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1 **Risk factors for sporadic salmonellosis: a systematic review and meta-analysis**

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23

24 **Short Title**

25 Meta-analysis on risk factors for sporadic salmonellosis

26 **Highlights** (*maximum 85 characters, including spaces, per bullet point*).

- 27 - Meta-analysis of 62 case-control studies about sporadic human salmonellosis
- 28 - Travel, environmental, animal and food exposures were significant risk factors
- 29 - Recent use of anti-acids or antibiotics and underlying disease increased the risk
- 30 - Known risk factors such as eggs and meat products were confirmed
- 31 - The role of consumption of raw or undercooked eggs and undercooked poultry is
- 32 underlined
- 33 - Produce and milk formula are risk factors of salmonellosis for children

34 **Keywords:** Research synthesis; Case-control studies; Meta-regression; *Salmonella*

35

36 **Abstract**

37 Non-typhoidal *Salmonella* is an important causative agent of diarrheal illness worldwide. A
38 systematic review and meta-analysis of case-control studies were performed to determine
39 the main risk factors associated with sporadic salmonellosis. Suitable scientific articles
40 published up to 2017 were identified through a systematic literature search and subject to
41 methodological quality assessment. From each study, odds ratios (OR) were extracted or
42 calculated, as well as study characteristics such as population type, design, type of model
43 used and risk factor categorization. Mixed-effects meta-analytical models were adjusted by
44 population type to appropriate data partitions. From 3858 identified references, the quality
45 assessment stage was passed by 62 case-control studies focusing on sporadic
46 salmonellosis which provided 1154 ORs for meta-analysis.

47 The meta-analysis identified host-specific factors, travel, environmental, animal and food
48 exposures as significant risk factors of salmonellosis in the mixed population. For the mixed
49 population, foods significantly associated with salmonellosis were eggs and egg products,
50 composite foods, and meat (pork, red meats other than beef and poultry meats). In the child

51 population, the main risk factors were found for person-to-person transmission, recent use of
52 gastric anti-acids or antibiotics, contact with pets and farm animals, environmental, and food
53 vehicles. Breastfeeding was found to be a protective factor for children. The food vehicles
54 identified in children comprised dairy (milk formula), produce, meat and eggs products.
55 Untreated drinking water was a risk factor for the children and mixed population. The result of
56 the meta-analysis conducted at the international level is very important in the context of
57 increasing international trade in foodstuffs and changes in food consumption patterns.

58 **Introduction**

59 Non-typhoid *Salmonella enterica* subsp. *enterica* is a major foodborne pathogen that causes
60 mild to moderate self-limiting gastroenteritis (WHO, 2018). Salmonellosis is usually
61 characterized by acute onset of fever, abdominal pain, diarrhea, nausea and sometimes
62 vomiting. The onset of disease symptoms occurs 6–72 hours (usually 12–36 hours) after the
63 ingestion of *Salmonella*, and the illness lasts 2–7 days (WHO, 2018). Patients will make a
64 recovery without specific treatment in most cases.

65 Salmonellosis is the second most frequently reported bacteriologically related zoonosis in
66 many European countries (EFSA and ECDC, 2018). In France, the annual community
67 incidence rate was estimated at 307 cases per 100,000 for salmonellosis (Van Cauteren et
68 al., 2015; Van Cauteren et al., 2017). Microbiological and epidemiological investigations
69 make it possible to identify outbreaks and to trace back the food at the origin of the human
70 cases (Inns et al., 2015; Ung et al., 2019). Although *Salmonella* outbreaks are identified, a
71 majority of salmonellosis cases is not associated with any known outbreak (Glass et al.,
72 2015) and are classified as sporadic cases. The question of specific food exposures and
73 respective weight for these specific forms arise.

74 There are several methodological approaches for salmonellosis source attribution (Pires et
75 al., 2010, Mughini-Gras et al., 2018), and the most appropriate approach depends on the
76 data availability and research question to be addressed. A large variety of approaches has
77 been explored, including microbial subtyping method (David et al., 2013 a,b; Barco et al.,
78 2013 & 2015; Mikkela et al., 2019), genomics approach (Zhang et al., 2019), comparative
79 exposure assessment (Christidis et al., 2020), outbreak data analysis (Pires et al., 2010;
80 Painter et al., 2013; IFASC, 2019), or expert elicitation (Havelaar et al., 2008).

81 Another way of identifying the sources of these sporadic cases is case-control studies
82 (Domingues et al., 2012). In case-control studies, the association of cases with various food
83 exposures is usually measured through odds ratios (ORs) (Pires et al., 2009). Meta-analyses
84 of these studies can provide information on exposure pathways of interest (Devleeschauwer
85 et al., 2019). Domingues et al (2012) conducted a meta-analysis comprising thirty-five

86 *Salmonella* case-control studies identified through a literature search conducted in February
87 2008.

88 The aim of the present study is to perform an updated systematic review of case-control
89 studies for human salmonellosis published internationally up to May 2017 and perform a
90 meta-analysis to synthesize data on factors associated with sporadic *Salmonella* infection,
91 combining the odds ratio from a selection of relevant studies (Gonzales-Barron et al., 2019).

92

93 **Methods**

94 The protocol of the systematic review and the meta-analysis model are described in depth in
95 the methodological paper of this special issue (Gonzales-Barron et al., 2019). The screening
96 criteria followed the Preferred Reporting Items for Systematic Reviews and Meta-analyses
97 (PRISMA).

98 **Systematic review**

99 The keywords were defined attending the review question which is to evaluate the
100 association between a (risk) factor and sporadic salmonellosis risk in a population exposed
101 to it. This review question was identified to have a typical PECO structure (Population,
102 Exposure, Comparator and Outcome as key elements). The literature search was conducted
103 in March 2017 using a combination of keywords related to (1) “*Salmonella* OR
104 salmonellosis”; (2) “case-control” OR “risk factor” OR “cohort (3) “infection” OR disease”;
105 joined by the logical connector AND.

106 Systematic searches using a combination of suitable keywords were conducted using the
107 bibliographic engines Science Direct, PubMed, Scielo, ISI Web of Science and Scopus. The
108 literature search was limited to the English, French, Portuguese and Spanish languages.

109 Each reference record was screened for relevance for inclusion in the meta-analysis study,
110 and subsequently, the methodological quality of the “candidate” studies was assessed using
111 preset quality criteria. Five criteria for inclusion were related to the definition of disease. First,
112 it had to refer to confirmed humans salmonellosis. The second criterion refers to the study
113 design whereby only case-control studies were considered. The third criterion is the
114 presence of information on cases definition. Finally, the quality and the completeness of
115 statistical analysis were assessed. Primary studies that passed the screening for relevance
116 were marked as having the potential for bias if they failed to meet at least one of the
117 methodological quality assessment criteria. Studies related to *S. Typhi* and *Paratyphi* were
118 excluded from the review.

119 Data from primary studies were then extracted using a standardised spreadsheet. Data
120 extracted included the relevant study characteristics (location, period, population, serotype,
121 case definition, design, sample size of the groups, type of model, etc.), the categorized risk
122 factors, the setting, the handling practices and the outcome of the study (Odds Ratio (OR)).
123 A data categorisation scheme was established to hierarchically group the risk factors into
124 travel, host-specific factors and pathways of exposure (see the methodological paper of this
125 issue Gonzales-Barron et al., 2019). The variable “population” was stratified into mixed
126 (adults, or undefined age), and children.

127 **Data synthesis**

128 As described in Gonzales-Barron et al. (2019). The joint meta-analytical data was first
129 described using basic statistics. Next, data was partitioned into subsets of categories of risk
130 factors. Meta-analysis models were then fitted to each of the data partitions or subsets in
131 order to estimate the overall OR for travel, host-specific factors and transmission pathways
132 related to person-to-person transmission, animal contact, environmental and food exposures.
133 The meta-analytical models were fitted separately by population type. For some food
134 classes, the effects of handling (i.e., eating raw, undercooked) and setting (i.e., eating out)
135 on the overall ORs were assessed by calculating the ratio of the mean ORs when food was
136 mishandled (or when food was prepared outside the home) to the base ORs.

137 The statistical analysis was designed to assess the effect of the geographical region, the
138 study period and the analysis type (univariate/multivariate) on the result. The objective of the
139 region-specific meta-analysis was to inform the decision on the geographical regions that
140 should be kept for the subsequent pooling of ORs. All meta-analytical models were
141 essentially weighted random-effects linear regression models. Once a meta-analytical model
142 was fitted, influential diagnostics statistics based on Cook’s distance were assessed to
143 remove any influential observation originating from studies marked as having potential-for-
144 bias. Publication bias was assessed by funnel plots and statistical tests investigating the
145 effect of the study sample size on the ORs (Gonzales-Barron et al., 2019). Heterogeneity

146 between studies was assessed by three indicators, the between-study variability (τ^2), the QE
147 test investigating residual heterogeneity, the variance of residuals and the intra-class
148 correlation I^2 (Gonzales-Barron et al., 2019).

