

Original Paper

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# Estimate of the annual burden of foodborne illness in nondeployed active duty US Army Service Members: five major pathogens, 2010–2015

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## Abstract

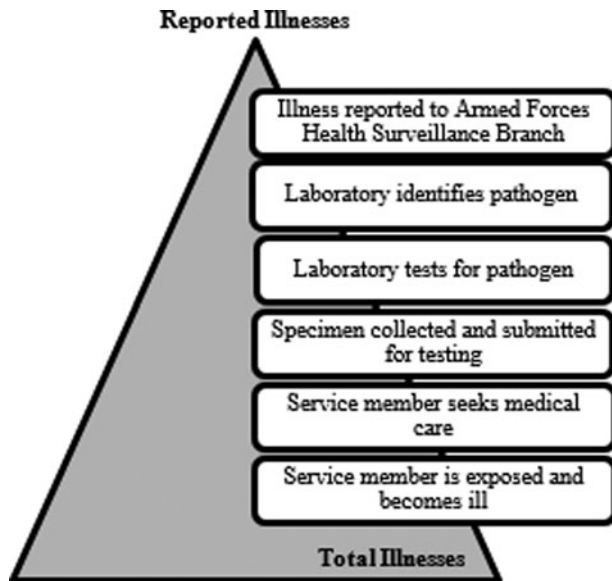
In this study, we estimate the burden of foodborne illness (FBI) caused by five major pathogens among nondeployed US Army service members. The US Army is a unique population that is globally distributed, has its own food procurement system and a food protection system dedicated to the prevention of both unintentional and intentional contamination of food. To our knowledge, the burden of FBI caused by specific pathogens among the US Army population has not been determined. We used data from a 2015 US Army population survey, a 2015 US Army laboratory survey and data from FoodNet to create inputs for two model structures. Model type 1 scaled up case counts of *Campylobacter jejuni*, *Shigella* spp., *Salmonella enterica* non-typhoidal and STEC non-O157 ascertained from the Disease Reporting System internet database from 2010 to 2015. Model type 2 scaled down cases of self-reported acute gastrointestinal illness (AGI) to estimate the annual burden of Norovirus illness. We estimate that these five pathogens caused 45 600 (5%–95% range, 30 300–64 000) annual illnesses among nondeployed active duty US Army Service members. Of these pathogens, Norovirus, *Campylobacter jejuni* and *Salmonella enterica* non-typhoidal were responsible for the most illness. There is a tremendous burden of AGI and FBI caused by five major pathogens among US Army Soldiers, which can have a tremendous impact on readiness of the force. The US Army has a robust food protection program in place, but without a specific active FBI surveillance system across the Department of Defence, we will never have the ability to measure the effectiveness of modern, targeted, interventions aimed at the reduction of specific foodborne pathogens.

## Introduction

Throughout military history, acute gastrointestinal illness (AGI) has been a significant cause of morbidity and mortality among US service members [1]. Despite advances in medicine and improvements in basic sanitation, modern day military operations still are affected by gastrointestinal illness. In 2012, diarrhoeal diseases were responsible for more than 17 000 healthcare encounters affecting over 15 000 US service members [2]. An outbreak of AGI caused by Shiga toxin-producing *Escherichia coli*, a major cause of foodborne illness, sickened 244 male recruits at the Marine Corps Recruit Depot, 15 of which had life threatening complications [3]. Symptoms of AGI include diarrhoea, vomiting, fever, malaise and/or weakness. Not only can AGI affect individual medical readiness, if a large proportion of the military population is affected by AGI, military operational effectiveness can be degraded [4].

One important preventable cause of AGI is foodborne illness. The WHO estimates that as much as 70% of diarrhoeal diseases worldwide can be attributed to foodborne pathogens [5]. Foodborne infections are an important cause of illness in the USA [6], with more than 48 million Americans becoming ill from contaminated foods annually [7]. Members of the US Army are also at risk for foodborne illness. The US Army is a unique population that is globally distributed, has its own food procurement system and a food protection system dedicated to the prevention of both unintentional and intentional contamination of food. To our knowledge, the burden of foodborne illness caused by specific pathogens among the nondeployed active duty US Army military population has not been determined. Foodborne illness burden measures are necessary for directing policy and interventions aimed at reducing the incidence of foodborne disease.

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**Fig. 1.** Burden of Illness pyramid illustrating the steps that must occur for an episode of illness in the active duty US army population to be reported through laboratory surveillance.

