

AKADÉMIAI KIADÓ

European Journal of
Microbiology and
Immunology

14 (2024) 4, 309–332

DOI:


10.1556/1886.2024.00093

© 2024 The Author(s)

ORIGINAL RESEARCH
PAPER



Spatial and temporal dynamics of the prevalence of resistance genes and gastrointestinal pathogens in stool samples of German deployment returnees

Vanessa Navabi¹, Dorothea Franziska Wiemer², Matthias Halfter², Ulrich Müseler³, Susann Dupke⁴, Anja Petrov-Salzwedel⁵, Ulrich Schotte⁵ and Hagen Frickmann^{1,6*} 

¹ Department of Microbiology and Hospital Hygiene, Bundeswehr Hospital Hamburg, Hamburg, Germany

² Infectious Disease and Tropical Medicine Department, Bundeswehr Hospital Hamburg, Hamburg, Germany

³ Medical Service, German Federal Police, Potsdam, Germany

⁴ Centre for Biological Threats and Special Pathogens/Highly Pathogenic Microorganisms, Robert Koch Institute, Berlin, Germany

⁵ Department A—Veterinary Medicine, Central Institute of the Bundeswehr Medical Service Kiel, Kronshagen, Germany

⁶ Institute for Medical Microbiology, Virology and Hygiene, University Medicine Rostock, 18057 Rostock, Germany

Received: August 27, 2024 • Accepted: October 6, 2024

Published online: October 29, 2024

ABSTRACT

Background: The exploratory study assessed trends in the abundance of CTX-M-type extended spectrum beta-lactamase (ESBL) and vancomycin-resistance genes *vanA* and *vanB* in the stool samples of German soldiers and police officers returning from predominantly tropical deployments next to the common diarrheagenic *Escherichia (E.) coli* pathovars enteropathogenic *Escherichia coli* (EPEC), enterotoxigenic *E. coli* (ETEC) and enteroaggregative *E. coli* (EAEC) as well as rarely imported *Vibrio* spp. between 2006 and 2024. **Methods:** Surveillance was performed applying real-time polymerase chain reaction and results were stratified by World Health Organization region of deployment as well as by deployment period. For the latter, the study interval was divided into three pre-COVID-19-pandemic periods, the COVID-19-pandemic period and the post-COVID-19-pandemic period. Averaged prevalences were used as references. **Results:** In stool samples of 1817 deployed German soldiers and 117 police officers, averaged prevalences were 47.9% and 24.8% for the ESBL-type beta-lactamase *bla*_{CTX-M}, 30.2% and 14.5% for *vanB*, 9.0% and 17.9% for EPEC, 3.4% and 12.8% for ETEC, 4.0% and 3.4% for EAEC as well as 2.0% and 3.4% for *Vibrio* spp., respectively. While resistance genes peaked during early deployments, maximum prevalences for enteropathogens were seen later. **Conclusions:** The assessment suggested time- and region-dependence of the assessed parameters.

KEYWORDS

antimicrobial resistance, military, police, surveillance, colonization

INTRODUCTION

As defined by the World Health Organization (WHO) [1], antimicrobial resistance is “one of the top global health and development threats”. Historically, the military as well as military

*Corresponding author. Department of Microbiology and Hospital Hygiene, Bundeswehr Hospital Hamburg, Bernhard-Nocht-Str. 74, 20359 Hamburg, Germany.
E-mail: Frickmann@bnitm.de

deployments have a relevant share in the acquisition, import and spread of microorganisms showing increased antimicrobial resistance (AMR) [2]. The relevance and dimension of the topic was early recognized by the US American armed forces in response to the experience of their military engagement in the Middle East and led to the implementation of a well-funded large-scale network-based multi-drug-resistance surveillance campaign called “Antimicrobial Resistance Monitoring and Research Program” more than 10 years ago [3, 4]. Also, large-scale molecular epidemiological assessments of resistant bacterial isolates based on next generation sequencing were early established by the US armed forces medical service [5].

Focusing on the situation in German soldiers, a previous culture-based AMR surveillance approach for German soldiers during post-deployment medical assessments [6, 7] has so far only shown low to moderate enteric colonization rates with ESBL-positive *Escherichia coli*. ESBL prevalence was unevenly distributed. In particular, deployment to tropical high endemicity settings and living under the local conditions of the deployment site, e.g., in case of United Nations (UN) observers, were observed as risk factors for increased prevalence compared to other deployment settings. Apart of ESBL-positive Enterobacterales, enteric colonization with vancomycin-resistant enterococci was found to be virtually negligible in German soldiers after their return from deployment in the culture-based approach [6].

In contrast to these previous works [6, 7], the presentation of molecular AMR surveillance results in stool samples of German deployment returnees was the aim of the here presented study. Thereby, the focus was on CTX-M-type ESBL genes, which were shown to be the major and predominant cause of third generation cephalosporin-resistance in Enterobacterales previously isolated from German deployment returnees [7], and the *vanA* and *vanB* genes as molecular markers for vancomycin-resistant enterococci. CTX-M-type ESBL beta-lactamases are the quantitatively dominating molecular determinants of ESBL-type beta-lactam resistance, which made them of interest for the here-described assessment. Thereby, the “CTX” element of the abbreviation stands for the third-generation cephalosporine ceftriaxone, which is a marker substance for ESBL-type resistance, while the letter “M” stands for the town Munich as the place of its first description [8]. The above-mentioned *van* genes mediate glycopeptide resistance and the acronym “van” stands for vancomycin, a glycopeptide drug commonly used for the treatment of several severe human infections with Gram-positive bacteria. In particular, *vanA* and *vanB* genes can occur in the enterococcal species *E. faecalis* and *E. faecium*, which are the enterococci most frequently associated with infections in human patients. This is why the genes were considered as interesting for the here-provided assessment. As detailed elsewhere, both ESBL-positive Enterobacterales and vancomycin-resistant enterococci are harmless in case of mere enteric colonization but can cause difficult-to-manage infections in case of translocation to sterile compartments [7, 9]. Such infections can comprise bacteremia and even sepsis but also urinary

tract infections due to both Enterobacterales and enterococci, less frequently, also infections of primarily sterile compartments like joints or cardiac valves [7, 9]. While young, healthy and immunocompetent soldiers are rarely affected apart from injury- or war wound-induced translocation risks to primarily non-sterile body compartments, increased infection risks may result from transmission events to severely ill and immunosuppressed individuals in close contact with colonized soldiers. Difficult-to-treat infections can then arise if causative bacterial agents are associated with genes associated with reduced susceptibility towards commonly used antibiotic drugs.

For beta-lactamase genes [10] and even more for vancomycin resistance-associated genes [9], previous studies had shown superior sensitivity of PCR compared to traditional culture-based detection with partly considerable influence of pre-analytic conditions. Molecular AMR detections were associated with WHO regions of deployment and colonization dynamics along the timeline were assessed. Special situations like the period of the COVID-19 pandemic were also considered, because a previous assessment by our group had suggested likely effects of associated infection prevention and control protocol enforcement on the occurrence of infectious gastroenteritis and thus on the fecal-oral transmission route in deployed soldiers [11]. From Germany as the home country of the deployed soldiers and police officers, reliable surveillance data on the abundance of CTX-M-type ESBL, *vanA* and *vanB* genes in stool samples of healthy individuals are not available. This makes specific risk assessments focusing on these parameters unfeasible so far.

For comparison purposes, results of the molecular detection dynamics of frequent and rare gastrointestinal pathogens were used. This was done to assess whether colonization with resistant bacteria shows comparable or discrepant prevalence patterns compared to infections with enteric pathogens on deployment. As pathogens frequently detected in the gut of deployed soldiers, not only in the United Kingdom (UK) [12] and in the USA [13–16] but also in Germany [17], enteropathogenic (EPEC), enterotoxigenic (ETEC) and enteroaggregative (EAEC) *E. coli* were chosen. EPEC and EAEC were primarily included as indicators of poor hygiene conditions. As detailed elsewhere [18], EPEC attaches on intestinal epithelial cells and causes lesions there associated with clinical diarrhea. However, EPEC-induced clinically apparent diarrhea primarily occurs in children, while adults are usually asymptotically colonized. EAEC [18] is characterized by the expression of aggregative adherence fimbriae, facilitating aggregative adhesion on enterocytes. EAEC’s etiological relevance for travelers’ diarrhea has recently been controversially debated, because a large-sized epidemiological study has shown virtually indistinguishable proportions of diarrhea in individuals with and without EAEC detections in their stool samples [19]. ETEC expresses genes coding for heat-stable and heat-labile enterotoxins [18] and is considered as a major cause of travelers’ diarrhea. In contrast to the frequently detected *E. coli* described above, *Vibrio* spp. were rarely reported in



stool samples of soldiers apart from outbreak scenarios [20, 21] in spite of the introduction of cholera in Haiti by UN peacekeepers more than a decade ago [22] and also in spite of the undeniable historic relevance of *Vibrio* spp. in previous armed conflicts like, e.g., the American Civil War [23]. Only round about a dozen among about 100 described *Vibrio* species are of medical relevance for human individuals. Toxin-expressing *Vibrio cholerae* isolates causes cholera, a life-threatening disease associated with diarrhea-associated massive loss of water. Non-cholera *Vibrio* spp. with etiological relevance for human individuals like *Vibrio haemolyticus*, *Vibrio alginolyticus* and *Vibrio vulnificus* can cause diarrhea as well. In case of *V. vulnificus*, however, severe wound infections with the potential of progression towards life-threatening systemic infections are considered as the more troublesome consequence of an infection [24].

In Germany as the home country of the deployed soldiers and police officers, prevalence for EPEC, ETEC, EAEC is not systematically assessed by surveillance programs. For *Vibrio* spp., only cases of cholera are obligatorily recorded with few imported cases per year in Germany [25]. These enteric pathogen-based control groups were added to evaluate a potential differential influence of the impact of periods of aggravated infection prevention and control schemes, e.g., during the COVID-19 pandemic, on the abundance of enteric pathogens and on the enteric resistance. As mentioned above, the COVID-19-pandemic was included as a separate stratum, because a previous assessment had indicated a reduced number of diarrhea events in deployed German soldiers during this period [11]. This finding suggests a potential impact of the pandemic-related enforcement of stricter infection prevention and control procedures on fecal-oral transmission events among deployed soldiers, an effect which could be of relevance for the here-assessed enteric colonization or infections events as well. Summarized, the study was explorative and hypothesis forming, as external reliable surveillance data for comparison purposes were not available. By doing so, a data-based holistic background for infection control and prevention assessments should be provided. Without surveillance data, it is difficult to assess effects of infection control and prevention procedures, especially if colonization with microorganisms which are not necessarily associated with clinically apparent infections is affected.

