1 **The global distribution of *Bacillus anthracis* and associated anthrax risk to humans,**

2 **livestock, and wildlife**

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37 **Running title:** Global anthrax distribution and risk

38

39   **Summary**

40   *Bacillus anthracis* is a spore-forming, Gram-positive bacterium responsible for anthrax, an acute

41   and commonly lethal infection that most significantly affects grazing livestock, wild ungulates

42   and other herbivorous mammals, but also poses a serious threat to human health[1,2]. The

43   geographic extent of *B. anthracis* endemism is still poorly understood, despite multi-decade

44   research on anthrax epizootic and epidemic dynamics around the world[3,4]. Several biogeographic

45   studies have focused on modeling environmental suitability for anthrax at local or national

46   scales[5–9], but many countries have limited or inadequate surveillance systems, even within

47   known endemic regions. Here we compile an extensive global occurrence dataset for *B.*

48   *anthracis*, drawing on confirmed human, livestock, and wildlife anthrax outbreaks. With these

49   records, we use boosted regression trees[10,11] to produce the first map of the global distribution of

50   *B. anthracis* as a proxy for anthrax risk. Variable contributions to the model support pre-existing

51   hypotheses that environmental suitability for *B. anthracis* depends most strongly on soil

52   characteristics such as pH that affect spore persistence, and the extent of seasonal fluctuations in

53   vegetation, which plays a key role in transmission for herbivores[12,13]. We apply the global model

54   to estimate that 1.83 billion people (95% credible interval: 0.59—4.16 billion) live within

55   regions of anthrax risk, but most of that population faces little occupational exposure to anthrax.

56   More informatively, a global total of 63.8 million rural poor livestock keepers (95% CI: 17.5—

57   168.6 million) and 1.1 billion livestock (95% CI: 0.4—2.3 billion) live within vulnerable regions.

58   Human risk is concentrated in rural areas, and human and livestock vulnerability are both

59   concentrated in rainfed systems throughout arid and temperate land across Eurasia, Africa, and

60   North America. We conclude by mapping where anthrax risk overlaps with vulnerable wild

61   ungulate populations, and therefore could disrupt sensitive conservation efforts for species like

62   bison, pronghorn, and saiga that coincide with anthrax-prone, mixed-agricultural landscapes.

63   Anthrax is a zoonotic disease caused by the Gram-positive bacterium *Bacillus anthracis,* a

64   generalist soil-transmitted pathogen found on every inhabited continent[14], and several islands

65   including Haiti and parts of the Philippines and Indonesia. Worldwide, an estimated 20,000 to

66   100,000 cases of anthrax occur annually, mostly in poor rural areas[15]. In clinical presentations of

67   anthrax, case fatality rates are a function of exposure pathway. Respiratory exposure from spore

68   inhalation is important the context of bioterrorism, but is highly uncommon, and accounts for a

69   negligible fraction of the global burden of anthrax cases. Cutaneous exposure to *B. anthracis*

70   accounts for the majority of human cases worldwide, and typically presents with low mortality;

71   gastrointestinal exposure accounts for the remainder and presents with intermediate to high

72   fatality rates. Cutaneous and gastrointestinal cases of anthrax are most commonly caused by

73   handling and slaughtering infected livestock, or butchering and eating contaminated meat;

74   untreated gastrointestinal cases likely account for most human mortality from anthrax.[14–16]

75   Human mortality from anthrax is driven by ecological dynamics at the wildlife-livestock

76   interface[17]. In nature, the enzootic cycle of anthrax is characterized by a combination of long-

77   term spore persistence in soil, and an obligate-lethal transmission route, primary in herbivorous

78   mammals[1,2,14]. Both wild herbivores and livestock are gastrointestinally exposed to *B. anthracis*

79   spores from soil while grazing, become infected, and usually return spores to the soil when they

80   die and decompose[13]. Because domesticated and wild herbivores frequently share grazing

81   grounds, wildlife epizootics can lead to downstream infections in livestock and humans. In some

82   regions, anthrax is hyperendemic, and cases follow regular seasonal trends; in other regions, the

83   disease re-emerges in major epidemics after years or decades without a single case[1].

