Table. Virulence genes associated with *Corynebacterium ulcerans* present in strain RAH1 isolated from patient with diphtheria-like disease, 2013, United Kingdom*

Gene	Strains	Strain RAH1	Potential function
tox	0102	P	Diphtheria-like toxin
rbp	809	A	Shiga toxin–like ribosome binding protein
cpp	809, BR-AD22, 0102	P	Corynebacterial protease CP40, protective antigen against caseous lymphadenitis
pld	809, BR-AD22, 0102	P	Toxic phospholipase D
spaF	809, BR-AD22, 0102	P	Surface-anchored protein, pilus tip protein
spaE	809, BR-AD22, 0102	P	Surface-anchored protein, minor pilin subunit
spaD	809, BR-AD22, 0102	P	Surface-anchored protein, major pilin subunit
spaC	809, BR-AD22, 0102	P†	Surface-anchored protein, pilus tip protein
spaB	809, BR-AD22, 0102	P	Surface-anchored protein, minor pilin subunit
rpfI	809, BR-AD22, 0102	P	Resuscitation-promoting factor interacting protein
cwlH	809, BR-AD22, 0102	P	Cell wall–associated hydrolase
nanH	809, BR-AD22, 0102	P	Neuraminidase, glycosyl hydrolases
vsp1	809, BR-AD22	P	Venom serine protease
vsp2	809	P	Venom serine protease
tspA	809, BR-AD22	P	Trypsin-like serine protease

*P, present; A, absent.
†≈700 bp deletion.

of easy-to-handle bioinformatics tools emphasize the suitability of deep-sequencing technology for rapid diagnostics and for the development of high-resolution genotyping. It is time for the wider introduction of this technology into public health investigations.

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Death of Woman with Peripartum Influenza B Virus Infection and Necrotizing Pneumonia

To the Editor: Pregnant women are at increased risk for severe influenza-related complications (*1*). Bacterial pneumonia with Panton-Valentine leukocidin-producing (PVL) *Staphylococcus aureus* is infrequently described in the literature as occurring concurrently with influenza B virus infection (*2–4*). Additionally, only 2 occurrences of peripartum PVL-methicillin-resistant *S. aureus* (MRSA) pneumonia have been described (*5*,*6*). We report a case of influenza B virus and PVL-MRSA coinfection during pregnancy.

In December 2012, a previously healthy pregnant woman, 38 years of age, at 37 weeks' gestation and in active labor, sought treatment in a New York hospital reporting 2 days of fever, productive cough, shortness of breath, and pleuritic chest pain. Household contacts included children with influenza-like illness. The patient had declined influenza vaccination while receiving prenatal care. On arrival, examination showed that her temporal temperature was 101.6°F, blood pressure was 122/71 mm Hg, pulse was 121 beats per minute, respiratory rate was 40 breaths per minute, and oxygen saturation was 89% on room air; bilateral inspiratory crackles were heard on lung auscultation. Rapid influenza screening of a nasopharyngeal swab sample by using ELISA was negative for influenza A and B viruses. Culture of the patient's nares was positive for MRSA colonization. Laboratory evaluation showed leukopenia of 1500/mL, and although imaging was limited by the patient's lead apron, a chest radiograph demonstrated bibasilar opacities (Figure, panel A).

The differential diagnosis for this patient included influenza pneumonia, community-acquired pneumonia, and MRSA pneumonia; treatment with oseltamivir, ceftriaxone, vancomycin, and azithromycin was started. Because of impending respiratory failure, she was admitted to the Medical Intensive Care Unit where mechanical ventilation was initiated and she underwent a spontaneous vaginal delivery of a live male infant. The patient's condition deteriorated and progressed to severe acute respiratory distress syndrome with multiple organ failure and required substantial inotropic support. Subsequent laboratory studies showed the following results: leukocyte count 400/mL, lactate 4.2 mmol/L, pH 7.16, $PaCO_2$ 36 mm Hg, PaO_2 68 mm Hg, HCO_3 12 mmol/L, and oxygen saturation of 87% at 1.0 FiO_2. Repeat imaging demonstrated diffuse infiltrates in all lung fields (Figure, panel B). Because the patient responded poorly to treatment, vancomycin was discontinued and linezolid was started.

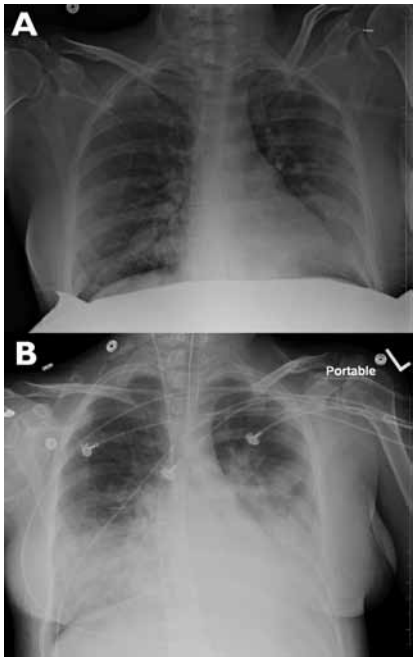

Figure. Course of influenza B virus infection and necrotizing pneumonia in peripartum woman, 2012, New York, USA. A) Chest radiograph at time of admission. B) Chest radiograph 1 day later, demonstrating progression of pneumonia.

Despite lung recruitment maneuvers and inhalation of nitric oxide, the patient remained hypoxemic. Extracorporeal membrane oxygenation was initiated and the patient was transferred to another institution.

