Emerging Multidrug-Resistant Hybrid Pathotype Shiga Toxin–Producing
*Escherichia coli* O80 and Related Strains of Clonal Complex 165, Europe

**Technical Appendix**

**GenBank Accession Numbers**


Nucleotide sequences of the 36 sequenced O80 strains (complete nucleotide sequence of RDEx444 and 35 draft nucleotide sequences) have been deposited in Genbank: Project PRJNA449634 under accession numbers: QBCG00000000, QBCH00000000, QBCI00000000, QBCJ00000000, QBCK00000000, QBCL00000000, QBCM00000000, QBCN00000000, QBCO00000000, QBCP00000000, QBCQ00000000, QBCR00000000, QBCS00000000, QBCT00000000, QBCU00000000, QBCV00000000, QBCW00000000, QBCX00000000, QBCY00000000, QBCZ00000000, QBDA00000000, QBDB00000000, QBDC00000000, QBDD00000000, QBDE00000000, QBDF00000000, QBDG00000000, QBDH00000000, QBDI00000000, QBDJ00000000, QBDK00000000, QBDL00000000, QBDM00000000, QBDN00000000, QBDO00000000, QBDP00000000.
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Technical Appendix Figure 1. Phylogeny (maximum likelihood method) of 36 O80 E. coli isolated from various sources and European countries between 1998 and 2016. The highlighted strains carry the Shiga toxin genes and the subtype of Stx is indicated by a color code as follows: purple, stx1a; yellow, stx2a; pink, stx2dactivable; brown, stx1a2a; dark green, stx1a2b. The presence of the pS88 like-plasmid is represented using a plasmid scheme next to the strain number. The “R” to the right of the plasmid indicates that the strain possesses at least two resistance genes that confer resistance to betalactams, kanamycin, or cotrimoxazole. R*: additional extended spectrum betalactamase (ESBL) gene. R**: additional resistance to colistin (mcr-1 gene). The strain origin (country and source of isolation) is represented by flags and human/animal/water symbols. HPI: presence of chromosomal locus encoding the siderophore yersiniabactin, also called the High Pathogenicicity Island.
Technical Appendix Figure 2. Summary of complete sequencing data of the 36 O80 strains isolated in various European countries between 1998 and 2016. The strain origin (country and source of isolation) is represented by flags and human/animal/water symbols as in Figure 2. Clinical features are indicated as follows: HUS for hemolytic uremic syndrome, BD for bloody diarrhea, NA for not applicable (animal strains), UK for unknown, and C for healthy carrier. Gray boxes indicate the presence of resistance genes, virulence genes, or the presence of cryptic plasmids similar to pR444_B. Resistance genes are classified by antibiotic family: BL for betalactams, AS for aminoglycoside, SXT for cotrimoxazole, TET for tetracycline, CHL for phenicols, MCRL for macrolide, CT for colistin, and AN for nalidixic acid and numbers indicate the variant of the resistance genes. *variant bla_{CTX-M-1} of extended spectrum betalactamase (ESBL) gene. Bacteriocins are indicated in yellow and the type of virulence factor is indicated by a color code as follows: purple, toxin; green, adhesion factor; light purple, hemolysin; beige, protectin; pink, iron uptake system.