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1 **Title: Quantitative assessment of microbiological risks due to red meat**
2 **consumption in France**

3 **Short title: Foodborne burden from red meat intake in France**

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22 **Abstract**

23 As reported by the European Centre for Disease Prevention and Control and the
24 European Food Safety Authority, red meat is a major food source that is responsible for
25 foodborne illnesses due to microbiological hazards. The first objective of this study was to
26 aggregate the available data in the literature in order to identify and characterise the main
27 microbiological hazards associated with red meat consumption in France. Next, the associated
28 numbers of foodborne illnesses, deaths and the subsequent burden of diseases, expressed in
29 Disability Adjusted Life Years (DALY), were estimated. Using the eight foodborne pathogens
30 kept in the assessment, a probabilistic risk model was built and uncertainty from the data was
31 considered. *Campylobacter* spp. was ranked as the worst pathogen in terms of the number of
32 human cases associated with red meat consumption, with 210 [95% confidence interval (CI) =
33 500–520] cases per 100,000 population. The pathogen that induced the highest mortality was
34 non-typhoidal *S. enterica*, with 0.04 [95% CI = 0.01–0.10] deaths per 100,000 population.
35 These cases were mostly related to pork consumption. However, the major contributor to the
36 number of years in good health lost from red meat consumption in France was hepatitis E,
37 with 33 [95% CI = 1-64] DALY per 100,000 population; this effect was mainly due to pork
38 liver consumption. In terms of foodborne bacteria, for beef and pork meat, *Campylobacter*
39 spp., non-typhoidal *S. enterica*, *C. perfringens* and STEC represented a mean of 2.2 [95% CI
40 = 1.0–4.0] DALY per 100,000 individuals per year. The estimations provided in this study
41 might help authorities to focus on these hazards and ultimately reduce their impact on the
42 health of the French population.

43 **Keywords:**

44 foodborne illnesses, risk ranking, public health, disability-adjusted life year, DALY

45 **1. Introduction**

46 In recent years, red meat consumption has become a public health concern in France and other
47 western countries [1]. In addition, unprocessed red meat, including beef, pork, lamb and other
48 small ruminants, is widely consumed in France. Indeed, in 2013, each adult consumed an
49 average of 52.5 g/day of red meat, from which 31 g/day was beef and 11 g/day was pork [2].
50 However, red meat has been classified by the World Cancer Research Found/Imperial College
51 of London and the World Health Organization (WHO) as “probably carcinogenic to humans”
52 for colorectal cancer [3,4]. On this basis, there are dietary recommendations to limit red meat
53 consumption to 500 g per week [5]. Red meat consumption was also associated with
54 cardiovascular disease (CVD) mortality risk [6] and suspected to increase the risk of breast
55 cancer, advanced prostate cancer, stroke, coronary heart diseases and heart failure [7,8].

56 Microbiological risks are also a major concern when preparing and consuming red meat. In
57 2017 in France, 10% of the total number of foodborne outbreaks declared to the Regional
58 Health Agency and Departmental Directorate of Social Cohesion and Population Protection
59 were due to red meat consumption. The main pathogens (confirmed or suspected) were
60 *Staphylococcus aureus* (13%), *Clostridium perfringens* (11%) and *Bacillus cereus* (10%) [9].

61 In Europe, the European Food Safety Authority (EFSA) and the European Centre for Disease
62 Prevention and Control (ECDC) are in charge of evaluating the annual trends and sources of
63 zoonoses, zoonotic agents and foodborne outbreaks. In 2017, they estimated that pork meat
64 was responsible for 4.2% of the total outbreaks and 6.9% of the total cases for strong-
65 evidence outbreaks in Europe. Beef meat was responsible for 2% of total outbreaks and 3% of
66 the total cases for strong-evidence outbreaks, with a reporting rate of 0.012 per 100,000 for
67 both types of meat [10].

68 Nevertheless, the number of confirmed cases was underestimated because notification
69 is not mandatory for every pathogen (e.g. campylobacteriosis in France [10]). Some studies
70 have attempted to estimate the real number of cases. The WHO estimated the number of
71 foodborne illness cases in 2010 by considering the effects of underestimation [11]. In France,
72 Van Cauteren et al. [12] and Vaillant et al. [13] performed this estimation for 2008–2013 and
73 1990–1999, respectively. Nevertheless, the number of cases provides an incomplete
74 estimation of the health impacts of foodborne diseases. Indeed, the severity and duration of
75 sequela vary according to the pathogenic species and the immune status of the consumer. For
76 example, salmonella infection may cause diarrhoea, with a duration of 8 days, while Guillain-
77 Barré syndrome—after campylobacteriosis—is assumed to last a lifetime [11]. To overcome
78 this limitation, the WHO has gone further than estimate the number of cases; it has used the
79 disability-adjusted life year (DALY) metric [11] to estimate the disability caused by
80 foodborne diseases. The use of the composite DALY metric enables to consider morbidity—
81 encompassing the duration and the disability induced by the sequelae—and the number of
82 years lost due to premature death [14,15]. The DALY metric was also used by ECDC through
83 a software tool for the estimation of the infectious disease burden in Europe (BCoDE) [16].
84 Disease models were built for each microbiological hazard and country. Information about
85 sequelae (health impact, death, proportion of people concerned, duration, etc.) were
86 integrated, and the user had to complete the requested information per age group and gender

87 Despite these substantial efforts, the burden of diseases induced by microbiological
88 pathogens on health that is exclusively attributable to red meat consumption in France
89 remains incomplete. In particular, the number of foodborne cases attributable to red meat
90 consumption, and its corresponding DALY values, has not yet been estimated. Moreover, the
91 uncertainty associated with the different types of data has not been aggregated into one model
92 to deliver final estimates of disease burdens with confidence intervals. Thus, the objective of

93 this study was to combine the available data in the literature to determine the main
94 microbiological hazards when consuming red meat and to estimate the associated number of
95 foodborne illness cases and deaths and the subsequent burden of diseases in France.
96 Moreover, this study aimed to estimate the burden of foodborne diseases attributable to red
97 meat consumption to enable comparison and balancing with nutritional risks and benefits of
98 red meat, expressed in DALYs, evaluated in recent publications [17,18].

