African swine fever (ASF) is an important disease of domestic pigs and wild boar. The disease is caused by African swine fever virus (ASFV). In 2014, ASFV was introduced into Eastern Europe, and it has since then continued to spread within various Eastern European countries. Investigating differences in sequences between ASFV isolates may be a valuable tool to understand differences in virulence among them, however currently, no complete genome sequences of the viruses responsible for the Eastern European outbreaks have been reported. In this study, the complete genome sequence of a highly virulent ASFV was determined directly from erythrocyte-associated nucleic acids obtained from a pig experimentally infected with an isolate from Poland (ASFV POL/2015/Podlaskie). The sequence (ca. 189 kb) of this recent European ASFV showed 95 nt differences (99.95 % identity) from the ASFV Georgia 2007/1 genome. The complete sequence of ASFV/POL/2015/Podlaskie should assist further studies on the genetic diversity and evolution of the European ASFVs.

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