

substantially lower case-fatality rate compared with classical RMSF (4,5,8–10). Other *Rickettsia* species could cause clinically similar diseases of varying severity and thereby account for historically recognized differences in severity described for RMSF in the western United States. Increasingly sensitive molecular detection methods, including mcfDNA sequencing, and access to expanding collections of whole genomes could aid in detection of otherwise unsuspected pathogens and contribute to a more nuanced understanding of SFGR epidemiology. Multidisciplinary partnerships among regional and federal health authorities, clinicians, and diagnostic laboratories led to recognition of *R. lanei* rickettsiosis in Oregon and could leverage identification of cases elsewhere. Clinicians should consider *R. lanei* when diagnosing patients with presumptive RMSF in the western United States, particularly in clinical scenarios that might appear unusual or atypical for classical RMSF.

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### About the Author

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### Correction: Vol. 31, No. 4

Some of the summary data included in Appendix 2 was incorrect in Foodborne Illness Acquired in the United States—Major Pathogens, 2019 (Elaine J. Scallan Walter et al.). The article has been corrected online ([https://wwwnc.cdc.gov/eid/article/31/4/24-0913\\_article](https://wwwnc.cdc.gov/eid/article/31/4/24-0913_article)).