99 **2. Methods**

100 **2.1. Selection of the available data**

101 The literature was searched using terms such as “foodborne disease(s)”, “foodborne
102 outbreak(s)”, “foodborne illness(es)”, “foodborne attribution” and “microbiological risk
103 assessment” to select the main foodborne pathogens in France and to estimate the incidence
104 and the associated burden of diseases when eating red meat (beef, pork and other small
105 ruminants). Official reports from the WHO, the EFSA, the French Agency for Food, the
106 Environmental and Occupational Health & Safety (ANSES), the ECDC and Santé Publique
107 France were searched. PubMed and Google Scholar searches identified complementary data
108 specific to the French population and the proportion of foodborne disease burden attributable
109 to each type of red meat.

110 **2.2. Determination of the main pathogens involved in foodborne outbreaks related** 111 **to red meat consumption in France**

112 To define the main foodborne pathogens of interest when eating red meat, three criteria
113 were considered.

114 *2.2.1. Incidence of foodborne illnesses in Europe and France for each pathogen,*
115 *regardless of the source*

116 To determine the hazards responsible for foodborne illness in Europe, a report from the
117 WHO, which estimated the number of foodborne illness cases in 2010 in countries in the
118 “EUR A” subregion, was used as a reference. It included Andorra, Austria, Belgium, Croatia,
119 Cyprus, the Czech Republic, Denmark, Finland, France, Germany, Greece, Iceland, Ireland,
120 Israel, Italy, Luxembourg, Malta, Monaco, Netherlands, Norway, Portugal, San Marino,
121 Slovenia, Spain, Sweden, Switzerland and the United Kingdom [11].

122 For the French incidence, the work of Van Cauteran et al. [12] was considered. These
123 authors estimated the number of French cases for the overall population. In order to make
124 comparisons with future and other countries’ estimations, the results were expressed per
125 100,000 population. The 2010 French population was considered to be 62,765,235 inhabitants
126 (Table 1).

127 2.2.2. *DALYs attributable to foodborne illnesses for each pathogen and for all sources*

128 The WHO evaluated the disease burdens associated with foodborne illnesses in terms of
129 DALYs [11]. To estimate this measure, data on the incidence, clinical outcomes, duration of
130 the health state, age distribution and mortality rate were collected for each hazard by the
131 WHO. The study estimated the number of years lived with disability (YLD) attributable to the
132 hazard health impact and multiplied it by the disability weight factor, which reflects the
133 severity of the health state [17]. Subsequently, the number of years of life lost (YLL)—due to
134 a premature death—was added [11].

135 Our calculation considered the WHO’s DALY estimations. For missing DALY values, the
136 estimations from Havelaar et al. [19], recently used by Mangen et al. [20], were considered.

137 2.2.3. *The proportion of foodborne illnesses attributable to red meat consumption for* 138 *each pathogen*

139 The burden that could be attributed to red meat consumption was mainly extracted from
 140 Hoffmann et al. [18], the most recent study on the attribution fraction per pathogen for beef,
 141 pork and other small ruminant meat. When data about the attribution fraction was missing
 142 from this latter study [18], attribution data from a French team was considered [19]. However,
 143 that source only estimated the attributable fraction to beef and pork. Finally, for the remaining
 144 missing data, the attributable fraction estimated by a Dutch team was utilised [20]. Attribution
 145 fractions per pathogen and type of meat is given in Table 1.

146 **2.3. Incidence, death and disease burden of foodborne pathogens in Europe and** 147 **France associated with red meat consumption**

148 The number of cases, deaths and disease burden attributable to red meat consumption were
 149 estimated. The number of illness cases were calculated as represented in Equation 1:

150 (1)

$$151 \quad Ncases.F_{rm} = \sum_{rm=1}^3 \frac{Ncases.F_p \times 100,000}{Pop_{2010}} \times PA_{p,rm},$$

152 where:

- 153 - rm is the type of red meat (1: beef; 2: pork; and 3: other small ruminant meat). For
 154 norovirus, $rm = 1$ also included lamb;
- 155 - p is the pathogen;
- 156 - $Ncases.F_{rm}$ is the number of cases of foodborne illness attributable to red meat
 157 consumption per 100,000 individuals in France;
- 158 - $Ncases.F_p$ is the number of cases of foodborne illness caused by a specific pathogen
 159 in France from Van Cauteren et al. [12];
- 160 - $PA_{p,rm}$ is the proportion of foodborne illness cases attributable to a pathogen and a
 161 type of red meat. *Campylobacter* spp., non-typhoidal *Salmonella enterica* and shiga-
 162 toxin producing *Escherichia coli* attribution fraction were extracted from Hoffmann et

163 al. [18]. The attribution fraction of hepatitis E and norovirus were extracted from
 164 Havelaar et al. [20] and *Staphylococcus aureus*, *Clostridium perfringens* and
 165 *Toxoplasma gondii* were extracted from Fosse et al. [19];
 166 - Pop_{2010} represents the 2010 population in France (62,765,235).