84   Environmental persistence facilitates these unusual dynamics; under optimal conditions, *B.*

85   *anthracis* spores are able to persist in the soil for long periods (i.e. decades). Alkaline, calcium-

86   rich soils are believed to facilitate sporulation, and therefore drive landscape-level patterns of

87   persistence; these patterns are usually hypothesized to drive the distribution of *B. anthracis* up to

88   the continental scale[2,14].

89   Global variation in anthrax endemism and outbreak intensity has been previously

90   characterized at extremely coarse scales[3,18], but anthrax is a neglected disease, and its global

91   distribution is still poorly characterized. In total, roughly a dozen studies have used ecological

92   niche models to develop regional (usually national-level) maps of suitability for *B. anthracis* (see

93   **Table S1**). These regional mapping efforts are a critical part of the public health planning

94   process[4], but are primarily conducted in isolation, and the results of these studies have yet to be

95   consolidated and synthesized. Furthermore, cross-validation of regional models has only been

96   recently attempted[19], and indicates either limitations in model transferability, or possible genetic

97   or ecological differences underlying distributional patterns of different regions; either way, this

98   highlights the limitations preventing regional models from being scaled up to a global estimate.

99   Moreover, the distribution of anthrax has yet to be modelled in several broad regions where it is

100 nevertheless pervasive, especially Western Europe, the Middle East, and South America. Cryptic

101 persistence of *B. anthracis* spores in the soil makes mapping efforts especially challenging, as

102 suitable and endemic regions could go years or potentially decades without a recorded outbreak.

103 This study consolidates clinical and ecological research on enzootic and epidemic anthrax

104 reports, compiling the largest global database of anthrax occurrences on record to map the global

105 suitability for *Bacillus anthracis* persistence. A total of 5,108 records were compiled describing

106 the global distribution of anthrax across 70 countries (**Figure 1**). Here we used a subset of 2,310

107 of these data points to describe the global distribution and eco-epidemiology of *Bacillus*

108 *anthracis*, exploring the relationship of anthrax outbreaks to environmental factors including soil

109 characteristics and climate, via boosted regression trees (BRTs) as a tool for species distribution

110 modelling. These maps provide a proxy for anthrax risk. We apply this global anthrax model to

111 provide a first estimate of the global human and livestock populations at risk from anthrax. We

112 compare the distribution of anthrax to that of critically threatened wildlife populations, and

113 identify areas where additional or new surveillance is needed to anticipate and prevent rare, but

114 likely catastrophic, threats to wildlife conservation efforts.

115 Our global ensemble distribution model (**Figure 2**) performed very well on validation

116 data (mean AUC = 0.9244), and regionally matches the well-established distribution of anthrax

117 in China[20], Kazakhstan[21], North America[5], and Australia[8], suggesting that it appropriately

118 captures the global range of *Bacillus anthracis*. These four regions, along with a band of

119 suitability in sub-Saharan Africa around roughly 15° S, represent the most geographically-

120 expansive zones of anthrax endemicity, and hotspots of human vulnerability. However, our study

121 also shows that perhaps the majority of the European continent, and a substantial part of the

122 Anatolian peninsula and surrounding region, are also highly suitable for *B. anthracis*. In some

123 cases, high risk areas match hyperendemic areas, such as Turkey and South Africa; but in other

124 cases (e.g., in Ethiopia), predicted areas of suitability were more limited than expected in

125 countries with a high anthrax burden. This may reflect sampling limitations in these areas, but
126 also likely reflects regional variation in anthrax control. Where food safety practices prevent
127 exposure and livestock vaccinations are affordable, high anthrax suitability may not translate into
128 high case burdens (supported by the vaccination data in the **Supporting Information**);
129 conversely, anthrax morbidity and mortality are usually exacerbated by limited local knowledge
130 about anthrax, limited access to healthcare, and conflicting pressures like food insecurity that
131 force local populations to handle and eat contaminated meat.