Estimating the number of foodborne illnesses caused by specific pathogens among US Army service members can be very challenging for a number of reasons. One challenge is that food can be simultaneously contaminated by a combination of agents that can cause illness including viruses, bacteria, parasites and chemicals [7]. Transmission of these agents can occur through nonfood routes such as consumption of contaminated water or contact with infected animals [7]. The number of infections transmitted by food depends on the level of contamination in the food, the environment in which the food is prepared, the pathogen itself and certain host factors such as immune status and age [7]. Finally, we generally rely on laboratory surveillance to detect cases of foodborne illness, which results in many cases going undetected [8]. Additionally, for the US Army, these issues are compounded by the fact that the US Army does not have a dedicated foodborne illness-specific surveillance system in place.

In the US Army, foodborne diseases are detected through the medical event reporting system (Disease Reporting System internet, DRSi) and only 17 of the 31 major causes of foodborne illness are included as reportable medical events [7, 9]. This system relies on laboratory confirmation of illness aetiology and is not an accurate reflection of the true burden of foodborne disease. For a reportable medical event to be documented, the ill service member must seek medical care and submit a stool specimen, the laboratory must isolate and identify the organism from the sample and positive results must be entered into DRSi (Fig. 1). If any one of these events does not occur, the illness is not recorded. To gain a more accurate estimate of the number of annual foodborne illnesses among US Army service members, we need to estimate the number of cases of disease that go unrecognised at each surveillance step. Scallan *et al.* calculated estimates of foodborne illness in the US through the use of telephone surveys of the population, laboratory surveys, FoodNet surveillance data and data from outbreak investigations [7]. Our current study uses similar methods to create pathogen-specific underreporting and underdiagnosis multipliers to estimate the true burden of disease caused by five major pathogens. Ultimately, the results of this study will be

used to make recommendations for a Department of Defence (DOD)-wide foodborne illness surveillance system, to identify strategies for foodborne illness intervention and to modernise the current US Army food protection program.

## Methods

In 2011, the Centers for Disease Control and Prevention provided estimates of foodborne illnesses in the USA caused by 31 known major pathogens and unspecified agents [7, 10]. We used a similar approach to estimate the annual number of foodborne illnesses among nondeployed active duty US Army service members for five major pathogens: *Campylobacter*, *Salmonella*, *Shigella*, non-O157 shiga-toxin-producing *E. coli* (STEC) and *Norovirus*. We used two different model structures depending on the pathogen. For all bacterial pathogens, we used models that began with the laboratory-confirmed cases counts and then scaled them up through the use of a series of underreporting and underdiagnosis multipliers (model type 1). For *Norovirus*, the model began with the total 2014 nondeployed active duty US Army population and used AGI incidence data to scale the population down to the estimated annual number of noroviral illnesses (model type 2).

For model type 1 we used a number of inputs, each with a measure of uncertainty. These inputs were derived from data obtained through surveys of the nondeployed active duty US Army population [11], US Army clinical laboratories [11] and data from FoodNet and Scallan *et al.* [7]. We chose program evaluation and review technique (PERT) distributions for the majority of the model inputs. The PERT distribution is used for modelling expert estimates using the expert's minimum, most likely and maximum estimates [12]. Similar to Scallan *et al.*, we chose this distribution because it works well when you have many estimates and sources of uncertainty that need to be combined into one model [7]. The general structure for model type 1 is shown in Figure 2, followed by a general description of how each input was ascertained. Tables 1–4 display detailed model input data descriptions for each of the bacterial pathogens.

### DRSi case count

Laboratory-confirmed case counts were ascertained from DRSi. The Army Public Health Center Epidemiology Service provided DRSi case counts of *Salmonella*, *Campylobacter*, STEC and *Shigella* from 2010 to 2015 (Z. McCormic, S. Gosine, email, 29 July 2014). All non-active duty US Army cases and all deployed cases were excluded. All cases were culture-confirmed positive. The STEC cases were not identified specifically as STEC O157:H7, so it was assumed that they were all non-O157:H7 cases. Histograms were constructed for each of the four bacterial pathogens for entry into the model. A non-parametric distribution was used because of the flexibility associated with these types of distributions [12]. The data did not meet the assumptions of parametric count distributions, such as the Poisson distribution [7, 12]. In particular, the annual case counts represented single count samples from distinct annual populations with different characteristics (not identically distributed) [7].

