different spatiotemporal dominance of SARS-CoV-2 variants; vaccination status of HCWs, considering lower efficacy of vaccines against Omicron (*9*); and different infection control measures applied among hospitals (*10*). Furthermore, the surveillance study we report was not a randomized controlled trial, does not provide data on asymptomatic courses or rates of false positive PCR results, nor does it provide detailed information regarding seroprevalence or symptoms that developed.

The finding that physicians and nurses who were at the frontline of the COVID-19 outbreak response at Klinikum Nürnberg were not overrepresented in infection numbers speaks in favor of an efficient hygiene regimen. Besides measures such as compulsory patient screening, high-quality protective equipment, or regular ventilation, we believe that effective identification of asymptomatic HCWs in a preinfectious status might be one cornerstone of SARS-CoV-2 infection prevention in hospitals.

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Six Extensively Drug-Resistant Bacteria in an Injured Soldier, Ukraine

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Blood and surveillance cultures from an injured service member from Ukraine grew *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Enterococcus faecium*, and 3 distinct *Pseudomonas aeruginosa* strains. Isolates were nonsusceptible to most antibiotics and carried an array of antibiotic resistant genes, including carbapenemases (bla_{IMP-1}, bla_{NDM-1}, bla_{OXA-23}, bla_{OXA-48}, bla_{OXA-72}) and 16S methyltransferases (*armA* and *rmtB4*).

The ongiong conflict in Ukraine has placed extraordinary pressure on medical infrastructure and health delivery services in the region (*1*). Previous reports from Eastern Ukraine have noted the emergence of multidrug-resistant (MDR) *Acinetobacter baumanii*, *Pseudomonas aeruginosa*, and Enterobacterales infections during hospitalization (*2*). Those strains encompassed a variety of clonal lineages, with many carrying carbapenemases, extended-spectrum β-lactamases (ESBLs), and 16S methyltransferases (*2*,*3*). We describe the isolation of 6 extensively drug-resistant (XDR) organisms from a single soldier from Ukraine.

A man in his mid-50s suffered multiple traumatic injuries after a vehicle fire, including full-thickness burns covering 60% of his total body surface. He was initially treated in a medical facility near Dnipro, Ukraine, before being transferred to a hospital in Kyiv, Ukraine, where healthcare practitioners performed burn wound debridement and escharotomies. Thereafter, the patient was transported to a US military hospital in Germany, where doctors obtained blood, urine, respiratory, and peri-rectal surveillance cultures. Surveillance cultures grew *A. baumannii*, *Enterococcus faecium*, *Klebsiella pneumoniae,* and 2 distinct morphologies of *P. aeruginosa*. Blood cultures grew a third *P. aeruginosa* (Table). By using the Vitek 2 automated system (bioMérieux, https://www.biomerieux.com), the gram-negative organisms were found to be nonsusceptible to almost every antibiotic tested (Appendix Table 1, https://wwwwnc.cdc.gov/EID/article/29/8/23-0567-App1.pdf), with the exception of *A. baumannii*, which was susceptible to tetracycline (MIC 2 μg/mL). The *E. faecium* was nonsusceptible to vancomycin. Researchers used a customized Sensititer panel (Thermo Scientific, https://www.thermofisher.com) to test the gram-negative organisms against colistin, eravacycline, imipenem/relebactam, meropenem/vaborbactam, omadacycline, and plazomicin; they used disk diffusion (Hardy Diagnostics, https://hardydiagnostics.com) to test against cefiderocol (Appendix Table 1). Researchers performed whole-genome sequencing of all isolates by using an Illumina Miseq and the MiSeq Reagent Kit version 3 (600 cycles, 2 × 300 bp) (Illumina, https://www.illumina.com).

The *K. pneumoniae* isolate, designated MRSN 110821, was nonsusceptible to every antibiotic tested (Appendix Table 1). Testing identified 24 antimicrobial resistance genes, including the carbapenemases bla_{NDM-1} and bla_{OXA-48}, the RMTase *armA*, and the ESBL $bla_{CTX-M-15}$ (Table). Five plasmid replicons were identified (Appendix Table 2), but long-read sequencing is underway to better understand the plasmid structure (data not shown). Colistin resistance likely resulted from a previously characterized E82K mutation in the 2-component transcriptional regulator PhoP (*4*). Cefiderocol resistance could be linked to mutations in the outer membrane protein OmpK36 combined with NDM (*5*). The isolate also carried several hypervirulence genetic markers, including *ybt*16 (yersiniabactin siderophore), *iuc*1 (aerobactin), and *rmpADC*/*rmpA2* (mucoviscosity and capsule).