132   Globally, we find an estimated 1.8 billion people live within anthrax-suitable areas, the
133 vast majority of whom live in rural areas in Africa, Europe and Asia (**Table 1**). However, most
134 of that population probably has no occupational exposure to infected animals, and direct
135 exposure from the soil has rarely been reported for human cases; in those few reported cases
136 patients had compromised immune systems and unknown or unusual exposure[22]. For a more
137 informative perspective on risk, we estimate that a total of 63.8 million rural poor livestock
138 keepers live in anthrax-affected areas (95% credible interval: 17.5—168.6 million; **Table 1**),
139 again primarily in Africa and Eurasia. Globally, we found that areas of anthrax risk contain 1.1
140 billion livestock (95% CI: 404 million—2.3 billion; **Table 2**), including 320 million sheep (95%
141 CI: 138—622 million), 294.9 million pigs (95% CI: 103—583 million), 268.1 million cattle
142 (95% CI: 87.4—639 million), 211.2 million goats (95% CI: 74.8—453 million), and 0.6 million
143 buffalo (95% CI: 0.16—1.6 million). Although arid and semi-arid ecosystems were a significant
144 source of vulnerable livestock across production systems (especially for cattle), the single most
145 significant across all four groups was rainfed mixed crop/livestock systems in temperate-
146 highland ecosystems, due to the disproportionate contribution from East Asia, especially China
147 (Table 1).

148   Most livestock at risk of anthrax are unvaccinated in any given year. Per reported data, an
149 average of 212.8 million live attenuated vaccines for anthrax are manufactured every year (2005-
150 2016) outside the United States (which reports no data but is also a major manufacturer); on
151 average, 198.2 million doses are used for livestock every year. Compared to the 1.1 billion
152 livestock at risk, vaccine coverage is patchy and regionally-variable; roughly 90% of cattle,
153 sheep, and goats are annually vaccinated in Eastern Europe and Central Asia, due to a strong
154 legacy of mass vaccination campaigns in the former Soviet Union. On the other hand,
155 vaccination rates are alarmingly low in sub-Saharan Africa (0-6%), East Asia (0-5%) and South

156   Asia (< 1%), where more than half of the livestock at risk and 48.5 million rural poor livestock

157   keepers are located. In these regions, livestock vaccination is commonly used reactively after a

158   major outbreak, rather than as a preventative measure[5,23]; improving proactive vaccination in

159   under-vaccinated, hyperendemic countries (in particular Afghanistan, Bangladesh, Ethiopia,

160   South Africa, Turkey, and Zimbabawe) could help bring anthrax outbreaks under control[24].

161   Vaccination may also be less effective than usual for the 31 million livestock and 4.6 million

162   poor livestock keepers in West Africa, where an endemic lineage of *B. anthracis* shares an

163   anthrose-deficiency mutation that has been hypothesized to lead to a vaccine escape[25]. Education

164   campaigns may be more cost-effective than mass vaccination, which is both cost-prohibitive and

165   logistically-challenging in inaccessible rural areas. However, livestock keepers may continue to

166   sell contaminated meat to recoup financial losses (which also contributes to underreporting); this

167   has increased cases urban settings[26]. In cases of extreme food insecurity, poor populations may

168   eat anthrax-infected meat despite understanding the risks.

169   Although risk is most commonly measured at the human-agriculture interface, anthrax

170   also has a major ecological impact; while *B. anthracis* is a stable part of some savannah

171   ecosystems, epizootics in other regions can have catastrophic impacts on wildlife

172   populations[14,27]. We note that several ungulate species could probably benefit from improved

173   epizootic surveillance, given range overlap with anthrax and limited coverage by protected areas,

174   which are a foundation of anthrax surveillance and control for most wildlife (**Table 3**).[28] Saiga

175   antelope (*Saiga tatarica*) in particular have a significant overlap with anthrax outside of

176   protected parts of their range, and the recent mass die-off of a third of the entire population of

177   saiga in three weeks highlights the vulnerability of threatened ungulates to sudden, disease-

178   induced population crashes. The anthrax vaccine may be used by conservationists in special

179   cases (e.g. with cheetahs and rhinoceros[29]), but the lack of an oral anthrax vaccine makes mass

180   vaccination more impractical for wildlife than for livestock, making surveillance all the more

181   important.