### Underreporting multiplier

In a study by Jordan *et al.* they found that DRSi case capture for *Chlamydia trachomatis* was 79% [13]. A study by Evans *et al.* found that DRSi captured only 30% of Lyme disease cases [14].

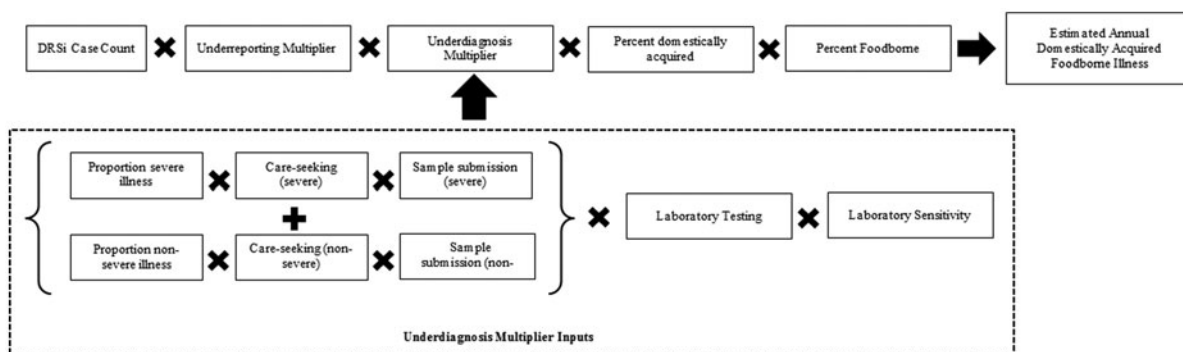


Fig. 2. Basic model structure for model type 1.

Table 1. Model inputs, data source, distribution and distribution values for *Campylobacter*

Pathogen: <i>Campylobacter</i>			
Model Input	Data source	Distribution	Distribution values
Reported illnesses	Laboratory confirmed positive clinical specimens from non-deployed active duty Army service members reported by the Disease Reporting System-internet (DRSi), 2010–2015.	Histogram	2010, 2011, 2012, 2013, 2014, 2015 values: 15, 47, 52, 58, 52, 63
Underreporting	Reports that DRSi captures 30% of Lyme disease cases and 79% of <i>Chlamydia trachomatis</i> cases. Most likely value based on average.	PERT	min, most likely, max values: 0.30, 0.54, 0.79
Percent severe	Proportion of cases by site reporting bloody diarrhoea from FoodNet case-control study of sporadic laboratory-confirmed <i>Campylobacter</i> infections.	PERT	min, most likely, max values: 0.36, 0.45, 0.52
Medical care seeking (severe)	Proportion (and 95% confidence interval (CI)) of survey respondents with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.14, 0.33, 0.52
Medical care seeking (mild)	Proportion (and 95% CI) of survey respondents with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.15, 0.19, 0.24
Specimen submission (severe)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.10, 0.13, 0.35
Specimen submission (mild)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.04, 0.12, 0.20
Laboratory testing	92.3% of clinical US Army clinical laboratories reported routinely testing stool samples for <i>Campylobacter</i> in the 2014 survey of Army clinical laboratories. Minimum value calculated based on if all other non-surveyed labs of same size do not routinely test. Max calculated based on if the one laboratory was the only lab that did not routinely test.	PERT	min, most likely, max values: 0.78, 0.92, 0.98
Test sensitivity	From the FoodNet study: they used a laboratory test sensitivity rate of 70% based on studies of <i>Salmonella</i> . They used a lower bound of 60% and an upper bound of 90%.	PERT	min, most likely, max values: 0.60, 0.70, 0.90
Proportion travel-related	From Scallan <i>et al.</i> [7, 10]; proportion of FoodNet cases of <i>Campylobacter</i> who reported travel outside the USA within 7 days of illness onset (2005–2008).	PERT	min, most likely, max values: 0.14, 0.20, 0.27
Proportion foodborne	From the FoodNet study: 1-total non-foodborne population attributable fractions from FoodNet case-control study.	PERT	min, most likely, max values: 0.73, 0.80, 0.86

Underreporting for the four bacterial pathogens of interest in this study likely falls somewhere between these two numbers and a PERT distribution was constructed accordingly. The same underreporting PERT distribution was used for all four bacterial pathogens. Detailed information for the underreporting model inputs are displayed in Tables 1–4.