METHODS

Study design

The study was conducted as a longitudinal surveillance assessment on diagnostic stool samples of German military and police officers returning from deployment. The stool samples were provided starting in 2006 until the end of June 2024. Returned police officers were assessed beginning in 2015 based on German interministerial administrative assistance (“Amtshilfe”). The assessment was stratified by deployment side on WHO (World Health Organization)

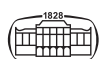
region level and deployment period. In deviation from the WHO region definitions, however, South Sudan was counted as part of the Eastern Mediterranean Region. The reason is that South Sudan did not yet exist as a sovereign state when the assessment was started in 2006. To avoid data inconsistency, South Sudan was assigned to the Mediterranean Region together with Sudan, to which it politically belonged until its independence in 2011. Focusing on deployment periods, the overall assessment period was sub-stratified into the period before 2010, the two five-year-periods 2010–2014 and 2015–2019, the COVID-19-pandemic period 2020–2022, and the post-pandemic period after 2022. The year 2023 was defined as part of the post-pandemic period for this assessment, because WHO declared the formal end of the pandemic at the beginning of May 2023, thus assigning the larger share of this year to the post-pandemic period. When timelines of individual deployments included time periods in two different assessment strata, the deployment was assigned to the stratum with the larger share.

Study population

The study population consisted of German soldiers and police officers providing stool samples for post-deployment diagnostic assessments between 2006 and the end of June 2024 after predominantly but not exclusively tropical deployments. Information on age, sex and geographic deployment sites were provided for the assessment.

Molecular diagnostics

The assessed stool samples were analyzed applying in-house real-time PCR for samples collected until 2022, while the diagnostic workflow was changed to commercial real-time PCR in 2022. Regarding the in-house approach, nucleic acids from the analyzed stool samples were extracted using the QIAamp stool DNA mini kit (Qiagen, Hilden, Germany) and the eluates were stored at -80°C afterwards. Using previously published oligonucleotides for the specific PCR targets, a 7-plex real-time PCR assay run on a LightCycler Pro device (Roche, Basel, Switzerland) comprised the ESBL gene *bla*_{CTX-M} [26], the vancomycin resistance-mediating genes *vanA* and *vanB* [27, 28], the diarrheagenic *E. coli* pathovars EPEC (enteropathogenic *E. coli*, *eae* gene and EAF plasmid sequence on the same fluorescence channel), ETEC (enterotoxigenic *E. coli*, *eltB* gene and *estB* genes on the same fluorescence channel) and EAEC (enteroaggregative *E. coli*, *aatA* gene) [17] as well as specific sequences of important *Vibrio* (*V.*) spp. with etiological relevance for human patients (both the *sodB* and *ctx* genes of *V. cholerae*, the *vvha* gene of *V. vulnificus* and the *toxR* gene of *Vibrio parahaemolyticus* on the same fluorescence channel) [29]. As detailed elsewhere, specificity estimations ranged between 94% and 100% for the applied assays [17, 24–29]. Details on the used oligonucleotides are provided in the [supplementary Table 1](#) for readers interested in reproducing the assessments. The reaction mix consisted of HotStarTaq master mix (Qiagen, Hilden, Germany), a Mg^{2+} concentration of



6.0 mM, primer and probe concentrations as indicated in the [supplementary Table 1](#) and 2 μ L sample DNA eluate in total reaction volumes of 20 μ L. Run conditions comprised initial denaturation at 95 °C for 15 min followed by 45 cycles of denaturation at 95°C for 15 s, annealing at 60 °C for 60 s and elongation at 72 °C for 30 s, followed by subsequent hold at 40 °C for 20 s. Typical sigmoid-shaped amplification curves were accepted as positive real-time PCR signals irrespective of the recorded cycle threshold value. In each run, quality control comprised the inclusion of plasmid-based positive controls (sequence inserts in pEX-A128 vector plasmid backbones (eurofins Genomics, Luxembourg) provided in the [supplementary Table 1](#)) and PCR-grade water-based negative controls. Ten-fold dilution steps of the positive control plasmids were also used to identify the technical detection threshold of each parameter (provided in the [supplementary Table 1](#)), which is necessary to decide how many target DNA copies will go undetected by the PCR approach. Further, PCR-inhibition in the samples was controlled with an in-house real-time PCR assay targeting a sequence fragment of Phocid Herpes Virus (PhHV) as described in detail elsewhere [30] in the diagnostic process. Starting in 2022, commercial real-time PCR assessment with assays accredited by the manufacturer for in-vitro diagnostic use in Europe replaced the in-house assays. In detail, after nucleic acid extraction using the STARMag 96 \times 4 Universal Cartridge kit (SeeGene, Seoul, Republic of Korea) on a Starlet extraction automate (SeeGene) as described by the manufacturer, real-time PCR results were obtained with the SeeGene assays Allplex GI Panels 1 (for *Vibrio* spp.) and 2 (for EPEC, ETEC, and EAEC) as well as Allplex Entero-DR (for *bla*_{CTX-M}, *vanA*, and *vanB*) on a Bio-Rad cycler CFX 96 (Bio-Rad Laboratories Inc., Hercules, CA, USA), again according to the manufacturer's instructions.

Statistics

The obtained real-time PCR surveillance data were mainly descriptively assessed. In line with the exploratory and hypothesis-forming study design, analytical statistical analyses were restricted to simple operations. In detail, averaged values over all deployment periods and sites for soldiers and police officers were used as references. Fisher's exact test or – in case of higher numbers – the Chi-squared test were used for binary results and the non-parametric Mann-Whitney U test in case of numeric results in order to compare deployment-specific findings for soldiers and police officers with those references. More complex statistical operations were not performed, keeping in mind the conditional dependence of the compared populations. *P*-values <0.05 were considered as significant without corrections for multiple testing with, e.g., the Holm-Bonferroni method [31].

Ethics

Anonymized retrospective assessment of surveillance data from the deployment returnees without informed consent was covered by the ethical clearance (reference number

WF-019/17) from the Ethics Committee of the Medical Association of Hamburg, Germany, in line with German national laws. The assessment was performed in line with the Declaration of Helsinki and all its amendments.

RESULTS

Population characteristics

Data from a total of 1817 soldiers and 117 police officers were included in the assessment; details are provided in the [Tables 1–5](#). The deployed forces were unevenly distributed over the assessed deployment periods and deployment areas as indicated in [Table 5](#). The soldiers were generally younger than the police officers with a mean age (\pm standard deviation (SD)) of 36.1 (\pm 10.4) years of age compared to 46.7 (\pm 9.8) years, respectively. Generally, there was a tendency towards higher age of soldiers in later deployment periods which became prominent in the period of the COVID-19 pandemic and did not vanish afterwards. For police forces, this trend was not detectable. Details of this shift are provided in the [Table 2](#), the raw data are in the [Table 1](#). African deployments were continuously associated with older deployed soldiers starting from 2010. For both the assessed soldiers and police forces, there was a quantitative dominance of male individuals on deployment, which was even more pronounced for police officers than for military personnel. The female : male-ratio was 1 : 10.8 for the assessed soldiers and 1 : 15.0 for the police forces. For soldiers, there was a particular predominance of males deployed to the Eastern Mediterranean Region until 2010, while slightly more military females were on the African deployments starting in 2015. For other deployment sites and periods as well as for police forces, no specific pattern was observed. In general, over the assessment periods, there was a tendency towards a higher proportion of deployed female individuals compared to the early assessment periods ([Tables 3 and 4](#)).

Surveillance results

Focusing on the assessed resistance genes in the stool samples of the screened soldiers and police officers, CTX-M-type beta-lactamase genes (*bla*_{CTX-M}) coding for enzymes which mediate the expression of ESBL were recorded in 47.9% of the stool samples collected from military personnel and in 24.8% of stool samples taken from police officers. Details are provided in the [Tables 6 and 7](#). Noteworthy, particularly high percentages ranging between 80% and 90% were observed in samples collected from soldiers from the very early deployments collected before 2010. Afterwards, the proportions of positive samples dropped to values below or equal to the references with the exemption of police officers in Africa between 2015 and 2019, for which increased proportions were observed as well. Deployment sites from the African, the Eastern Mediterranean and the European Region associated with deployments before 2010 most prominently contributed to the high prevalence in soldiers, while



Table 1. Temporal and spatial age distribution of deployed forces (raw data)

Assessment period	Population	African Region, mean value (\pm SD)	Region of the Americas, mean value (\pm SD)	South-East Asia Region, mean value (\pm SD)	European Region, mean value (\pm SD)	Eastern Mediterranean Region, mean value (\pm SD)	Western Pacific Region, mean value (\pm SD)	Multiple WHO regions, mean value (\pm SD)	Total, mean value (\pm SD)
Age (years)									
Before 2010	Soldiers	33.1 (\pm 8.8)	55 (–)	n.a.	31.5 (\pm 8.8)	32.4 (\pm 8.8)	n.a.	n.a.	32.4 (\pm 8.5)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	37 (\pm 11.7)	33.2 (\pm 13.1)	33.1 (\pm 16.1)	26 (\pm 2.2)	37.3 (\pm 13.3)	27 (\pm 8.7)	38.3 (\pm 18.1)	36.7 (\pm 12.8)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	37.7 (\pm 6.3)	38.3 (\pm 17.1)	31.1 (\pm 9.5)	36.5 (\pm 9.5)	28.9 (\pm 13.8)	27 (–)	43.2 (\pm 14.7)	34.4 (\pm 13.3)
	Police officers	41.4 (\pm 6.1)	n.a.	n.a.	45.9 (\pm 8.2)	42.3 (\pm 11.7)	n.a.	n.a.	43.8 (\pm 9)
2020–2022	Soldiers	41.5 (\pm 11.0)	38 (\pm 17.0)	n.a.	45 (–)	46.7 (\pm 9.7)	53 (\pm 7.1)	n.a.	42.6 (\pm 10.9)
	Police officers	48.2 (\pm 9.5)	n.a.	n.a.	45.5 (\pm 10.2)	50.5 (\pm 0.7)	48 (–)	n.a.	47 (\pm 9.5)
After 2022	Soldiers	37.6 (\pm 8.9)	26 (–)	n.a.	47.3 (\pm 12.8)	27 (–)	26 (–)	46.8 (\pm 10.4)	40.7 (\pm 10.8)
	Police officers	48.2 (\pm 10.5)	n.a.	n.a.	47.3 (\pm 11.8)	48.0 (\pm 10.5)	57 (–)	51.0 (\pm 5.6)	48.4 (\pm 10.3)
Total	Soldiers	37.9 (\pm 10.0)	39.1 (\pm 19.9)	31.9 (\pm 12.2)	32.1 (\pm 9.5)	35.4 (\pm 9.7)	35.5 (\pm 15.0)	43.8 (\pm 13.6)	36.1 (\pm 10.4)
	Police officers	47.0 (\pm 10.1)	n.a.	n.a.	46.0 (\pm 9.7)	45.9 (\pm 10.3)	52.5 (\pm 6.4)	51.0 (\pm 5.6)	46.7 (\pm 9.8)

SD = standard deviation, n.a. = not applicable.





