How Many Foodborne Outbreaks of *Salmonella* Infection Occurred in France in 1995?

Application of the Capture-Recapture Method to Three Surveillance Systems

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Despite prevention and control efforts, foodborne outbreaks of non-*typhi* *Salmonella* infection continue to occur in developed countries (1–3). Changes in dietary habits, changes in modes of food production and distribution, and increases in the size of more vulnerable populations have been implicated as contributing factors (3–9). In humans, *Salmonella* may cause sporadic disease, family outbreaks, and community outbreaks either limited to a defined population or spread community-wide (10). In outbreaks, and community outbreaks either limited to a

human and economic burden of *Salmonella* infection, particularly outbreaks, requires a precise knowledge of its incidence. This is particularly true in France, where data on *Salmonella* outbreaks are derived from passive mandatory notification of foodborne outbreaks, which is known from anecdotal data to have a very low sensitivity (11). In this study, we quantified the level of underascertainment of foodborne *Salmonella* outbreaks by estimating the true number of outbreaks that occurred in France in 1995, using the capture-recapture method applied to three different sources of information.

MATERIALS AND METHODS
Data sources and characteristics

We used data collected by the three French surveillance systems for foodborne outbreaks in 1995: 1) the National Public Health Network (NPHN), to which notification is mandatory through the district public health departments; 2) the Ministry of Agriculture (MA), to which notification is mandatory through the district veterinary departments; and 3) the National *Salmonella* and *Shigella* Reference Center (NRC). Any foodborne outbreak must be reported by the physician, the head of the family, or the chief of the affected community to the district public health department (Direction Départementale des Affaires Sanitaires et Sociales (DDASS)) or the district veterinary service (Direction des Services Vétérinaires (DSV)). After an investigation, the
Identification of matches

Because foodborne outbreaks are not recorded in each system with a common identifier, we developed matching criteria between the three systems (NPHN, MA, and NRC) according to data common to all systems. A match between the NPHN and the MA had to have the same postal code of occurrence and the same date of onset (1 day). Potential matches were confirmed if the investigation reports sent to the NPHN and the MA had similar characteristics (date, place of occurrence, number of patients, serotype, and implicated food). Date of onset is not recorded at the NRC (dates of isolation and/or receipt at the NRC). If the isolate is associated with an outbreak, information on the number of patients affected and the type of outbreak (family or community) is also collected. The NRC defines a foodborne Salmonella outbreak as the isolation of Salmonella associated with the occurrence of other cases of gastroenteritis in a defined population or community. A common food origin is not always reported in the NRC data.

Capture-recapture estimates

According to the hypothesis of independence between the sources and the equal catchability in each source, estimates of the total number of foodborne Salmonella outbreaks were calculated for each pair of sources using Hook and Regal’s (24) unbiased formula. Two sources are considered independent when the probability of notification of one event in one source is not dependent on its probability of notification in the other source. Equal catchability is fulfilled when the probability of notification of one event is not influenced by its characteristics (i.e., age, gender, severity of symptoms, circumstances of the diagnosis, etc.) in each source. This probability may vary from one source to another or be constant overall. The dependence between two sources was assessed by comparing the estimates obtained for each pair of sources and by calculating the odds ratio (and its 95% confidence interval) between the cell counts of the two sources within the third one, as proposed by Wittes and colleagues (20, 21).

To take into account the dependencies between the sources and potential variable catchability, we estimated the number of outbreaks by log-linear modeling (22, 23). We used a stepwise procedure with the BMDP 4F program (BMDP Statistical Software, Inc., Los Angeles, California). The choice of the final model was based on the likelihood ratio statistic ($G^2$), the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC), which are functions of the likelihood ratio statistic, with $AIC = G^2 - 2 df$ and $BIC = G^2 - \log N/2\pi df$, where $df$ is degrees of freedom and $N$ is the number of foodborne outbreaks observed (24). The optimal model was the model with the lowest AIC and BIC values. The weighted average of the BIC (“weighted BIC”) of all estimates provided by each model was calculated as suggested by Draper (25).

We also stratified the analysis by serotype (S. enteritidis, S. typhimurium, and other serotypes) and type of outbreak (family or community). The total variance was calculated by adding the variance of each stratum. The 95% confidence interval was calculated using the method suggested by Hook and Regal (24). The sensitivity of each source is the number of foodborne outbreaks reported to the source divided by the total number of foodborne outbreaks.