### Underdiagnosis multiplier

The underdiagnosis multiplier is made up of eight different model inputs (Fig. 2). PERT distributions were constructed for each of the eight inputs using the minimum, most likely and maximum values.

**Table 2.** Model inputs, data source, distribution and distribution values for *Salmonella enterica* non-typhoidal serotypes

Pathogen: <i>Salmonella enterica</i>			
Model input	Data source	Distribution	Distribution values
Reported illnesses	Laboratory confirmed positive clinical specimens from non-deployed active duty Army service members reported by the Disease Reporting System-internet (DRSi), 2010–2015.	Empirical	2010, 2011, 2012, 2013, 2014, 2015 values: 2, 18, 8, 12, 13, 21
Underreporting	Reports that DRSi captures 30% of Lyme disease cases and 79% of <i>Chlamydia trachomatis</i> cases. Most likely value based on average.	PERT	min, most likely, max values: 0.30, 0.54, 0.79
Per cent severe	Proportion of cases by site reporting bloody diarrhoea from FoodNet case-control study of sporadic laboratory-confirmed <i>Salmonella</i> infections.	PERT	min, most likely, max values: 0.17, 0.35, 0.53
Medical care seeking (severe)	Proportion (and 95% confidence interval (CI)) of survey respondents with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.14, 0.33, 0.52
Medical care seeking (mild)	Proportion (and 95% CI) of survey respondents with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.15, 0.19, 0.24
Specimen submission (severe)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.10, 0.13, 0.35
Specimen submission (mild)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.04, 0.12, 0.20
Laboratory testing	100% of clinical US Army clinical laboratories reported routinely testing stool samples for <i>Shigella</i> in the 2014 survey of Army clinical laboratories. Based on expert opinion from US Army Laboratory personnel, assumed 94% and 97% min and most likely estimate.	PERT	min, most likely, max values: 0.94, 0.97, 1.00
Test sensitivity	From the FoodNet study: they used a laboratory test sensitivity rate of 70% based on studies of <i>Salmonella</i> . They used a lower bound of 60% and an upper bound of 90%.	PERT	min, most likely, max values: 0.60, 0.70, 0.90
Proportion travel-related	From Scallan <i>et al.</i> [7, 10]; proportion of FoodNet cases of <i>Salmonella</i> who reported travel outside the USA within 7 days of illness onset (2005–2008)	PERT	min, most likely, max values: 0.10, 0.15, 0.21
Proportion foodborne	From Scallan <i>et al.</i> [7, 10]; 31% based on FoodNet enhanced surveillance.	PERT	min, most likely, max values: 0.23, 0.31, 0.40

### Proportion severe illness and proportion non-severe illness

The data for proportion severe illness and non-severe illness were obtained from Scallan *et al.*, Technical Appendix 3 [7]. Depending on the pathogen, these data were based on FoodNet case-control studies or FoodNet surveillance data. Detailed information and model inputs for each pathogen are displayed in Tables 1–4.

### Care seeking and stool specimen submission

To adjust for medical care seeking and specimen submission, results from the 2015 survey of nondeployed active duty US Army service members were used [11]. The proportion of respondents who reported acute diarrhoeal illness in the last 30 days and sought medical care and submitted a stool sample were calculated. People with more severe illness are more likely to seek care and bloody diarrhoea is an indicator of severe disease [15]. Therefore, medical care seeking and stool sample submission for bloody and non-bloody diarrhoea as surrogates for medical care-seeking and stool sample submission for severe and mild cases of illness were used. These four inputs scale up mild and severe illness care-seekers to all mild and severe illnesses in the population and scale up submitted samples from mild and severe illness care-seekers to all ill medical visits [7]. Detailed information and model inputs for each pathogen are displayed in Tables 1–4.

### Laboratory testing

The number of laboratories routinely testing for each of the four bacterial pathogens varied [11]. PERT distributions for each of the pathogens based on the 2014 survey of US Army clinical laboratories were constructed [11]. This factor scales tests performed up to samples submitted [7]. Detailed information and model inputs for each pathogen are displayed in Tables 1–4.

### Laboratory sensitivity

Laboratory specimen handling and practices across the surveyed Army laboratories met most of the recommended guidelines [11]. There were some practices that could result in decreased sensitivity, though quantification of the impact these variations in specimen handling and transport had on the number of positive samples was unable to be performed. The findings were similar to the 2004 survey of FoodNet laboratories, so the Scallan *et al.* data found in Technical Appendix 3 were used to construct the PERT distributions for this model input [7, 16]. The data are based on studies of the laboratory test sensitivity rate of *Salmonella*. This model input scales up positive tests to true positive specimens [7]. Detailed information and model inputs for each pathogen are displayed in Tables 1–4.