The isolate belonged to clade B1 of the clonal lineage sequence type (ST) 395 (*6*) and was K-antigen capsular biosynthesis loci, K39, and O-antigen

Table. Characteristics of 6 isolates cultured from an injured service member from Ukraine*

MRSN ID	Species	ST†	Antimicrobial resistance genes‡
110819	*Acinetobacter baumannii*	78	*aph(3')-Via*, *aac(6')-Ian*, ***armA***, *aadA5*, *ant(3'')-IIa*, ***bla*$_{OXA-23}$**, ***bla*$_{OXA-72}$**, bla_{OXA-90}, $bla_{ADC-152}$, ***bla*$_{CTX-M-115}$**, $bla_{CARB-16}$, *catA1*, *mph(E)*, *msr(E)*, *sul1*, *sul2*
110818	*Pseudomonas aeruginosa*	357	*aac(6')-II*, *aph(3')-IIb*, *aadA1*, bla_{OXA-10}, $bla_{OXA-846}$, bla_{PDC-11}, ***bla*$_{VEB-9}$**, *catB7*, *sul1*, *tet(A)*, *dfrB2*
110817	*P. aeruginosa*	773	*aph(3')-IIb*, *aadA11*, ***bla*$_{NDM-1}$**, bla_{PDC-16}, $bla_{OXA-395}$, *catB7*, *qnrVC1*, ***rmtB4***, *sul1*, *tet(G)*
110606§	*P. aeruginosa*	1047	*aac(6')-Ib3*, *aph(3')-IIb*, *aph(3'')-Ib*, *aph(6)-Id*, ***bla*$_{IMP-1}$**, bla_{OXA-10}, $bla_{OXA-488}$, bla_{PDC-12}, *catB7*, *sul1*
110821	*Klebsiella pneumoniae*	395	*aac(6')-Ib-cr5*, *aph(3')-VI*, *ant(2'')-Ia*, *aadA1*, ***armA***, ***bla*$_{NDM-1}$**, ***bla*$_{OXA-48}$**, ***bla*$_{CTX-M-15}$**, bla_{OXA-1}, bla_{SHV-11}, bla_{TEM-1}, *catA1*, *dfrA1*, *dfrA5*, *fosA*, *mph(A)*, *mph(E)*, *msr(E)*, *oqxA*, *oqxB*, *qnrS1*, *sul1*, *sul2*, *tet(A)*
110820	*Enterococcus faecium*	117	*aac(6')-Ie*, *aacA-ENT1*, *aph(2'')-Ia*, *catA7*, *dfrG*, *erm(B)*, *msr(C)*, ***vanA*** (operon)

*Bold indicates high-impact genes. MRSN, The Multidrug-Resistant Organism Repository and Surveillance Network; ID, identification; ST, sequence type.
† **In silico**–derived multilocus STs.
‡**In silico**–derived antimicrobial resistance gene content generated using MIGHT, a customized script wrapping ARIBA (https://github.com/sanger-pathogens/ariba) and AMRfinder (https://github.com/ncbi/amr).
§Blood culture isolate.