167 The number of deaths (Equation 2) was calculated by multiplying the number of
 168 foodborne illness cases per pathogen and red meat type by the proportion of deaths per
 169 pathogen-case. These latter values were obtained from the ratio between the number of deaths
 170 and the number of illness cases per pathogen from Van Cauteren et al [12].

171 (2)

$$172 \quad Ndeath.F_{rm} = \sum_{rm=1}^3 \frac{Ncases.F_p \times 100,000}{Pop_{2010}} \times PA_{p,rm} \times Rdeath.F_p$$

173 Where:

- 174 - $Ndeath.F_{rm}$ is the number of deaths after of foodborne illness attributable to red meat
 175 consumption per 100,000 population in France;
- 176 - $Rdeath.F_p$ is the ratio of deaths after a foodborne illness per pathogen-case from Van
 177 Cauteren et al. [12].

178 DALYs issued from the WHO (2015) [11] were considered in the estimation, except for *C.*
 179 *perfringens*, *S. aureus*, hepatitis E and norovirus. For those cases, DALY values attributable
 180 to foodborne diseases were not available in the WHO estimations. Therefore, DALYs per
 181 1,000 cases from a Dutch study were used as reference [21]. DALYs were estimated as
 182 follows (Equation 3):

183 (3)

$$\begin{aligned}
184 \quad DALY.F_{rm} &= \left(\sum_{rm=1}^3 DALY.EUR A_{p=Camp.,Salm,E.coli,Toxo} \times PA_{p=Camp.,Salm,E.coli,Toxo} \right) \\
185 \quad &+ \left(\frac{Ncases.F_{p=C.perf,HepE,Noro,S.aureus} \times 100,000}{Pop_{2010}} \times DALY.case_{p=C.perf,HepE,Noro,S.aureus} \right),
\end{aligned}$$

186 Where:

- 187 - $DALY.F_{rm}$ is the number of DALYs caused by a specific pathogen and attributable to
- 188 red meat consumption per 100,000 population in France;
- 189 - $DALY.EUR A_p$ is the number of DALYs in the “EUR A” region due to the pathogen
- 190 per 100,000 population from WHO [11];
- 191 - $DALY.case_p$ is the number of DALYs in the Netherlands due to the pathogen per
- 192 1,000 cases;
- 193 - Pop_{2010} is the 2010 population in France (62,765,235).

194 To compare the disease severity from any pathogen, considering the type of sequelae and their
195 duration, the DALYs per case was estimated by dividing the number of DALYs by the
196 number of cases.

197 **2.4. Uncertainty propagated in the model**

198 In literature and report, the data were expressed by their median values and corresponding
199 95% confidence intervals (CIs). Therefore, the probability distributions were re-built using
200 these initial data, as explained hereafter:

- 201 - The number of foodborne disease cases was extracted from a previous study [12],
- 202 specifically the median value of the estimations and the associated 95% CI. These data
- 203 were integrated into our model with a lognormal distribution, which was the same
- 204 distribution law used by Van Cauteren et al. [12]. The latter study did not specify
- 205 whether this confidence interval reflected uncertainty or variability. Therefore, it was

206 considered to represent uncertainty. The mean was approximated by the median value
207 reported (on a ln scale), the standard deviation was estimated by using the interval
208 confidence bounds. As an example, for *Campylobacter* spp., the estimated median
209 incidence from Van Cauteren et al. study [12] was 392,177 with a confidence interval
210 between 215,216 at the 5% limit and 862,747 at the 95% limit. The mean of the
211 lognormal distribution was estimated to 12.88 and to match the confidence interval
212 bounds, the standard deviation was approximated to 0.375. This gave a lognormal
213 distribution with a 5th percentile of 12.27 and a 95th percentile of 13.51. Once
214 expressed in cell count, this interval was close to the one given in Van Cauteren et al.
215 [12].

216 - The attribution fraction of foodborne illnesses per pathogen and type of meat followed
217 a beta distribution; the available mean or the median was used to estimate the beta
218 distribution parameters. When the value of the attributable proportion was expressed
219 by the mean, the parameters were estimated using the equation $\text{mean} = \alpha / (\alpha + \beta)$. When
220 the value of the attributable proportion was expressed by the median, the parameters
221 were estimated using the equation $\text{median} = (\alpha - 1/3) / (\alpha + \beta - 2/3)$. Therefore, the values of
222 α and β were estimated by approximation. As an example, for *Campylobacter* spp., the
223 median of the attributable fraction from beef was 0.16 with a confidence interval
224 between 0 at the 5% limit, and 0.37 at the 95% limit [18]. The best fit of α and β
225 parameters were 3 and 14.3, respectively. This resulted to an estimation of beef
226 *Campylobacter* spp. attribution by a beta distribution having a median of 0.16, a 5th
227 percentile of 0.05 and a 95th percentile of 0.34, close to results given in Hoffmann et
228 al. [18].

229 - Finally, the probability distributions of DALY, acquired from the literature, were
230 assumed to follow normal distributions.

231 The implementation of the inputs in the model are represented in Table 1. Our models used
232 10,000 iterations to capture the uncertainty. This action was performed using R software
233 (version 3.6.2). To verify the stability of the outputs, three simulations were performed. The
234 variation between these three simulations was less than 5% for the mean of the DALY
235 whatever the pathogen and type of meat.