**Table 3.** Model inputs, data source, distribution and distribution values for *Shigella* spp

Pathogen: <i>Shigella</i> spp.			
Model input	Data source	Distribution	Distribution values
Reported illnesses	Laboratory confirmed positive clinical specimens from non-deployed active duty Army service members reported by the Disease Reporting System-internet (DRSi), 2010–2015.	Empirical	2010, 2011, 2012, 2013, 2014, 2015 values: 2, 18, 8, 12, 13, 21
Underreporting	Reports that DRSi captures 30% of Lyme disease cases and 79% of <i>Chlamydia trachomatis</i> cases. Most likely value based on average.	PERT	min, most likely, max values: 0.30, 0.54, 0.79
Percent severe	Proportion of cases by site reporting bloody diarrhoea from FoodNet case-control study of sporadic laboratory-confirmed <i>Salmonella</i> infections.	PERT	min, most likely, max values: 0.17, 0.35, 0.53
Medical care seeking (severe)	Proportion (and 95% confidence interval (CI)) of survey respondents with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.14, 0.33, 0.52
Medical care seeking (mild)	Proportion (and 95% CI) of survey respondents with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.15, 0.19, 0.24
Specimen submission (severe)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.10, 0.13, 0.35
Specimen submission (mild)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.04, 0.12, 0.20
Laboratory testing	100% of clinical US Army clinical laboratories reported routinely testing stool samples for <i>Shigella</i> in the 2014 survey of Army clinical laboratories. Based on expert opinion from US Army Laboratory personnel, assumed 94% and 97% min and most likely estimate.	PERT	min, most likely, max values: 0.94, 0.97, 1.00
Test sensitivity	From the FoodNet study: they used a laboratory test sensitivity rate of 70% based on studies of <i>Salmonella</i> . They used a lower bound of 60% and an upper bound of 90%.	PERT	min, most likely, max values: 0.60, 0.70, 0.90
Proportion travel-related	From Scallan <i>et al.</i> [7, 10]; proportion of FoodNet cases of <i>Salmonella</i> who reported travel outside the USA within 7 days of illness onset (2005–2008)	PERT	min, most likely, max values: 0.10, 0.15, 0.21
Proportion foodborne	From Scallan <i>et al.</i> [7, 10]; 31% based on FoodNet enhanced surveillance.	PERT	min, most likely, max values: 0.23, 0.31, 0.40

### Percent domestically acquired

This model input is a contractive factor to scale down case counts to those cases that are domestically acquired, excluding those cases acquired while traveling overseas [7]. The data for this model input was obtained from Scallan *et al.*, Technical Appendix 3 and is based on FoodNet studies that looked at the number of infected individuals who reported travel outside of the US within 7 days of illness to determine the number acquired during travel [7]. Those who reported no travel were considered to have domestically acquired foodborne illness. This data were not available for our population, the assumption was made that our population is similar. Detailed information and model inputs for each pathogen are displayed in Tables 1–4.

### Percent foodborne

This factor scales down overall illness counts to illness counts that are foodborne [7]. The data for this model input were obtained from Scallan *et al.* Technical Appendix 3, based on FoodNet case-control studies, outbreak data and surveillance data, as outlined for each pathogen in Tables 1–4 [7].

Figure 3 illustrates the model structure for *Norovirus*. The annual incidence of AGI among nondeployed US Army service members was estimated previously [11]. The data showed variation in

incidence among geographical US Army medical regions. Estimates of the region-level incidence for each of the five different regions were calculated. Using ModelRisk 5 (VOSE Software), normal distributions of AGI incidence from each site were overlaid using the point estimate and standard error as inputs to the distribution. The distributions were averaged for entry into the model as the annual incidence of AGI. The remaining model inputs and data sources are described in detail in Table 5.

