Supplementary information

Table S1. Ecology of Diabetic Foot Infections during the inclusion period of the study in Nîmes University Hospital

Microorganism(s)	N (%)	Multidrug-resistant bacteria* (%)
Aerobic Gram-positive cocci	327 (46.5)	
Staphylococcus aureus	162 (23.0)	28 (17.3)
Enterococcus faecalis	27 (3.8)	—
Other *Enterococcus*	3 (0.4)	—
Coagulase-negative Staphylococcus	57 (8.1)	—
Streptococcus spp.	78 (11.1)	—
Aerobic Gram-negative bacilli	203 (28.8)	
Enterobacteria	181 (25.7)	15 (8.3)
Escherichia coli	36 (5.1)	3 (8.3)
Proteus mirabilis	33 (4.7)	3 (9.1)
Enterobacter cloacae	30 (4.3)	4 (13.3)
Morganella morganii	27 (3.8)	2 (7.4)
Klebsiella oxytoca	14 (2.0)	1 (7.1)
Citrobacter spp.	13 (1.9)	1 (7.7)
Serratia spp.	11 (1.6)	1 (9.1)
Proteus spp.	7 (1.0)	—
Others	10 (3.2)	—
Stenotrophomonas maltophila	5 (0.7)	5 (100)
Pseudomonas spp.	7 (1.0)	3 (42.9)
Others	10 (3.2)	1 (10)
Gram positive aerobic bacilli	37 (5.3)	
Corynebacterium striatum	24 (3.4)	
Anaerobes	134 (19.0)	
Fungi	3 (0.4)	

*Multidrug resistant bacteria included methicillin-resistant *S. aureus*, *Enterobacteriaceae* resistant to third-generation cephalosporins, *P. aeruginosa* or *Acinetobacter baumannii* resistant to ceftazidime and *Stenotrophomonas maltophilia*.

Table S2. *Escherichia coli* toxin/antitoxin and virulence factors encoding ORF

Strain	Toxin/Antitoxin ORF	Other virulence ORF
NECS21	Toxin HokB (x2) Antitoxin Ccda Antitoxin HigA-2 (x3) Cytoskeleton-binding toxin CbtA (x2) Persistence and stress-resistance antitoxin PasI Ribosome association toxin RatA Toxin GhoT (x2) Antitoxin PrlF Toxin YhaV Toxin-antitoxin biofilm protein TabA (x3) Antitoxin ChpS Antitoxin RelB	Glutamate decarboxylase (x2) Salmonella HilA homolog Enteroaggregative immunoglobuline repeat protein Long polar fimbriae
NECS50	Toxin HokB (x2) Antitoxin Ccda Antitoxin HigA-2 (x3) Cytoskeleton-binding toxin CbtA (x2) Persistence and stress-resistance antitoxin PasI Ribosome association toxin RatA Toxin GhoT (x2) Antitoxin PrlF Toxin YhaV Toxin-antitoxin biofilm protein TabA (x3) Antitoxin ChpS Antitoxin RelB	Glutamate decarboxylase (x2) Salmonella HilA homolog Enteroaggregative immunoglobuline repeat protein Long polar fimbriae
NECR70	Toxin HokB (x2) Antitoxin HigA-2 (x2) Cytoskeleton-binding toxin CbtA (x2) Persistence and stress-resistance antitoxin PasI	Glutamate decarboxylase Salmonella HilA homolog Enteroaggregative immunoglobuline repeat protein

	Ribosome association toxin RatA Toxin GhoT (x2) Antitoxin PrlF Toxin YhaV Toxin-antitoxin biofilm protein TabA (x2) Antitoxin MqSA	Long polar fimbriae
NECR107	Toxin HokB (x2) Antitoxin HigA-2 (x2) Cytoskeleton-binding toxin CbtA (x2) Persistence and stress-resistance antitoxin PasI Ribosome association toxin RatA Toxin GhoT (x2) Antitoxin PrlF Toxin YhaV Toxin-antitoxin biofilm protein TabA (x2) Antitoxin MqSA	Glutamate decarboxylase (x2) Salmonella HilA homolog Enteroaggregative immunoglobuline repeat protein Long polar fimbriae

Table S3. Effect of single-nucleotide polymorphism on the *Escherichia coli* strain firstly isolated.

		High effect		Moderate effect	Low effect
Strain	**SNP**	**Start lost**	**Stop gained**	**Missense**	**Synonymous**
NECS21	1,764 (1,277 genes)	1 (1 gene)	29 (22 genes)	561 (127 genes)	472 (121 genes)
NECR70	6,874 (2,198 genes)	6 (6 genes)	132 (99 genes)	2,721 (373 genes)	2,155 (358 genes)

Numbers represent the count of identified single-nucleotide polymorphism