149 All analyses were conducted in the R software implemented with the *metafor* package
150 (Viechtbauer, 2010).

151 Pooled ORs were considered as significant when the lower bound of the 95% CI was equal
152 or greater than one, except for breastfeeding where the upper bound of the confidence
153 interval had to be below one for it to be deemed as significant (protective).

154

155 **Results**

156 **Descriptive statistics of the case-control studies**

157 From 3858 identified and analyzed references, 460 passed the relevance screening and 62
158 passed the quality assessment stage (Fig. 1). Appendix 1 summarizes the 62 bibliographic
159 references. Appendix 2 summarizes the main features (country, population, period, design,
160 model, number of cases/controls, quality and numbers of ORs) of the 62 case-control studies
161 used in this meta-analysis. These case-control studies constitute a set of 1,154 ORs from
162 risk factors (above 0.5 except for breastfeeding).

163 These published studies were conducted in years spanning from 1987 and 2013 (51.6 % are
164 after 2000). Most publications concerned Europa (29 publications), North America (25
165 publications), followed by Oceania (5 publications), Asia (2 publications) and South America
166 (1 publication). Europe provided 51% of the ORs (588/1154) while North America (United
167 States, Canada) is also highly represented with 40% of ORs (455/1154).

168 Most studies investigated exposures in the mixed population (adults or non-precise age, 48
169 publications), followed by **child population** (16 publications) and susceptible (HIV infected
170 patients) (1 publication) (Appendix 1) (Taconelli et al., 1998). This last publication only
171 contributes to the analysis with one OR concerning antibiotics in host-specific factors.

172 Except for one study (Bellido-Blasco et al., 2007), salmonellosis cases were confirmed by
173 isolation of the bacterium. A diversity of serotypes is considered in the 62 studies but the
174 majority (50%) retained only *S. Enteritidis* and *S. Typhimurium*.

175 The risk factors studied concerned the following routes of exposure: person-to-person (19
176 OR), environmental (84 OR), contact with animals (175 OR), and food or handling practices
177 (700 OR). Host-specific factor (122 OR) or travel (54 OR) are also studied in this work.

178 After methodological quality assessment, 13 case-control studies were marked as being
179 below standards (as example controls have campylobacteriosis) and corresponding ORs
180 were removed from the meta-analysis if sensitivity analysis found an influence on the pooled
181 estimate (Gonzales-Barron et al., 2019).

182 **Meta-analysis**

183 For every data partition, the meta-analysed risk factors are presented in summary tables only
184 when significant (Tables 1, 2 and 3). Non-significant results or significant pooled ORs coming
185 from a single study for main risk factors are given in Table 4.

186 **Significant risk factors associated with travel, host-related factors, contact with the** 187 **environment and animals**

188 Table 1 presents the significant risk factors for these main factors explored. In all
189 geographical regions, except for case-control studies carried out in Asia, travel was a
190 significant risk factor for salmonellosis. Thus, for the estimation of the travel subcategories,
191 the data points from Asia were removed. Both inside and abroad travels were found to be
192 associated with an increased risk of sporadic salmonellosis (pooled OR of 3.612 95% CI
193 [2.839 - 4.593] and 2.195 95% CI [1.054 - 4.572] respectively. It is worth noticing that before
194 the year 2000, the travel associated OR was significantly higher ($p=0.005$).

195 Several host-specific factors were associated with the risk of salmonellosis. The use of
196 gastric anti-acids or antibiotics had ORs above 3.0 in the mixed population (Table 1) (anti-
197 acids: pooled OR 3.184 95% CI [2.449 - 4.139]). Patients with chronic diseases (i.e.
198 allergies, stomach ulcer, cancer, diabetes, endocrine disease, heart disease, kidney disease,

199 intestinal disorders, alcoholism, autoimmune disease, and blood disorder) had also
200 significantly higher odds of acquiring salmonellosis (pooled OR=3.289 95% CI [2.449 -
201 4.416]). The same level of odds was observed in patients receiving other medications, such
202 as NSAID, corticosteroids, thyroid and hormone drugs (pooled OR=4.655 95% CI [3.458 -
203 6.266]). When focusing on children, the use of anti-acids (pooled OR=3.413 95% CI [1.851 -
204 6.296]) and antibiotics (pooled OR=2.376 95% CI [1.618 - 3.489]) produced a similar degree
205 of salmonellosis risk. In the population of infants, breastfeeding was proven to be protective
206 against *Salmonella* infection. Combining the results from seven case-control studies, 747
207 infants of age lower than 2 years had a pooled OR of 0.249 95% CI [0.165 -0.377] times the
208 odds of becoming ill than those who were not breastfed.

209 Person-to-person transmission was a significant risk factor for both the mixed population and
210 children, but it was much higher in the latter, with a pooled OR of 1.692 95% CI [1.145 -
211 2.500] and 3.811 [1.977 - 7.348], respectively. Person-to-person transmission was described
212 in the mixed population as contact with patient or contact household member with diarrhea
213 (or confirmed cases). For the **child population**, contacts were described as contact with
214 diarrhea in household or creche with an ill child.

215 Contact with animals (farm, pet or wild) for children as well as in the mixed population was an
216 exposure pathway widely explored in the different studies (127 ORs for 30 studies in the
217 mixed population, and 44 ORs from 9 studies for children). In the mixed population, the
218 pooled ORs for this route of exposure ranged from 1.471 to 2.619 (contact with pets, on-farm
219 activities, or professional activities related to animals and carcasses, and contact with wild
220 animals). Farm environment was also found to be a risk factor in the mixed population
221 (pooled OR 1.900 95% CI [1.251 - 2.885]). For children, the pooled ORs associated with
222 contact with pets and farm animals were 3.035 95% CI [1.938 - 4.756] and 2.658 95% CI
223 [1.431 - 4.938], respectively. When exploring in more detail the pet factor, for both
224 populations, the diversity of animals was important (reptiles, dogs, cats, pets with diarrhea,
225 etc.). The categories of farm animals and wild animals were also very diverse.

226 For the mixed population, salmonellosis cases occurred more frequently among people
227 exposed to water-related activities (fishing, swimming, sailing, etc.) (pooled OR=2.221 95%
228 CI [1.339 - 3.681]). Drinking water practice was also significantly associated with increased
229 salmonellosis risk. Within this category, the consumption of untreated water was associated
230 with salmonellosis for the mixed population (pooled OR=1.753 95% CI [1.109 - 2.770]) and
231 represented a risk factor specifically for children too (pooled OR=2.130 95% CI [1.285 -
232 3.532]) (Figure 2). For children, outdoor activities (activities in parks, playground sandboxes,
233 contact with soil, etc.) were strongly associated with salmonellosis (pooled OR=3.055 95% CI
234 [2.243 - 4.160]). Childcare attendance was significantly associated with salmonellosis
235 (pooled OR=2.738 95% CI [2.243 - 4.160]) in children, but strength or ORs were very
236 different in different childcare settings (e.g. school, daycare).

237 **Significant risk factors associated with food-related transmission pathways**

238 Significant factors associated with food are given in Tables 1, 2 and 3. The studies explored
239 a wide range of foods and food preparation/consumption practices (e.g. hygiene, cooking,
240 and place of consumption). For the mixed population foods significantly associated with
241 salmonellosis were eggs and egg products (pooled OR=1.774 95% CI [1.351 - 2.329]),
242 composite foods (pooled OR=1.731 95% CI [1.258 -2.381]), and meat (pooled OR=1.489
243 95% CI [1.137 - 1.951]) (Table 1). Within eggs category, higher pooled OR values were
244 obtained for egg products (pooled OR=2.736 95% CI [1.502 - 4.987]) compared to eggs
245 (pooled OR= 1.976 95% CI [1.138 - 3.431]).