182   Our study has proposed the first global map of *B. anthracis* suitability as a proxy for

183   anthrax risk, and while this is a major step forward, several important directions remain to make

184   these models actionable for public health practitioners. Although some estimates have been

185   proposed for the annual global burden of anthrax, these estimates range by several orders of

186   magnitude. Most regional assessments, especially in rural Africa, agree that anthrax cases are

187   severely underreported despite mandatory reporting. Similar studies to ours have used suitability

188   maps to extrapolate global case burden for diseases like dengue fever or melioidosis

189   (*Burkholderia pseudomallei*)[11,30]; however, this approach seems inadequate for anthrax, given

190   that human incidence is just as strongly determined by anthrax dynamics in wildlife, local

191   agricultural intensity, knowledge about anthrax transmission, access to healthcare and

192   vaccination, and complicating factors like food insecurity. At national and local levels, One

193   Health approaches to surveillance have had promising results, but a more globally-coordinated

194   network among these programs might help address some of the major data gaps.

195   Our work also sets a foundation for investigating how climate change will impact the

196   distribution and burden of anthrax. Published work suggests anthrax suitability may decrease in

197   parts of Kazakhstan and the southern United States in a changing climate, but other work

198   anticipates warming-driven emergence at higher latitudes[31,32]. Our study includes recent records

199   from the Yamalo-Nemets area of Russia, where outbreaks in reindeer have led to massive

200   economic losses and threaten the livelihood of traditional pastoralists. However, our model made

201   limited predictions of suitability in the sub-Arctic in current climates. Even though anthrax cases

202   are regularly reported throughout Sweden, northern Russia, and other cold, high-latitude

203   countries, high-latitude outbreaks are proportionally under-represented in our database (and are

204   often poorly documented). Persistence at higher latitudes may also be better predicted by a

205   slightly different set of climatic constraints on persistence. A recently-published model trained

206   on high-latitude cases in the Northern Hemisphere seems to under-predict known areas of

207   endemism in warmer climates, possibly supporting this explanation[32]. Feedback between local

208   modelling efforts and updated global consensus mapping will improve our overall understanding

209   of what drives different anthrax dynamics, and the likely impact of climate change.

210   Finally, we observe increasing interest, by microbiologists and ecologists alike, in the

211   closely related "anthrax-like" *Bacillus cereus* biovar. *anthracis.* Whereas *Bacillus cereus* is a

212   typically non-pathogenic soil bacterium, the pathogenic *B. cereus* biovar. *anthracis* (*Bcbva*)

213   carries variants of the pXO1 and pXO2 plasmids that allow capsule production, which are both

214   required for full virulence in *B. anthracis.* A recent study in Taï National Park in Cote D'Ivôire

215   showed that *Bcbva* accounted for 40% of wildlife mortality in a 26-year survey, and could

216   potentially drive the local extinction of chimpanzees in the Taï Forest within the next century.[33]

217   The geographic distribution of *Bcbva* is still unknown, and it is plausible that different climatic

218   and environmental factors determine the spatial patterns of its transmission; though improved

219   diagnostics will be necessary to differentiate the role of the two pathogens in anthrax infections

220   beyond Taï National Park. Mapping *Bcbva* across West Africa may be an important next step for

221   measuring the threat of anthrax and anthrax-like disease to wildlife conservation (and,

222   potentially, to human health down the road).

223

224   **Methods**

225

226   **Occurrence & Pseudoabsence Data**

227   We assembled a global occurrence database for *Bacillus anthracis* out of a combination of (i)

228   outbreak data collected in the field by the authors or their extended team of collaborators, (ii)

229   national passive surveillance and reporting infrastructures, (iii) online records from ProMed

230   Mail, and (iv) georeferenced records or (v) digitized maps from peer-reviewed publications

231   documenting anthrax outbreaks. Our final database of 5,018 unique records spanning 70

232   countries and more than a century (1914 – 2018), thinned to 2,310 distinct localities after

233   removing uncertain sightings and thinning to a single point per unique 10 arcminute (~20 km at

234   the equator) cell, to correct for sampling bias[34]. For background environmental data, a total

235   dataset of 10,000 pseudoabsences were randomly generated from countries where anthrax

236   occurrence records were collected, an upper sample commonly used for similar disease

237   distribution mapping studies[35]. Of these 10,000, an equal 1:1 sample was randomly selected to

238   match the presence points in submodels, as is recommended for boosted regression tree

239   models[36].