Table 2. Temporal and spatial age distribution of deployed forces. Mean values over all deployed military and police forces (reference values) are shown in yellow. Lower mean values ($P < 0.05$) are indicated in green, higher mean values ($P < 0.05$) in red. No color is used in case of lacking significance for difference or lacking values

Assessment period	Population	African Region, mean value (\pm SD), P	Region of the Americas, mean value (\pm SD), P	South-East Asia Region, mean value (\pm SD), P	European Region, mean value (\pm SD), P	Eastern Mediterranean Region, mean value (\pm SD), P	Western Pacific Region, mean value (\pm SD), P	Multiple WHO regions, mean value (\pm SD), P	Total, mean value (\pm SD), P
Age (years)									
Before 2010	Soldiers	33.1 (\pm 8.8), P=0.2586	55 (-), P=n.e.	n.a.	31.5 (\pm 8.8), P=0.0006	32.4 (\pm 8.8), P=0.0028	n.a.	n.a.	32.4 (\pm 8.5), P=0.0002
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010-2014	Soldiers	37 (\pm 11.7), P=0.0002	33.2 (\pm 13.1), P=0.3343	33.1 (\pm 16.1), P=0.1777	26 (\pm 2.2), P=0.0343	37.3 (\pm 13.3), P<0.0001	27 (\pm 8.7), P=0.1522	38.3 (\pm 18.1), P=0.2004	36.7 (\pm 12.8), P<0.0001
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015-2019	Soldiers	37.7 (\pm 6.3), P<0.0001	38.3 (\pm 17.1), P=0.4841	31.1 (\pm 9.5), P=0.1119	36.5 (\pm 9.5), P=0.4464	28.9 (\pm 13.8), P<0.0001	27 (-), P=n.e.	43.2 (\pm 14.7), P=0.1396	34.4 (\pm 13.3), P=4623
	Police officers	41.4 (\pm 6.1), P=0.0557	n.a.	n.a.	45.9 (\pm 8.2), P=0.5384	42.3 (\pm 11.7), P=0.2841	n.a.	n.a.	43.8 (\pm 9), P=0.0647
2020-2022	Soldiers	41.5 (\pm 11.0), P<0.0001	38 (\pm 17.0), P=0.7348	n.a.	45 (-), P=n.e.	46.7 (\pm 9.7), P<0.0001	53 (\pm 7.1), P=0.0325	n.a.	42.6 (\pm 10.9), P<0.0001
	Police officers	48.2 (\pm 9.5), P=0.4759	n.a.	n.a.	45.5 (\pm 10.2), P=0.7215	50.5 (\pm 0.7), P=0.6155	48 (-), P=n.e.	n.a.	47 (\pm 9.5), P=0.7600
After 2022	Soldiers	37.6 (\pm 8.9), P=0.0076	26 (-), P=n.e.	n.a.	47.3 (\pm 12.8), P=0.0055	27 (-), P=n.e.	26 (-), P=n.e.	46.8 (\pm 10.4), P<0.0001	40.7 (\pm 10.8), P<0.0001
	Police officers	48.2 (\pm 10.5), P=0.4052	n.a.	n.a.	47.3 (\pm 11.8), P=0.7709	48.0 (\pm 10.5), P=0.6637	57 (-), P=n.e.	51.0 (\pm 5.6), P=5596	48.4 (\pm 10.3), P=0.2600
Total	Soldiers	37.9 (\pm 10.0), P<0.0001	39.1 (\pm 19.9), P=0.8614	31.9 (\pm 12.2), P=0.0386	32.1 (\pm 9.5), P=0.0054	35.4 (\pm 9.7), P=0.0191	35.5 (\pm 15.0), P=0.6542	43.8 (\pm 13.6), P<0.0001	36.1 (\pm 10.4), ref.
	Police officers	47.0 (\pm 10.1), P=0.8392	n.a.	n.a.	46.0 (\pm 9.7), P=0.6668	45.9 (\pm 10.3), P=0.6946	52.5 (\pm 6.4), P=0.4300	51.0 (\pm 5.6), P=5596	46.7 (\pm 9.8), ref.

SD = standard deviation, n.a. = not applicable. ref. = reference. n.e. = not estimable. P = significance level.

Table 3. Temporal and spatial distribution of the female: male-ratio of deployed forces (raw data)

Assessment period	Population	African Region, n : n	Region of the Americas, n : n	South-East Asia Region, n : n	European Region, n : n	Eastern Mediterranean Region, n : n	Western Pacific Region, n : n	Multiple WHO regions, n : n	Total, n : n
Female : male-ratio									
Before 2010	Soldiers	1 : 9.9	0 : 1.0	n.a.	1 : 74.0	1 : 25.4	n.a.	n.a.	1 : 22.9
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	1 : 14.4	1 : 5.5	1 : 4.5	1 : 4.0	1 : 54.7	3.0 : 0	1 : 4	1 : 14.8
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	1 : 5.9	1 : 3.8	1 : 1.3	1 : 1.7	1 : 27.0	0 : 1.0	0 : 5	1 : 7.3
	Police officers	1 : 9.0	n.a.	n.a.	1 : 14.0	0 : 6	n.a.	n.a.	1 : 14.5
2020–2022	Soldiers	1 : 5.2	0 : 2.0	n.a.	0 : 1.0	1 : 10.5	0 : 2.0	n.a.	1 : 6.1
	Police officers	1 : 16.0	n.a.	n.a.	1 : 5.0	0 : 2	0 : 1.0	n.a.	1 : 8.5
After 2022	Soldiers	1 : 4.6	1.0 : 0	n.a.	1 : 6.0	0 : 1.0	0 : 1.0	1 : 3.2	1 : 4.0
	Police officers	1 : 8.7	n.a.	n.a.	1 : 3.5	1 : 5.0	0 : 1.0	0 : 3.0	1 : 7.0
Total	Soldiers	1 : 7.0	1 : 4.1	1 : 1.9	1 : 23.4	1 : 27.9	1 : 1.3	1 : 4.0	1 : 10.8
	Police officers	1 : 12.8	n.a.	n.a.	1 : 6.0	1 : 13.0	0 : 2.0	0 : 3.0	1 : 15.0

n = number, n.a. = not applicable.

deployments to the African Region between 2015 and 2019 were the only ones with significantly increased colonization rates in police forces.

When looking at the assessed *vanA* and *vanB* genes, which mediate vancomycin resistance in enterococci, an even more differentiated picture was seen. While *vanA* genes were not recorded at all, *vanB* prevalences of 30.2% and 14.5% were seen in the collected stool samples of deployed soldiers and police officers, respectively. Similar as observed for the *bla*_{CTX-M} genes, soldiers showed particularly high colonization rates in the very early deployment periods, comprising deployments to the African, the European and the Eastern Mediterranean Region, which dropped in later deployments to intermediate or even lower levels compared to the reference value. For police officers, no significances were seen. Details are provided in the Tables 8 and 9 below.

Surveillance data on diarrheagenic *E. coli* and *Vibrio* spp. were included to compare resistance trends in stool samples with colonization rates of both frequently and less frequently observed bacterial enteric pathogens. Thereby, contrasting patterns were recorded as shown in the Tables 6–9. In total, recorded prevalences for soldiers and police officers were 9.0% and 17.9% for enteropathogenic EPEC, 3.4% and 12.8% for enterotoxigenic ETEC, 4.0% and 3.4% for enteroaggregative EAEC as well as 2.0% and 3.4% for *Vibrio* spp. in samples obtained from deployed soldiers and police officers, respectively. For EPEC and ETEC, in particular, there was a tendency for increased prevalence values in the pre-pandemic period 2015–2019 and during the COVID-19 pandemic. For EAEC and *Vibrio* spp., the tendencies were less obvious but pointed towards a similar direction, quite different from the pattern of assessed molecular resistance

determinants. Geographically, increased prevalence rates for all assessed enteric bacterial pathogens were recorded associated with deployments to the African Region, while a pathogen-specific distribution pattern over the other WHO regions was seen. Details are provided in the Tables 10–17.

Recorded cycle threshold (Ct) values of the real-time PCRs are shown in the supplementary Tables 2–7. Obvious shifts in recorded Ct values over the assessed deployment periods and regions were not observed. Of note, Ct-values from the post-pandemic assessment period (after 2022) cannot be directly compared with the Ct values from the earlier collected samples due to a change in the applied real-time PCR approach as stated in the methods chapter.

DISCUSSION

The assessment was conducted to investigate the temporal and spatial dynamics of *bla*_{CTX-M} genes commonly mediating ESBL-type resistance in Enterobacterales and of *vanA* as well as *vanB* genes mediating vancomycin-resistance in enterococci in stool samples collected from deployed German soldiers and police officers. In comparison, respective dynamics for diarrheagenic *E. coli* as common bacterial pathogens and for *Vibrio* spp. as less common ones were co-assessed. The study provided a number of results.

First, the assessment confirmed the above-mentioned suspicion that previous merely culture-based screening approaches for resistant bacteria in stool samples of returnees from deployment [6, 7] might have underestimated the abundance of resistance-associated genes. This is well in line with previous reports on inferior sensitivity of merely





Table 4. Temporal and spatial distribution of the likelihood of deployed forces for being female compared to the totals of deployed soldiers and police officers (references). Higher odds ratios values are indicated in green, lower ones in red. No color is used in case of lacking significance or lacking values

Assessment period	Population	African Region, odds ratio (P)	Region of the Americas, odds ratio (P)	South-East Asia Region, odds ratio (P)	European Region, odds ratio (P)	Eastern Mediterranean Region, odds ratio (P)	Western Pacific Region, odds ratio (P)	Multiple WHO regions, odds ratio (P)	Total, odds ratio (P)
Female : male-ratio									
Before 2010	Soldiers	1.1 (P=0.8603)	3.6 (P=1.0000)	n.e.	0.1 (P=0.0004)	0.4 (P=0.0005)	n.e.	n.e.	0.4 (P<0.0001)
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	0.8 (P=0.5233)	2.0 (P=0.3056)	2.4 (P=0.2403)	2.7 (P=0.3592)	0.2 (P=0.0008)	75.4 (P=0.0006)	2.7 (P=0.2077)	0.7 (P=0.2201)
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2015-2019	Soldiers	1.8 (P=0.0014)	2.8 (P=0.0498)	8.6 (P<0.0001)	3.3 (P=0.0520)	0.4 (P=0.0184)	3.6 (P=1.0000)	1.0 (P=1.0000)	1.5 (P=0.0176)
	Police officers	1.7 (P=0.5001)	n.e.	n.e.	1.1 (P=1.0000)	1.1 (P=1.0000)	n.e.	n.e.	1.0 (P=1.0000)
2020-2022	Soldiers	1.8 (P=0.0456)	2.2 (P=1.0000)	n.e.	3.6 (P=1.0000)	0.9 (P=1.0000)	2.2 (P=1.0000)	n.e.	1.6 (P=0.0648)
	Police officers	1.0 (P=1.0000)	n.e.	n.e.	3.1 (P=0.3450)	2.9 (P=1.0000)	4.8 (P=1.0000)	n.e.	1.8 (P=0.6179)
After 2022	Soldiers	2.4 (P=0.0356)	32.3 (P=0.0853)	n.e.	1.8 (P=0.4635)	3.6 (P=1.0000)	3.6 (P=1.0000)	3.4 (P=0.0172)	2.7 (P=0.0013)
	Police officers	1.2 (P=0.7526)	n.e.	n.e.	4.3 (P=0.1348)	3.0 (P=0.3500)	4.7 (P=1.0000)	2.0 (P=1.0000)	2.1 (P=0.2120)
Total	Soldiers	1.5 (P=0.0025)	2.7 (P=0.0221)	5.7 (P<0.0001)	0.5 (P=0.0548)	0.4 (P<0.0001)	8.1 (P=0.0169)	2.7 (P=0.3592)	ref.
	Police officers	1.2 (P=0.7526)	n.e.	n.e.	2.6 (P=0.1886)	1.2 (P=1.0000)	2.8 (P=1.0000)	2.0 (P=1.0000)	ref.

n = number, n.e. = not estimable. ref. = reference. P = significance level.