236 3. Results

237 3.1. Main microbiological hazards associated with red meat consumption

238 From our literature search, 16 foodborne pathogens were identified to be involved in
239 foodborne diseases associated with red meat consumption:

- 240 - 12 bacteria: *Bacillus cereus*, *Brucella* spp., *Campylobacter* spp., *Clostridium*
241 *botulinum*, *C. perfringens*, Shiga-toxin producing *Escherichia coli* (STEC), *Listeria*
242 *monocytogenes*, *Salmonella* spp. (mostly *Salmonella enterica*), *Shigella* spp., *S.*
243 *aureus*, *Vibrio* spp. and *Yersinia* spp.;
- 244 - Two viruses: hepatitis E and norovirus;
- 245 - Two parasites: *Taenia saginata* and *Toxoplasma gondii*.

246 Some of these pathogens were discarded according to the criteria described below.

- 247 - *B. cereus*, *Shigella* spp., *Vibrio* spp. and *T. saginata* were excluded due to the lack
248 of data about the proportion attributable to red meat. *Brucella* spp. was excluded
249 due to the lack of information about the number of French cases. *C. botulinum* was
250 excluded due to the lack of quantified DALYs.
- 251 - Foodborne illnesses due to *L. monocytogenes* and *Yersinia* spp. were not
252 considered because these pathogens were mostly associated with ready-to-eat
253 foods [22,23].

254 After the above exclusions, the selected pathogens associated with red meat consumption
255 were *Campylobacter* spp., *C. perfringens*, *S. enterica*, *S. aureus*, STEC, *T. gondii*, hepatitis E
256 virus and norovirus.

257 3.2. Estimation of the foodborne disease burden in France

258 In France, the number of foodborne diseases due to red meat consumption was estimated to
259 have a mean of 670 [95% CI = 380–1100] illness cases per 100,000 inhabitants.
260 *Campylobacter* spp. was responsible for 32% of foodborne incidents due to red meat
261 consumption, with a mean of 210 [95% CI = 50–520] cases per 100,000 population (Figure
262 1). *C. perfringens* was the second pathogen responsible of the highest number of cases with a
263 mean of 150 [95% CI = 40–420] cases per 100,000 population, followed by non-typhoidal *S.*
264 *enterica* with a mean of 110 [95% CI = 30–280] per 100,000 population. The least frequent
265 foodborne pathogen was *T. gondii*, which contributed to 12 [95% CI = 4–25] cases (estimated
266 mean values) per 100,000 population. The pathogen that induced the highest mortality was
267 non-typhoidal *S. enterica*, with a mean of 0.04 [95% CI = 0.01-0.10] death per 100,000
268 population (Table 2), followed by hepatitis E, *T. gondii* and *Campylobacter* spp., with means
269 of 0.02 death per 100,000 population (Figure 2). The total number of deaths was estimated to
270 a mean value of 0.12 [95% CI = 0.07–0.19] per 100,000 population.

271 Our study estimated a mean of 39 [95% CI = 8–71] DALYs per 100,000 population
272 due to foodborne diseases in France. The major contributor to the loss of years in good health
273 from red meat consumption in France was hepatitis E (mean: 33 [95% CI = 1–64] DALYs per
274 100,000 population), specifically due to pork consumption, even though it was ranked fourth
275 in terms of the overall incidence of foodborne illnesses from red meat consumption (Table 2,
276 Figure 1 and Figure 3). The main bacteria associated with burden of disease in terms of
277 DALY from pork consumption were non-typhoidal *S. enterica*, which was three times higher
278 than *C. perfringens* or *Campylobacter* spp. For beef, the main bacteria contributor of
279 foodborne burden was *Campylobacter* spp., *C. perfringens*, STEC and non-typhoidal *S.*
280 *enterica* (Table 2).

281 The severity of each pathogen was estimated by dividing the number of DALY by the
282 number of cases. As an example, the severity of *T. gondii* per case was estimated by dividing
283 the number of DALY per 100,000 population (3.86 DALY) by the number of cases per
284 100,000 population (12 cases). The most severe pathogen per case was hepatitis E, with 0.46
285 DALY per case, followed by *T. gondii* (0.32 DALY per case), STEC (0.02 DALY per case)
286 and non-typhoidal *S. enterica* (0.01 DALYs per case). *C. perfringens*, *Campylobacter* spp.
287 and *S. aureus* had similar impacts in terms of severity, with 0.003 DALY per case. The least
288 severe pathogen was norovirus, with 0.002 DALY per case.

289 4. Discussion

290 The first objective of the present study was to aggregate data available in the literature to
291 identify and characterise the main microbiological hazards when consuming red meat in
292 France. These sources included muscle and offal from beef, pork and other small ruminants,
293 but not dairy products. Subsequently, a risk assessment model was built to estimate the
294 associated number of foodborne illnesses and deaths. Finally, the goal was to estimate the
295 consequent burden of diseases, considering the severity of the illness, and perform further
296 comparisons with other health effects and compare consumption scenarios.

