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Rickettsioses in South Korea, Materials and Methods

To the Editor: We read with interest the article by Choi et al. (1), which describes the molecular detection of *Rickettsia typhi* and 4 spotted fever group rickettsiae by nested polymerase chain reaction (PCR) in the serum of febrile Korean patients. The value of the study, however, is limited by imprecision, inconsistencies, and the impossibility of verifying data. First, neither epidemiologic nor clinical data are provided for studied patients, although these are essential for interpreting PCR results. Second, multiplex nested PCR is hampered by a high risk of contamination (2). Alternatively, nested PCR techniques that use a closed assay or single-use primers without positive controls limit such a risk (3). In all cases, the use of negative controls is critical (2,3). In this study, negative controls are neither described in the Materials and Methods section nor shown on the gels. In addition, the authors used as positive controls 4 of the 5

Rickettsia species they detected. Therefore, apart from *R. felis*, which was not used as a positive control, positive products may result from cross-contamination. Finally, technically, the data are impossible to reproduce: 1) primer sets WJ77/80 and WJ79/83/78 cited in the legends of Figures 2 and 3 are neither described nor referenced in the text, 2) sequence of the RpCS.877p primer in Table 1 differs from that in the referenced article (4), 3) described sequences have not been deposited in GenBank, and 4) all *rompB* primers described in Table 1 exhibit 1–6 nucleotide mismatches with *ompB* sequences of at least 1 of the detected species. Based on these errors, the 7 cases of dual infections with *R. conorii* and *R. typhi*, which have never been reported before, are doubtful, and these data need to be confirmed.

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Rickettsioses in South Korea, Data Analysis

To the Editor: Choi et al. (1) conducted a study on sequence analysis of a partial *rompB* gene amplified from sera of humans who were seropositive for spotted fever group (SFG) and typhus group rickettsioses. They write, “These finding suggested that several kinds of rickettsial diseases, including boutonneuse fever, rickettsialpox, *R. felis* infection, and Japanese spotted fever... are occurring in Korea.”

These claims propagate some errors and may lead to an inadequate conclusion. First, *rompB* is conserved in *Rickettsia* spp. and consists of 4,968 bp with respect to the published sequence of the *R. conorii* strain Seven (2,3). Fournier et al. (4) amplified 4,682 bp of *rompB* and showed a high degree of nucleotide sequence similarity (99.2%) between *R. africae* and *R. sibirica*, *R. pakeri*, and *R. slovaca*. Choi et al. amplified ≈420 bp of *rompB* (position 3562–4077) for sequence analysis. This segment is located in a highly conserved region of the gene, which may decrease the ability to differentiate particular species from other SFG rickettsiae. This study cannot prove the existence of specific SFG rickettsioses until the results are confirmed further by, for example, isolating these SFG rickettsiae from humans, animals, or ticks in South Korea. Recently, the authors analyzed nucleotide sequences of 267-bp amplicons of *rompB* (position 4762–4496) obtained from patient sera and found that *R. conorii* could not be differentiated from *R. sibirica* (5). This finding also supports our concerns.

Second, although partial *rompB* nucleotide sequence analysis of rickettsiae obtained from 1 patient's serum showed 98.87% similarity with *R. conorii* strain Seven, the finding does not indicate boutonneuse fever is