240

241   **Environmental Predictors**

242   Global layers of environmental predictors were selected based on successful variables used in

243   previously published anthrax distribution modelling studies at regional scales[5,21,37], as well as

244   from other distribution modelling studies on soil-borne pathogens[30]. Climate data were taken

245   from version 1.4 of the WorldClim dataset, which includes nineteen bioclimatic variables

246   characterizing average and seasonal trends in temperature and precipitation[38]. In addition to

247   climate data, we included layers describing elevation, soil, and two vegetation indices.

248   Elevational data was taken from the Global Multi-resolution Terrain Elevation Data

249   (GMTED2010) dataset provided by the US Geological Service. Soil layers were taken from the

250   Global Soil Information Facilities (GSIF) SoilGrids database at 250 m resolution; four layers

251   were included: soil pH, and the predicted soil content of sand, humult, and calcic vertisols at a

252   depth of 0-5 cm[39]. The mean and amplitude of the normalized difference vegetation index

253   (NDVI) were taken from the Trypanosomiasis & Land Use in Africa (TALA) dataset[40]. To

254 prevent overfitting and reduce correlation among predictor variables, the variable set was

255 reduced down using an automated procedure within the boosted regression tree implementation.

256

257 **Distribution Modelling**

258 Boosted regression trees (BRTs) are currently considered a best practices method for modelling

259 the global distribution of infectious diseases[11,41], including other soil-transmitted pathogens like

260 *Burkholderia pseudomallei*[30]. In our study, BRTs were implemented using the 'gbm' package in

261 R to develop a global species distribution model for *Bacillus anthracis*. Automated variable set

262 reduction procedures selected a total of seventeen predictor layers: ten bioclimatic variables, two

263 vegetation indices, elevation, and four soil variables. Presence, absence, and environmental data

264 were run through the 'gbm.step' procedure on default settings (tree complexity = 4, learning rate

265 = 0.005), following the established template of other studies. A total of 500 submodels were run;

266 for each, presence points were bootstrapped, and pseudoabsences were randomly selected from

267 the total 10,000 to achieve a 1:1 ratio[36]. Separate from the internal cross-validation (75%-25%

268 split) of the BRT procedure, both presence and pseudoabsence points were split into an 80%

269 training and 20% test dataset in each submodel, and model AUC was evaluated based on the

270 independent test dataset. A final average model was calculated across the 500 submodels, and the

271 5th and 95th percentile were retained for use in the population at risk analyses. Models performed

272 very well on the withheld test data (mean submodel AUC = 0.9244).

273

274 **Estimation of Human and Livestock Populations-at-Risk**

275 We estimated the vulnerability of human and livestock populations by overlaying population

276 datasets with maps of anthrax-suitable areas[42]. We mapped global anthrax suitability by

277 dichotomizing model predictions with a threshold of 0.565 for suitable versus unsuitable

278 predictions, with the threshold selected to maximize the true skill statistic (which weights

279 sensitivity and specificity equally) of mean predictions across the entire dataset of all sightings

280 and pseudoabsences. We estimated global population at risk using human population counts for

281 2015 from the Gridded Population of the World (GPW) dataset, version 4.0. We dichotomized

282 "urban" and "rural" areas using the Global Human Built-up and Settlement Extent (HBASE)

283 Dataset, version 1.0. We further split "urban" areas into urban and peri-urban based on the GPW

284 population dataset, where we used a density under 1,000 persons per km^2 as the threshold for

285   classification as peri-urban. To measure possible occupational exposure, we used a global dataset