297 From the literature search, 17 foodborne pathogens were identified as involved in
298 foodborne diseases attributable to red meat consumption. This number was less than the main
299 zoonotic agents identified by Haddad et al. [24], who identified more than 31 agents from red
300 meat, but those authors included additional transmission pathways of infection (e.g.
301 occupational transmission, animal bites, etc.). A team from the Centre d'Information des
302 Viandes (Meat Information Center) identified four bacterial diseases associated with meat
303 product consumption (foodborne outbreaks, listeriosis, botulism and haemolytic uraemic
304 syndrome [HUS]), three parasitic diseases (taeniasis, toxoplasmosis and trichinellosis) and
305 one viral disease (hepatitis E) [25]. However, for *L. monocytogenes* and *C. botulinum*
306 identified in that study, the main meat products were processed and consumed without pre-
307 cooking [25]. In 2014, ANSES classified the main hazard-food pathogen couples. Meat was
308 associated with STEC, *T. gondii*, non-typhoidal *Salmonella* spp., *Y. enterocolitica* and *T.*
309 *saginata*. *Campylobacter* was mostly from poultry meat and hepatitis E with raw pork liver
310 [23].

311 The incidence, attribution source and data availability were considered when selecting
312 the pathogens to quantify the disease burden due to red meat consumption. Eight pathogens

313 were selected for this study: *Campylobacter* spp., *C. perfringens*, non-typhoidal *S. enterica*,
314 STEC, *S. aureus*, *T. gondii*, hepatitis E and norovirus. In the Netherlands, 12 pathogens were
315 identified for red meat—including beef, lamb and pork—with the same criteria. In addition to
316 the pathogens chosen in our study, *L. monocytogenes*, rotavirus, *C. parvum* and *Giardia*
317 *lamblia* were considered in that study [26].

318 To estimate the attribution of foodborne diseases to red meat consumption, our
319 estimations were mostly based on WHO data, which aggregated the judgments from 73
320 international experts [18]. Hereby, per 100,000 inhabitants, our study's estimated number of
321 cases was 670 [95% CI = 380–1,100] illnesses, 0.12 [95% CI = 0.07–0.19] deaths and 39
322 [95% CI = 8–71] DALYs. These latter figures corresponded to 418,380 [95% CI = 238,480–
323 691,800] illnesses, 73 [95% CI = 41–118] deaths and 24,750 [95% CI = 4,900–44,720]
324 DALYs for the French population per year. Knowing the total number of foodborne illnesses
325 estimated by the WHO in EUR A region [11,27] (2431 cases per 100,000 population) and the
326 sum of the mean number of illnesses cases associated with *Campylobacter* spp., non-
327 typhoidal *S. enterica*, STEC and *T. gondii*, attributable to red meat estimated here (353 per
328 100,000 French population), it could be concluded that *Campylobacter* spp., non-typhoidal *S.*
329 *enterica*, STEC and *T. gondii* in red meat accounted for 15% of the total foodborne illnesses
330 estimated. These pathogens infection associated with red meat also accounted for 16% of the
331 total deaths and 15 % of the total DALYs due to foodborne pathogens

332 From our estimations, the major contributor of foodborne illness cases attributable to
333 red meat consumption was *Campylobacter* spp. This pathogen has been the most commonly
334 reported hazard that induced gastrointestinal issues in the European Union since 2005 [22].
335 Indeed, infection with this pathogen may cause diarrhoea, abdominal pain, bloody stools,
336 fever, headaches, vomiting and acute enteritis. Moreover, campylobacteriosis was responsible
337 for 30.1% of the total cases of Guillain-Barré syndrome according to a WHO study [28]. Even

338 though the main reservoir of *Campylobacter jejuni* is birds—including poultry—beef and
339 pork can also serve as a *Campylobacter* reservoir (essentially *Campylobacter coli*) [29]. In
340 2017, the EFSA/ECDC reported that 51% of the strong-evidence foodborne outbreaks caused
341 by *Campylobacter* were due to milk consumption, versus 3% for meat and meat products
342 (excluding strong-evidence waterborne outbreaks) [10]. However, this pathogen was reported
343 to be present in fresh pork and beef meat (8.3% of positive units) [10]. In addition, in our
344 study, it was estimated that 30% of foodborne illnesses from red meat were due to
345 *Campylobacter* spp., from which 55% were attributable to beef meat. In terms of incidence, it
346 was also determined that the second pathogen inducing the highest number of cases was *C.*
347 *perfringens* (22%), followed by non-typhoidal *S. enterica* (17%) and hepatitis E (11%). *S.*
348 *aureus* accounted for 6% of the cases related to red meat consumption.

349 The proportion of foodborne illnesses associated with the distinct pathogens in our
350 study was different from Dutch studies. Indeed, in the same years in the Netherlands, the
351 National Institute for Public Health and the Environment (RIVM) estimated that *C.*
352 *perfringens* was the major contributor of foodborne illness from red meat consumption, with
353 56% of foodborne illness cases [26]. Moreover, the proportion of *Campylobacter* spp., *S.*
354 *aureus* and *S. enterica* cases were approximately two-times higher in our study compared to
355 the Dutch studies [20,30]. The strategy used to estimate incidence of foodborne illnesses in
356 Van Cauteran et al. [12] was not the same as the Dutch studies. The former used an
357 underestimation factor to calculate the number of illness from the reported cases [12], while
358 the Dutch study based the incidence estimates for gastro-enteritis on population-based cohort
359 studies [30]. Moreover, the disease surveillance system coverage is not the same in France as
360 in the Netherlands, a factor that makes comparison difficult. For example, the
361 campylobacteriosis and salmonellosis surveillance system coverage in 2016 was estimated to
362 be 20% and 48%, respectively, in France, versus 52% and 64%, respectively, in the

363 Netherlands [10]. In addition, the list of mandatory notifiable infectious diseases is not the
364 same for all countries. For instance, STEC infection is required to be reported in the
365 Netherlands but not in France [10].