246 Among meats, poultry (pooled OR=1.474 95% CI [1.167 - 1.861]), pork (pooled OR=1.563
247 95% CI [1.111 - 2.200]), red meats other than beef (pooled OR=1.680 95% CI [1.044 -
248 2.703])(as lamb, mutton or venison meat), and other meats (pooled OR = 1.938 95%CI
249 [1.215 - 3.091]) were the most important risk factors in the mixed population (Table 2).The
250 category “others” is very heterogeneous containing meats of non-specified origin. The food
251 vehicles identified in children also comprised meat and eggs categories (Table 1). For meat
252 products, pork had the highest pooled OR (pooled OR=3.089 95% CI [1.348 - 7.078])

253 followed by processed meat products (pooled OR=2.122 95% CI [1.538 - 2.928]) and beef
254 (pooled OR=1.623 [1.072 - 2.473]). Produce and dairy were also significantly associated with
255 increased risk of salmonellosis in children (Table 1). The association with dairy, here
256 described as milk formula, was explained by a pooled OR of 3.324 95% CI [2.136 - 5.172]
257 (Figure 3 and Table 2).

258 The consumption of undercooked pork and poultry meat multiplied the basic ORs by a factor
259 of 3.038 and 3.986, respectively (Table 3). Consumption of raw or undercooked eggs
260 increased the basic ORs by a factor of 3.642 and 2.182, respectively. Out-of-home
261 consumption of poultry, eggs or processed meats increased the basic ORs by factors
262 ranging from 1.5 to 2 (Table 3).

263 For most of the meta-analytical models (models) reported in legends of Tables 1, 2 and 3,
264 the statistical tests indicated the absence of potential significant publication bias is above
265 5%. An exception is observed in the partitions related to host-specific and food in the mixed
266 population (Table 1), dairy in children (Table 2), and the effect of handling on the
267 consumption of poultry and processed meat (Table 3). For better assessing the publication
268 bias (above 5%), the funnel plot for those models is given in Figure 4. All of them exhibited
269 asymmetry, as lack of non-significant studies with smaller ORs which could lead to OR
270 overestimation. Moreover, the intraclass correlation I^2 were for all partitions below high
271 heterogeneity (<75%). However, residual between-study heterogeneity (p-value often below
272 0.05 for Q or QE) was observed for the data partitions.

273 **Discussion**

274 In this study, the aim was to perform an updated systematic review of case-control studies
275 for human salmonellosis and to synthesize data in order to reveal the weight of common
276 factors associated with sporadic *Salmonella* infection, among them the relative importance of
277 travel, host-related factors, contact with animals and the environment, as well as food-related
278 factors. Based on the results of the meta-analysis, the ORs associated with non-food risk
279 factors (ORs between 2 and 6) were higher than those associated with exposures to main
280 foods categories (ORs between 1.4 and 2.9). In agreement with the scientific literature
281 (Domingues et al., 2012; Johnson et al., 2011), the present study identified international
282 travel as a significant risk factor for salmonellosis. Although the number of studies was
283 relatively small, the meta-analysis also allowed for the identification of within-country travel
284 as a significant risk factor; the considered case-control studies concerned large countries, i.e.
285 Australia (Ashbolt and Kirk, 2006) and the US (Passaro et al, 1996, Trepka et al, 1999).
286 Another hypothesis to explain this risk factor is associated with the consumption habits
287 during travelling. Indeed, this risk factor might be a reflection of more frequent eating out
288 practices, which have been also found to be a significant risk factor.

289 The present meta-analysis also confirmed the findings of Domingues et al. (2012) in the
290 relation to the importance of medication and chronic diseases. Concerning the latter factor, it
291 is worth mentioning that Teunis et al. (2010) did not observe significant differences between
292 the salmonellosis dose-response relations obtained for general and susceptible populations.

293 The evidenced strong effects of non-food exposures in this meta-analysis suggest that the
294 risk of acquiring salmonellosis is multi-factorial and that other sources than the foodborne
295 ones, such as contact with animals (Hoelzer et al., 2011; Lambertini et al., 2016) and
296 environmental waters (Guillier et al. 2020), are worth investigating too.

297 The food risk factors identified in the meta-analysis were corroborated by the analysis of
298 epidemiological data. Consumption of raw eggs, undercooked pork, poultry, beef, and milk
299 formula regularly cause outbreaks (Guillier et al., 2013; Dallman et al., 2016; Jones et al.,
300 2016; Dewey-Mattia et al., 2018). The data collected by the European RASFF (Rapid Alert

301 System for Food and Feed) system also confirm the importance of these categories. Of the
302 170 notifications from the EU Member States, poultry meat ranks first in terms of number of
303 alerts, followed by other meat and eggs and egg products (RASFF 2017). Similar to
304 Domingues et al. (2012), the consumption of dairy products was not found to be significant in
305 the mixed population despite the frequent link between raw milk cheese consumption
306 and *Salmonella* outbreaks (Yoon et al., 2016).

307 A potential difficulty to interpret the results of the meta-analysis could be due to the strong
308 host specificity of some serovars (Vila-Nova et al., 2019). Indeed, the salmonellosis cases in
309 the considered case-control studies are either caused by specific and frequently occurring
310 serovars (i.e. Typhimurium and Enteritidis, in particular) or by many different serovars. While
311 some serovars are not strongly associated with a unique animal reservoir (e. g. Typhimurium
312 or Agona), others display strong associations with reservoirs, such as Enteritidis and layers,
313 Derby and pigs, Dublin and cattle (Langridge et al., 2014). This may partly explain the
314 variability in ORs in the different case-control studies, and the remaining heterogeneity
315 between studies. For example, the ORs associated with egg consumption in studies focusing
316 only on Enteritidis were likely to be higher than those from studies of other serovars. The
317 importance of serovar in risk factor analysis has been shown recently (MacDonald et al.,
318 2018); their results supported the notion that the epidemiology of *S. Typhimurium* may differ
319 from other *Salmonella* types leading to differences in risk factors.

320 Besides, the relative importance of serovars in sporadic cases may differ between continents
321 and reflect very different epidemiological situations (Ferrari et al., 2019). For example, the
322 Heidelberg and Newport serovars are important and original in their representation in
323 salmonellosis cases for the North American continent (Jackson et al., 2013), while they are
324 not very important in the EU. Moreover, the different food consumption behaviors and habits
325 in the countries where the case-control studies were carried out may have had an impact, as
326 e.g. some kinds of meat may be mostly consumed undercooked by some, but not by others.
327 For example, in France, the consumption of undercooked beef is a common
328 practice (ANSES, 2017) and this consumption practice has been described as a major risk

329 factor for Typhimurium and Enteritidis serovars (Delarocque-Astagneau et al., 2000;
330 Delarocque-Astagneau et al., 1998). Snary et al. (2016) have shown that there is large
331 variability concerning the type and frequency of consumption of pork products within the EU.
332 These consumption patterns greatly impact the level of risk of pork products. On the other
333 hand, the results of the meta-analysis conducted at the international level is very important in
334 the context of increasing international trade in foodstuffs (Ercsey-Ravasz et al., 2012; Garre
335 et al., 2019) and changes in food consumption patterns (Smith and Fazil, 2019). Indeed, this
336 internationalization of trade and changes in consumer attitudes may lead to a change in risk.
337 In this context, the identification of risk factors at the international level is, therefore, an
338 important element for epidemiologists who often have a historical view of the different routes
339 of transmission and specific to their country.

340 At this stage, the ORs cannot be used to estimate the population attributable fraction in a risk
341 assessment. Indeed, the overall values of ORs might have been modulated by the different
342 regulatory measures at the international level (e.g. for the table egg sector in Europe versus
343 other continents) or within Europe (e.g. Sweden applies more stringent management
344 measures for cattle herds than those adopted by European regulations (Ågren et al., 2015)).

345 The published case-control studies included this meta-analysis are stored in a database,
346 which will be updated with other relevant studies published in the future. This opens the way
347 for further analyses, providing a basis for comparison between different countries about the
348 risk for salmonellosis associated with exposure to a given risk factor. Analysis of ORs
349 observed in different countries in relation to their regulations might also indicate the
350 appropriateness of management measures to be adopted. This basis should also make it
351 possible to carry out various studies focusing on specific serovars, in particular Enteritidis
352 and Typhimurium, in the future. Examination at this level would be a key element for tracing
353 the sources of sporadic cases.

354 **Conclusion**

355 The results of this meta-analysis confirm the outcomes obtained in a previous systematic
356 review of case-controls studies of salmonellosis (Domingues et al., 2012). Moreover, they
357 help going beyond the usual suspect of egg products being always the source and stress the
358 importance of refining the assessment of other food vehicles and consumption practices, and
359 routes such as environmental and animal contact.

360 The contribution of environmental or animal contact to the risk of sporadic salmonellosis
361 should be better documented in dedicated studies. It may be appropriate to include factors
362 related to professional activities, and those relating to contact with pets. Finally, risk factors
363 should be investigated by *Salmonella* serovars. Such investigations could enable for the
364 identification of source-specific risk factors and underlying transmission pathways.