TABLE 1. Delays (in days) between the dates of onset of foodborne Salmonella outbreaks and the dates of isolation and receipt of Salmonella by the National Salmonella and Shigella Reference Center (NRC), by quartile (Q), France, 1995

<table>
<thead>
<tr>
<th>Delay</th>
<th>Q1</th>
<th>Q1–Q2</th>
<th>Q2–Q3</th>
<th>&gt;Q3</th>
</tr>
</thead>
<tbody>
<tr>
<td>From date of onset to date of isolation (delay 1)</td>
<td>0–3</td>
<td>4–7</td>
<td>8–14</td>
<td>15–30</td>
</tr>
<tr>
<td>From date of onset to date of receipt by the NRC (delay 2)</td>
<td>0–10</td>
<td>11–13</td>
<td>14–30</td>
<td>31–45</td>
</tr>
</tbody>
</table>
by the total number estimated by the final log-linear model. Sensitivity was also calculated for each stratum of serotype and type of outbreak. The representativeness was assessed by comparing, by stratification variables, the distribution of each source to the distribution estimated by log-linear modeling using the goodness-of-fit $\chi^2$ test (26).

**Qualitative assessment of the dependency between the NPHN and the MA**

In addition to the log-linear method, we evaluated the dependency between the two mandatory notification systems through a survey of a random sample of 22 districts, for both public health (DDASS) and veterinary (DSV) departments. In each district selected, officers of the DDASS and DSV were interviewed independently by telephone, using a standardized questionnaire, on their handling of foodborne outbreak notifications and their collaboration.

**Positive predictive value of the definition used by the NRC**

Because notifications to the NPHN and the MA are validated by a systematic procedure, we assumed that their positive predictive value was 100 percent. For the NRC, information about the index meal is not always complete and validated. Therefore, we estimated the positive predictive value of a prospective sample of foodborne Salmonella outbreaks reported to the NRC between February 1 and May 31, 1997. We contacted laboratories of isolation and case physicians by telephone to collect further information on the reported outbreaks. An outbreak was considered truly foodborne if it fulfilled the case definition used for mandatory notification. The positive predictive value obtained was used to correct the estimate of the total number of foodborne Salmonella outbreaks estimated by the capture-recapture analysis, as suggested by LaPorte et al. (27).

**RESULTS**

Among the 780 foodborne Salmonella outbreaks recorded by the three sources in 1995, 64 notifications were excluded from the analysis: 33 were multiple notifications to the same source, 13 had no identification criteria, and 18 did not include information on the serotype or type of outbreak. Of the 716 outbreaks that remained for analysis, 114 had been reported to the NPHN, 73 had been reported to the MA, and 529 had been reported to the NRC; 108 were matches. Of the latter outbreaks, 30 were matches between the NPHN and the MA, 59 were matches between the NPHN and the NRC, 39 were matches between the MA and the NRC, and 20 were matches between all three sources.

The median delay 1 for matched outbreaks was 3.5 days (range, 0–19 days) between the NPHN and the NRC and 3 days (range, 1–18 days) between the MA and the NRC. Delay 2 was similar (10 days) for matches between the NPHN and the NRC (range, 2–37 days) and matches between the MA and the NRC (range, 2–33 days).

In the two-source capture-recapture analysis, the estimate of the total number of foodborne Salmonella outbreaks for the NPHN-MA pair was 3.5 times smaller than the estimates for NPHN-NRC and MA-NRC (table 2). This indicates a strong dependence between the NPHN and the MA, with, among the outbreaks notified to the NRC, an odds ratio between NPHN and MA data of 12.2 (95 percent confidence interval (CI): 5.7, 26.2). The survey of the DDASS and DSV confirmed the strong positive dependency between the two mandatory notification systems: Of the 22 districts surveyed, 10 DDASS and DSV districts indicated that very good collaboration for community outbreaks only, and in two districts the DDASS and the DSV did not collaborate.

The estimate obtained with the saturated log-linear model was approximately 2–3 times greater than the estimates obtained with the other model, and it had a wide 95 percent confidence interval. The model with an interaction term between the NPHN and the MA had the best adequacy ($p = 0.1$), the best BIC (−4.7), and an AIC (0.4) superior to the AIC of the saturated model and gave an estimate of 1,065 outbreaks (95 percent CI: 910, 1,220) (table 3). Two interaction terms were further identified, one between the serotype and the NPHN and the other between the type of outbreak and the MA (table 3). With these interaction terms added to the previous model, the BIC and AIC values became −103.2 and −23.2, respectively. The analysis gave the same estimate of number of outbreaks (1,065; 95 percent CI: 913, 1,217), which is also similar to the “weighted BIC” (table 3).