Table 5. Temporal and spatial distribution of deployment sites

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n/n (%)
Deployment sites									
Before 2010	Soldiers	120/720 (16.7%)	1/41 (2.4%)	0/29 (0%)	150/171 (87.7%)	422/809 (52.2%)	0/7 (0%)	0/40 (0%)	693/1817 (38.1%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	139/720 (19.3%)	13/41 (31.7%)	11/29 (37.9%)	5/171 (2.9%)	167/809 (20.6%)	3/7 (42.9%)	10/40 (25.0%)	348/1817 (19.2%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	305/720 (42.4%)	24/41 (58.5%)	18/29 (62.1%)	8/171 (4.7%)	196/809 (24.2%)	1/7 (14.3%)	5/40 (12.5%)	557/1817 (30.7%)
	Police officers	10/56 (17.9%)	n.a.	n.a.	15/42 (35.7%)	6/14 (42.9%)	0/7 (0%)	0/3 (0%)	31/117 (26.5%)
2020–2022	Soldiers	106/720 (14.7%)	2/41 (4.9%)	0/29 (0%)	1/171 (0.6%)	23/809 (2.8%)	2/7 (28.6%)	0/40 (0%)	134/1817 (7.4%)
	Police officers	17/56 (30.4%)	n.a.	n.a.	18/42 (42.9%)	2/14 (14.3%)	1/2 (50.0%)	0/3 (0%)	38/117 (32.5%)
After 2022	Soldiers	50/720 (6.9%)	1/41 (2.4%)	0/29 (0%)	7/171 (4.1%)	1/809 (0.1%)	1/7 (14.3%)	25/40 (62.5%)	85/1817 (4.7%)
	Police officers	29/56 (51.8%)	n.a.	n.a.	9/42 (21.4%)	6/14 (42.9%)	1/2 (50.0%)	3/3 (100%)	48/117 (41.0%)
Total	Soldiers	720 (100%)	41 (100%)	29 (100%)	171 (100%)	809 (100%)	7 (100%)	40 (100%)	1817 (100%)
	Police officers	56 (100%)	n.a.	n.a.	42 (100%)	14 (100%)	2 (100%)	3 (100%)	117 (100%)

n = number, n.a. = not applicable.





Table 6. Temporal and spatial distribution of CTX-M-type ESBL genes in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
CTX-M-type ESBL genes									
Before 2010	Soldiers	109/120 (90.8%)	0/1 (0%)	n.a.	128/150 (85.3%)	340/422 (80.6%)	n.a.	n.a.	577/693 (83.3%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	36/139 (25.9%)	7/13 (53.8%)	2/11 (18.2%)	1/5 (20%)	27/167 (16.2%)	0/3 (0%)	1/10 (10%)	74/348 (21.3%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	91/305 (29.8%)	11/24 (45.8%)	10/18 (55.6%)	1/8 (12.5%)	44/196 (22.4%)	1/1 (100%)	4/5 (80%)	162/557 (29.1%)
	Police officers	6/10 (60%)	n.a.	n.a.	3/15 (20%)	2/6 (33.3%)	n.a.	n.a.	11/31 (35.5%)
2020–2022	Soldiers	34/106 (32.1%)	0/2 (0%)	n.a.	0/1 (0%)	9/23 (39.1%)	1/2 (50%)	n.a.	44/134 (32.8%)
	Police officers	2/17 (11.8%)	n.a.	n.a.	6/18 (33.3%)	0/2 (0%)	1/1 (100%)	n.a.	9/38 (23.7%)
After 2022	Soldiers	8/50 (16.0%)	0/1 (0%)	n.a.	1/7 (14.3%)	0/1 (0%)	0/1 (0%)	4/25 (16.0%)	13/85 (15.3%)
	Police officers	6/29 (20.7%)	n.a.	n.a.	0/9 (0%)	1/6 (16.7%)	1/1 (100%)	1/3 (33.3%)	9/48 (18.8%)
Total*	Soldiers	278/720 (38.6%)	18/41 (43.9%)	12/29 (41.4%)	131/171 (76.6%)	420/809 (51.9%)	2/7 (28.6%)	9/40 (22.5%)	870/1817 (47.9%)
	Police officers	14/56 (25.0%)	n.a.	n.a.	9/42 (21.4%)	3/14 (21.4%)	2/2 (100%)	1/3 (33.3%)	29/117 (24.8%)

n = number. n.a. = not applicable.

Table 7. Odds ratios of CTX-M-type ESBL genes in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, odds ratio (P)	Region of the Americas, odds ratio (P)	South-East Asia Region, odds ratio (P)	European Region, odds ratio (P)	Eastern Mediterranean Region, odds ratio (P)	Western Pacific Region, odds ratio (P)	Multiple WHO regions, odds ratio (P)	Total, odds ratio (P)
CTX-M-type ESBL genes									
Before 2010	Soldiers	10.8 (5.8 , 20.2), P<0.0001	0.4 (<0.1 , 8.9), P=1.0000	n.e.	6.3 (3.9 , 10.1), P<0.0001	4.5 (3.5 , 5.8), P<0.0001	n.e.	n.e.	6.5 (5.2 , 8.1), P<0.0001
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	0.4 (0.3 , 0.6), P<0.0001	1.3 (0.4 , 3.8), P=0.7833	0.2 (<0.1 , 1.1), P=0.0677	0.3 (<0.1 , 3.4), P=0.3767	0.2 (0.1 , .03), P<0.0001	0.2 (<0.1 , 3.0), P=0.2510	0.1 (<0.1 , 1.0), P=0.0225	0.3 (0.2 , 0.4), P<0.0001
	Police officers	n.e.	n.e.	n.a.	n.e.	n.e.	n.e.	n.e.	n.e.
2015-2019	Soldiers	0.5 (0.4 , 0.6), P<0.0001	0.9 (0.4 , 2.1), P=1.0000	1.4 (0.5 , 3.5), P=0.6372	0.2 (<0.1 , 1.3), P=0.0720	0.3 (0.2 , 0.4), P<0.0001	3.3 (0.1 , 80.3), P=0.4791	4.4 (0.5 , 39.1), P=0.2007	0.5 (0.4 , 0.5), P<0.0001
	Police officers	4.6 (1.2 , 17.3), P=0.0262	n.e.	n.e.	0.8 (0.2 , 2.9), P=1.0000	1.5 (0.3 , 8.7), P=0.6412	n.e.	n.e.	1.7 (0.7 , 3.9), P=0.2589
2020-2022	Soldiers	0.5 (0.3 , 0.8), P<0.0001	0.2 (<0.1 , 4.5), P=0.5007	n.e.	0.4 (<0.1 , 8.9), P=1.0000	0.7 (0.3 , 1.6), P=0.5296	1.1 (<0.1 , 17.4), P=1.0000	n.e.	0.5 (0.4 , 0.8), P=0.0008
	Police officers	0.4 (<0.1 , 1.9), 0.3581	n.e.	n.e.	1.5 (0.5 , 4.4), P=0.5634	0.6 (<0.1 , 12.9), P=1.0000	9.0 (0.4 , 227.2), P=0.2542	n.e.	0.9 (0.4 , 2.2), P=1.0000
After 2022	Soldiers	0.2 (0.1 , 0.4), P<0.0001	0.4 (<0.1 , 8.9), P=1.0000	n.e.	0.2 (<0.1 , 1.5), P=0.1269	0.4 (<0.1 , 8.9), P=1.0000	0.4 (<0.1 , 8.9), P=1.0000	0.2 (<0.1 , 0.6), P=0.0018	0.2 (0.1 , 0.4), P<0.0001
	Police officers	0.8 (0.3 , 2.1), P=0.8091	n.e.	n.e.	0/9 (0%), P=1.0000	0.6 (<0.1 , 5.4), P=1.0000	9.0 (0.4 , 227.2), P=0.2542	1.5 (0.1 , 17.4), P=1.0000	0.7 (0.3 , 1.6), P=0.5417
Total*	Soldiers	0.7 (0.6 , 0.8), P<0.0001	0.9 (0.5 , 1.6), P=0.6388	0.8 (0.4 , 1.6), P=0.5756	3.6 (2.5 , 5.1), P<0.0001	1.2 (1.0 , 1.4), P=0.0619	0.4 (<0.1 , 2.3), P=0.4554	0.3 (0.1 , 0.7), P=0.0020	ref.
	Police officers	1.0 (0.5 , 2.1), P=1.0000	n.e.	n.e.	0.8 (0.4 , 1.9), P=0.8333	0.8 (0.2 , 3.2), P=1.0000	15.0 (0.7 , 321.7), P=0.0662	1.5 (0.1 , 17.4), P=1.0000	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.



Table 8. Temporal and spatial distribution of *vanB*-type vancomycin resistance genes in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
<i>vanB</i> -type vancomycin resistance genes									
Before 2010	Soldiers	55/120 (45.8%)	1/1 (100%)	n.a.	68/150 (45.3%)	206/422 (48.8%)	n.a.	n.a.	330/693 (47.6%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	48/139 (34.5%)	4/13 (30.8%)	2/11 (18.2%)	1/5 (20%)	44/167 (26.3%)	0/3 (0%)	2/10 (20%)	101/348 (29.0%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	68/305 (22.3%)	2/24 (8.3%)	2/18 (11.1%)	3/8 (37.5%)	25/196 (12.8%)	0/1 (0%)	1/5 (20%)	101/557 (18.1%)
	Police officers	1/10 (10%)	n.a.	n.a.	1/15 (6.7%)	1/6 (16.7%)	n.a.	n.a.	3/31 (9.7%)
2020–2022	Soldiers	4/106 (3.8%)	0/2 (0%)	n.a.	0/1 (0%)	2/23 (8.7%)	1/2 (50%)	n.a.	7/134 (5.2%)
	Police officers	3/17 (17.6%)	n.a.	n.a.	3/18 (16.7%)	0/2 (0%)	0/1 (0%)	n.a.	6/38 (15.8%)
After 2022	Soldiers	4/50 (8.0%)	0/1 (0%)	n.a.	0/7 (0%)	0/1 (0%)	0/1 (0%)	5/25 (20.0%)	9/85 (10.6%)
	Police officers	4/29 (13.8%)	n.a.	n.a.	3/9 (33.3%)	1/6 (16.7%)	0/1 (0%)	0/3 (0%)	8/48 (16.7%)
Total	Soldiers	179/720 (24.9%)	7/41 (17.1%)	4/29 (13.8%)	72/171 (42.1%)	277/809 (34.2%)	1/7 (14.3%)	8/40 (20.0%)	548/1817 (30.2%)
	Police officers	8/56 (14.3%)	n.a.	n.a.	7/42 (16.7%)	2/14 (14.3%)	0/2 (0%)	0/3 (0%)	17/117 (14.5%)

n = number. n.a. = not applicable.