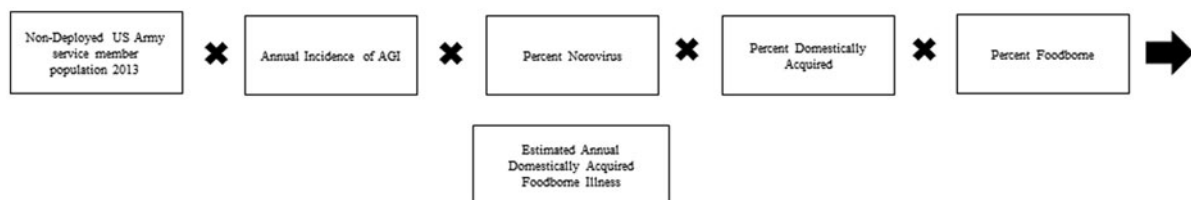
For both model types 1 and 2, once all model input distributions were constructed, Monte Carlo simulation was performed using ModelRisk 5 (Vose Software, 2013, Ghent, Belgium) with 100 000 iterations for each estimation. The results of each simulation were reported as a mean and range between the 5th and 95th percentile. Sensitivity analysis investigating the uncertainty introduced by each model input was conducted. All statistical analysis was performed using ModelRisk 5 (Vose Software, 2013, Ghent, Belgium).

## Results

Distribution inputs and model outputs for each pathogen are displayed in Supplementary Figures S1–S9. Estimated annual number of episodes of domestically acquired foodborne illness among nondeployed active duty Army service members caused

**Table 4.** Model inputs, data source, distribution, and distribution values for Shiga-toxin producing *Escherichia coli*, non-O157

Pathogen: Shiga-toxin producing <i>Escherichia coli</i> , non-O157			
Model input	Data source	Distribution	Distribution values
Reported illnesses	Laboratory confirmed positive clinical specimens from non-deployed active duty Army service members reported by the Disease Reporting System-internet (DRSi), 2010–2015.	Empirical	2010, 2011, 2012, 2013, 2014, 2015 values: 0, 0, 0, 1, 0, 3
Underreporting	Reports that DRSi captures 30% of Lyme disease cases and 79% of <i>Chlamydia trachomatis</i> cases. Most likely value based on average.	PERT	min, most likely, max values: 0.30, 0.54, 0.79
Percent severe	Proportion of cases by site reporting bloody diarrhoea from FoodNet case-control study of sporadic laboratory-confirmed <i>Salmonella</i> infections.	PERT	min, most likely, max values: 0.44, 0.54, 0.64
Medical care seeking (severe)	Proportion (and 95% confidence interval (CI)) of survey respondents with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.14, 0.33, 0.52
Medical care seeking (mild)	Proportion (and 95% CI) of survey respondents with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.15, 0.19, 0.24
Specimen submission (severe)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.10, 0.13, 0.35
Specimen submission (mild)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.04, 0.12, 0.20
Laboratory testing	84.6% of clinical US Army clinical laboratories reported routinely testing stool samples for STEC in the 2014 survey of Army clinical laboratories. Max value based on if the two laboratories not routinely testing were the only two out of 41. Minimum value based on if all laboratories of the same size did not test.	PERT	min, most likely, max values: 0.66, 0.85, 0.95
Test sensitivity	From the FoodNet study: they used a laboratory test sensitivity rate of 70% based on studies of <i>Salmonella</i> . They used a lower bound of 60% and an upper bound of 90%.	PERT	min, most likely, max values: 0.60, 0.70, 0.90
Proportion travel-related	From Scallan <i>et al.</i> [7, 10]; proportion of FoodNet cases of non-O157 STEC who reported travel outside the USA within 7 days of illness onset (2005–2008)	PERT	min, most likely, max values: 0.13, 0.18, 0.25
Proportion foodborne	From Scallan <i>et al.</i> [7, 10]; proportion of non-O157 STEC outbreak-associated illnesses due to foodborne transmission from outbreaks reported to CDC (1990–2008)	PERT	min, most likely, max values: 0.75, 0.82, 0.87

**Fig. 3.** Basic model structure for *Norovirus*.

by *Campylobacter jejuni*, *Shigella* spp., *Salmonella enterica* nontyphoidal, STEC non-O157 and *Norovirus* are presented in Table 6. Due to differences in care-seeking and stool sample submission behaviours among nondeployed active duty Army service members when compared with the general US population, our under-diagnosis multipliers were much higher for the four bacterial pathogens than in the Scallan *et al.* study [7]. Estimates are that these five major pathogens caused 158 500 (5%–95% range: 105 600–220 300) illnesses, of which 156 200 (5%–95% range: 103 600–217 800) were domestically acquired and 45 600 (5%–95% range: 30 300–64 200) were foodborne. Out of these pathogens, *Norovirus* (38 900, 85%) and *Campylobacter* (3650, 8%) caused the most illness in this population.

