < 0.05$). With the 10- and 2-fold dilution series of the *C. burnetii* inoculum, the real-time assay consistently detected more bac-
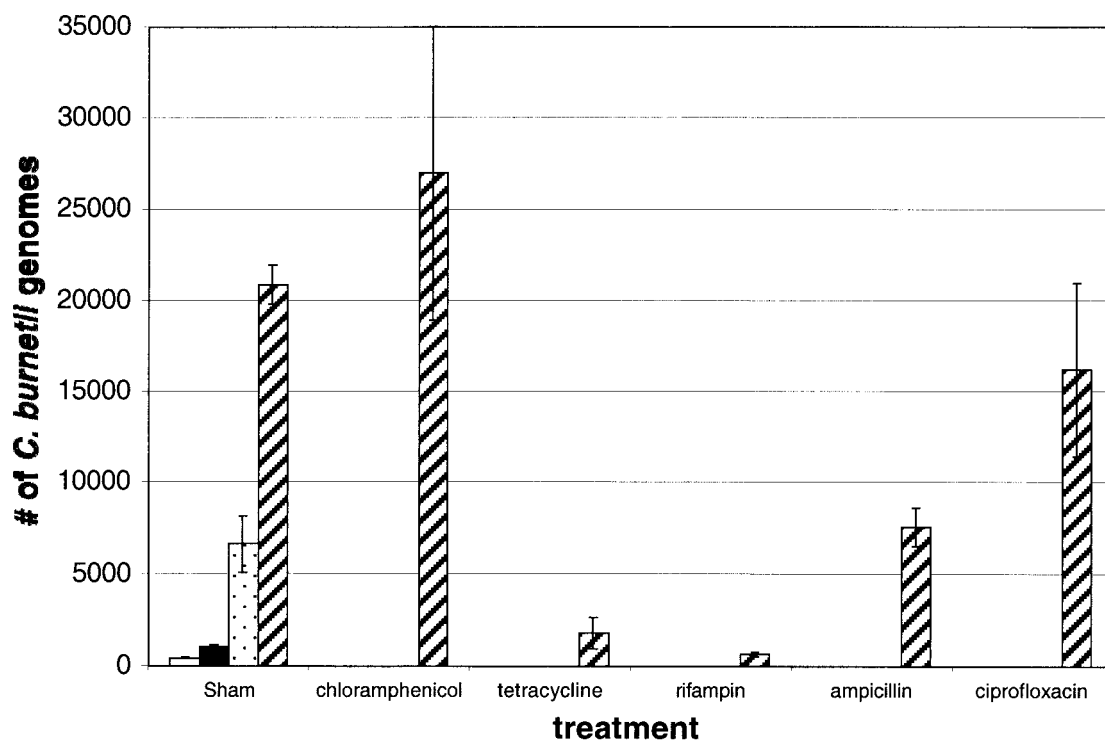

FIG. 4. Effects of chloramphenicol, tetracycline, rifampin, ampicillin, and ciprofloxacin on *C. burnetii* replication in J774.16 cells. Antibiotic-treated cells were assayed on day 7. Sham-treated cells were assayed on days 1, 2, 4, and 7 postinoculation and served as a control for bacterial replication. Open bar, day 1; black bar, day 2; stippled bar, day 4; striped bars, day 7. Results are reported as the means and standard errors for three replicates.

teria at each dilution, suggesting that this assay is more sensitive. This finding may be attributed in part to the inherent difficulty of accurately counting the number of bacteria in a three-dimensional cell when only one dimension is accessible. Thus, the traditional immunofluorescence staining method (IFA) may ultimately result in underestimation of the number of intracellular bacteria.