286   of rural poor livestock keeper density.[43] Finally, we estimated the number of livestock (cattle,

287   sheep, goats, and swine) using a database of global livestock density at a spatial resolution of

288   ~1km x 1km (http://www.livestock.geo-wiki.org/).[44] Those livestock populations at risk were

289   further stratified by each of the livestock production zones using the livestock production

290   systems data version 5 (http://www.livestock.geo-wiki.org/).[43–45] For all human and livestock

291   analyses, we obtained vulnerability estimates by overlaying population counts with dichotomized

292   anthrax suitable areas from the BRT models; 95% credibility intervals were calculated by using

293   the 5% (lower) and 95% (upper) bounds of the averaged BRT model prediction, in place of the

294   mean prediction.[42]

295

296   **Delineating Wildlife at Risk**

297   We identified ungulate species of interest based on species of conservation concern with known

298   range overlap with anthrax, and measured the degree of range overlap with our global *B.*

299   *anthracis* model, as a proxy for anthrax exposure. We selected seven candidate species of

300   interest: pronghorn (*Antilocapra americana*), roan (*Hippotragus equinus*), saiga (*Saiga tatarica*),

301   moose (*Alces alces*), reindeer (*Rangifer tarandus*), wild yak (*Bos mutus*), and bison (*Bison*

302   *bison*). Of the seven, saiga are most threatened, and are listed on the IUCN red list as critically

303   endangered. Yak are listed as vulnerable; bison are listed as near threatened; and pronghorn,

304   roan, and moose are listed as least concern. We use the Global Protected Areas Database and

305   official IUCN range maps, though we note that these range maps tend to overestimate ranges and

306   can be misleading for conservation work[46]. (At least for saiga, we note that telemetry studies are

307   currently underway to reassess the boundaries of the species' range.)

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317

318   **Author Contributions**

319   CJC, ITK and JKB conceived of the study. JKB, MEHJ, ITK, and CJC collected and

320   georeferenced data. CJC, ITK and JKB designed the models, and CJC ran models and analyses.

321   NR contributed R code. All authors contributed to the writing and editing of the draft, and

322   approved the study before submission.

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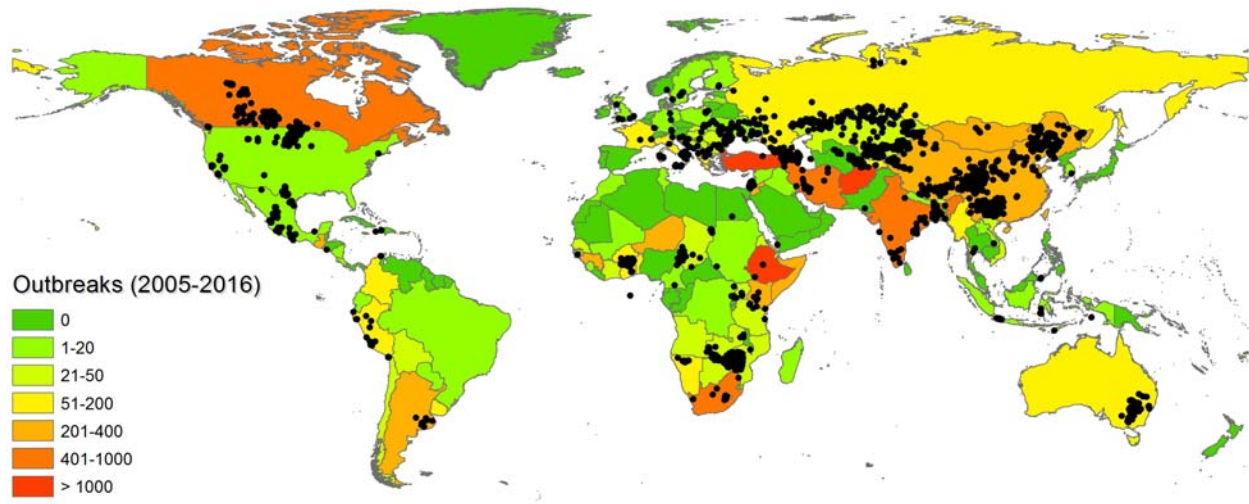408   birds in the Western Ghats. *Biol. Conserv.* **210,** 205–221 (2017).