For the sensitivity analysis, we calculated the variance and coefficient of variance for each of the model inputs to assess how much uncertainty each input added to the model. Overall, the under-diagnosis multiplier as a whole contributed the most uncertainty to the models and this was due to three model inputs: sample submission (non-severe), proportion severe illness and care-seeking (severe).

## Discussion

To our knowledge, this is the first time the burden of foodborne illness caused by specific bacterial and viral pathogens has been estimated in the nondeployed active duty US Army population.

**Table 5.** Model inputs, data source, distribution and distribution values for *Norovirus*

Pathogen: <i>Norovirus</i>			
Model input	Data source	Distribution	Distribution values
Population at risk	Estimated 2013 non deployed active duty US Army service member population	–	528 070
Norovirus fraction	From Scallan <i>et al.</i> [7, 10]; the proportion of all acute gastroenteritis illnesses was estimated from published studies of the proportion of acute gastroenteritis illnesses due to <i>Norovirus</i> in the Netherlands, England and Wales, and Australia. The proportions from these studies were used to define min, most likely, and maximum values.	PERT	min, most likely, max values: 0.06, 0.11, 0.2
Norovirus illnesses	Norovirus fraction (above) applied to the estimated number of acute gastroenteritis illness (below)		
Acute gastroenteritis illnesses	Estimated rate per person year by US Army medical region using data from the 2015 survey of non-deployed active duty US Army service members. We assumed that site estimates were normally distributed with standard deviations equal to survey standard errors.	Normal Distributions	By US Army medial region: 3.3, 2.16, 2.16, 2.32, 2.1
Proportion travel-related	From Scallan <i>et al.</i> [7, 10]; assumed to be low	PERT	0.00, 0.00, 0.02
Proportion foodborne	From Scallan <i>et al.</i> [7, 10]; based on 179 <i>Norovirus</i> outbreaks examined by CDC from 2000 to 2005. Of 13 955 person ill, 3628 (26%) were in foodborne outbreaks.	PERT	min, most likely, max values: 0.19, 0.26, 0.35
Specimen submission (mild)	Proportion (and 95% CI) of survey respondents who submitted a stool specimen among persons with a non-bloody diarrhoea who sought medical care from the 2015 survey of nondeployed US Army service members	PERT	min, most likely, max values: 0.04, 0.12, 0.20

**Table 6.** Estimated annual number of episodes of domestically acquired foodborne illnesses caused by five major pathogens among nondeployed active duty US Army service members

Pathogen	Multipliers				Travel Related, %	Foodborne, %	Estimated domestically acquired foodborne illnesses, mean (5%–95% range)
	Laboratory Confirmed	Under-reporting	Under-diagnosis				
<b>Bacteria</b>							
<i>Campylobacter jejuni</i>	56	1.5	70.1	20	80	3650 (2100–5800)	
<i>Shigella</i> spp.	14	1.5	70	15	31	350 (100–700)	
<i>Salmonella enterica</i> non-typhoidal	32	1.5	63.7	11	93.8	2500 (900–4800)	
STEC non-O157	3	1.5	70.8	18	82	150 (90–300)	
Subtotal						6700 (4200–9700)	
<b>Virus</b>							
<i>Norovirus</i>	NA	NA	NA	<1	26.3	38 900 (24 000– 57 000)	
Total						45 600 (30 300– 64 000)	

Our study shows that underdiagnosis multipliers are higher in this population than in the general US population. The sensitivity analysis revealed three inputs to the underdiagnosis multipliers are contributing the most uncertainty in the models. These data come from a population-based survey of the US Army population and the uncertainty is introduced due to the small number of respondents with non-severe AGI who submitted a sample, the small number of respondents who reported severe illness and the small number of respondents with severe illness who sought

medical care [11]. As previously described, repeating the survey, possibly through face-to-face administration, or through a higher level authority could improve response rate and improve the robustness of the data. This would help to reduce uncertainty in the model and improve model estimates. In addition, DRSi data are collected passively, so underreporting multipliers were required for the four bacterial pathogens of interest. This should be considered in future burden of illness calculations for the US Army population. Similar to other studies, of the five pathogens