Due to the acidic nature of the intracellular environment in which *C. burnetii* resides, it has been difficult but critical to find drugs effective for the treatment of Q fever, especially chronic manifestations of infection. Several studies have been done to evaluate the effectiveness of a wide range of antibiotics against *C. burnetii* (11, 12, 15, 17). However, the shell vial assay used in those studies to determine the effectiveness of a specific antibiotic requires at least 6 days to determine the effect of antibiotic treatment on replication rates. The real-time PCR based assay described here provides an alternative method that can be used to rapidly evaluate the effectiveness of antibiotics against *C. burnetii*. Results can be obtained within 24 h after the completion of drug treatments. Our results indicate that *C. burnetii* Nine Mile, phase I, was susceptible to tetracycline and rifampin at concentrations of 4 μg/ml, which is in accordance with the results of a previous study (17). Our results also indicate that this strain was not susceptible to chloramphenicol at a concentration of 8 μg/ml or to ciprofloxacin at a concentration of 1 μg/ml, which is not in complete agreement with the results of the previous study (17). Previous work demonstrated that the efficacies of chloramphenicol and ciprofloxacin against *C. burnetii* varied (14, 17, 25, 26), depending on the dose, the culture model, and the *C. burnetii* strain used to test the antimicrobials. The ability of ampicillin to inhibit *C. burnetii* growth supports prior evidence presented by Suhan et al. (21) that *C. burnetii* Nine Mile, phase I, is susceptible to ampicillin at 50 μg/ml. At present, the recommended treatments for *C. burnetii* infections involve doxycycline for 2 weeks for acute infections and doxycycline plus chloroquine for at least 18 months for chronic infections. There are, however, several drawbacks to these treatments. Neither of these regimens has been proven to be bactericidal in vitro, and no reliable treatment is available for children and pregnant women (13). Therefore, it is important to continue to evaluate alternative treatments for Q fever. We propose that a real-time PCR-based approach to rapid screening of multiple antibiotic candidates is an appropriate alternative to the present methodology.

In conclusion, the real-time PCR assay described in this study provides a rapid and reliable way to quantify *C. burnetii* infectious units in tissue culture models. This assay offers several advantages over traditional staining techniques, including the elimination of subjectivity, reduced labor, and the ability to standardize reporting of results. In addition to studies that are screening potential antimicrobial agents, studies that use this assay to evaluate bactericidal host responses against *C. burnetii* are in progress.