Forty outbreaks reported to the NRC were included in the study of the positive predictive value of the NRC outbreak case definition. Of the 40 laboratories and physicians con-
tacted, one refused to participate, and no information was available for seven outbreaks. Of the 32 events investigated, 21 were confirmed as foodborne outbreaks, for a positive predictive value of 65.6 percent (95 percent CI: 50, 82). Positive predictive values were similar by serotype. Because the 11 “false positive” outbreaks (sporadic cases associated or not associated with secondary transmission) could not be classified as being of either the family type or the community type, it was not possible to estimate the positive predictive value by type of outbreak and thus to obtain corrected values by type of outbreak.

After correction with the positive predictive value of the NRC, we estimated that 757 (95 percent CI: 651, 863) foodborne Salmonella outbreaks had occurred in France in 1995 (table 4). The sensitivity of the three surveillance systems was estimated at 15 percent for the NPHN, 10 percent for the MA, and 50 percent for the NRC. S. enteritidis outbreaks were reported more often to the NPHN (19 percent) than outbreaks of S. typhimurium (8 percent) and other serotypes (11 percent) (table 4). There were almost three times fewer reports of family outbreaks (5 percent) reported to the MA than community outbreaks (13 percent). Compared with the estimates obtained by the capture-recapture analysis (table 5), there was a statistically significant difference in the serotype distribution for the NPHN \((p = 0.001)\), with an overrepresentation of S. enteritidis (71 percent vs. 54 percent), and in the types of outbreaks for the MA \((p = 2 \times 10^{-7})\), with many fewer family outbreaks reported (52 percent vs. 74 percent).

A total of 753 (95 percent CI: 649, 857) outbreaks were obtained in a two-source analysis after we merged the two dependent sources (NPHN and MA) and adjusted the estimate for the positive predictive value of the NRC. The sensitivity was then 21 percent for the two sources combined and 50 percent for the NRC.

**DISCUSSION**

To the best of our knowledge, this is the first study that used the capture-recapture method to estimate the true number of foodborne Salmonella outbreaks in a given country and year. Despite the lack of a common identifier between the three sources, it was possible to identify matches between the three sources based on the date, place of occurrence, and serotype of each outbreak. In addition, we completed the capture-recapture approach with a qualitative investigation to better understand the mechanisms of dependencies between two of the sources. Furthermore, we estimated the positive predictive value of the case definition of the surveillance system (NRC), which was thought to have a positive predictive value less than 100 percent. After adjusting for the estimated positive predictive value, we concluded that 757 foodborne Salmonella outbreaks occurred in France in 1995, of which only 15 percent (NPHN), 10 percent (MA), and 50 percent (NRC) had been reported to the three surveillance systems, respectively. The sensitivity of 15 percent for the mandatory notification to the NPHN is similar to the one (12.5 percent) found in 1994 during an exhaustive survey of reports of foodborne Salmonella outbreaks in one district of France (28). We also showed that notification was not homogeneous in two of the sources: S. enteritidis was better reported to the NPHN than other serotypes, while family outbreaks were far less often

### Table 3. Characteristics of log-linear models fitted to three sources of data on foodborne Salmonella outbreaks and their estimates of the total number of outbreaks, France, 1995