After transfer, culture of 1 peripheral blood sample obtained at admission identified MRSA, and viral culture of the patient's nasal swab sample isolated influenza B virus. Genetic testing of the MRSA isolate identified a PVL-producing USA300 *spa*1 clone carrying staphylococcal cassette chromosome *mec* type IV. The patient died 2 weeks later from overwhelming sepsis. The neonatal course was notable for a birth weight of the infant of 2,825 g and Apgar scores of 5 and 8 at 1 and 5 minutes, respectively. He was intubated and transferred to the Neonatal Intensive Care Unit with an arterial cord blood pH of 6.78 and base deficit of 16 mmol/L. Nasal swab culture isolated methicillin-sensitive *S. aureus*. Viral culture of endotracheal aspirate was negative for influenza A and B viruses. Blood cultures were sterile. He received vancomycin for 1 week and was discharged home to the family on day 8 of life.

This case emphasizes the potential lethality of respiratory complications related to seasonal influenza. Colonization of the patient's nares with MRSA, possibly PVL-producing, may have predisposed her to a bacterial co-infection, consequentially increasing her risk for death from influenza (*1*). *S. aureus* clones USA300 and USA400 are emerging causes of community-acquired pneumonia in healthy adults and are leading to a rise in co-infections with influenza and MRSA. These 2 infections have been shown to act synergistically in animal models to induce a rapidly progressive necrotizing pneumonia associated with severe leukopenia (*7*). This is unlike classic secondary bacterial pneumonia, which typically occurs in a biphasic course with influenza (*2*).

Although methicillin susceptibility does not influence the mortality rate of PVL-*S. aureus* pneumonia (*8*), antibiotic drugs should be administered early and selection should reflect local resistance patterns. When making the diagnosis, physicians should recognize that the sensitivity of rapid influenza diagnostic tests is low and should not be relied on when a high level of clinical suspicion exists (*1*). Despite trivalent vaccine correspondence with circulating influenza B virus in 5 of 10 influenza seasons during 2001–2011 (*9*), vaccination against seasonal influenza is still the most effective way to prevent this potentially fatal condition. Availability of a quadrivalent influenza vaccination, introduced for the 2013–14 influenza season, should improve future incidence of influenza B virus infection. Because PVL-MRSA colonization is becoming more prevalent (*10*), necrotizing pneumonia must be considered in critically ill patients during influenza season.

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MERS-Related Betacoronavirus in *Vespertilio superans* Bats, China

To the Editor: Middle East respiratory syndrome coronavirus (MERS-CoV), a novel lineage C betacoronavirus, was first described in September 2012, and by April 16, 2014, the virus had caused 238 infections and 92 deaths in humans worldwide (*1*). Antibodies against MERS-CoV in dromedary camels were recently reported (*2*), as was the full genome of MERS-CoV from dromedary camels (*3*). Finding the natural reservoir of MERS-CoV is fundamental to our ability to control transmission of this virus to humans (*4*).

We report a novel lineage C betacoronavirus identified from *Vespertilio superans* bats in China. The full-length genome of this betacoronavirus showed close genetic relationship with MERS-CoV. Together with other evidence of MERS-CoV–related viruses in bats (*5–8*), our findings suggest that bats might be the natural reservoirs of MERS-related CoVs.

In June 2013, we collected anal swab samples from 32 *V. superans* bats from southwestern China. A small proportion of each sample was pooled (without barcoding) and processed by using virus particle–protected nucleic acid purification and sequence-independent PCR for next-generation sequencing analysis with the Illumina (Solexa) Genome Analyzer II (Illumina, San Diego, CA, USA). Redundant reads were filtered, as described (*9*), from the raw sequencing reads generated by the genome analyzer and then aligned with the nonredundant protein database of the National Center for Biotechnology Information (ftp://ftp.ncbi.nlm.nih.gov/blast/db/) by using BLAST (http://blast.ncbi.nlm.nih.gov). The taxonomy of these aligned reads was parsed by using MEGAN 4 (http://ab.inf.uni-tuebingen.de/software/megan/).

On the basis of the BLAST results, 8,751,354 sequence reads 81 nt in length were aligned with the protein sequences of the nonredundant protein database: 72,084 of the reads were uniquely matched with virus proteins. Of these 72,084 reads, 32,365 were assigned to the family *Coronaviridae*, primarily to lineage C of the genus *Betacoronavirus*, and found to share 60%–97% aa identity with MERS-CoV.

The MERS-CoV–related reads were extracted and assembled by using SeqMan software from the Lasergene 7.1.0 program (DNASTAR, Madison, WI, USA), resulting in a draft CoV genome. Reverse transcription PCR selective for the partial RNA-dependent RNA polymerase (RdRp) gene of this novel lineage C betacoronavirus suggested that 5 of the 32 samples (≈16%) were positive for the novel betacoronavirus, and the PCR amplicons shared >98% nt identity with each other. Using a set of overlapped nested PCRs and the rapid amplification of cDNA ends method, we determined the full-length genome of 1 strain of this *V. superans* bat–derived betacoronavirus (referred to as BtVs-BetaCoV/SC2013, GenBank accession no. KJ473821).

The betacoronavirus strain had a genome length of 30,413 nt, excluding the 3′poly (A) tails, and a G+C content of 43.1%. Pairwise genome sequence alignment, conducted by the EMBOSS Needle software (http://www.ebi.ac.uk/Tools/psa/emboss_needle/) with default parameters, suggested that the genome sequence of BtVs-BetaCoV/SC2013 showed 75.7% nt identity with that of human MERS-CoV (hCoV-MERS); this shared identity is higher than that for other lineage C betacoronaviruses (from bats and hedgehogs) with full genomes available. hCoV-MERS showed 69.9% nt identity with bat CoV (BtCoV) HKU4-1, 70.1%