Table 9. Odds ratios of *vanB*-type vancomycin resistance genes in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, odds ratio (P)	Region of the Americas, odds ratio (P)	South-East Asia Region, odds ratio (P)	European Region, odds ratio (P)	Eastern Mediterranean Region, odds ratio (P)	Western Pacific Region, odds ratio (P)	Multiple WHO regions, odds ratio (P)	Total, odds ratio (P)
<i>vanB</i> -type vancomycin resistance genes									
Before 2010	Soldiers	2.0 (1.4 , 2.8), P=0.0005	6.9 (0.3 , 170.9), P=0.3020	n.e.	1.9 (1.4 , 2.7); P=0.0002	2.2 (1.8 , 2.7), P<0.0001	n.e.	n.e.	2.1 (1.8 , 2.5), P<0.0001
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	1.2 (0.8 , 1.8), P=0.2933	1.0 (0.3 , 3.4), P=1.0000	0.5 (0.1 , 2.4), P=0.5214	0.6 (<0.1 , 5.2), P=1.0000	0.8 (0.6 , 1.2), P=0.3315	0.3 (<0.1 , 6.4), P=0.5584	0.6 (0.1 , 2.7), P=0.7324	0.9 (0.7 , 1.2), P=0.7188
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2015-2019	Soldiers	0.7 (0.5 , 0.9), P=0.0063	0.2 (<0.1 , 0.9), P=0.0225	0.3 (<0.1 , 1.3), P=0.1177	1.4 (0.3 , 5.9), P=0.7041	0.4 (0.2 , 0.5), P<0.0001	0.8 (<0.1 , 19.0), P=1.0000	0.6 (<0.1 , 5.2), P=1.0000	0.5 (0.4 , 0.7), P<0.0001
	Police officers	0.7 (<0.1 , 5.5), P=1.0000	n.e.	n.e.	0.4 (<0.1 , 3.4), P=0.6922	1.2 (0.1 , 10.7), P=1.0000	n.e.	n.e.	0.6 (0.2 , 2.3), P=0.7675
2020-2022	Soldiers	0.1 (<0.1 , 0.2), P<0.0001	0.5 (<0.1 , 9.7), P=1.0000	n.e.	0.8 (<0.1 , 19.0), P=1.0000	0.2 (<0.1 , 0.9), P=0.0223	2.3 (0.1 , 37.1), P=0.5127	n.e.	0.1 (<0.1 , 0.3), P<0.0001
	Police officers	1.3 (0.3 , 4.9), P=0.7194	n.e.	n.e.	1.2 (0.3 , 4.5), P=0.7311	1.1 (<0.1 , 25.0), P=1.0000	1.9 (<0.1 , 49.0), P=1.0000	n.e.	1.1 (0.4 , 3.0), P=0.7987
After 2022	Soldiers	0.2 (<0.1 , 0.6), P=0.0004	0.8 (<0.1 , 19.0), P=1.0000	n.e.	0.2 (<0.1 , 2.7), P=0.1103	0.8 (<0.1 , 19.0), P=1.0000	0.8 (<0.1 , 19.0), P=1.0000	0.6 (0.2 , 1.6), P=0.3797	0.3 (0.1 , 0.6), P<0.0001
	Police officers	0.5 (0.1 , 2.2), P=0.5284	n.e.	n.e.	3/9 (33.3%)	0.2 (<0.1 , 0.9), P=0.0223	0.9 (<0.1 , 49.0), P=1.0000	0.8 (<0.1 , 16.6), P=1.0000	1.2 (0.5 , 2.9), P=0.8117
Total	Soldiers	0.8 (0.6 , 0.9), P=0.0090	0.5 (0.2 , 1.0), P=0.0621	0.5 (0.2 , 1.1), P=0.0838	1.7 (1.2 , 2.3), P=0.0018	1.2 (1.0 , 1.4), P=0.0419	0.4 (<0.1 , 3.2), P=0.6819	0.6 (0.3 , 1.3), P=0.2210	ref.
	Police officers	1.0 (0.4 , 2.4), P=1.0000	n.e.	n.e.	1.2 (0.5 , 3.1), P=0.8026	1.0 (0.2 , 4.8), P=1.0000	1.1 (<0.1 , 25.0), P=1.0000	0.8 (<0.1 , 16.6), P=1.0000	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.





Table 10. Temporal and spatial distribution of EPEC (enteropathogenic *E. coli*) in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
EPEC (enteropathogenic <i>E. coli</i>)									
Before 2010	Soldiers	7/120 (5.8%)	0/1 (0%)	n.a.	7/150 (4.7%)	23/422 (5.5%)	n.a.	n.a.	37/693 (5.3%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	5/139 (3.6%)	0/13 (0%)	0/11 (0%)	0/5 (0%)	8/167 (4.8%)	1/3 (33.3%)	0/10 (0%)	14/348 (4.0%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	60/305 (19.7%)	3/24 (12.5%)	1/18 (5.6%)	3/8 (37.5%)	20/196 (10.2%)	0/1 (0%)	2/5 (40%)	89/557 (16.0%)
	Police officers	2/10 (20%)	n.a.	n.a.	7/15 (46.7%)	1/6 (16.7%)	n.a.	n.a.	10/31 (32.3%)
2020–2022	Soldiers	17/106 (16.0%)	0/2 (0%)	n.a.	0/1 (0%)	0/23 (0%)	0/2 (0%)	n.a.	17/134 (12.7%)
	Police officers	2/17 (11.8%)	n.a.	n.a.	4/18 (22.2%)	0/2 (0%)	1/1 (100%)	n.a.	7/38 (18.4%)
After 2022	Soldiers	4/50 (8.0%)	0/1 (0%)	n.a.	0/7 (0%)	0/1 (0%)	0/1 (0%)	2/25 (8.0%)	6/85 (7.1%)
	Police officers	4/29 (13.8%)	n.a.	n.a.	0/9 (0%)	0/6 (0%)	0/1 (0%)	0/3 (0%)	4/48 (8.3%)
Total	Soldiers	93/720 (12.9%)	3/41 (7.3%)	1/29 (3.4%)	10/171 (5.8%)	51/809 (6.3%)	1/7 (14.3%)	4/40 (10.0%)	163/1817 (9.0%)
	Police officers	8/56 (14.3%)	n.a.	n.a.	11/42 (26.2%)	1/14 (7.1%)	1/2 (50.0%)	0/3 (0%)	21/117 (17.9%)

n = number. n.a. = not applicable.

Table 11. Odds ratios of EPEC (enteropathogenic *E. coli*) in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n
EPEC (enteropathogenic <i>E. coli</i>)									
Before 2010	Soldiers	0.6 (0.3 , 1.4), P=0.3161	3.4 (<0.1 , 83.2), P=1.0000	n.e.	0.5 (0.2 , 1.1) P=0.0940	0.6 (0.4 , 0.9), P=0.0237	n.e.	n.e.	0.6 (0.4 , 0.8), P=0.0035
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	0.4 (0.2 , 0.9), P=0.0270	0.4 (<0.1 , 6.3), P=0.6208	0.4 (<0.1 , 7.5), P=0.6134	0.9 (<0.1 , 16.7), P=1.0000	0.5 (0.2 , 1.1), P=0.0819	5.1 (0.5 , 56.3), P=0.2468	0.5 (<0.1 , 8.3), P=1.0000	0.4 (0.2 , 0.7), P=0.0029
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2015-2019	Soldiers	2.5 (1.8 , 3.4), P<0.0001	1.5 (0.4 , 4.9), P=0.4717	0.6 (<0.1 , 4.5), P=1.0000	6.1 (1.4 , 25.7), P=0.0294	1.2 (0.7 , 1.9), P=0.6601	3.4 (<0.1 , 83.2), P=1.0000	6.9 (1.1 , 40.8), P=0.0679	1.9 (1.5 , 2.5), P<0.0001
	Police officers	1.1 (0.2 , 5.8), P=1.0000	n.e.	n.e.	4.0 (1.3 , 12.2), P=0.0178	0.9 (0.1 , 8.2), P=1.0000	n.e.	n.e.	2.2 (0.9 , 5.3), P=0.0886
2020-2022	Soldiers	1.9 (1.1 , 3.3), P=0.0239	2.0 (<0.1 , 42.4), P=1.0000	n.e.	3.4 (<0.1 , 83.2), P=1.0000	0.2 (<0.1 , 3.6), P=0.2568	2.0 (<0.1 , 42.4), P=1.0000	n.e.	1.5 (0.9 , 2.5), P=0.1625
	Police officers	0.6 (0.1 , 2.9), P=0.7362	n.e.	n.e.	1.3 (0.4 , 4.4), P=0.7445	0.9 (<0.1 , 19.4), P=1.0000	13.5 (0.5 , 342.2), P=0.1864	n.e.	1.0 (0.4 , 2.7), P=1.0000
After 2022	Soldiers	0.9 (0.3 , 2.5), P=1.0000	3.4 (<0.1 , 83.2), P=1.0000	n.e.	0.7 (<0.1 , 11.9), P=1.0000	3.4 (<0.1 , 83.2), P=1.0000	3.4 (<0.1 , 83.2), P=1.0000	0.9 (0.2 , 3.8), P=1.0000	0.8 (0.3 , 1.8), P=0.6969
	Police officers	0.7 (0.2 , 2.3), P=0.7847	n.e.	n.e.	0.2 (<0.1 , 4.2), P=0.3541	0.3 (<0.1 , 6.4), P=0.5884	1.5 (<0.1 , 38.0), P=1.0000	0.6 (<0.1 , 12.9), P=1.0000	0.4 (0.1 , 1.3), P=0.1531
Total	Soldiers	1.5 (1.1 , 2.0), P=0.0037	0.8 (0.2 , 2.6), P=1.0000	0.4 (<0.1 , 2.7), P=0.5088	0.6 (0.3 , 1.2), P=0.2010	0.7 (0.5 , 0.9), P=0.0258	1.7 (0.2 , 14.1), P=0.4835	1.1 (0.4 , 3.2), P=0.7783	ref.
	Police officers	0.8 (0.3 , 1.8), P=0.6654	n.e.	n.e.	1.6 (0.7 , 3.7), P=0.2675	0.4 (<0.1 , 2.8), P=0.4629	4.6 (0.3 , 76.1), P=0.3368	0.6 (<0.1 , 12.9), P=1.0000	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.