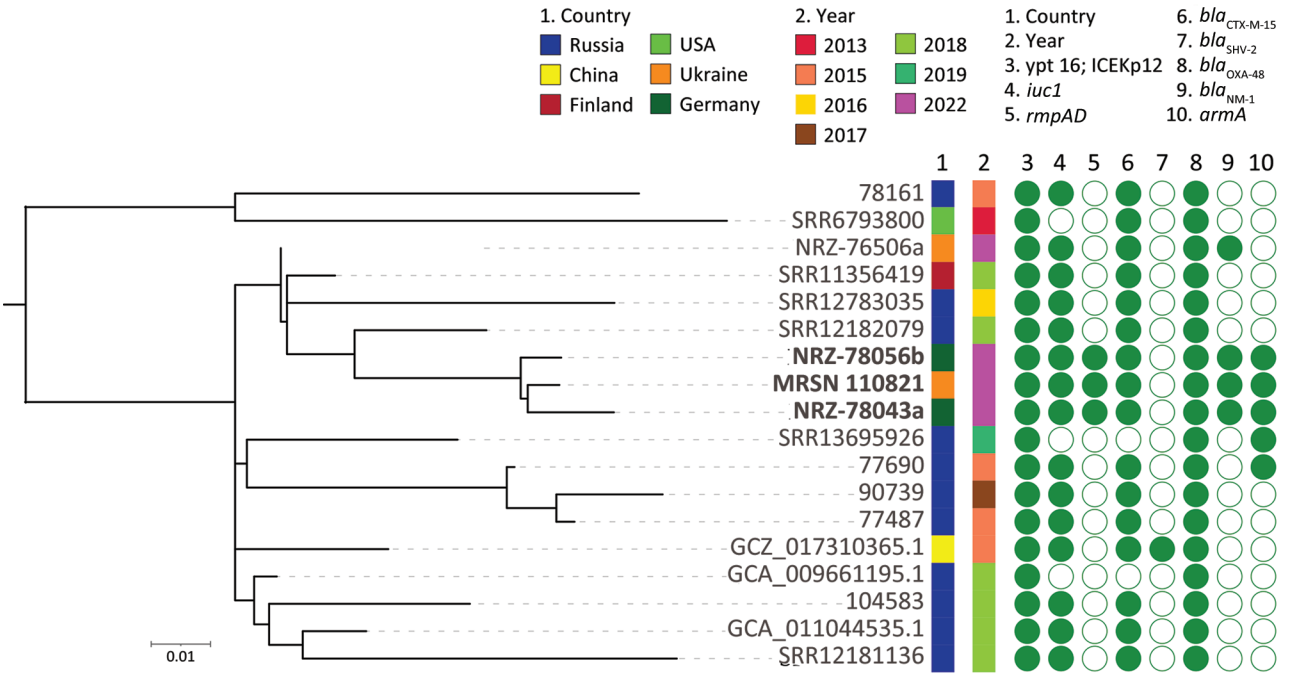

Figure. Core genome, SNP-based phylogenetic tree for *Klebsiella pneumoniae* from an injured service member from Ukraine (MRSN 110821) and 17 closely related sequence type 395 *K. pneumoniae*. In addition to MRSN 110821, the dataset included 14 subclade B2 isolates and 3 NDM-1/OXA-48–producing isolates available in public databases. Country of origin, year of collection, and presence (closed circle) or absence (open circle) of selected virulence and antimicrobial resistance genes are indicated. The midpoint was used as a root for the phylogenetic tree. *K. pneumoniae* MRSN 110821 from this study and the 2 highly related strains from Germany are highlighted in boldface. Scale bar indicates the ratio of substitutions per site for a 1,665 bp alignment of variable sites in the core genomes of the 18 strains.

type O2 variant 1 (O2v1). ST395 was first described in France in 2010, and carbapenemase-producing strains are increasingly being reported across Europe (*6*). We downloaded all clade B1 ST395 isolates from Pathogenwatch (https://pathogen.watch) and constructed a phylogenetic tree (Figure). We included 3 ST395 genomes identified by Sandfort et al, which they cultured from patients from Ukraine who were hospitalized in Germany (*7*). Of note, MRSN 110821 was separated by just 20 single nucleotide polymorphisms from NRZ-78043a from the Sandfort study and by just 19 from NRZ-78056b from that same study (Figure). Those 3 isolates clustered more broadly with isolates from Russia and Finland (Figure), but have since acquired *armA*, $bla_{\text{NDM-1}}$, and the mucoviscosity and capsule loci *rmpADC*, further increasing their antibiotic resistance profile and virulence potential.

We found *A. baumannii* MRSN 110819 to be resistant to all antibiotics except cefiderocol, colistin, eravacycline, and omadacycline (Appendix Table 1). The isolate carried 18 AMR genes, including the RMTase *armA*, the ESBL $bla_{\text{CTX-M-115}}$, and 2 carbapenemases, $bla_{\text{OXA-23}}$ and $bla_{\text{OXA-72}}$ (Table). The isolate was assigned to ST78, a clonal group known as the Italian clone because it emerged in Italy in the mid-2000s (*8*). This clonal group has also been identified in war wounds of service members from Ukraine during the earlier conflict in Eastern Ukraine (*2*).

The 3 *P. aeruginosa* isolates belonged to 3 distinct strains (Table). All 3 isolates had high MICs to 20 of the 23 antibiotics tested (Appendix Table 1). Only colistin and cefiderocol appeared effective in vitro, although MRSN 110818 was susceptible to imipenem/relebactam using US Food and Drug Administration breakpoints (MIC 2 mg/L). All 3 carried carbapenemases, ESBLs, and 16S methyltransferases (Table). MRSN 110818 and 110817 belonged to well-known (ST357) and emerging (ST773) epidemic, high-risk clones that are increasingly associated with horizontally acquired β-lactamases (*9*). The single blood isolate was assigned to ST1047.