365

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374 **References**

375 Ågren, E.C.C., Johansson, J., Frössling, J., Wahlström, H., Emanuelson, U., Sternberg-
376 Lewerin, S., 2015. Factors affecting costs for on-farm control of *Salmonella* in Swedish dairy
377 herds. *Acta Veterinaria Scandinavica* 57. <https://doi.org/10.1186/s13028-015-0118-y>

378 Ashbolt, R., Kirk, M. D., 2006. *Salmonella* Mississippi infections in Tasmania: the role of
379 native Australian animals and untreated drinking water. *Epidemiology & Infection*, 134(6),
380 1257-1265. <https://doi.org/10.1017/S0950268806006224>

381 ANSES, 2017. Third national study of individual food consumption: Changes in consumption
382 habits and patterns, new issues in the areas of food safety and nutrition.
383 [https://www.anses.fr/en/content/inca-3-changes-consumption-habits-and-patterns-new-](https://www.anses.fr/en/content/inca-3-changes-consumption-habits-and-patterns-new-issues-areas-food-safety-and-nutrition)
384 [issues-areas-food-safety-and-nutrition.](https://www.anses.fr/en/content/inca-3-changes-consumption-habits-and-patterns-new-issues-areas-food-safety-and-nutrition)

385 Barco, L., Barrucci, F., Olsen, J. E., Ricci, A., 2013. *Salmonella* source attribution based on
386 microbial subtyping. *International Journal of Food Microbiology*, 163(2-3), 193-203.
387 <https://doi.org/10.1016/j.ijfoodmicro.2013.03.005>

388 Barco, L., Barrucci, F., Cortini, E., Ramon, E., Olsen, J.E., Luzzi, I., Lettini, A.A., Ricci, A.,
389 2015. Ascertaining the relationship between *Salmonella* Typhimurium and *Salmonella*
390 4,[5],12:i:- by MLVA and inferring the sources of human salmonellosis due to the two
391 serovars in Italy. *Frontiers in Microbiology* 6. <https://doi.org/10.3389/fmicb.2015.00301>

392 Bellido-Blasco, J.B., González-Cano, J.M., Galiano-Arlandis, J.V., Herrero-Carot, C., Tirado-
393 Balaguer, M.D., Arnedo-Pena, A., Safont-Adsuara, L., Romeu-García, M.A., 2007. Risk
394 factors for the occurrence of sporadic *Campylobacter*, *Salmonella* and rotavirus diarrhea in
395 preschool children. *Anales de pediatria* 66(4), 367-374. <https://doi.org/10.1157/13101241>

396 Christidis, T., Hurst, M., Rudnick, W., Pintar, K. D., Pollari, F. (2020). A comparative
397 exposure assessment of foodborne, animal contact and waterborne transmission routes of
398 *Salmonella* in Canada. *Food Control*, 109, 106899.
399 <https://doi.org/10.1016/j.foodcont.2019.106899>

400 Dallman, T., Inns, T., Jombart, T., Ashton, P., Loman, N., Chatt, C., Messelhaeusser, U.,
401 Rabsch, W., Simon, S., Nikisins, S., Bernard, H., le Hello, S., Jourdan-da-Silva, N.,
402 Kornschober, C., Mossong, J., Hawkey, P., de Pinna, E., Grant, K., Cleary, P., 2016.
403 Phylogenetic structure of European *Salmonella* Enteritidis outbreak correlates with national
404 and international egg distribution network. *Microbial Genomics* 2.
405 <https://doi.org/10.1099/mgen.0.000070>

406 David, J. M., D. Guillemot, N. Bemrah, A. Thebault, A. Brisabois, M. Chemaly, F. X. Weill, P.
407 Sanders and Watier, L. 2013a. The Bayesian microbial subtyping attribution model:
408 robustness to prior information and a proposition. *Risk Analysis* 33(3): 397-408.
409 <https://doi.org/10.1111/j.1539-6924.2012.01877.x>

410 David, J.M., Sanders, P., Bemrah, N., Granier, S. A., Denis, M., Weill, F.X., Guillemot,
411 D., Watier, L., 2013. Attribution of the French human salmonellosis cases to the main food-
412 sources according to the type of surveillance data. *Preventive veterinary medicine*, 110(1),
413 12-27. <https://doi.org/10.1016/j.prevetmed.2013.02.002>

414 Delarocque-Astagneau, E., Bouillant, C., Vaillant, V., Bouvet, P., Grimont, P.A.D.,
415 Desenclos, J.-C., 2000. Risk Factors for the Occurrence of Sporadic *Salmonella enterica*
416 serotype Typhimurium infections in children in France: a national case-control study. *Clinical*
417 *Infectious Diseases* 31, 488–492. <https://doi.org/10.1086/313990>

418 Delarocque-Astagneau, E., Desenclos, J.-C., Bouvet, P., Grimont, P.A.D., 1998. Risk factors
419 for the occurrence of sporadic *Salmonella enterica* serotype Enteritidis infections in children
420 in France: a national case-control study. *Epidemiology and Infection* 121, 561–567.
421 <https://doi.org/10.1017/s0950268898001460>

422 Devleeschauwer, B., Pires, S.M., Young, I., Gill, A., and, S.E.M., 2019. Associating sporadic
423 foodborne illness caused by Shiga toxin-producing *Escherichia coli* with specific foods: a
424 systematic review and meta-analysis of case-control studies. *Epidemiology and Infection*
425 147. <https://doi.org/10.1017/s0950268819001183>

426 Dewey-Mattia, D., Manikonda, K., Hall, A.J., Wise, M.E., Crowe, S.J., 2018. Surveillance for
427 foodborne disease outbreaks United States 2009-2015. *MMWR. Surveillance Summaries* 67,
428 1–11. <https://doi.org/10.15585/mmwr.ss6710a1>

429 Domingues, A. R., Pires, S. M., Halasa, T., Hald, T., 2012. Source attribution of human
430 salmonellosis using a meta-analysis of case-control studies of sporadic infections.
431 *Epidemiology & Infection*, 140(6), 959-969. <https://doi.org/10.1017/S0950268811002172>

432 EFSA, ECDC, 2018. The European Union summary report on trends and sources of
433 zoonoses, zoonotic agents and food-borne outbreaks in 2017. *Efsa Journal* 16.

434 Ercsey-Ravasz, M., Toroczkai, Z., Lakner, Z., Baranyi, J., 2012. Complexity of the
435 international agro-food trade network and its impact on food safety. *PLoS ONE* 7, e37810.
436 <https://doi.org/10.1371/journal.pone.0037810>

437 Ferrari, R.G., Rosario, D.K.A., Cunha-Neto, A., Mano, S.B., Figueiredo, E.E.S., Conte-Junior,
438 C.A., 2019. Worldwide epidemiology of *Salmonella* serovars in animal-based foods: a meta-
439 analysis. *Applied and Environmental Microbiology* 85. <https://doi.org/10.1128/aem.00591-19>

440 Garre, A., Fernandez, P.S., Brereton, P., Elliott, C., Mojtahed, V., 2019. The use of trade
441 data to predict the source and spread of food safety outbreaks: An innovative mathematical
442 modelling approach. *Food Research International* 123, 712–721.
443 <https://doi.org/10.1016/j.foodres.2019.06.007>

444 Glass, K., Fearnley, E., Hocking, H., Raupach, J., Veitch, M., Ford, L., Kirk, M.D., 2015.
445 Bayesian source attribution of salmonellosis in South Australia. *Risk Analysis* 36, 561–570.
446 <https://doi.org/10.1111/risa.12444>

447 Gonzales-Barron, U., Thébault, A., Kooh, P., Watier, L., Sanaa, M., Cadavez, V., 2019.
448 Strategy for systematic review of observational studies and meta-analysis modelling of risk
449 factors for sporadic foodborne diseases. *Microbial Risk Analysis* 100082.
450 <https://doi.org/10.1016/j.mran.2019.07.003>

451 Guillier, L., Danan, C., Bergis, H., Delignette-Muller, M.-L., Granier, S., Rudelle, S., Beaufort,
452 A., Brisabois, A., 2013. Use of quantitative microbial risk assessment when investigating
453 foodborne illness outbreaks: The example of a monophasic *Salmonella* Typhimurium
454 4,5,12:i:- outbreak implicating beef burgers. *International Journal of Food Microbiology* 166,
455 471–478. <https://doi.org/10.1016/j.ijfoodmicro.2013.08.006>

456 Guillier, L., Gourmelon, M., Lozach, S., Cadel-Six, S., Vignaud, M.-L., Munck, N. S., Hald, T.,
457 Palma, F., 2020. AB_SA: Accessory genes-Based Source Attribution – tracing the source of
458 *Salmonella enterica* Typhimurium environmental strains. *Microbial Genomics*.
459 <https://doi.org/10.1099/mgen.0.000366>

