Multigenotype Q Fever Outbreak, the Netherlands

To the Editor: Q fever is a zoonosis caused by Coxiella burnetii (1). An ongoing Q fever outbreak has occurred in the Netherlands since 2007; incidence rates have increased >50-fold compared with the baseline rate (2). The source of this outbreak is unknown. Identifying the source of an infection is complicated because of difficulties in obtaining sufficient clinical and/or environmental samples for testing. Molecular diagnosis of Q fever has focused on the use of serum samples. Up-to-date genotyping of C. burnetii has depended on cultivation and enrichment of the isolate before analysis (3). We report multiple-locus variable-number tandem repeat analysis (MLVA) typing of C. burnetii for a variety of human and animal clinical samples obtained from different locations in the Netherlands (Table).

Severe pneumonia developed in patient 1 after close contact with sheep (ewes) and intimate cuddling with a newborn lamb. Patients 2 and 3 (a dairy goat farmer and his wife from another village) tested positive for Q fever after a large part of their goat herd aborted offspring. The farmer had no clinical symptoms; his wife had mild symptoms that disappeared spontaneously within 2 days. No samples from any of the goats were available. Two additional patients were tested, 1 of which lived in the same village as patients 2 and 3.

Swab specimens from all sheep and lambs tested in the first case yielded identical MLVA genotypes. The same genotype was also found in patient 1 but not in the other examined samples, implicating sheep as the origin of patient 1’s infection. Although patients 2 and 3 lived together, the genotype found in patient 2 differed from the (partial) genotype found in patient 3. Yet another genotype was found in a patient from the same village (patient 4). However, an identical genotype found in patient 2 was found in a patient from a distant village (patient 5). The village had only 1 goat farm, and if this herd of goats was the source of infection for the farmer, his wife, and patient 4, it would have contained >1 genotype. At least 1 of the obtained genotypes has spread over a wider surface area in the Netherlands.

Our results show that the unprecedented, ongoing Q fever outbreak in the Netherlands involves multiple genotypes of C. burnetii. Because most of the genotypes differ only by a single repeat difference, they might represent microvariants of a hypervirulent strain that has been introduced in the Dutch animal population. MLVA schemes with up to 17 markers have been previously reported (3). In this “proof of concept” (applying direct genotyping of C. burnetii on clinical samples), we focused on the 3 shortest repeat units because we believed that these units might have the highest a priori chance of successful amplification in clinical samples (especially in serum/plasma). Similar genotypes as those reported here were found in the MLVA database (http://mlva.u-psud.fr), but these similarities need confirmation by using more markers. Although using only 3 markers may lead to poor discriminatory power, we were still able to distinguish 4 different genotypes in a relatively small collection of serum samples. We are currently exploring the use of additional MLVA markers.

Our results also show a poor correlation between DNA load and clinical symptoms. Multiple human and animal clinical samples, including serum and plasma, throat or genital swabs, or sputum and urine, may be useful for direct genotyping and outbreak source tracking.

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Letters

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References


Correlation between Buruli Ulcer and Vector-borne Notifiable Diseases, Victoria, Australia

To the Editor: Buruli ulcer (BU) is a destructive skin disease caused by the toxin-producing environmental pathogen Mycobacterium ulcerans. Since the 1980s, BU has emerged as a major public health problem in rural West and Central Africa (1), where some researchers have suggested a role for aquatic insects as either reservoirs or vectors of M. ulcerans (2,3). However, this hypothesis remains unproven (4).

In contrast to the emerging BU–endemic areas in tropical rural West Africa, the climate of the Australian state of Victoria is temperate, yet locally acquired BU also has increased there in recent years (5). In addition, notifications have varied markedly from year to year for reasons not yet explained.

During the investigation of a new outbreak of BU in Victoria, we demonstrated that M. ulcerans is detectable by PCR in mosquitoes and that being bitten by mosquitoes increases the odds of being diagnosed with BU (6,7). However, M. ulcerans–positive mosquitoes might reflect only the presence of M. ulcerans in the local environment and play no role in transmission. To further investigate links between BU and mosquitoes, we compared patterns of notifications of BU with other notifiable diseases in Victoria. In particular, we were interested in any association between BU and the locally transmitted vector-borne alphaviruses Ross River virus (RRV) and Barmah Forest virus (BFV). Areas of BU and RRV/BFV endemicity overlap geographically, but areas with RRV and BFV are more extensive and include inland river systems where BU has not so far been reported.