Table 12. Temporal and spatial distribution of ETEC (enterotoxigenic *E. coli*) in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
ETEC (enterotoxigenic <i>E. coli</i>)									
Before 2010	Soldiers	0/120 (0%)	0/1 (0%)	n.a.	3/150 (2%)	3/422 (0.7%)	n.a.	n.a.	6/693 (0.9%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	4/139 (2.9%)	0/13 (0%)	1/11 (9.1%)	0/5 (0%)	0/167 (0%)	1/3 (33.3%)	0/10 (0%)	6/348 (1.7%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	13/305 (4.3%)	3/24 (12.5%)	3/18 (16.7%)	1/8 (12.5%)	4/196 (2%)	0/1 (0%)	0/5 (0%)	24/557 (4.3%)
	Police officers	1/10 (10%)	n.a.	n.a.	0/15 (0%)	0/6 (0%)	n.a.	n.a.	1/31 (3.2%)
2020–2022	Soldiers	14/106 (13.2%)	0/2 (0%)	n.a.	0/1 (0%)	1/23 (4.3%)	0/2 (0%)	n.a.	15/134 (11.2%)
	Police officers	2/17 (11.8%)	n.a.	n.a.	2/18 (11.1%)	1/2 (50%)	0/1 (0%)	n.a.	5/38 (13.2%)
After 2022	Soldiers	2/50 (4.0%)	0/1 (0%)	n.a.	0/7 (0%)	0/1 (0%)	0/1 (0%)	0/25 (0%)	2/85 (2.4%)
	Police officers	6/29 (20.7%)	n.a.	n.a.	0/9 (0%)	1/6 (16.7%)	1/1 (100%)	1/3 (33.3%)	9/48 (18.8%)
Total	Soldiers	33/720 (4.6%)	3/41 (43.9%)	4/29 (7.3%)	4/171 (2.3%)	8/809 (1.0%)	1/7 (14.3%)	0/40 (0%)	61/1817 (3.4%)
	Police officers	9/56 (16.1%)	n.a.	n.a.	2/42 (4.8%)	2/14 (14.3%)	1/2 (50.0%)	1/3 (33.3%)	15/117 (12.8%)

n = number. n.a. = not applicable.

Table 13. Odds ratios of ETEC (enterotoxigenic *E. coli*) in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n
ETEC (enterotoxigenic <i>E. coli</i>)									
Before 2010	Soldiers	0.1 (<0.1 , 1.9), P=0.0301	9.5 (0.4 , 236.3), P=1.0000	n.e.	0.6 (0.2 , 1.9), P=0.4779	0.2 (<0.1 , 0.7), P=0.0055	n.e.	n.e.	0.3 (0.1 , 0.6), P=0.0009
2010-2014	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
	Soldiers	0.9 (0.3 , 2.4), P=1.0000	1.1 (<0.1 , 18.0), P=1.0000	2.9 (0.4 , 22.9), P=0.3166	2.6 (0.1 , 47.5), P=1.0000	0.1 (<0.1 , 1.4), P=0.0081	14.4 (1.3 , 161.0), P=0.0988	1.4 (<0.1 , 23.5), P=1.0000	0.5 (0.2 , 1.2), P=0.1491
2015-2019	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
	Soldiers	1.0 (0.5 , 1.8), P=0.8812	4.1 (1.2 , 14.2), P=0.0482	5.8 (1.6 , 20.4), P=0.0227	4.1 (0.5 , 34.0), P=0.2420	0.6 (0.2 , 1.7), P=0.4367	9.5 (0.4 , 236.3), P=1.0000	2.6 (0.1 , 47.5), P=1.0000	1.3 (0.8 , 2.1), P=0.3538
2020-2022	Police officers	0.8 (<0.1 , 6.4), P=1.0000	n.e.	n.e.	0.2 (<0.1 , 3.8), P=0.2161	0.5 (<0.1 , 9.5), P=1.0000	n.e.	n.e.	0.2 (<0.1 , 1.8), P=0.1940
	Soldiers	4.4 (2.4 , 8.1), P<0.0001	5.7 (0.3 , 120.3), P=1.0000	n.e.	9.5 (0.4 , 236.3), P=1.0000	1.3 (0.2 , 9.9), P=0.5476	5.7 (0.3 , 120.3), P=1.0000	n.e.	3.6 (2.0 , 6.6), P=0.0001
After 2022	Police officers	0.9 (0.2 , 4.4), P=1.0000	n.e.	n.e.	0.9 (0.2 , 4.1), P=1.0000	6.8 (0.4 , 114.7), P=0.2518	2.2 (<0.1 , 56.6), P=1.0000	n.e.	1.0 (0.3 , 3.1), P=1.0000
	Soldiers	1.2 (0.3 , 5.1), P=0.6849	9.5 (0.4 , 236.3), P=1.0000	n.e.	1.9 (0.1 , 33.7), P=1.0000	9.5 (0.4 , 236.3), P=1.0000	9.5 (0.4 , 236.3), P=1.0000	0.6 (<0.1 , 9.3), P=1.0000	0.7 (0.2 , 2.9), P=1.0000
Total	Police officers	1.8 (0.6 , 5.1), P=0.3730	n.e.	n.e.	0/9 (0%), P=1.0000	1.4 (0.1 , 12.5), P=0.5747	19.8 (0.8 , 509.4), P=0.1356	3.4 (0.3 , 39.9), P=0.3516	1.6 (0.3 , 3.9), P=0.3381
	Soldiers	1.4 (0.9 , 2.1), P=0.1746	2.3 (0.7 , 7.6), P=0.1652	4.6 (1.6 , 13.6), P=0.0171	0.7 (0.2 , 1.9), P=0.6525	0.3 (0.1 , 0.6), P=0.0007	4.8 (0.6 , 40.1), P=0.2153	0.4 (<0.1 , 5.8), P=0.6402	ref.
	Police officers	1.3 (0.5 , 3.2), P=0.6395	n.e.	n.e.	0.3 (<0.1 , 1.6), P=0.2426	1.1 (0.2 , 5.6), P=1.0000	6.8 (0.4 , 114.7), P=0.2518	3.4 (0.3 , 39.9), P=0.3516	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.





Table 14. Temporal and spatial distribution of EAEC (enteroaggregative *E. coli*) in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
EAEC (enteroaggregative <i>E. coli</i>)									
Before 2010	Soldiers	8/120 (6.7%)	0/1 (0%)	n.a.	4/150 (2.7%)	11/422 (2.6%)	n.a.	n.a.	23/693 (3.3%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	11/139 (7.9%)	0/13 (0%)	3/11 (27.3%)	0/5 (0%)	5/167 (3.0%)	0/3 (0%)	0/10 (0%)	19/348 (5.5%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	13/305 (4.3%)	0/24 (0%)	2/18 (11.1%)	0/8 (0%)	9/196 (4.6%)	0/1 (0%)	1/5 (20%)	25/557 (4.5%)
	Police officers	1/10 (10%)	n.a.	n.a.	0/15 (0%)	0/6 (0%)	n.a.	n.a.	1/31 (3.2%)
2020–2022	Soldiers	2/106 (1.9%)	0/2 (0%)	n.a.	0/1 (0%)	0/23 (0%)	0/2 (0%)	n.a.	2/134 (1.5%)
	Police officers	2/17 (11.8%)	n.a.	n.a.	0/18 (0%)	0/2 (0%)	0/1 (0%)	n.a.	2/38 (5.3%)
After 2022	Soldiers	2/50 (4.0%)	0/1 (0%)	n.a.	0/7 (0%)	0/1 (0%)	0/1 (0%)	1/25 (4.0%)	3/85 (3.5%)
	Police officers	1/29 (3.4%)	n.a.	n.a.	0/9 (0%)	0/6 (0%)	0/1 (0%)	0/3 (0%)	1/48 (2.1%)
Total	Soldiers	36/720 (5.0%)	0/41 (0%)	5/29 (17.2%)	4/171 (2.3%)	25/809 (3.1%)	0/7 (0%)	2/40 (5.0%)	72/1817 (4.0%)
	Police officers	4/56 (7.1%)	n.a.	n.a.	0/42 (0%)	0/14 (0%)	0/2 (0%)	0/3 (0%)	4/117 (3.4%)

n = number. n.a. = not applicable.

Table 15. Odds ratios of EAEC (enteroaggregative *E. coli*) in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n
EAEC (enteroaggregative <i>E. coli</i>)									
Before 2010	Soldiers	1.7 (0.8 , 3.7), P=0.1525	8.0 (0.3 , 198.9), P=1.0000	n.e.	0.7 (0.2 , 1.8), P=0.6567	0.6 (0.3 , 1.2), P=0.2360	n.e.	n.e.	0.8 (0.5 , 1.3), P=0.5231
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	2.1 (1.1 , 4.0), P=0.0445	0.9 (<0.1 , 15.2), P=1.0000	9.1 (2.4 , 35.0), P=0.0086	2.2 (0.1 , 40.0), P=1.0000	0.7 (0.3 , 1.9), P=0.6772	3.4 (0.2 , 67.3), P=1.0000	1.1 (<0.1 , 19.8), P=1.0000	1.4 (0.8 , 2.4), P=0.2588
	Police officers	n.e.	n.e.	n.e.	n.a.	n.e.	n.a.	n.e.	n.e.
2015-2019	Soldiers	1.1 (0.6 , 2.0), P=0.9289	0.5 (<0.1 , 8.2), P=1.0000	3.0 (0.7 , 13.4), P=0.1622	1.4 (<0.1 , 24.8), P=1.0000	1.2 (0.6 , 2.4), P=0.8145	8.0 (0.3 , 198.9), P=1.0000	6.1 (0.7 , 54.9), P=0.1851	1.1 (0.7 , 1.8), P=0.6701
	Police officers	3.1 (0.3 , 31.1), P=0.3410	n.e.	n.e.	0.8 (<0.1 , 15.9), P=1.0000	1.9 (<0.1 , 40.1), P=1.0000	n.e.	n.e.	0.9 (0.1 , 8.7), P=1.0000
2020-2022	Soldiers	0.5 (0.1 , 1.9), P=0.4328	4.8 (0.2 , 101.2), P=1.0000	n.e.	8.0 (0.3 , 198.9), P=1.0000	0.5 (<0.1 , 8.5), P=1.0000	4.8 (0.2 , 101.2), P=1.0000	n.e.	0.4 (<0.1 , 1.5), P=0.2352
	Police officers	3.8 (0.6 , 22.4), P=0.1675	n.e.	n.e.	0.7 (<0.1 , 13.2), P=1.0000	5.0 (0.2 , 121.3), P=1.0000	8.4 (0.3 , 236.6), P=1.0000	n.e.	1.6 (0.3 , 8.9), P=0.6354
After 2022	Soldiers	1.0 (0.2 , 4.2), P=1.0000	8.0 (0.3 , 198.9), P=1.0000	n.e.	1.6 (<0.1 , 28.4), P=1.0000	8.0 (0.3 , 198.9), P=1.0000	8.0 (0.3 , 198.9), P=1.0000	1.0 (0.1 , 7.6), P=1.0000	0.9 (0.3 , 2.9), P=1.0000
	Police officers	1.0 (0.1 , 9.4), P=1.0000	n.e.	n.e.	0/9 (0%)	1.9 (<0.1 , 40.1), P=1.0000	8.4 (0.3 , 236.6), P=1.0000	3.6 (0.2 , 80.8), P=1.0000	0.6 (<0.1 , 5.5), P=1.0000
Total	Soldiers	1.3 (0.8 , 1.9), P=0.2901	0.3 (<0.1 , 4.8), P=0.4045	5.0 (1.9 , 13.6), P=0.0060	0.6 (0.2 , 1.6), P=0.4027	0.8 (0.5 , 1.2), P=0.3260	1.6 (<0.1 , 28.4), P=1.0000	1.3 (0.3 , 5.4), P=0.6722	ref.
	Police officers	2.2 (0.5 , 9.0), P=0.2752	n.e.	n.e.	0.3 (<0.1 , 5.6), P=0.5738	0.9 (<0.1 , 17.0), P=1.0000	5.0 (0.2 , 121.3), P=1.0000	3.6 (0.2 , 80.8), P=1.0000	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.