460 Havelaar, A.H., Ángela Vargas Galindo, Kurowicka, D., Cooke, R.M., 2008. Attribution of
461 foodborne pathogens using structured expert elicitation. *Foodborne Pathogens and Disease*
462 5, 649–659. <https://doi.org/10.1089/fpd.2008.0115>

463 Hoelzer, K., Switt, A.M., Wiedmann, M., 2011. Animal contact as a source of human non-
464 typhoidal salmonellosis. *Veterinary Research* 42, 34. [https://doi.org/10.1186/1297-9716-42-](https://doi.org/10.1186/1297-9716-42-34)
465 [34](https://doi.org/10.1186/1297-9716-42-34)

466 IFSAC (Interagency Food Safety Analytics Collaboration), 2019. Foodborne illness source
467 attribution estimates for 2017 for *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*,
468 and *Campylobacter* using multi-year outbreak surveillance data, United States. GA and D.C.:
469 U.S. Department of Health and Human Services, CDC, FDA, USDA-FSIS.
470 <https://www.cdc.gov/foodsafety/ifsac/pdf/P19-2017-report-TriAgency-508.pdf>

471 Inns, T., Lane, C., Peters, T., Dallman, T., Chatt, C., McFarland, N., Crook, P., Bishop, T.,
472 Edge, J., Hawker, J., Elson, R., Neal, K., Adak, G.K., Cleary, P., on behalf of the Outbreak

473 Control T, 2015. A multi-country *Salmonella* Enteritidis phage type 14b outbreak associated
474 with eggs from a German producer: 'near real-time' application of whole genome sequencing
475 and food chain investigations United Kingdom, May to September 2014. *Eurosurveillance* 20.
476 <https://doi.org/10.2807/1560-7917.es2015.20.16.21098>

477 Jackson, B.R., Griffin, P.M., Cole, D., Walsh, K.A., Chai, S.J., 2013. Outbreak-associated
478 *Salmonella enterica* serotypes and food commodities United States, 1998-2008. *Emerging*
479 *Infectious Diseases* 19, 1239–1244. <https://doi.org/10.3201/eid1908.121511>

480 Johnson, L.R., Gould, L.H., Dunn, J.R., Berkelman, R., Mahon, B.E., 2011. *Salmonella*
481 infections associated with international travel: A Foodborne Diseases Active Surveillance
482 Network (FoodNet) Study. *Foodborne Pathogens and Disease* 8(9), 1031-1037.

483 Jones, G., Pihier, N., Vanbockstael, C., Hello, S.L., Six, S.C., Fournet, N., Jourdan-da Silva,
484 N., 2016. Outbreak of *Salmonella* Enteritidis linked to the consumption of frozen beef burgers
485 received from a food bank and originating from Poland: northern France December 2014 to
486 April 2015. *Eurosurveillance* 21. <https://doi.org/10.2807/1560-7917.es.2016.21.40.30363>

487 Jourdan-da Silva, N., Fabre, L., Robinson, E., Fournet, N., Nisavanh, A., Bruyand, M.,
488 Mailles, A., Serre, E., Ravel, M., Guibert, V., Issenhuth-Jeanjean, S., Renaudat, C.,
489 Tourdjman, M., Septfons, A., de Valk, H., Le Hello, S., 2018. Ongoing nationwide outbreak of
490 *Salmonella* Agona associated with internationally distributed infant milk products, France,
491 December 2017. *Eurosurveillance*, 23(2). [https://doi.org/10.2807/1560-](https://doi.org/10.2807/1560-7917.ES.2018.23.2.17-00852)
492 [7917.ES.2018.23.2.17-00852](https://doi.org/10.2807/1560-7917.ES.2018.23.2.17-00852)

493 Lambertini, E., Buchanan, R.L., Narrod, C., Ford, R.M., Baker, R.C., Pradhan, A.K., 2016.
494 Quantitative assessment of human and pet exposure to *Salmonella* associated with dry pet
495 foods. *International Journal of Food Microbiology* 216, 79–90.
496 <https://doi.org/10.1016/j.ijfoodmicro.2015.09.005>

497 Langridge, G.C., Fookes, M., Connor, T.R., Feltwell, T., Feasey, N., Parsons, B.N., Seth-
498 Smith, H.M.B., Barquist, L., Stedman, A., Humphrey, T., Wigley, P., Peters, S.E., Maskell,

499 D.J., Corander, J., Chabalgoity, J.A., Barrow, P., Parkhill, J., Dougan, G., Thomson, N.R.,
500 2014. Patterns of genome evolution that have accompanied host adaptation in *Salmonella*.
501 Proceedings of the National Academy of Sciences 112, 863–868.
502 <https://doi.org/10.1073/pnas.1416707112>

503 MacDonald, E., White, R., Mexia, R., Bruun, T., Kapperud, G., Brandal, L.T., Lange, H.,
504 Nygård, K., Vold, L., 2018. The role of domestic reservoirs in domestically acquired
505 *Salmonella* infections in Norway: epidemiology of salmonellosis 2000-2015, and results of a
506 national prospective case-control study, 2010-2012. Epidemiology and Infection 147.
507 <https://doi.org/10.1017/s0950268818002911>

508 Mikkela, A., Ranta, J., Tuominen, P., 2019. A modular bayesian *Salmonella* source
509 attribution model for sparse data. Risk Analysis. <https://doi.org/10.1111/risa.13310>

510 Mughini-Gras, L., Franz, E., van Pelt, W., 2018. New paradigms for *Salmonella* source
511 attribution based on microbial subtyping. Food Microbiology 71, 60–67.
512 <https://doi.org/10.1016/j.fm.2017.03.002>

513 Painter, J.A., Hoekstra, R.M., Ayers, T., Tauxe, R.V., Braden, C.R., Angulo, F.J., Griffin,
514 P.M., 2013. Attribution of foodborne illnesses, hospitalizations, and deaths to food
515 commodities by using outbreak data, United States, 1998-2008. Emerging infectious
516 diseases, 19(3), 407. <https://doi.org/10.3201/eid1903.111866>

517 Passaro, D.J., Reporter, R., Mascola, L., Kilman, L., Malcolm, G.B., Rolka, H., Werner, S.B.,
518 Vugia, D.J., 1996. Epidemic *Salmonella* Enteritidis infection in Los Angeles county,
519 California. The predominance of phage type 4. Western journal of medicine, 165(3), 126.

520 Pires, S.M., Vigre, H., Makela, P., Hald, T., 2010. Using outbreak data for source attribution
521 of human salmonellosis and campylobacteriosis in Europe. Foodborne pathogens and
522 disease, 7(11), 1351-1361. <https://doi.org/10.1089/fpd.2010.0564>

523 Pires, S. M., Vieira, A. R., Hald, T., Cole, D., 2014. Source attribution of human
524 salmonellosis: an overview of methods and estimates. *Foodborne pathogens and disease*,
525 11(9), 667-676. <https://doi.org/10.1089/fpd.2014.1744>

526 Pires, S.M., Evers, E.G., van Pelt, W., Ayers, T., Scallan, E., Angulo, F.J., Havelaar, A.,
527 Hald, T., 2009. Attributing the human disease burden of foodborne infections to specific
528 sources. *Foodborne Pathogens and Disease* 6, 417–424.
529 <https://doi.org/10.1089/fpd.2008.0208>

530 Smith, B.A., Fazil, A., 2019. How will climate change impact microbial foodborne disease in
531 Canada? *Canada Communicable Disease Report* 45, 108–113.
532 <https://doi.org/10.14745/ccdr.v45i04a05>

533 Snary, E.L., Swart, A.N., Simons, R.R.L., Domingues, A.R.C., Vigre, H., Evers, E.G., Hald,
534 T., Hill, A.A., 2016. A Quantitative Microbiological Risk Assessment for *Salmonella* in Pigs for
535 the European Union. *Risk Analysis* 36, 437–449. <https://doi.org/10.1111/risa.12586>

536 Teunis, P.F., Kasuga, F., Fazil, A., Ogden, I.D., Rotariu, O., Strachan, N.J., 2010. Dose–
537 response modeling of *Salmonella* using outbreak data. *International journal of food*
538 *microbiology*, 144(2), 243-249. <https://doi.org/10.1016/j.ijfoodmicro.2010.09.026>