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411   **Figures**

412   **Figure 1.** Global database of anthrax occurrences (points), versus outbreaks of anthrax by

413   country (Jan. 2005-Aug. 2016; data digitized from United Nations Food & Agriculture

414   Organization report).

415

416   **Figure 2.** Global environmental suitability (probability of occurrence) for *Bacillus anthracis*

417   modelled by an ensemble of 500 boosted regression trees.

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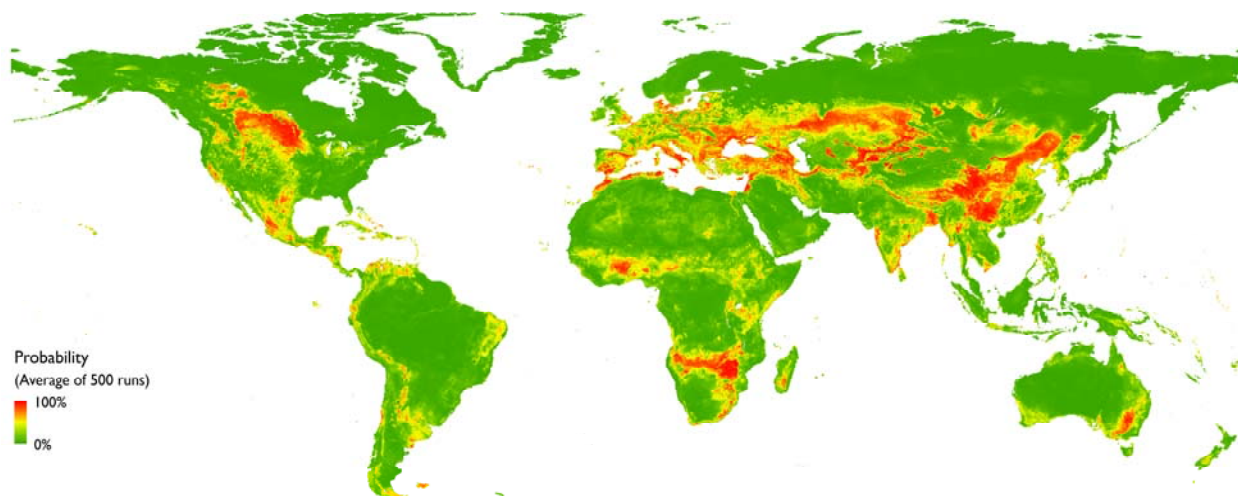
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420

421   **Figure 3.** Average vaccination rates for all livestock (cattle, sheep, goats, buffalo, and pigs)

422   reported to WAHIS over the interval 2005-2016, as a function of doses administered and