**Table 7.** List of pathogens, incubation period, length of illness, clinical symptoms and possible complications

Pathogen	Incubation Period	Length of Illness	Clinical Symptoms	Post-infection Complications
<b>Bacteria</b>				
<i>Campylobacter jejuni</i>	2–5 days	2–10 days	Diarrhoea (often bloody), abdominal pain, fever	Guillain-Barre syndrome, reactive arthritis
<i>Shigella</i> spp.	1–2 days	5–7 days	Diarrhoea (often bloody), often accompanied by fever and abdominal cramps	Post-infection arthritis
<i>Salmonella enterica</i> non-typhoidal	12–72 h	4–7 days	Diarrhoea, often with fever and abdominal cramps	Reactive arthritis
STEC non-O157	1–10 days	5–10 days	Diarrhoea (often bloody), abdominal cramps (often severe), little or no fever	Hemolytic Uremic Syndrome (HUS)
<b>Virus</b>				
<i>Norovirus</i>	12–48 h	1–3 days	Diarrhoea, vomiting, nausea, abdominal cramps, low-grade fever	Rare complications due to severe dehydration

assessed, *Norovirus* was the leading cause of foodborne illness in our population [17]. In the present study, of the four bacterial pathogens, *Campylobacter* and *Salmonella* caused the most illnesses. This finding is similar to studies in England, Wales, Australia and the USA [7, 17, 18]. The estimated number of illnesses caused by these five major pathogens is alarming. Overall, these five pathogens cause an estimated 8600 illness per 100 000 population (range: 5800–12 200 per 100 000). The illnesses caused by these pathogens can vary in duration, severity and post-infection complications (Table 7) and can impact mission readiness if numerous individuals in a unit are affected, especially in outbreak situations.

### Limitations

The DRSi database system only captures individuals seeking care at military medical treatment facilities. If an ill service member sought care at a civilian location, DRSi will not capture the case. It is possible that cases of illness caused by the four bacterial pathogens were missed for this reason, resulting in lower burden estimates, which were not accounted for in the models. The data for this study came from a number of sources, including our own surveys and from FoodNet surveillance and outbreak data. Limitations of our population and laboratory surveys are discussed elsewhere [11]. Limitations of the FoodNet data are discussed in the 2011 Scallan *et al.* burden of illness study [7]. Using the FoodNet data for the US Army population may have resulted in inaccurate estimates. However, the US Army does not have an active surveillance system in place (like FoodNet), so using the FoodNet data was the best option to provide estimates. One input in particular, percent domestically acquired, may have particularly affected the outcomes. The PERT distribution for this model input came directly from FoodNet studies of cases that reported travel outside the USA within 7 days of illness onset [7]. There was no access to patient records where travel history may (or may not) have been recorded. The US Army population is located worldwide and may be more likely than the general US population to travel to countries where risk of foodborne disease is higher. They also may live in overseas locations where the risk of foodborne disease is higher or even lower. That means the actual percent domestically acquired input for the US Army population could either be higher or lower than

the FoodNet estimates. Regardless of these limitations, these data serve as an important baseline of the estimate of foodborne illness caused by five major pathogens. This study also shows that the military population is unique with respect to care-seeking for AGI, stool sample submission and exposure risk, so calculating military-specific underdiagnosis and underreporting multipliers to make foodborne illness burden estimates for the military population is a worthwhile undertaking. The next logical step is to start active surveillance for foodborne illness in the military population so more accurate burden estimates can be calculated in the future.

There are more than 200 known diseases transmitted through food [6]. Foodborne illness can be attributed to viruses, bacteria, parasites, toxins, metals and prions [6]. Estimating the burden of foodborne illness for all causes of foodborne illness was beyond the scope of this present study. Future studies to estimate the burden of illness for all causes of foodborne illness would be helpful to get a better idea of the total burden in the US Army population. Before this lofty undertaking is performed, however, limitations of the current study and previous should be addressed so the most accurate data are produced. Recommendations include: a DoD-sponsored survey of active duty service members across all branches of the military (Air Force, Marines, Navy, etc.); survey of deployed service members to identify unique risk factors for foodborne illness in this population; implementation of a DoD-wide active laboratory-based foodborne illness surveillance system that can monitor trends in the burden of specific foodborne illnesses in the military population over time, detect foodborne illness outbreaks in the military population and attribute the burden of foodborne illness in the military to specific foods and settings; cohort and case-control studies to provide military-specific data for disease burden model inputs; and implementation of specific foodborne illness interventions to modernise the current US Army food protection program aimed at preventing foodborne illness among members of the military.

**Supplementary material.** The supplementary material for this article can be found at <https://doi.org/10.1017/S0950268818003199>.

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