Invasive meningococcal disease is usually defined by the occurrence of meningitis or sepsis. Pericarditis might occur during the course of invasive infection. This clinical picture, defined as disseminated meningococcal disease with pericarditis (1) or secondary meningococcal pericarditis, was reported in 1918 (2). In 1939, primary or isolated meningococcal pericarditis (1,3) was described. In this form of pericarditis, pericardial or blood cultures are positive for Neisseria meningitidis. This finetype has been reported in the United States meningococcal disease cases in Italy in 2015 (http://www.iss.it/). Serogroup C was associated with 53 (41%) of 132 invasive meningococcal disease cases. Multilocus sequence typing (MLST) and typing of Neisseria meningitidis ST increase was observed. A blood culture was positive for N. meningitidis. Whole-genome sequencing was conducted to obtain molecular data and enable comparison with other meningococci of the same serogroup that were isolated in Italy. Multilocus sequence typing (MLST) and typing of Neisseria meningitidis porA and fetA genes and Bexsero (meningococcal group B vaccine) antigen genes (http://www.fda.gov/Biologics BloodVaccines/Vaccines/ApprovedProducts/ucm431374.htm) were conducted as described (http://neisseria.org/). Whole-genome sequence was analyzed by using the BIGSdb Genome Comparator Tool (http://pubmlst.org/neisseria/). Genomes of meningococci belonging to the same type were compared by using the core genome MLST (cgMLST) approach.

The N. meningitidis strain was susceptible to all antimicrobial drugs tested. Although serogroup C was associated with 53 (41%) of 132 invasive meningococcal disease cases in Italy in 2015 (http://www.iss.it/binary/mabi/content/Report_MBI_20151223_v4.pdf), this serogroup has not been detected in Sardinia since 2010.

Molecular analyses showed that the strain belonged to the hypervirulent clonal complex (cc) 11, sequence type (ST) 11. The complete finetype was C:5–1,10–8:F3–6:ST-11(cc11). This finetype has been reported in the United States meningococcal disease cases in Italy in 2015 (http://www.iss.it/). Serogroup C was associated with 53 (41%) of 132 invasive meningococcal disease cases. Multilocus sequence typing (MLST) and typing of Neisseria meningitidis ST increase was observed. A blood culture was positive for N. meningitidis. Whole-genome sequencing was conducted to obtain molecular data and enable comparison with other meningococci of the same serogroup that were isolated in Italy. Multilocus sequence typing (MLST) and typing of Neisseria meningitidis porA and fetA genes and Bexsero (meningococcal group B vaccine) antigen genes (http://www.fda.gov/Biologics BloodVaccines/Vaccines/ApprovedProducts/ucm431374.htm) were conducted as described (http://neisseria.org/). Whole-genome sequence was analyzed by using the BIGSdb Genome Comparator Tool (http://pubmlst.org/neisseria/). Genomes of meningococci belonging to the same type were compared by using the core genome MLST (cgMLST) approach.

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States and several countries in Europe (7), including Italy, and is responsible for several disease outbreaks. In Italy, this finetype represents 61% (70/115) of all serogroup C strains collected during 2012–2015. Two outbreaks caused by this strain were reported in Italy in 2007 (8) and in 2012 (9). The N. meningitidis factor H binding protein and heparin binding protein alleles were 1.13 and 20, respectively. The N. meningitidis adhesin A variant had an insertion sequence that disrupted this gene, as described for ET-15 meningococci (10). On the basis of results of cgMLST, the strain was determined to be related to strains responsible for an outbreak in Italy in 2015.

In summary, we report a case of meningococcal pericarditis caused by a strain of N. meningitidis. This strain belongs to hyperinvasive clonal complex cc11 and was identified as C:P1.5–1,10–8:F3–6:ST-11(cc11), an emerging strain in Italy and worldwide. Timely diagnosis and complete molecular characterization of this strain, which causes a rare form of invasive disease (4), is needed for appropriate management of patients with this disease.

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Ecologic Study of Meningococcal B Vaccine and Neisseria gonorrhoeae Infection, Norway

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To the Editor: Gonorrhea is a sexually transmitted disease that can cause pelvic inflammatory disease, ectopic pregnancy, and salpingitis in women and infertility in men and women. Rates vary; incidence is 12.5 cases/100,000 population in Europe (1) and ≈6,000 cases/100,000 population in parts of sub-Saharan Africa (2). Recurrent infection is common, antimicrobial drug resistance is growing, and no licensed vaccine is available to protect against gonorrhea infection. Components of some meningococcal B (MenB) vaccines could provide protection against the causative bacterium, Neisseria gonorrhoeae (M. Pizza, pers. comm.), because the meningococcus bacterium is of the same Neisseria genus and the 2 bacteria share key protein antigens, such as the outer membrane vesicle (OMV). Ecologic evidence from Cuba supports a decline in gonococcus

*Now a GlaxoSmithKline company.