Table 16. Temporal and spatial distribution of *Vibrio* spp. in deployed forces (raw data)

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n (%)
<i>Vibrio</i> spp.									
Before 2010	Soldiers	0/120 (0%)	0/1 (0%)	n.a.	0/150 (0%)	0/422 (0%)	n.a.	n.a.	0/693 (0%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2010–2014	Soldiers	1/139 (0.7%)	1/13 (7.7%)	0/11 (0%)	0/5 (0%)	1/167 (0.6%)	0/3 (0%)	0/10 (0%)	3/348 (0.9%)
	Police officers	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
2015–2019	Soldiers	22/305 (7.2%)	1/24 (4.2%)	0/18 (0%)	1/8 (12.5%)	4/196 (2.0%)	0/1 (0%)	0/5 (0%)	28/557 (5.0%)
	Police officers	0/10 (0%)	n.a.	n.a.	1/15 (6.7%)	2/6 (33.3%)	n.a.	n.a.	3/31 (9.7%)
2020–2022	Soldiers	5/106 (4.7%)	0/2 (0%)	n.a.	0/1 (0%)	0/23 (0%)	0/2 (0%)	n.a.	5/134 (3.7%)
	Police officers	0/17 (0%)	n.a.	n.a.	0/18 (0%)	0/2 (0%)	0/1 (0%)	n.a.	0/38 (0%)
After 2022	Soldiers	0/50 (0%)	0/1 (0%)	n.a.	0/7 (0%)	0/1 (0%)	0/1 (0%)	0/25 (0%)	0/85 (0%)
	Police officers	0/29 (0%)	n.a.	n.a.	0/9 (0%)	1/6 (16.7%)	0/1 (0%)	0/3 (0%)	1/48 (2.1%)
Total	Soldiers	28/720 (3.9%)	2/41 (4.9%)	0/29 (0%)	1/171 (0.6%)	5/809 (0.6%)	0/7 (0%)	0/40 (0%)	36/1817 (2.0%)
	Police officers	0/56 (0%)	n.a.	n.a.	1/42 (2.4%)	3/14 (21.4%)	0/2 (0%)	0/3 (0%)	4/117 (3.4%)

n = number. n.a. = not applicable.

Table 17. Odds ratios of *Vibrio* spp. in deployed forces by WHO region of deployment site and assessment period compared to the totals of deployed soldiers and police officers (references). Lower odds ratios are indicated in green, higher odds ratios in red. No color coding is applied in case of lacking significance or lacking values

Assessment period	Population	African Region, n/n (%)	Region of the Americas, n/n (%)	South-East Asia Region, n/n (%)	European Region, n/n (%)	Eastern Mediterranean Region, n/n (%)	Western Pacific Region, n/n (%)	Multiple WHO regions, n/n (%)	Total, n
<i>Vibrio</i> spp.									
Before 2010	Soldiers	0.2 (<0.1 , 3.3), P=0.1655	16.3 (0.7 , 406.4), P=1.0000	n.e.	0.2 (<0.1 , 2.7), P=0.1073	0.1 (<0.1 , 0.9), P=0.0069	n.e.	n.e.	<0.1 (<0.1 , 0.6), P=0.0004
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2010-2014	Soldiers	0.4 (<0.1 , 2.6), P=0.5139	4.1 (0.5 , 32.6), P=0.2339	2.1 (0.1 , 36.7), P=1.0000	4.4 (0.2 , 81.8), P=1.0000	0.3 (<0.1 , 2.1), P=0.3630	7.0 (0.4 , 137.6), P=1.0000	2.3 (0.1 , 40.4), P=1.0000	0.4 (0.1 , 1.4), P=0.2232
	Police officers	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.	n.e.
2015-2019	Soldiers	3.8 (2.2 , 6.6), P<0.0001	2.1 (0.3 , 15.7), P=0.3999	1.3 (<0.1 , 22.3), P=1.0000	7.1 (0.8 , 59.0), P=0.1514	1.0 (0.4 , 2.9), P=0.9548	16.3 (0.7 , 406.4), P=1.0000	4.4 (0.2 , 81.8), P=1.0000	2.6 (1.6 , 4.3), P=0.0002
	Police officers	1.2 (<0.1 , 23.9), P=1.0000	n.e.	n.e.	2.0 (0.2 , 19.4), P=0.4583	14.1 (2.0 , 101.2), P=0.0274	n.e.	n.e.	3.0 (0.6 , 14.3), P=0.1600
2020-2022	Soldiers	2.4 (0.9 , 6.4), P=0.0714	9.8 (0.5 , 207.1), P=1.0000	n.e.	16.3 (0.7 , 406.4), P=1.0000	1.0 (<0.1 , 17.4), P=1.0000	9.8 (0.5 , 207.1), P=1.0000	n.e.	1.9 (0.7 , 5.0), P=0.1983
	Police officers	0.7 (<0.1 , 14.0), P=1.0000	n.e.	n.e.	0.7 (<0.1 , 13.2), P=1.0000	5.0 (0.2 , 121.3), P=1.0000	8.4 (0.3 , 236.6), P=1.0000	n.e.	0.3 (<0.1 , 6.3), P=0.5726
After 2022	Soldiers	0.5 (<0.1 , 8.0), P=0.6234	16.3 (0.7 , 406.4), P=1.0000	n.e.	3.3 (0.2 , 58.1), P=1.0000	16.3 (0.7 , 406.4), P=1.0000	16.3 (0.7 , 406.4), P=1.0000	1.0 (<0.1 , 16.0), P=1.0000	0.3 (<0.1 , 4.7), P=0.4053
	Police officers	0.4 (<0.1 , 8.1), P=0.5847	n.e.	n.e.	1.3 (<0.1 , 26.6), P=1.0000	5.7 (0.5 , 60.3), P=0.2246	8.4 (0.3 , 236.6), P=1.0000	3.6 (0.2 , 80.8), P=1.0000	0.6 (<0.1 , 5.5), P=1.0000
Total	Soldiers	2.0 (1.2 , 3.3), P=0.0087	2.5 (0.6 , 10.9), P=0.2037	0.8 (<0.1 , 13.8)	0.3 (<0.1 , 2.1), P=0.3670	0.3 (0.1 , 0.8), P=0.0150	3.3 (0.2 , 58.1), P=1.0000	0.6 (<0.1 , 10.0), P=1.0000	ref.
	Police officers	0.2 (<0.1 , 4.2), P=0.3059	n.e.	n.e.	0.7 (<0.1 , 6.3), P=1.0000	7.7 (1.5 , 38.9), P=0.0266	5.0 (0.2 , 121.3), P=1.0000	3.6 (0.2 , 80.8), P=1.0000	ref.

n = number. n.e. = not estimable. ref. = reference. P = significance level.



culture-based assessments [9, 10]. While low colonization rates for ESBL-positive Enterobacterales and virtual non-abundance of vancomycin-resistant enterococci in stool samples of German returnees from deployment had been described previously [6], the here presented assessment provides evidence for high prevalence of associated molecular resistance determinants. Admittedly, the approach did not necessarily measure the abundance of vital resistant bacteria, because the applied molecular diagnostic approach might have resulted in the identification of DNA detritus from already dead bacteria as well [32]. Even in this case, however, the obtained data provide evidence on very high exposure rates of deployed German military and police forces compared to previously reported culture-based results [6, 7].

Second, the assessment indicates a both geographically as well as periodically uneven detection rate of molecular resistance determinants in the stool samples collected during the post-deployment investigations. In case of *vanB* gene assessment, for example, even contradictory tendencies for colonization rates with vancomycin-resistant enterococci in the gut of deployed soldiers and of police officers over time could be demonstrated. For CTX-M-type beta-lactamase genes, a tendency for declining prevalence over the assessment periods could be observed for deployed military personnel, although the international spread of ESBL-positive Enterobacterales is still ongoing and evolving [33]. These findings indicate that not only geographic but also mission-specific characteristics may affect colonization rates of deployed soldiers with resistant bacteria. This issue makes direct conclusions from the local epidemiology challenging and encourages mission-tailored surveillance approaches.

Third, there were marked differences in the temporal and spatial dynamics of assessed molecular resistance determinants over the various assessed deployment periods and regions compared to the co-assessed enteropathogenic bacteria. The lacking parallelism in these developments makes simple explanations like, e.g., better or worse compliance with standard infection prevention and control procedures, considerably less likely. Enteric colonization with bacterial enteric pathogens on the one hand as well as ESBL-positive Enterobacterales and vancomycin-resistant enterococci on the other hand is mediated via the fecal-oral transmission route. However, even the COVID-19-pandemic period 2020–2022, when comparably strict hygiene protocols were enforced on deployment, was not associated with a marked and stable decrease of recorded colonization rates with both enteropathogenic bacteria and resistant enteric bacterial colonizers. This finding is in line with previous observations on deployment-associated infections in German soldiers and police officers, suggesting only minor influence of the COVID-19 pandemic period [11].

Of note, the observed detection rates of *Vibrio* spp. in the assessed returnees from deployment were in a similar range like the EAEC detection rates. High recorded cycle threshold values mostly >35 (see also [supplementary Table 7](#)

for details) suggested most likely pathogen DNA residuals from previous, already cleared infections on deployment. Nevertheless, the findings encourage ongoing consideration of *Vibrio* spp. as a potential causative agent of diarrhea on deployment. Noteworthy, oral whole cell vaccines against cholera [34] contain target DNA of the *Vibrio* spp. PCR and so, residual DNA from very recent oral vaccination can be an alternative explanation of positive *Vibrio* spp. PCR rather than true infection. Within biological matrices like stool, DNA of dead microorganisms as, e.g., associated with the oral cholera vaccine, is preserved for several days [32].

From the point of view of individual medicine, the observed enteric colonization rates with ESBL-positive Enterobacterales or vancomycin-resistant enterococci are usually not harmful for healthy deployed forces. However, it can contribute to the further spread of such resistant bacteria and associated infections in more vulnerable populations. Historic investigations have indicated that at least culturally detectable quantities of ESBL-positive Enterobacterales in the human gut after travelling abroad have a good prognosis of spontaneous vanishing in the course of several months after travel [35, 36]. At least within the first months after return from deployment, thorough compliance with standard hygiene procedures is nevertheless advisable in order not to facilitate an avoidable spread of resistant bacteria, which is quite likely in the household setting as reported elsewhere [36].

Our study has several limitations. The number and composition of available samples was limited by the number of individuals who provided specimens for voluntary post-deployment assessments. Insofar, the study population is not fully representative for the total of deployed German soldiers and police officers which needs to be considered when interpreting the results. This also contributed to the above-mentioned uneven distribution of assessed specimens over the different deployment periods and regions. For the same reason, the investigation was designed as a holistic exploratory, hypothesis-forming assessment only, without elaborated statistical analyses. Future confirmatory studies should be performed with a well-defined and standardized study population.

