Initial Costs of Ebola Treatment Centers in the United States

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Academy (Table). Of these specimens, 12 (41%) were P1 type 1, 15 (52%) were P1 type 2a, and only 2 (7%) were P1 type 2c. A polycolonal distribution with 8 distinct MLV A types was observed, with the MLVA type M representing 11 (38%) of the identified MLVA types. Without the MPN1 marker, 3 MLVA types were observed. No macrolide resistance–associated mutation was detected, similar to what was observed in the 32 specimens collected in 2013. This finding is consistent with the low prevalence of macrolide resistance reported in northern Europe (6,7).

We report 2 outbreaks of M. pneumoniae infections that occurred in the first and last quarter of 2013 in western Russia (Smolensk region). Despite the high predominance of P1 type 1 strains reported in the recent literature (1,2,7), these 2 outbreaks, reported in semiclosed settings involved only the newly described P1 type 2c variant; 1 outbreak represented a monoclonal phenomenon. In the Smolensk region, the circulation of both type 1 and 2 strains was observed a few years before the outbreak; most of these strains were P1 type 2a variants, and only a minority were type 2c variants, suggesting that the new type 2c variant had spread throughout this region of Russia since at least 2006. In other parts of the world, a switch between type 1 and type 2 strains might be occurring. Indeed, in the United States, P1 type 1 isolates predominated before 2010 but dropped to 50% of isolates in 2013, and type 2 and type 2 variant strains increased (9). This cyclic pattern of type 1 or type 2 predominance in the population has previously been reported (10).

In conclusion, we detected no macrolide resistance in western Russia. The P1 type 2c variant spread throughout this region and can be responsible for monoclonal outbreaks. The epidemiologic monitoring of M. pneumoniae P1 types will assess the potential switch to P1 type 2 in the United States and other parts of the world and detect the possible emergence of the P1 type 2c variant. This study was supported by internal funding.

References


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To the Editor: The 2014–2015 outbreak of Ebola virus disease (EVD) in West Africa was unprecedented in scale and scope. During the outbreak, 11 patients with
EVD were cared for in the United States (1). Safely caring for patients with suspected EVD requires specialized protocols and training for hospital staff in the use of personal protective equipment (PPE) and isolation precautions (2,3). The care of a hospitalized patient with confirmed EVD in high-level isolation units requires large specialized teams of nurses, physicians, laboratory technologists, environmental service workers, and waste management specialists, and inpatient care may continue for weeks (3,4). The staff-to-patient ratio necessary to care for a patient with EVD in high-level isolation is much higher than that in a typical intensive care unit because of the extensive PPE used and the need for partners to assist with PPE donning and doffing.

In response to preparedness challenges in the United States, the Centers for Disease Control and Prevention recommended a multiterritorial framework of hospitals with advanced capabilities for Ebola care: frontline facilities, Ebola assessment hospitals, and Ebola treatment centers (ETCs) (2). Within this federal framework, 55 hospitals in the United States have been designated by their states as ETCs, which have the advanced capabilities required to provide medical care to patients with confirmed EVD throughout their illness (5). Although the cost of preparing these healthcare facilities to care for EVD patients was believed to be substantial (5–7), we aimed to directly survey ETCs to determine the costs incurred to prepare their facilities to manage and treat EVD patients.

In April 2015, we sent a 19-question electronic survey to all 55 ETCs, including the 3 preexisting biocontainment patient care units (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/22/2/15-1431-Techapp1.pdf). Participation was voluntary, and individual responses were confidential. The survey assessed the ETCs’ general expenses incurred by public and private public health organizations funded ETCs but were not included in this survey (8). The costs of EVD programs underscore the need for specialized

| Table. Initial costs in US$ incurred by 45 Ebola treatment centers in the United States* |
|-----------------------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| Cost scale | Total costs | Construction/ facility modifications | PPE supplies | Staff training | Unit planning | Laboratory equipment |
| Average | 1,197,993 | 420,502 | 213,347 | 267,075 | 176,713 | 99,106 |
| Median | 1,000,000 | 202,980 | 110,000 | 150,000 | 82,000 | 84,000 |
| High | 6,556,457 | 3,839,000 | 1,067,573 | 1,624,639 | 1,200,000 | 317,406 |
| Low | 51,500 | 8,500 | 10,000 | 10,000 | 0 | 3,000 |
| Sum† | 53,909,701 | 16,820,080 | 8,747,240 | 10,950,072 | 4,947,966 | 3,865,124 |

*PPE, personal protective equipment.
†Summarized data were collected through self-report by individual treatment centers through an electronically administered survey.
facilities to treat EVD (9,10). A tiered nationwide network of healthcare facilities that can rapidly identify, isolate, and treat patients with EVD has been established to improve the nation’s preparedness for EVD and can serve as a valuable resource for future outbreaks of other highly infectious diseases. Ongoing resources will be needed to sustain the readiness of such a network.

References


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Detection of Influenza D Virus among Swine and Cattle, Italy

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To the Editor: Recent studies have identified a new genus of the Orthomyxoviridae family (1–5). The virus, distantly related to human influenza C virus, has been provisionally designated as influenza D virus. This novel virus was identified for the first time in pigs with influenza-like illness (1), but subsequent serologic and virologic surveys have suggested cattle as a possible reservoir (2–4). Moreover, the virus was shown to infect ferrets used in laboratories as surrogates for humans when investigating influenza infection (1). In a serologic study conducted on 316 human samples, low antibody titers and a low level of positive samples (1.3%) were detected (1), suggesting that humans are a possible host to be studied in depth. To investigate the circulation of influenza D viruses among pigs and cattle in Italy, we performed molecular and virological tests on clinical samples collected from respiratory outbreaks in Po Valley, the area in Italy with the highest density of swine and cattle farms.

We screened clinical specimens from swine (n = 150) and cattle (n = 150) for influenza D virus by reverse transcription quantitative PCR (1). Three nasal swab samples were found positive: 1 from a sow and 2 from cattle, collected from 3 farms located at linear distances ranging from 47 to 80 km. All positive samples were confirmed by partial polymerase basic 1 gene sequencing and submitted to viral isolation in cell cultures as previously described (5,6). The virus was isolated on CACO-2 and HRT18 cell cultures only from the sow sample (D/swine/Italy/199723-3/2015). Cell cultures were tested by using reverse transcription quantitative PCR. Viral RNA was isolated from clinical samples or cell culture by using One-For-All Vet Kit (QIAGEN, Milan, Italy). Full-genome amplification from influenza D virus–positive samples was achieved as previously described (3). A sequencing library of the purified amplicons was prepared by using NEXTERA-XT kit and

1These authors contributed equally to this article.