366 Among microbiological hazards relevant to beef consumption, STEC is the most
367 studied[31]. In 2010, 122 cases of HUS, which is characterised by acute kidney and renal
368 failure in young children [32], were reported in France [23] following STEC ingestion from
369 ground beef [23,33]. Ground beef is considered the most common source of STEC foodborne
370 illnesses, along with raw milk [23]. In a previous report, ANSES estimated a probability of
371 HUS between 0.02 and 0.05 of illness after STEC infections [34]. In our estimations, 19 cases
372 per 100,000 population were due to STEC infections attributable to red meat consumption,
373 from which the incidence due to beef consumption was estimated at 14 [3–34] per 100,000
374 population. This finding suggests between 0.3 (14 x 0.02) and 0.7 (14 X 0.05) HUS cases per
375 100,000 population are attributed to beef. In other words, between 190 and 440 HUS cases in
376 France in 2010 resulted from beef consumption. The slightly lower number of HUS cases
377 reported in 2010 (122) compared with our beef estimations (190–440) might be due to under-
378 reporting because there is no surveillance of the whole population. Rather, only individuals
379 less than 15 years old are monitored [23]. Indeed, in Havelaar et al., 72% of all HUS cases
380 were in individuals under 15 years of age [35]. If we assumed the same proportion
381 distribution as in the Dutch study, then the HUS estimation reported in 2010 in France (122)
382 would be around 170 cases, which is close to the lower bound of our estimations.

383 The major contributor of deaths due to red meat consumption was non-typhoidal *S.*
384 *enterica* associated with pork, followed by hepatitis E, *T. gondii* and *Campylobacter* spp. In
385 terms of DALYs, hepatitis E was responsible for the highest loss of years in good health
386 resulting from consumption of red meat. In France, this loss was exclusively due to pork
387 meat, specifically pork liver. After hepatitis E, *T. gondii* and non-typhoidal *S. enterica* were

388 responsible for the greatest loss of years in good health. This reversal of ranking can be
389 explained by an overestimation of the hepatitis E severity. Indeed, the majority of the DALYs
390 estimated for hepatitis E by the Dutch team were from deaths [30]. However, the proportion
391 of deaths due to this virus in the Netherlands (1.4% [30]), which was the reference study, was
392 higher than that observed in France (0.03% [12]). Havelaar et al. [30] assumed that mortality
393 from hepatitis E resulted in 33.4 years of life lost. Therefore, if we considered mortality in
394 France (0.02 deaths [95% CI: 0–0.04] per 100,000 population) and the number of years lost
395 from hepatitis E estimated by the Dutch study, the most probable DALY from hepatitis E in
396 France would be 0.7 per 100,000 population.

397 Without considering hepatitis E, the mean number of DALYs due to consumption of
398 red meat muscle was 6.6 [95% CI: 3.4–11.1] per 100,000 population, from which 2.8 [95%
399 CI: 1.2–5.2] per 100,000 population were associated with beef meat. Pork meat accounted for
400 1.5 [95% CI: 0.4–3.8] DALYs per 100,000 population per year. These values were of the
401 same order of magnitude as the estimations from the Netherlands based upon the following
402 calculations: 934 DALY for beef & lamb and 1280 DALY for pork in 2012 for the all
403 Netherlands population [26] (16.73 million of inhabitants considered according Eurostat),
404 corresponding to 5.6 DALYs per 100,000 population and 7.7 DALYs per 100,000 population,
405 respectively

406 *T. gondii* infection was ranked second in terms of DALYs. The burden of this parasite
407 might affect the general population (but mostly in a benign form). The most severe forms in
408 France, including deaths, concern immunosuppressed populations (acquired form) [36,37]
409 [38]; congenital forms have a lower effect on burden. In fact, in the French population,
410 pregnant women are very aware of the toxoplasmosis risk, and blood samples are taken from
411 the beginning of pregnancy for the detection of immunisation following possible
412 contamination. Indeed, it is one of the four infectious diseases—with rubella, syphilis and

413 hepatitis B and maternal anti D-fetal allo—for which screening is mandatory. This protocol
414 has been a part of prenatal screening programmes in France since the late 1970s [39]. Almost
415 all of the congenital forms of *T. gondii* infection are identified in France, in contrast to other
416 European countries where the screening is not performed or is not mandatory [40]. When fetal
417 infection occurs, the treatment against toxoplasmosis infection in utero was demonstrated to
418 allow children to have a similar quality of life to those not infected [41]. The proportion of
419 congenital toxoplasmosis sequela in France might be lower than estimated by WHO [11,28].
420 Therefore, the burden estimated in our study is likely to be overestimated.

421 In this study, red meat consumption was responsible for a mean of 0.37 [95% CI:
422 0.10–0.77] DALY per 100,000 population from STEC infection. This value corresponded to a
423 mean of 232 [95% CI: 62–489] DALYs annually for the population in France, which is one-
424 half the DALYs estimated by the ANSES (465 years in good health lost) [33]. This
425 discrepancy might be due to the higher proportion of deaths considered by the BCoDE toolkit,
426 which was used for the ANSES estimations, compared to the proportion of deaths considered
427 for the 2015 WHO estimations. However, we could not use the BCoDE toolkit for
428 comparison with our estimations due to the lack of foodborne illness incidence data per age
429 class and gender, which is required for BCoDE estimations. The estimations from Havelaar et
430 al. [35] were also higher than ours, even though the considered disability weight was lower
431 than the one used by the WHO (0.123 versus 0.210, respectively). This finding might be
432 explained by the duration of the sequelae, which was considered to be longer in the Dutch’s
433 study, i.e. 1 year against 28 days in the Hoffmann study [28,35].