539 Ung, A., Baidjoe, A.Y., Cauteren, D.V., Fawal, N., Fabre, L., Guerrisi, C., Danis, K., Morand,
540 A., Donguy, M.-P., Lucas, E., Rossignol, L., Lefèvre, S., Vignaud, M.-L., Cadel-Six, S.,
541 Lailier, R., Jourdan-da Silva, N., Hello, S.L., 2019. Disentangling a complex nationwide
542 *Salmonella* Dublin outbreak associated with raw-milk cheese consumption France, 2015 to
543 2016. *Eurosurveillance* 24. <https://doi.org/10.2807/1560-7917.es.2019.24.3.1700703>

544 Trepka, M. J., Archer, J. R., Altekruse, S. F., Proctor, M. E., Davis, J.P., 1999. An increase in
545 sporadic and outbreak-associated *Salmonella* Enteritidis infections in Wisconsin: the role of
546 eggs. *The Journal of infectious diseases*, 180(4), 1214-1219. <https://doi.org/10.1086/314984>

547 Van Cauteren, D., Strat, Y.L., Sommen, C., Bruyand, M., Tourdjman, M., Jourdan-da Silva,
548 N., Couturier, E., Fournet, N., de Valk, H., Desenclos, J.-C., 2017. Estimated annual
549 numbers of foodborne pathogen-associated illnesses, hospitalizations, and deaths, France,
550 2008-2013. *Emerging Infectious Diseases* 23, 1486–1492.
551 <https://doi.org/10.3201/eid2309.170081>

552 Van Cauteren, D., Valk, H.D., Sommen, C., King, L.A., Jourdan-da Silva, N., Weill, F.-X.,
553 Hello, S.L., Mégraud, F., Vaillant, V., Desenclos, J.C., 2015. Community incidence of
554 campylobacteriosis and non-typhoidal salmonellosis France, 2008-2013. *Foodborne*
555 *Pathogens and Disease* 12, 664–669. <https://doi.org/10.1089/fpd.2015.1964>

556 Viechtbauer, W., 2010. Conducting meta-analyses in R with the metaphor package. *Journal*
557 *of Statistical Software* 36. <https://doi.org/10.18637/jss.v036.i03>

558 Vila-Nova, M., Durimel, K., La, K., Felten, A., Bessières, P., Mistou, M.-Y., Mariadassou, M.,
559 & Radomski, N., 2019. Genetic and metabolic signatures of *Salmonella enterica* subsp.
560 *enterica* associated with animal sources at the pangenomic scale. *BMC genomics*, 20(1),
561 814. <https://doi.org/10.1186/s12864-019-6188-x>

562 Yoon, Y., Lee, S., & Choi, K.H. (2016). Microbial benefits and risks of raw milk cheese. *Food*
563 *Control*, 63, 201-215. <https://doi.org/10.1016/j.foodcont.2015.11.013>

564 Zhang, S., Li, S., Gu, W., den Bakker, H., Boxrud, D., Taylor, A., Roe, C., Driebe, E.,
565 Engelthaler, D.M., Allard, M., Brown, E., McDermott, P., Zhao, S., Bruce, B.B., Trees, E.,
566 Fileds, P.I., Deng, X., 2019. Zoonotic source attribution of *Salmonella enterica* serotype
567 Typhimurium using genomic surveillance data, United States. *Emerging infectious diseases*,
568 25(1), 82. <https://doi.org/10.3201/eid2501.180835>

569 **Appendix**

570 **Appendix-1. Bibliographic references of the case-control studies for *Salmonella* spp**

571 **Appendix- 2. Characteristics of the 62 case-control studies investigating sources of**

572 **sporadic human salmonellosis included in the meta-analysis**

573 **Figure captions**

574 **Figure 1. PRISMA flow chart of the literature search for case-control studies of human**
575 **salmonellosis**

576

577 **Figure 2. Forest plot of the associations of salmonellosis with consumption of**
578 **untreated /not enough treated drinking water in the mixed population (horizontal axis**
579 **is expressed as OR in logarithm scale).**

580

581 **Figure 3. Forest plot of the associations of salmonellosis with consumption of dairy**
582 **products in children (OR in logarithm scale)**

583

584 **Figure 4: Funnel plots of studies investigating categorized risk factors (host specific**
585 **in mixed population, food in mixed population, dairy in children, handling poultry and**
586 **handling processed meat)**

587

588

590 Table 1. Results of the meta-analysis for the main risk factors

Population	Geographical area	Risk factor	Pooled OR [IC95%]	N/n*	p-value of risk factor	Publication bias p-value	Points removed**	Heterogeneity analysis***
Travel								
Mixed(y)	Asia excluded	Abroad	3.612 [2.839 - 4.593]	18/47	<.0001	0.408	1	τ ² =0.0624 QE(df = 49) = 123.6, p-val < .0001 s ² =0.925 ; I ² =6.319%
		Inside	2.195 [1.054 - 4.572]	3/3	0.036			
Host specific								
Mixed(y)	All	Antiacids	3.184 [2.449 - 4.139]	12/31	<.0001	<.0001	0	τ ² =0.6956 QE(df = 88) = 866.970, p-val < .0001 s ² =0.533; I ² =56.626%
		Antibiotics	3.348 [2.657 - 4.219]	14/30	<.0001			
		Chronic diseases	3.289 [2.449 - 4.416]	8/21	<.0001			
		Other medical conditions	4.655 [3.458 - 6.266]	5/11	<.0001			
Children	All	Antiacids	3.413 [1.851 - 6.296]	2/3	<.0001	0.501	0	τ ² =0.278 QE(df = 24) = 31.053, p-val = 0.152 s ² =0.500; I ² =35.724%
		Antibiotics	2.376 [1.618 - 3.489]	6/12	<.0001			
		Breastfeeding	0.249 [0.165 - 0.377]	7/12	<.0001			
Person to person								
Mixed	All		1.692 [1.145 - 2.500]	7/10	0.008	0.056	0	τ ² =0.557 QE(df = 17) = 58.734, p-val < .0001 ; s ² =0.82; I ² =40.425%
Children			3.811 [1.977 - 7.348]	7/9	<.0001			
Animals								
Mixed	All	Pets	1.471 [1.189 - 1.821]	26/71	<.0001	0.283	1	τ ² =1.1449 QE(df = 123) = 464.3872, p-val < .0001 ; s ² =0.605; I ² =65.420
		Exotic (new) pets	2.619 [1.763 - 3.894]	7/25	<.0001			
		Farm animals	1.937 [1.394 - 2.693]	9/19	0.0004			
		Occupational exposure	1.737 [1.175 - 2.567]	5/12	0.0056			
Children	All	Pets	3.035 [1.938 - 4.756]	9/36	<.0001	0.731	1	τ ² =0.369 QE(df = 41) = 76.2961, p-val = 0.0007; s ² =0.540; I ² =40.63%
		Farm animals	2.658 [1.431 - 4.938]	2/5	0.002			
Environment								
Mixed	All	Recreational water	2.221 [1.339 - 3.681]	9/12	0.0020	0.088	0	τ ² =0.7714 QE(df = 45) = 132.6221, p-val < .0001; s ² =0.594; I ² =56.48%
		Untreated drinking water	1.753 [1.109 - 2.770]	11/19	0.0162			
		Farm environment	1.900 [1.251 - 2.885]	8/17	0.0026			
Children (at)	All	Untreated drinking water	2.130 [1.285 - 3.532]	5/8	0.0034	0.199	0	τ ² = 0 QE(df = 27) = 31.5105, p-val = 0.2507 ;s ² =0.431 I ² = 0
		Daycare attendance	2.738 [1.658 - 4.522]	5/10	<.0001			

		Playground	3.055 [2.243 - 4.160]	6/13	<.0001			
Food								
Mixed	All	Meat	1.489 [1.137 - 1.951]	37/231	0.0039	0.035	8	τ ² =0.215 QE(df = 537) = 1971.5989, p- val < .0001 ; s ² =0.792; I ² =21.34%
		Eggs	1.774 [1.351 - 2.329]	35/139	<.0001			
		Composite	1.731 [1.258 - 2.381]	16/66	0.0008			
Children	All	Meat	1.794[1.548 - 2.079]	8/34	<.0001	0.072	2	τ ² = 0.6705 QE(df = 76) = 93.1415, p-val = 0.0884 s ² =0.482 ; I ² =58.178
		eggs	1.669[1.295 - 2.150]	7/20	<.0001			
		Dairy	2.828[2.067 - 3.870]	6/10	<.0001			
		Produce	2.099[1.169 - 3.768]	2/13	0.0130			

591

592 *N/n Number of studies/number of OR;** points removed by sensitivity analysis, all results are given after
593 removing data concerned; ***Between-study variability (τ^2), test for residual heterogeneity (QE), variance of
594 residuals (s^2), intra-class correlation (I^2). (y): year is significant (before/after 2000) in this model and the
595 estimates are taking this effect into account; (at) analysis type is significant