<table>
<thead>
<tr>
<th>Log-linear model</th>
<th>df (^\ast)</th>
<th>G (^\dagger)</th>
<th>p (^\ddagger)</th>
<th>AIC (^\star)</th>
<th>BIC (^\ddagger)</th>
<th>x (\dagger)</th>
<th>N (\ddagger)</th>
<th>95% confidence interval for N</th>
</tr>
</thead>
<tbody>
<tr>
<td>NPHN (\ast) × MA (\ast), NPHN (\ast) × NRC (\ddagger), MA (\ast) × NRC</td>
<td>0</td>
<td>0</td>
<td>1.00</td>
<td>0.00</td>
<td>0.00</td>
<td>1,309</td>
<td>1,917</td>
<td>523, 3,311</td>
</tr>
<tr>
<td>NPHN (\ast) × MA, NPHN (\ast) × NRC</td>
<td>1</td>
<td>3.69</td>
<td>0.05</td>
<td>41.7</td>
<td>39.2</td>
<td>569</td>
<td>1,177</td>
<td>827, 1,527</td>
</tr>
<tr>
<td>NPHN (\ast) × MA, MA (\ast) × NRC</td>
<td>1</td>
<td>3.40</td>
<td>0.05</td>
<td>1.6</td>
<td>–0.9</td>
<td>520</td>
<td>1,128</td>
<td>896, 1,360</td>
</tr>
<tr>
<td>NPHN (\ast) × NRC, MA (\ast) × NRC</td>
<td>1</td>
<td>43.73</td>
<td>0.00</td>
<td>1.7</td>
<td>–0.9</td>
<td>108</td>
<td>716</td>
<td>628, 804</td>
</tr>
<tr>
<td>NPHN (\ast) × MA, NRC</td>
<td>2</td>
<td>4.40</td>
<td>0.11</td>
<td>0.4</td>
<td>–4.7</td>
<td>457</td>
<td>1,065</td>
<td>910, 1,220</td>
</tr>
<tr>
<td>NPHN (\ast) × NRC, MA</td>
<td>2</td>
<td>49.77</td>
<td>0.00</td>
<td>45.8</td>
<td>42.3</td>
<td>262</td>
<td>870</td>
<td>736, 1,004</td>
</tr>
<tr>
<td>MA (\ast) × NRC, NPHN</td>
<td>2</td>
<td>51.41</td>
<td>0.00</td>
<td>47.4</td>
<td>42.3</td>
<td>322</td>
<td>940</td>
<td>811, 1,069</td>
</tr>
<tr>
<td>NPHN, MA, NRC</td>
<td>3</td>
<td>51.66</td>
<td>0.00</td>
<td>45.7</td>
<td>37.9</td>
<td>342</td>
<td>950</td>
<td>843, 1,057</td>
</tr>
<tr>
<td>Weighted BIC estimate</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>533</td>
<td>1,141</td>
<td></td>
</tr>
<tr>
<td>NPHN (\ast) × MA, NRC, NPHN (\ast) × serotype, MA (\ast) × type of foodborne outbreak</td>
<td>12</td>
<td>15.0</td>
<td>0.2</td>
<td>–8.9</td>
<td>–39.8</td>
<td>457</td>
<td>1,065</td>
<td>802, 1,328</td>
</tr>
<tr>
<td>NPHN (\ast) × MA, NRC, MA (\ast) × serotype, MA (\ast) × type of foodborne outbreak</td>
<td>7</td>
<td>11.1</td>
<td>0.1</td>
<td>–2.9</td>
<td>–20.8</td>
<td>457</td>
<td>1,065</td>
<td>862, 1,268</td>
</tr>
<tr>
<td>NPHN (\ast) × MA, NRC, NPHN (\ast) × serotype, MA (\ast) × type of foodborne outbreak</td>
<td>31</td>
<td>38.5</td>
<td>0.2</td>
<td>–23.2</td>
<td>–103.2</td>
<td>457</td>
<td>1,065</td>
<td>913, 1,217</td>
</tr>
<tr>
<td>Weighted BIC estimate</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>456</td>
<td>1,065</td>
<td></td>
</tr>
</tbody>
</table>

\(^\ast\) df, degrees of freedom; AIC, Akaike Information Criterion; BIC, Bayesian Information Criterion; NPHN, National Public Health Network; MA, Ministry of Agriculture; NRC, National Salmonella and Shigella Reference Center.  
\(^\dagger\) p value for the likelihood ratio statistic.  
\(^\ddagger\) Estimate of the number of outbreaks not reported to any source.  
\(\ddagger\) Estimate of the total number of outbreaks.
TABLE 4. Sensitivity of surveillance systems for foodborne Salmonella outbreaks, by serotype and type of outbreak, France, 1995

<table>
<thead>
<tr>
<th>Serotype</th>
<th>Type of outbreak</th>
<th>NPHN N</th>
<th>MA N</th>
<th>NRC N</th>
<th>% sensitivity NPHN</th>
<th>% sensitivity MA</th>
<th>% sensitivity NRC N</th>
<th>Estimate not corrected by the NRC* positive predictive value</th>
<th>Estimate corrected by the NRC positive predictive value</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. enteritidis</td>
<td>Family</td>
<td>789</td>
<td>645</td>
<td>933</td>
<td>10 (8, 12)</td>
<td>5 (4, 6)</td>
<td>49 (42, 6)</td>
<td>1065 910, 1220 (11, 9, 13)</td>
<td>757 651, 863 (15, 13, 17)</td>
</tr>
<tr>
<td>S. typhimurium</td>
<td>Community</td>
<td>276</td>
<td>210</td>
<td>342</td>
<td>14 (11, 18)</td>
<td>13 (10, 17)</td>
<td>51 (41, 67)</td>
<td>1065 910, 1220 (11, 9, 13)</td>
<td>757 651, 863 (15, 13, 17)</td>
</tr>
<tr>
<td>Other</td>
<td>Community</td>
<td>276</td>
<td>210</td>
<td>342</td>
<td>14 (11, 18)</td>
<td>13 (10, 17)</td>
<td>51 (41, 67)</td>
<td>1065 910, 1220 (11, 9, 13)</td>
<td>757 651, 863 (15, 13, 17)</td>
</tr>
</tbody>
</table>

* NRC, National Salmonella and Shigella Reference Center; CI, confidence interval; NPHN, National Public Health Network; MA, Ministry of Agriculture.
† Estimate of the number of outbreaks.
‡ Numbers in parentheses, 95% confidence interval for the sensitivity.

reported to the MA than community outbreaks.