434 Using existing studies in the literature allowed us to estimate the number of cases and
435 deaths and the foodborne disease burden in France attributable to red meat consumption,
436 without generating new data with additional monitoring costs. The estimations might be
437 improved by considering the effect of age on outcomes of foodborne diseases, such as sequela

438 and mortality. Indeed, if deaths or permanent sequela occur during childhood, the number of
439 years lost will be higher than if death occurs at an advanced age. However, this estimation
440 was not possible in this study because all the information was given for a global population.

441 The study by Hoffmann et al. [18] was chosen to determine the attribution fraction of a
442 pathogen to a red meat type because it is the most recent and reliable study conducted by the
443 WHO with expert elicitation. Although it did not specifically refer to France, data from the
444 “EUR A” region included France. Nevertheless, we are aware that the estimations provided
445 by this study are somewhat different from other published estimates [18]. This discrepancy
446 introduced unquantifiable uncertainty into our results. Moreover, to increase the reliability of
447 this work, the existing French attribution study might be updated. Additionally, considering
448 other red meat types, including a larger number of pathogens selected and separate attribution
449 of unprocessed and processed red meat types, might improve the reliability.

450 Our study estimates the number of foodborne illnesses and DALYs dedicated to red
451 meat in France, with French incidence data. In terms of foodborne bacteria, for beef and pork
452 meat, *Campylobacter* spp., non-typhoidal *Salmonella enterica*, *C. perfringens* and STEC
453 represented a mean of 2.2 [95% CI = 1.0–4.0] DALYs per 100,000 individuals per year.
454 Overall, the estimations provided in this study might help authorities to focus on these hazards
455 and ultimately reduce their impact on the health of the French population.

456 With the use of the DALY metric, we were able to compare our estimates to include
457 the effects of other foods components on health. The burden estimated in this study was lower
458 than the burden caused by diet high in sugar-sweetened beverages (46 DALYs [95% CI = 15–
459 83] per 100,000 population) and the use of alcohol (1,818 [95% CI = 1,359–2,368] DALYs
460 per 100,000 population) [42]. In future studies, the microbiological burden will be balanced
461 by nutritional risks and benefits brought by red meat consumption in a broader risk-benefit
462 assessment as done by other studies [43–45]. It was recently estimated that a mean of 19 [95%

463 CI = 8–33] DALYs per 100,000 people per year were due to colorectal cancer, and a mean of
464 21 [95% CI = 12–32] DALYs per 100,000 people per year due to cardiovascular disease,
465 were associated with the consumption of red meat [46]. Red meat consumption does have
466 some benefits with regard to the nutrients it provides, especially iron, which may help
467 decrease the major nutritional deficiency in the world [47]. This condition accounts for a
468 mean of 16 [95% CI = 11–20] DALYs per 100,000 individuals per year [48].

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613

614 **Figure captions:**

615

616 **Fig. 1.** Mean number of foodborne cases per 100,000 French population per year and per
617 pathogen attributable to red meat estimated in this study. The full lines represent the 95%
618 uncertainty around the mean value.

619

620 **Fig. 2.** Mean number of deaths per 100,000 French population per year and per pathogen
621 attributable to red meat estimated in this study. The full lines represent the 95% uncertainty
622 around the mean value.

623

624 **Fig. 3.** Mean number of disease-adjusted life years (DALYs) per 100,000 French population
625 per year and per pathogen attributable to red meat estimated in this study. The full lines
626 represent the 95% uncertainty around the mean value.

627

628 **Table 1:** Implementation of the model inputs per hazard in the quantification model and data sources.