596

Table 2: Results of the meta-analysis on disaggregated risk factors (food)

Risk Factor	Population	Geographical area	Risk factor precise	Pooled OR [IC95%]	N/n*	p-value of risk factor	Publication bias p-value	Points removed**	Heterogeneity analysis***
Meat	Mixed	Asia and south America removed	Poultry	1.474[1.167 - 1.861]	29/93	0.0011	0.202	2	$\tau^2=1.93$ QE(df = 218) = 917.4944, p-val < .0001 $s^2=0.812$; $I^2=70.408\%$
			Other red Meats	1.680 [1.044 - 2.703]	5/10	0.0325			
			Pork	1.563 [1.111 - 2.200]	8/19	0.0103			
			Others	1.938 [1.215 - 3.091]	7/20	0.0054			
Meat (y)	Children	All	Beef	1.623 [1.072 - 2.473]	5/12	0.022	0.117	0	$\tau^2=0.567$ QE(df = 28) = 38.496, p-val = 0.089 $s^2=0.54941$ $I^2=50.788$
			Processed Meat	2.122 [1.538 - 2.928]	2/5	<.0001			
			Pork	3.089 [1.348 - 7.078]	2/4	0.007			
Eggs (at,y)	Mixed	Asia and south America removed	Eggs	1.976[1.138 - 3.431]	32/115	0.0155	0.592	0	$\tau^2= 0.219$ QE(df = 127) = 386.5163, p-val < .0001 ; $s^2=0.769$ $I^2=22.197\%$
			Egg products	2.736[1.502 - 4.987]	7/16	0.0010			
Eggs (at)	Children	All	Multivariate analysis	1.557 [1.233 - 1.967]	3/5	0.0002	0.915	0	$\tau^2=0$ QE(df = 18) = 10.733, p-val = 0.905 $s^2=0.228$ $I^2=0$
			Univariate Analysis	1.464[1.272 - 1.685]	6/15	<.0001			
Dairy	Children	All	Milk formula	3.324 [2.136 - 5.172]	5/8	<.0001	0.014	0	$\tau^2=0.111$ Q(df = 7) = 9.665, p-val = 0.208 $s^2=0.22810$ $I^2 : 0.228$
Produce	Children	All		1.545 [1.314 - 1.819]	2/10	<.0001	0.535	0	$\tau^2=0$ Q(df = 9) = 8.4746, p-val = 0.4871 $s^2=0.805$; $I^2=0$
Composite	Children+mixed (all)	Asia removed	Dishes	1.609 [1.206 - 2.147]	16/46	0.0012	0.121	0	$\tau^2=0.742$ QE(df = 64) = 201.7201, p-val < .0001 $s^2=0.569$ $I^2=56.574\%$
			Fast Food	1.443[1.053 - 1.977]	7/16	0.0226			
BBQ	All	All		1.952 [1.003 - 3.798]	4/7	0.0491	0.221	0	$\tau^2=0.274$ Q(df = 6) = 15.967, p-val = 0.0139 $s^2=0.669$; $I^2=29.059\%$

598 *N/n Number of studies/number of OR;** points removed by sensitivity analysis, all results are given
599 after removing data concerned; ***Between-study variability (τ^2), test for residual heterogeneity (QE),
600 variance of residuals (s^2), intra-class correlation (I^2). (y): year is significant (before/after 2000) in this
601 model and the estimates are taking this effect into account; (at) analysis type is significant.

602 **Table 3. Effect of food handling on the pooled OR**

Risk Factor	Risk factor precise	Pooled OR [IC95%]	N/n*	p-value of risk factor	OR ratios and CI95%	Points removed **	Publication bias p-value	Heterogeneity analysis***
Poultry (at)	Eating Out	3.038 [1.965 - 4.697]	12/24	<.0001	1.961 [1.583- 2.429]	3	0.032	$\tau^2=0.124$ QE(df = 102) = 243.7902, p-val < .0001 $s^2=0.593$; $I^2=17.311\%$
	Undercooked	3.986 [1.641 - 9.681]	6/8	0.0054	2.572 [1.322 - 5.005]			
	Poultry (base)	1.549 [1.241 - 1.934]	32/82 (ref eating out) 34/98 (ref handling)	0.0001	-			
Processed Meat	Eating out	1.919 [0.922 - 3.994]	7/13	0.021	1.635 [1.074 - 2.487]	2	0.009	$\tau^2=0.303$ QE(df = 58) = 207.632, p-val < .0001 $s^2=0.715$ $I^2=29.755\%$
	Processed Meat (base)	1.174 [0.858 - 1.606]	17/48	0.315	-			
Eggs (at)	Eating Out	2.575 [1.465 - 4.527]	10/29	0.0011	1.575 [1.199 - 2.069]	3	0.787	$\tau^2=0.174$ QE(df = 135) = 423.730, p-val < .0001 $s^2=0.818$ $I^2=17.574\%$
	Undercooked	2.182 [1.388 - 3.428]	22/49	0.0004	1.335 [1.136 - 1.567]			
	Raw	3.642 [1.776 - 7.469]	10/12	0.0002	2.228 [1.454 - 3.414]			
	Base eggs	1.635 [1.221 - 2.188]	39/111(s) 31/79(h)	0.0009	-			
Pork meat	Undercooked	3.039 [1.289 - 7.163]	5/12	<.0001	3.578 [2.132- 6.002]	0	p= 0.259	$\tau^2=0.1051$ QE(df = 20) = 36.145, p-val = 0.0148 $s^2=0.440$ $I^2=19.274\%$
	Base	0.849 [0.605 - 1.193]	7/11	0.3475	-			
Vegetables	Unwashed	1.542 [0.773- 3.073]	2/4	0.112	1.551 [1.002 - 2.399]	0	p= 0.378	$\tau^2=0.136$ QE(df = 36) = 113.719, p-val < .0001 $s^2=0.477$ $I^2=22.273\%$
	Base	0.994 [0.772- 1.281]	10/27	0.964	-			

603 *N/n Number of studies/number of OR;** points removed by sensitivity analysis, all results are given
604 after removing data concerned; ***Between-study variability (τ^2), test for residual heterogeneity (QE),
605 variance of residuals (s^2), intra-class correlation (I^2). (y): year is significant (before/after 2000) in this
606 model and the estimates are taking this effect into account; (at) analysis type is significant

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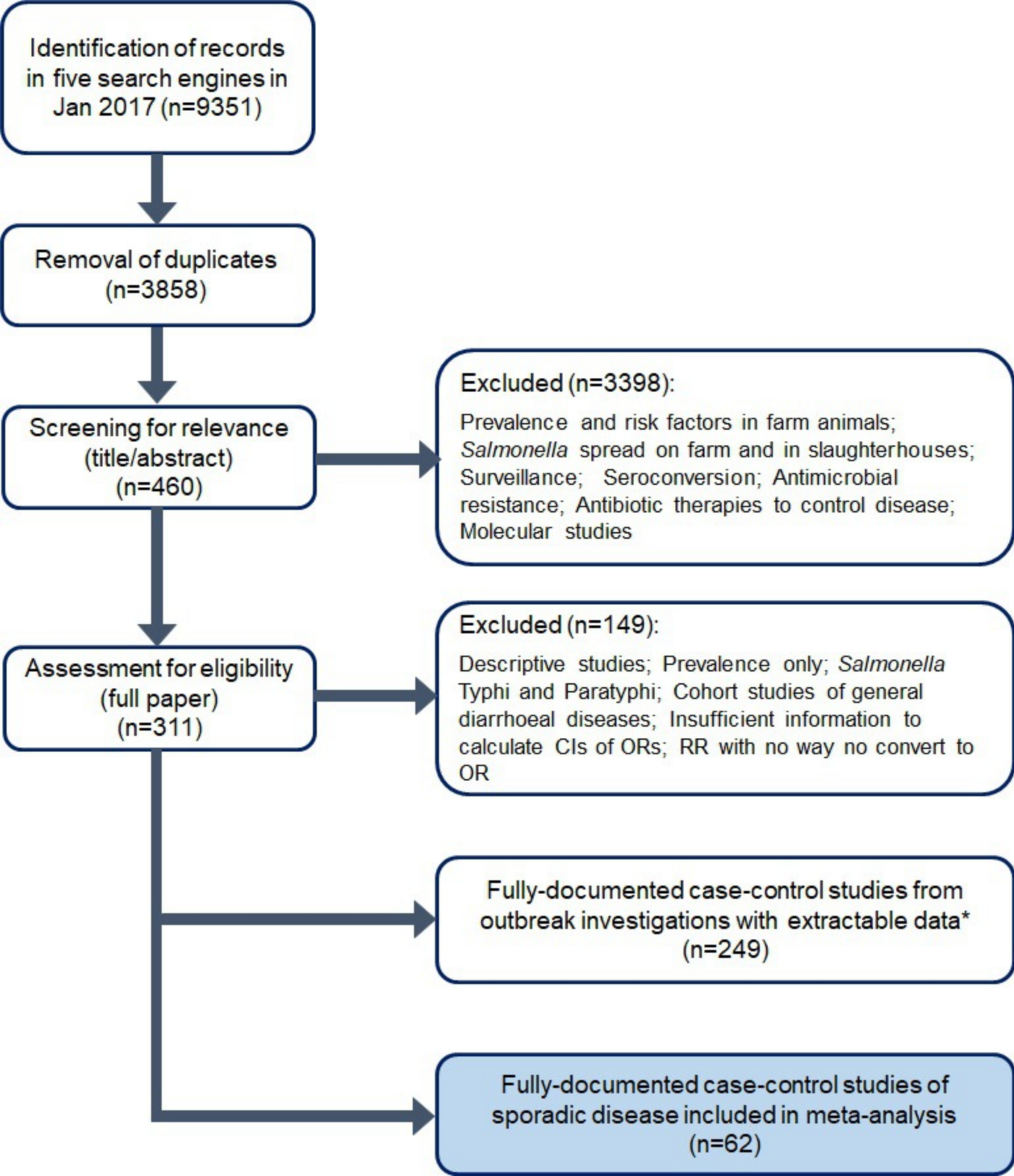
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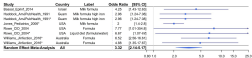
611 Table 4. Non significant or isolated *ORs* (1 publication) in main risk factors.