423   reported livestock populations at risk, excluding years with no reported vaccination.
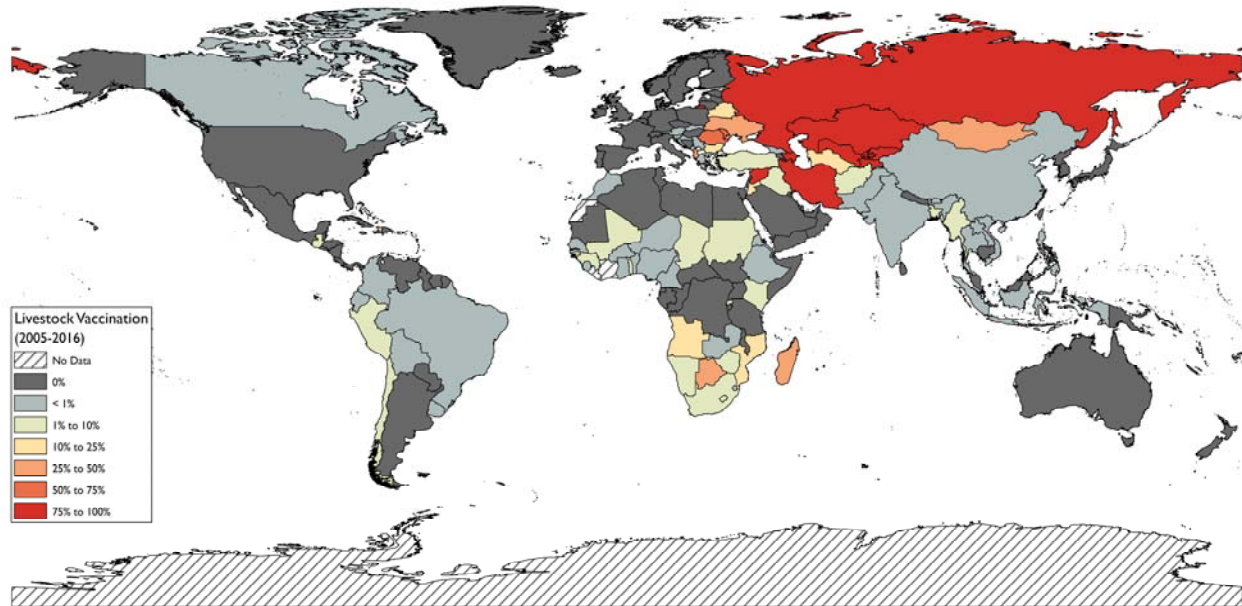
424

425   **Tables.**

426

427   **Table 1.** Population at risk (in millions) by region, land use, and occupational exposure.

Region	Poor livestock keepers	Rural	Peri-urban	Urban	Total
East Asia and the Pacific	5.7	458.5	15.0	162.4	635.9
South Asia	26.6	345.0	1.9	55.1	401.9
Western and Central Europe	0.26	125.3	14.0	79.6	218.8
North Africa and the Middle East	6.6	152.9	6.1	51.7	210.7
Eastern Europe and Central Asia	5.6	112.7	3.4	26.5	142.7
Sub-Saharan Africa	16.2	84.2	1.5	16.6	102.3
Latin America and the Caribbean	2.9	38.1	2.6	42.0	82.7
North America	< 0.1	5.6	3.6	21.5	30.8
Australia and Oceania	< 0.1	0.74	0.24	0.7	1.76
World Total	**63.8**	**1,323.1**	**48.4**	**456.1**	**1,827.5**

428

429   **Table 2.** Estimated global livestock at risk (by millions), by species & region.

Region	Cattle	Pigs	Goats	Sheep	Buffalo	Total
East Asia and the Pacific	63.2	190.9	79.9	108.1	0.24	442.4
South Asia	61.6	1.8	72.5	18.7	0.33	154.8
Western and Central Europe	22.2	60.9	7.5	42.2	< 0.1	132.8
North Africa and the Middle East	15.8	0.2	13.4	65.2	< 0.1	94.6
Eastern Europe and Central Asia	26.6	12.0	8.9	40.4	< 0.1	87.8
Sub-Saharan Africa	30.5	5.3	22.4	14.5	0	72.8
Latin America and the Caribbean	21.9	8.0	5.7	8.1	0	43.7
North America	23.0	15.2	0.45	0.29	0	39.0
Australia and Oceania	3.1	0.61	0.47	22.7	0	26.9
World Total	**268.1**	**294.9**	**211.2**	**320.1**	**0.58**	**1,094.9**

430

431   **Table 3.** Overlap between wildlife species of concern and the global distribution of anthrax,

432   including overlap with the protected areas database.

Wildlife Species	Geographic Overlap	Anthrax suitable area overlap with protected areas	IUCN Red List Status
Bison (*Bison bison*)	32.2%	64.6%	NT
Pronghorn (*Antilocapra americana*)	26.6%	3.9%	LC
Roan (*Hippotragus equinus*)	23.9%	30.5%	LC
Saiga (*Saiga tatarica*)	17.5%	2.8%	CE (A2acd)
Moose (*Alces alces*)	6.0%	9.9%	LC
Reindeer (*Rangifer tarandus*)	1.6%	14.9%	LC
Yak (*Bos mutus*)	0.7%	0%	VU (C10)

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