To use the capture-recapture method accurately, several conditions must be met (24). The definition of the event studied should be the same for each source (29, 30), a condition that was not met for the NRC. The lower specificity of the definition of the NRC would have induced false positive notifications and therefore an overestimate of outbreaks. This was corrected with the positive predictive value of the case definition of the NRC, as suggested by LaPorte et al. (27). Since the notifications to the two mandatory notification sources were routinely validated, we assumed that their positive predictive values were 100 percent.

Since none of the three notification systems shared a unique identifier, we identified matches according to the postal code and delays unique identifier, we identified matches according to the their positive predictive values were 100 percent.

Furthermore, as Egeland et al. did in another study (32), we were able to validate all identified matches by comparing the reports of the two sources. This method allowed us to minimize the number of false positives, but it did not rule the false negatives out.

The qualitative investigation confirmed the positive dependency found statistically between the NPHN and the MA in the capture-recapture analysis. Such studies are recommended for assessment of the dependency between two sources when this dependency cannot be assessed using statistical analysis (33). Furthermore, it was useful to understand the mechanisms of the dependency. Since the respective and complementary roles of the NPHN and the MA are both defined by the same regulatory act, we expected to find a strong positive dependency between both sources.

To take into account the dependencies between the three sources and the variable catchability in the different sources, we performed a log-linear analysis. To select the final model, we did not use the “principle of parsimony” (24), which would have ignored the interactions between the NPHN and the serotype and between the MA and the type of foodborne outbreak. The model that included these two interaction terms had the best BIC and AIC criteria and gave the same estimate as the one without these two interaction terms. In addition, the “weighted BIC” proposed by Hook and Regal (24, 34) gave the same estimate. A two-source analysis between the NRC and the NPHN-MA merged together gave an estimate similar to that of the final log-linear model. This simple approach developed by Wittes and colleagues (20, 21) could be used in future analyses. However, the log-linear
model remains relevant for analysis of the dependencies between sources and the interactions with covariates, when at least three sources are considered (24).

Serotype and type of outbreak (community and family) introduced variable catchability within the NPHN and MA data, respectively. *S. enteritidis* was better reported to the NPHN than *S. typhimurium* or other serotypes, and community outbreaks were more often reported to the MA than family outbreaks. This observation may be explained by more systematic requesting of stool cultures by district health officers when the assumed index meal contains eggs or egg products. In the same way, the DSV probably pays less attention to family outbreaks than to community outbreaks. Analysis of the variable catchability by region would be of interest; however, this was not possible because of the low number of outbreaks in some regions. Moreover, it was not possible to stratify on the size of the outbreaks. Although the data were available in each source, information on this variable was not considered valid, because there were important variations in numbers of patients for the same foodborne outbreak reported to at least two sources (laboratory-confirmed cases versus clinical cases, for example).

Our study estimated the number of outbreaks in which at least one patient had a positive *Salmonella* stool culture. Therefore, it still underestimated the true number of foodborne *Salmonella* outbreaks, because it did not take into account outbreaks in which patients did not visit a clinical practitioner or did not have a stool culture, or those for which a common food exposure was not identified (35). This estimation does not include the number of sporadic cases. In France, it is estimated that 4–6 percent of patients who consult a general practitioner for acute gastroenteritis have a stool culture, and *Salmonella* is the most frequently isolated agent (36, 37). Using the algorithm proposed by Chalker and Blaser (38), which adjusts for the problems mentioned above, the true estimate is probably in excess of 2,000 foodborne *Salmonella* outbreaks yearly.

Assessment of the actual number of foodborne *Salmonella* outbreaks is a necessary preliminary step for assessing its public health burden. Whatever the design used, studies of the burden of foodborne *Salmonella* infection, including estimation of the number of sporadic cases and the economic impact, are needed to foster prevention and control efforts in food production, distribution, and consumption (39). Analyses conducted according to characteristics such as the type of outbreak are very helpful for adjusting the targeting of prevention and control. Because routine surveillance underestimates the number of family outbreaks more than community outbreaks, less priority is given by public health and food safety authorities for the control of the former. Our quantitative approach, based on routine surveillance data, is a first step in the assessment of the true burden of this unresolved public health problem in France.

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