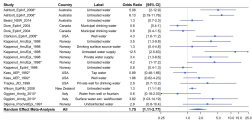
Population	Geographical area	Risk factor	Pooled OR [IC95%]	N/n*
Travel				
Mixed(y)	Asia excluded	Any	0.909[0.528- 1.565]	2/3
Animals				
Children	All	Exotic (new) pets	1.433[1.046- 1.962]	1/3
Food				
Mixed	All	Produce	1.228[0.892- 1.690]	12/63
		Seafood	1.224 [0.795- 1.884]	6/10
		Dairy	1.187[0.850- 1.658]	13/31
		Beverages	1.535[0.887- 2.655]	3/4
Children	All	Seafood	1.387[0.637- 3.019]	2/4

612 N/n Number of studies/number of OR; if N=1 isolated studies: the result is not considered of significant

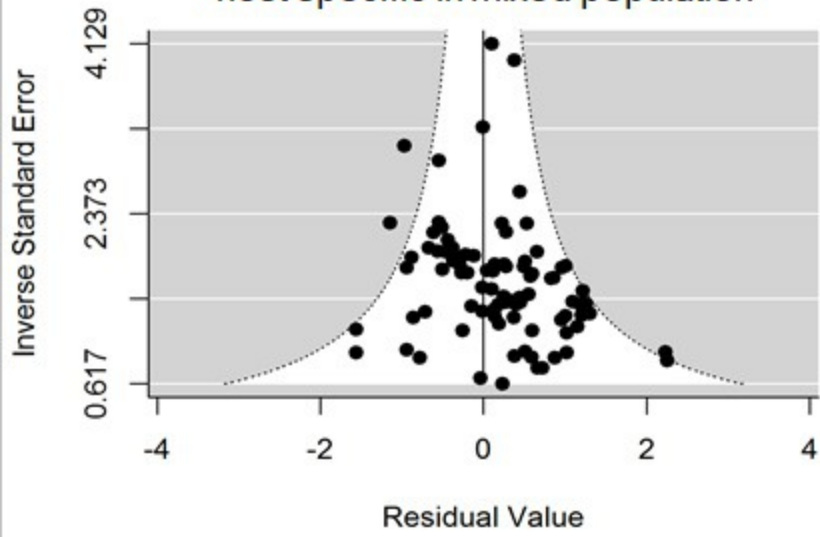
613 due to the lack of studies



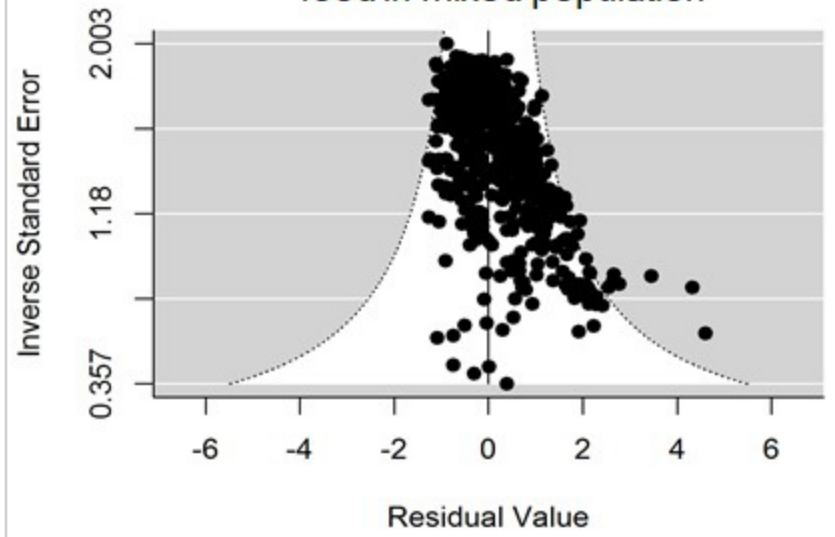




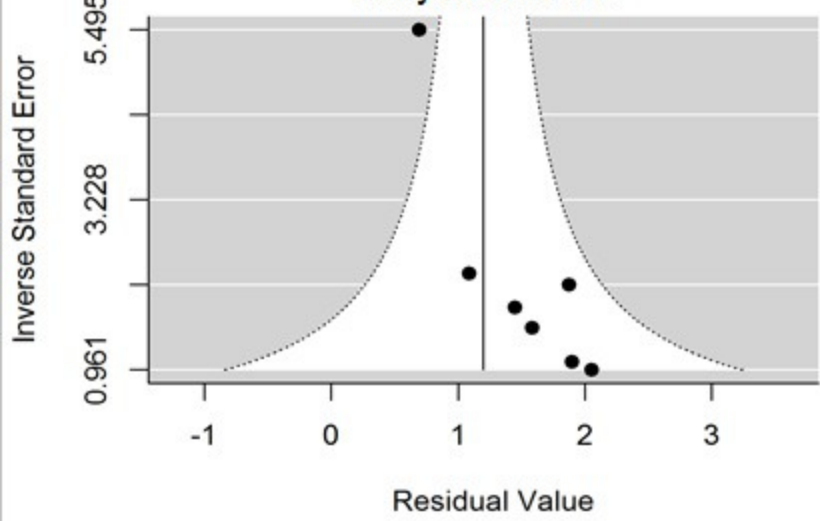
host specific in mixed population



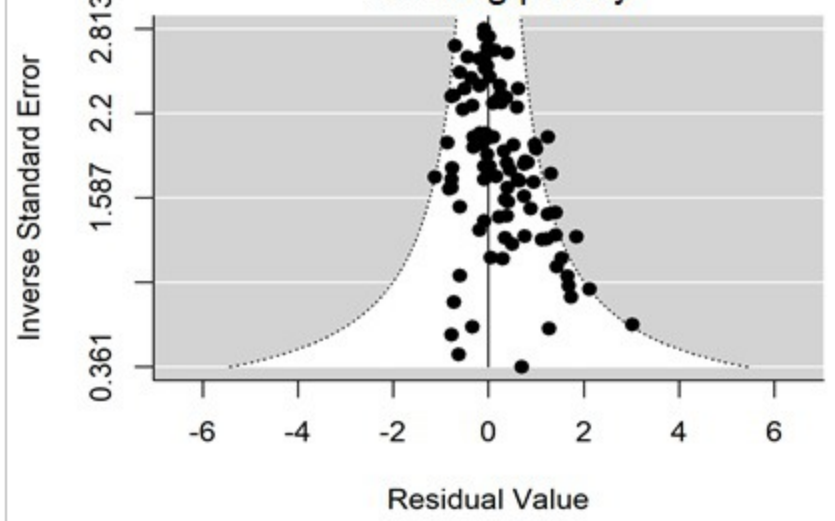
food in mixed population



dairy in children



handling poultry



handling processed meat

