Quantifying the Contribution of Animal-food Sources to Human Salmonellosis in Denmark in 1999

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Abstract: A risk assessment model quantifying the importance of the major animal-food sources was developed. For modelling purposes, we combined Bayesian inference and Monte Carlo simulation. The principle was to compare the registered number of human cases caused by different Salmonella sero- and phage types with the prevalence of these types in the different sources, weighted by the amount of food source consumed. A prior distribution was included to account for the presumed differences between serotypes and food sources with respect to causing human salmonellosis. A Poisson likelihood function was used for the probability of observing the actual number of human cases given the prevalence in the sources. Based on the posterior distribution, the number of human cases attributable to each food source was estimated. The described method may prove to be an alternative to the "traditional" stable-to-table risk assessment, which often involves making a large number of assumptions.

Keywords: Epidemiological typing, Monte Carlo simulation, QRA modelling

Introduction: In order to get a better understanding of the mechanisms behind the dynamics in the occurrence of Salmonella infections in humans, we developed a quantitative risk assessment model based on principles described earlier (Hald and Wegener, 1999). The model quantifies the importance of the major animal-food sources of domestic and sporadic cases of human salmonellosis.

Materials and Methods: Data from the national Salmonella surveillance of animals, foods and humans in Denmark in 1999 were included as input in the model (Anonymous, 2000). For modelling purposes, we applied a technique called Bayesian Monte Carlo (Vose, 2000), which combines Bayesian inference and Monte Carlo simulation. The principle behind the model is to compare the number of domestic and sporadic cases, broken down by sero- and phage types, with the prevalence of these Salmonella types in different animal-food sources, weighted by the amount of food...
source consumed. First, the number of domestic and sporadic cases per *Salmonella* type was estimated based on available information regarding epidemiological typing results, travelling history and the extent of reported outbreaks. A Poisson likelihood function was then used to calculate the probability of observing these numbers of cases given the prevalence in the various food sources and the amount of food consumed. To account for the presumed but undefined differences between *Salmonella* serotypes and food sources with respect to causing human salmonellosis, a multiparameter prior was introduced. We also added an unknown parameter (non-se) recognising that *S. Enteritidis*, because of its predilection for contaminating the egg content, presumably causes more egg-born infections than other serotypes, which primarily are located on the egg shell. The equation used to estimate the number of human cases per source and *Salmonella* type was defined as follows:

\[ \lambda_{ij} = M_j \times p_{ij} \times q_i \times a_j \times (\text{non-se}), \]

where \( \lambda_{ij} \) = the expected no. of cases; \( M_j \) = the amount of food source consumed; \( p_{ij} \) = the prevalence; \( q_i \) = the serotype-dependent factor; \( a_j \) = the source-dependent factor; non-se = estimated when serotype \( \neq S. Enteritidis \) and source = eggs, else non-se = 1; \( i \) = subscript indicating *Salmonella* type; \( j \) = subscript indicating food source. It was assumed, that the \( \{q_i\} \) for phage types within the same serotype were equal.

The maximum likelihood estimators (MLEs) were determined for the unknown parameters (\( \{q_i\} \) \( \{a_j\} \), and non-se) and uniform priors were constructed centred around the MLEs. The joint posterior distribution was estimated by the Bayesian Monte Carlo technique. The uniform prior distribution was then replaced with the posterior in the final model.

**Results:** Of the 3,268 registered cases in Denmark in 1999, 2,629 (90% C.I.: 2,613 – 2,641) were estimated to be both domestic and sporadically occurring. The final result of quantifying the contribution of animal-food sources to human salmonellosis is presented in Figure 1. The most important sources were found to be table eggs, followed by domestically produced pork and imported poultry. Approximately 19% of the cases could not be associated with any of the sources.
**Discussion:** Any successful control of *Salmonella* requires an extensive and integrated quantitative risk-based approach that documents a programme’s needs as well as its effect. Being able to quantify the contribution of the various food sources is therefore an important tool in risk management. In addition to evaluate the trends and dynamics of sources to human salmonellosis, it will support risk managers in their decision of allocating resources in order to achieve the highest possible benefit. We believe that the described method may prove to be an alternative to the “traditional” stable-to-table risk assessment, which often involves making a large number of assumptions with variable plausibility.

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**References**