CONCLUSIONS

In spite of the abovementioned limitations, the investigations confirmed two-digit prevalence rates for the resistance-mediating genes *bla*_{CTX-M} and *vanB* in stool samples of deployed German soldiers and police officers. This prevalence shows a variance depending on the region and period of deployment which is not matched with detection dynamics of bacterial enteropathogenic microorganisms in spite of a comparable transmission route. Multiple factors on deployment may have affected specific resistance prevalence values, as, e.g., recently demonstrated for co-occurring travelers' diarrhea as well as its therapy with antibiotic drugs [37].



Conflicts of interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Author contributions: Conceptualization, V.N., H.F.; methodology, V.N., S.D., A.P.S., U.S., H.F.; software, V.N.; validation, V.N., H.F.; formal analysis, V.N.; investigation, V.N., D.F.W., M.H., H.F.; resources, D.F.W., H.F.; data curation, V.N.; writing—original draft preparation, V.N., H.F.; writing—review and editing, V.N., D.F.W., M.H., U.M., S.D., A.P.S., U.S., H.F.; visualization, V.N., H.F.; supervision, H.F.; project administration, H.F.; funding acquisition, H.F. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

ACKNOWLEDGEMENTS

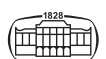
Annett Michel and Simone Priesnitz are gratefully acknowledged for excellent technical assistance, Nancy Schumacher for excellent data management assistance.

SUPPLEMENTARY DATA

Supplementary data to this article can be found online at <https://doi.org/10.1556/1886.2024.00093>.

REFERENCES

1. Antimicrobial resistance 21 November 2023 key facts. Available online: <https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance> (accessed on 01 June 2024).
2. Hutley EJ, Matheson AS, Biswas J, Green AD. Rapid intelligence and failing weapons: meeting the challenges of 21st century infections in the deployed clinical environment. *J R Army Med Corps.* 2013;159:144–9.
3. Waterman P, Kwak Y, Clifford R, Julius M, Onmus-Leone F, Tsurgeon C, et al. A multidrug-resistance surveillance network: 1 year on. *Lancet Infect Dis.* 2012;12:587–8.
4. Chandrasekera RM, Lesho EP, Chukwuma U, Cummings JF, Waterman PE. The state of antimicrobial resistance surveillance in the military health system: a review of improvements made in the last 10 years and remaining surveillance gaps. *Mil Med.* 2015;180:145–50.
5. Lesho E, Clifford R, Onmus-Leone F, Appalla L, Snesrud E, Kwak Y, et al. The challenges of implementing next generation sequencing across a large healthcare system, and the molecular epidemiology and antibiotic susceptibilities of carbapenemase-producing bacteria in the healthcare system of the U.S. Department of Defense. *PLoS One.* 2016;11:e0155770.
6. Frickmann H, Wiemer D, Frey C, Hagen RM, Hinz R, Podbielski A, et al. Low enteric colonization with multidrug-resistant pathogens in soldiers returning from deployments- experience from the years 2007–2015. *PLoS One.* 2016;11:e0162129.
7. Pankok F, Fuchs F, Loderstädt U, Kaase M, Balczun C, Scheithauer S, et al. Molecular epidemiology of *Escherichia coli* with resistance against third-generation cephalosporines isolated from deployed German soldiers-A retrospective assessment after deployments to the African Sahel region and other sites between 2007 and 2016. *Microorganisms.* 2022;10:2448.
8. Castanheira M, Simner PJ, Bradford PA. Extended-spectrum β -lactamases: an update on their characteristics, epidemiology and detection. *JAC Antimicrob Resist.* 2021;3:dlab092.
9. Trick WE, Paule SM, Cunningham S, Cordell RL, Lankford M, Stosor V, et al. Detection of vancomycin-resistant enterococci before and after antimicrobial therapy: use of conventional culture and polymerase chain reaction. *Clin Infect Dis.* 2004;38:780–6.
10. Singh K, Mangold KA, Wyant K, Schora DM, Voss B, Kaul KL, et al. Rectal screening for *Klebsiella pneumoniae* carbapenemases: comparison of real-time PCR and culture using two selective screening agar plates. *J Clin Microbiol.* 2012;50:2596–600.
11. Wiemer DF, Halfter M, Müseler U, Schawaller M, Frickmann H. Effects of COVID-19-associated infection control on the pattern of infections imported by German soldiers and police officers returning from predominantly tropical deployment sites. *Infect Dis Rep.* 2023;15:778–94.
12. Biswas JS, Lentaigne J, Hill NE, Harrison JJ, Mackenzie H, Akorli E, et al. Epidemiology and etiology of diarrhea in UK military personnel serving on the United Nations Mission in South Sudan in 2017: a prospective cohort study. *Trav Med Infect Dis.* 2019;28:34–40.
13. Velasco JM, Valderamat MT, Nogrado K, Wongstitwilairoong T, Swierczewski B, Bodhidatta L, et al. Diarrheal and respiratory illness surveillance during US-RP Balikpapan 2014. *MSMR.* 2015;22:20–3.
14. Ashbaugh HR, Early JM, Johnson ME, Simons MP, Graf PCF, Riddle MS, et al. A multisite network assessment of the epidemiology and etiology of acquired diarrhea among U.S. Military and Western travelers (global travelers' diarrhea study): a principal role of norovirus among travelers with gastrointestinal illness. *Am J Trop Med Hyg.* 2020;103:1855–63.
15. Walters WA, Reyes F, Soto GM, Reynolds ND, Fraser JA, Aviles R, et al. Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea. *PLoS One.* 2020;15:e0236703.
16. Ashbaugh HR, Early JM, Johnson ME, Simons MP, Graf PCF, Riddle MS, et al. A prospective observational study describing severity of acquired diarrhea among U.S. military and Western travelers participating in the Global Travelers' Diarrhea Study. *Trav Med Infect Dis.* 2021;43:102139.
17. Hahn A, Luetgehetmann M, Landt O, Schwarz NG, Frickmann H. Comparison of one commercial and two in-house TaqMan multiplex real-time PCR assays for detection of enteropathogenic, enterotoxigenic and enteroaggregative *Escherichia coli*. *Trop Med Int Health.* 2017;22:1371–6.
18. Denamur E, Clermont O, Bonacorsi S, Gordon D. The population genetics of pathogenic *Escherichia coli*. *Nat Rev Microbiol.* 2021;19:37–54.
19. Tisdale MD, Tribble DR, Mitra I, Telu K, Kuo HC, Fraser JA, et al. TaqMan Array Card testing of participant-collected stool smears to



- determine the pathogen-specific epidemiology of travellers' diarrhoea. *J Trav Med.* 2022;29:taab138.
20. Begue RE, Meza R, Castellares G, Cabezas C, Vasquez B, Ballardo A, et al. Outbreak of diarrhea due to *Vibrio parahaemolyticus* among military personnel in Lima, Peru. *Clin Infect Dis.* 1995;21:1513–4.
 21. Oyofe BA, Peruski LF, Ismail TF, el-Etr SH, Churilla AM, Wasfy MO, et al. Enteropathogens associated with diarrhea among military personnel during Operation Bright Star 96, in Alexandria, Egypt. *Mil Med.* 1997;162:396–400.
 22. Enserink M. Haiti's cholera outbreak. Cholera linked to U.N. forces, but questions remain. *Science.* 2011;332:776–7.
 23. Barbieri R, Aboudharam G, Raoult D, Drancourt M. *Vibrio vulnificus* casualties during the American Civil War. *Lancet Infect Dis.* 2020;20:170–1.
 24. Baker-Austin C, Oliver JD, Alam M, Ali A, Waldor MK, Qadri F, et al. *Vibrio* spp. infections. *Nat Rev Dis Primers.* 2018;4:8.
 25. Robert Koch-Institut. Infektionsepidemiologisches Jahrbuch meldepflichtiger Krankheiten für 2022, Berlin 2024: 1–210.
 26. van der Zee A, Roorda L, Bosman G, Fluit AC, Hermans M, Smits PH, et al. Multi-centre evaluation of real-time multiplex PCR for detection of carbapenemase genes OXA-48, VIM, IMP, NDM and KPC. *BMC Infect Dis.* 2014;14:27.
 27. Fang H, Ohlsson AK, Jiang GX, Ullberg M. Screening for vancomycin-resistant enterococci: an efficient and economical laboratory-developed test. *Eur J Clin Microbiol Infect Dis.* 2012;31:261–5.
 28. Both A, Berneking L, Berinson B, Lütgehetmann M, Christner M, Aepfelbacher M, et al. Rapid identification of the *vanA/vanB* resistance determinant in *Enterococcus* sp. from blood cultures using the Cepheid Xpert *vanA/vanB* cartridge system. *Diagn Microbiol Infect Dis.* 2020;96:114977.
 29. Messelhäusser U, Colditz J, Thäringen D, Kleih W, Höller C, Busch U. Detection and differentiation of *Vibrio* spp. in seafood and fish samples with cultural and molecular methods. *Int J Food Microbiol.* 2010;142:360–4.
 30. Niesters HG. Quantitation of viral load using real-time amplification techniques. *Methods.* 2001;25:419–29.
 31. Giacalone M, Agata Z, Cozzucoli PC, Alibrandi A. Bonferroni-Holm and permutation tests to compare health data: methodological and applicative issues. *BMC Med Res Methodol.* 2018;18:81.
 32. Monteiro L, Gras N, Vidal R, Cabrita J, Mégraud F. Detection of *Helicobacter pylori* DNA in human feces by PCR: DNA stability and removal of inhibitors. *J Microbiol Methods.* 2001;45:89–94.
 33. Karlowsky JA, Lob SH, DeRyke CA, Siddiqui F, Young K, Motyl MR, et al. Prevalence of ESBL non-CRE *Escherichia coli* and *Klebsiella pneumoniae* among clinical isolates collected by the SMART global surveillance programme from 2015 to 2019. *Int J Antimicrob Agents.* 2022;59:106535.
 34. Saif-Ur-Rahman KM, Mamun R, Hasan M, Meiring JE, Khan MA. Oral killed cholera vaccines for preventing cholera. *Cochrane Database Syst Rev.* 2024;1:CD014573.
 35. Ruppé E, Armand-Lefèvre L, Estellat C, Consigny PH, El Mniai A, Boussadia Y, et al. High rate of acquisition but short duration of carriage of multidrug-resistant enterobacteriaceae after travel to the tropics. *Clin Infect Dis.* 2015;61:593–600.
 36. Arcilla MS, van Hattem JM, Haverkate MR, Bootsma MCJ, van Genderen PJJ, Goorhuis A, et al. Import and spread of extended-spectrum β -lactamase-producing Enterobacteriaceae by international travellers (COMBAT study): a prospective, multi-centre cohort study. *Lancet Infect Dis.* 2017;17:78–85.
 37. Kantele A, Lääveri T, Mero S, Vilkkman K, Pakkanen SH, Ollgren J, et al. Antimicrobials increase travelers' risk of colonization by extended-spectrum betalactamase-producing Enterobacteriaceae. *Clin Infect Dis.* 2015;60:837–46.