629

Characteristic	Initials	Equations	Distribution or deterministic value implemented	Hazard	Values implemented per type of hazard and meat ¹	Reference from which raw data was obtained	
Number of illness cases	N_{cases}, F_p	(1)	$LogNormal(\mu, \sigma)$	<i>Campylobacter</i> spp.	$\mu = 12.88$ $\sigma = 3.75 \times 10^{-1}$	[12]	
				Non-typhoidal <i>Salmonella enterica</i>	$\mu = 12.12$ $\sigma = 3.55 \times 10^{-1}$		
				<i>Staphylococcus aureus</i>	$\mu = 11.20$ $\sigma = 6.5 \times 10^{-1}$		
				Shiga-toxin producing <i>Escherichia coli</i> (STEC)	$\mu = 9.79$ $\sigma = 4.60 \times 10^{-1}$		
				<i>Clostridium perfringens</i>	$\mu = 11.69$ $\sigma = 6.00 \times 10^{-1}$		[12]
				Hepatitis E	$\mu = 10.99$ $\sigma = 2.45 \times 10^{-1}$		
				Norovirus	$\mu = 13.16$ $\sigma = 1.50 \times 10^{-1}$		
				<i>Toxoplasma gondii</i>	$\mu = 9.37$ $\sigma = 2.00 \times 10^{-1}$		
Proportion of foodborne diseases attributable to red meat	PA	(1), (2) and (3)	$Beta(\alpha, \beta)$	<i>Campylobacter</i> spp.	Beef $\alpha = 3$ $\beta = 14.3$	[18]	
					Pork $\alpha = 1$ $\beta = 10.78$		
					Other $\alpha = 1$ $\beta = 16.33$		
				Non-typhoidal <i>Salmonella enterica</i>	Beef $\alpha = 0.7$ $\beta = 9.13$		
					Pork $\alpha = 2.5$ $\beta = 7.19$		
					Other $\alpha = 0.8$ $\beta = 23.2$		
				<i>Staphylococcus aureus</i>	Beef $\alpha = 200$ $\beta = 954$		[49]
					Pork $\alpha = 15$ $\beta = 107,95$		
				Shiga-toxin producing <i>Escherichia coli</i> (STEC)	Beef $\alpha = 5$ $\beta = 6.8$		[18]
					Pork $\alpha = 0.5$ $\beta = 5.72$		
					Other $\alpha = 1.1$ $\beta = 9.15$		
				<i>Clostridium perfringens</i>	Beef $\alpha = 8.5$ $\beta = 13.52$		[49]
					Pork $\alpha = 240$ $\beta = 655.52$		
				Hepatitis E	Pork $\alpha = 0.74$ $\beta = 0.26$		[20]
				Norovirus	Beef and Lamb $\alpha = 1$ $\beta = 32.3$		
					Pork $\alpha = 0.6$ $\beta = 19.4$		
					<i>Toxoplasma gondii</i>		Beef $\alpha = 2.5$ $\beta = 6.96$
				Other $\alpha = 1.6$ $\beta = 5.4$			
Proportions of deaths after foodborne illness	R_{death}, F_p	(3)	Deterministic value	<i>Campylobacter</i> spp.	1.04×10^{-4}	[12]	
				Non-typhoidal <i>Salmonella enterica</i>	3.66×10^{-4}		
				<i>Staphylococcus aureus</i>	0.16×10^{-4}		
				Shiga-toxin producing <i>Escherichia coli</i> (STEC)	2.23×10^{-4}		
				<i>Clostridium perfringens</i>	0.17×10^{-4}		[12]
				Hepatitis E	3.03×10^{-4}		
				Norovirus	0.15×10^{-4}		
				<i>Toxoplasma gondii</i>	18.67×10^{-4}		
Number of DALYs per 100,000 population	$DALY.EURA$	(3)	$Normal(\mu, \sigma)$	<i>Campylobacter</i> spp.	$\mu = 10$ $\sigma = 2.04$	[28]	
				Non-typhoidal <i>Salmonella enterica</i>	$\mu = 12$ $\sigma = 2.81$		
				Shiga-toxin producing <i>Escherichia coli</i> (STEC)	$\mu = 0.6$ $\sigma = 2.04 \times 10^{-1}$		
				<i>Toxoplasma gondii</i>	$\mu = 6$ $\sigma = 1.53$		
Number of DALYs per case	$DALY.case$	(3)	Deterministic value	<i>Staphylococcus aureus</i>	2.6×10^{-3}	[30]	
				<i>Clostridium perfringens</i>	3.2×10^{-3}		
				Hepatitis E	4.6×10^{-1}		
				Norovirus	2.5×10^{-3}		

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631 ¹ Following R parametrisation: μ = mean; σ = standard deviation; α = shape 1 of the beta distribution, β = shape 1 of the beta distribution

632 **Table 2:** Mean deaths and disability-adjusted life years (DALYs) per 100,000 population
 633 attributable to red meat estimated in this study. The means are presented with the 2.5 and 97.5

Hazard	Beef		Pork		Other small ruminants	
	Deaths	DALY	Deaths	DALY	Deaths	DALY
<i>Campylobacter spp.</i>	0.012 (0.002–0.033)	0.37 (0.04–1.03)	0.006 (0–0.023)	0.18 (0–0.74)	0.004 (0–0.015)	0.12 (0–0.49)
Non-typhoidal <i>Salmonella enterica</i>	0.008 (0–0.035)	0.20 (0–0.88)	0.029 (0.005–0.078)	0.73 (0.10–1.89)	0.004 (0–0.016)	0.09 (0–0.41)
<i>Staphylococcus aureus</i>	0 (0–0.001)	0.07 (0.01–0.19)	0 (0–0.001)	0.05 (0.01–0.14)	-	-
Shiga-toxin producing <i>Escherichia coli</i> (STEC)	0.003 (0.001–0.008)	0.25 (0.06–0.53)	0 (0–0.001)	0.05 (0–0.24)	0.001 (0–0.003)	0.07 (0–0.23)
<i>Clostridium perfringens</i>	0.001 (0–0.004)	0.28 (0.06–0.83)	0.001 (0–0.003)	0.20 (0.05–0.54)	-	-
Hepatitis E	-	-	0.023 (0.001–0.042)	32.82 (1.46–63.79)	-	-
Norovirus	0 (0–0.001)	0.06 (0–0.23)	0 (0–0.002)	0.06 (0–0.29)	-	-
<i>Toxoplasma gondii</i>	0.009 (0.001–0.022)	1.59 (0.29–3.82)	0.005 (0–0.018)	0.90 (0.03–3.51)	0.008 (0.001–0.022)	1.37 (0.13–3.79)
Total	0.035 (0.015–0.068)	2.80 (1.24–5.19)	0.064 (0.026–0.119)	34.96 (3.58–66.69)	0.017 (0.005–0.037)	1.65 (0.33–4.12)

634 percentiles in parentheses.

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