E. faecium MRSN 110820 carried 8 AMR genes, including the *vanA* operon (Table). The strain was assigned to ST117, a member of clonal complex 78.

Gaps in such services as infection control, caused by limited resources and personnel, are

exacerbating the transmission of MDR organisms in Ukraine. As a result, healthcare networks in Europe now consider prior hospitalization in Ukraine to be a critical risk factor for colonization of MDR organisms (*7*,*10*). Healthcare practitioners treating citizens of Ukraine need to be cognizant of the increased risk for MDR organism transmission and infection imposed by the conflict in Ukraine and implement appropriate infection control measures to mitigate their spread.

Isolates for this study were collected under the auspices of routine public health surveillance. Sequences have been deposited into GenBank (BioProject nos. PRJNA950448, PRJNA950449, PRJNA950450, and PRJNA950451). The Multidrug-Resistant Organism Repository and Surveillance Network (MRSN) is a department within Walter Reed Army Institute of Research's Bacterial Diseases Branch, a unique entity that serves as the primary surveillance organization for antibiotic-resistant bacteria across the Army, Navy, and Air Force.

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Six Extensively Drug-Resistant Bacteria in an Injured Soldier, Ukraine

Appendix

Appendix Table 1. Antibiotic susceptibility data*

	MIC†				
	110606	**110817**	**110818**	**110819**	**110821**
Antibiotic	**PSA**	**PSA**	**PSA**	**ACB**	**KPN**
Amikacin	≥64	≥64	32	NA	≥64
Gentamicin	≥16	≥16	8	≥16	≥16
Tobramycin	≥16	≥16	≥16	≥16	≥16
Ampicillin/Sulbactam	NA	NA	NA	≥32	≥32
Cefazolin	≥64	≥64	≥64	≥64	≥64
Cefepime	≥32	≥32	≥32	NA	≥32
Cefotaxime	NA	NA	NA	≥64	≥64
Ceftazidime	≥64	≥64	≥64	≥64	≥64
Ceftazidime/Avibactam	>32	>32	32	32	>32
Ceftolozane/Tazobactam	>8	>8	>8	>8	>8
Imipenem	≥16	≥16	≥16	≥16	≥16
Meropenem	≥16	≥16	≥16	≥16	≥16
Piperacillin/Tazobactam	≥128	≥128	≥128	NA	≥128
Ticarcillin/Clavulanic Acid	≥128	≥128	≥128	NA	NA
Ciprofloxacin	≥4	≥4	≥4	≥4	≥4
Levofloxacin	≥8	≥8	≥8	4	≥8
Tetracycline	NA	NA	NA	2	≥16
Trimethoprim/Sulfameth	NA	NA	NA	≥320	≥320
Colisitin	2	1	1	≤0.25	16
Eravacycline	>8	8	>8	0.25	4
Imipenem	>16	>16	16	>16	>16
Imipenem/Relebactam	>16	>16	2	>16	>16
Meropenem	>8	>8	>8	>8	>8
Meropenem/Vaborbactam	>16	>16	8	>16	>6
Omadacycline	>8	>8	>8	2	>8
Plazomicin	>4	>4	4	>4	>4
Cefiderocol‡	20	21	24	20	8

* PSA, Pseudomonas aeruginosa; ACB, Acinetobacter baumannii, KPN, *Klebsiella pneumoniae*
† Interpretation is based on CLSI (2020) where available. Blue, Resistant; Yellow, Intermediate; Green, susceptible; Orange, Not Interpretable
‡ Performed by Disk diffusion; Results are the Zone of Inhibition expressed in millimeters (mm)

Appendix Table 2. Basic genomic data of Gram-negative strains in this study

MRSN ID	Species	Genome size (Mb)	%G/C	Plasmid Replicons*
110819	*A. baumannii*	3.96	38.9	None
110818	*P. aeruginosa*	6.51	66.0	None
110817	*P. aeruginosa*	6.63	66.1	None
110606	*P. aeruginosa*	6.7	65.9	None
110821	*K. pneumoniae*	5.49	56.7	Col440II, ColRNAI, IncFIB, IncHI1B, IncR

* Plasmid replicons detected using the Plasmid Finder tool (https://bio.tools/PlasmidFinder).
"None" indicates that no replicons present in the database were detected in the strains.