ACKNOWLEDGMENTS

REFERENCES

1. Acar, J., E. Bergogne-Berezin, Y. Chabbert, R. Cluzel, A. Courtieu, P. Courvalin, H. Dabernat, H. Drugeon, J. Duval, J. P. Flandrois, J. Fleurette, F. Goldstein, M. Meyran, C. Morel, A. Philippon, J. Sirot, C. J. Soussy, A. Thabaut, and M. Verus. 1990. Communique du comitte de l'antibiogramme. Pathol. Biol. 38:749–752.
2. Brouqui, P., H. T. Dupont, M. Drancourt, Y. Berland, J. Etienne, C. Leport, F. Goldstein, P. Massip, M. Micoud, A. Bertrand, et al. 1993. Chronic Q fever: ninety-two cases from France, including 27 cases without endocarditis. Arch. Intern. Med. 153:642–648.
3. Dellacasagrande, J., C. Capo, D. Raoult, and J.-L. Mege. 1999. IFN-γ-mediated control of *Coxiella burnetii* survival in monocytes: the role of cell apoptosis and TNF. J. Immunol. 176:2259–2265.
4. Fink, L., W. Seeger, L. Ermert, J. Hanze, U. Stahl, F. Grimminger, W. Kummer, and R. M. Bohle. 1998. Real-time quantitative RT-PCR after laser-assisted cell picking. Nat. Med. 4:1329–1333.
5. Gikas, A., D. P. Kofteridis, A. Manios, J. Pediaditis, and Y. Tselentis. 2001. Newer macrolides as empiric treatment for acute Q fever infection. Antimicrob. Agents Chemother. 45:3644–3646.
6. Gikas, A., I. Spyridaki, A. Psaroulaki, D. Kofterithis, and Y. Tselentis. 2001. In vitro susceptibility of *Coxiella burnetii* to trovafloxacin in comparison with susceptibilities to pefloxacin, ciprofloxacin, ofloxacin, doxycycline, and clarithromycin. Antimicrob. Agents Chemother. 42:2747–2748.
7. Htwe, K. K., T. Yoshida, S. Hayashi, T. Miyake, K.-I. Amano, C. Morita, T. Yamaguchi, H. Fukushi, and K. Hirai. 1993. Prevalence of antibodies to *Coxiella burnetii* in Japan. J. Clin. Microbiol. 31:722–723.
8. Huebner, R. J., G. A. Hottle, and E. B. Robinson. 1948. Action of streptomycin in experimental infection with Q fever. Public Health Rep. 63:357–362.
9. Jackson, E. R. 1951. Comparative efficacy of several antibiotics on experimental rickettsial infections in embryonnated eggs. Antibiot. Chemother. 1:231–235.
10. Marrie, T. J., and D. Raoult. 1997. Q fever—a review and issues for the next century. Int. J. Antimicrob. Agents 8:145–161.
11. Maurin, M., A. M. Benoliel, P. Bongrand, and D. Raoult. 1992. Phagolysosomal alkalinization and the bactericidal effect of antibiotics: the *Coxiella burnetii* paradigm. J. Infect. Dis. 166:1097–1102.
12. Maurin, M., and D. Raoult. 1997. Bacteriostatic and bactericidal activity of levofloxacin against *Rickettsia rickettsii*, *Rickettsia conorii*, 'Israeli spotted fever group rickettsia' and *Coxiella burnetii*. J. Antimicrob. Chemother. 39:725–730.
13. Maurin, M. R., and D. Raoult. 1999. Q fever. Clin. Microbiol. Rev. 12:518–553.
14. Ormsbee, R. A., H. Parker, and E. G. Pickens. 1955. The comparative effectiveness of aureomycin, terramycin, chloramphenicol, erythromycin, and thiocymetin in suppressing experimental rickettsial infections in chick embryos. J. Infect. Dis. 96:162–167.
15. Raoult, D., M. Drancourt, and G. Vestris. 1990. Bactericidal effect of doxycycline associated with lysosomotropic agents on *Coxiella burnetii* in P388D1 cells. Antimicrob. Agents Chemother. 34:1512–1514.
16. Raoult, D., and T. Marrie. 1995. Q fever. Clin. Infect. Dis. 20:489–496.
17. Raoult, D., H. Torres, and M. Drancourt. 1991. Shell-vial assay: evaluation of a new technique for determining antibiotic susceptibility, tested in 13 isolates of *Coxiella burnetii*. Antimicrob. Agents Chemother. 35:2070–2077.
18. Samuel, J. E., M. E. Frazier, and L. P. Mallavia. 1985. Correlation of plasmid type and disease caused by *Coxiella burnetii*. Infect. Immun. 49:775–779.
19. Sawyers, L. A., D. B. Fishbein, and J. E. McDade. 1987. Q fever: current concepts. Rev. Infect. Dis. 9:935–946.
20. Stewart, R. D. 1997. Ph.D. dissertation. Kansas State University, Manhattan.
21. Suhan, M. L., C. Shu-Yin, and H. A. Thompson. 1996. Transformation of *Coxiella burnetii* to ampicillin resistance. J. Bacteriol. 178:2701–2708.
22. Whitten, K. W., R. E. Davis, and M. L. Peck. 1996. General chemistry. Harcourt Brace College Publishing, New York, N.Y.
23. Wike, D. A., G. Tallent, M. G. Peacock, and R. A. Ormsbee. 1972. Studies of the rickettsial plaque assay technique. Infect. Immun. 5:715–722.
24. Yeaman, M. R., and O. G. Baca. 1990. Antibiotic susceptibility of *Coxiella burnetii*, p. 213–223. In T. J. Marrie (ed.), Q fever. The disease, vol. 1. CRC Press, Boca Raton, Fla.
25. Yeaman, M. R., M. J. Roman, and O. G. Baca. 1989. Antibiotic susceptibilities of two *Coxiella burnetii* isolates implicated in distinct clinical syndromes. Antimicrob. Agents Chemother. 33:1052–1057.
26. Yeaman, M. R., L. A. Mitscher, and O. G. Baca. 1987. In vitro susceptibility of *Coxiella burnetii* to antibiotics, including several quinolones. Antimicrob. Agents Chemother. 31:1079–1084.
27. Zhang, G. Q., H. To, T. Yamaguchi, H. Fukushi, and K. Hirai. 1997. Differentiation of *Coxiella burnetii* by sequence analysis of the gene (*com*1) encoding a 27-kDa outer membrane protein. Microbiol. Immunol. 41:871–877.