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Supporting document 2

Quantitative risk model: development of a base model for *Salmonella* Enteritidis in eggs – Proposal P1060

P1060 – Egg Food Safety & Primary Production Requirements

Executive summary

SUMMARY

The risk posed by *Salmonella* Enteritidis (SE) in eggs is complex, involving multiple factors from farm management practices through to consumer behaviour. To better understand and mitigate these risks a quantitative microbial risk assessment model has been developed.

SE is a nationally notifiable animal disease in Australia and is not endemic in the national layer flocks. Evidence gathered since the 2018-19 SE in eggs incident (see P1060 SD1) found that SE continues to appear sporadically in layer flocks leading to infrequent cases of human illness.

The model simulates the journey of individual eggs laid on either a small (1,000 laying hens) or medium-size (20,000 laying hens) farm that becomes SE-positive during a production cycle. The model has been used to answer the risk assessment questions relating to through-chain temperature control and testing for SE in layer environments. The model predicts the number of actual and notified illnesses for different scenarios to inform the cost benefit analysis. Two mitigations are considered: environmental testing regimes (once or regular 13 week tests (91 days) per production cycle) and temperature control (refrigeration or ambient storage after egg grading). The baseline is the number of illnesses before the SE-contaminated farm is identified using passive human surveillance (epidemiological traceback).

Model simplifications include that there is successful traceback following epidemiological traceback, and perfect environmental testing.

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1. Introduction

The risk to consumers posed by *Salmonella* Enteritidis (SE) in eggs is complex, involving multiple factors from farm management practices through to consumer behaviour. To better understand and mitigate these risks a quantitative microbial risk assessment (QMRA) model has been developed. This model simulates the various stages of egg production, distribution, and consumption, estimating the likelihood of contamination and subsequent illness under different scenarios. Models developed by the EFSA (European Food Safety Authority, EFSA 2014) and ANSES (French Agency for Food, Environmental and Occupational Health & Safety) with BfR (Federal Institute for Risk Assessment in Germany) (Desvignes et al. 2019) have provided a foundational framework for estimating the probability of SE-related illness from egg consumption in the European context. FSANZ has previously collaborated with EFSA to modify an Australian risk assessment model for eggs (Thomas et al. 2006).

Supporting Document 1 (SD1) provides an overview of the current situation for SE in Australian layer flocks. Until the 2018-19 SE in eggs incident a SE strain capable of vertical transmission (i.e. deposition of SE cells within the egg during egg development) had not been found in commercial layer flocks. Evidence from national surveillance systems of poultry demonstrates that the SE 2018/19 strain is infrequently being detected in layer flocks.

In response to the need for a more contemporary, comprehensive and context-specific model for Australia, FSANZ developed an enhanced QMRA model. Building upon the ANSES/BfR framework, the new model incorporates additional features to reflect the unique characteristics of the Australian egg production and supply chain. The model considers a single farm. Key additions in the FSANZ model include the integration of environmental monitoring, passive human surveillance, and detailed modelling of multiple supply chain pathways. These enhancements allow for a more granular assessment of SE risks, accounting for factors such as farm-level contamination, storage conditions, and the impact of regulatory interventions.

2. Development of the QMRA

2.1 Previous work that informed the QMRA

A simulation model of a complex system is only ever an approximation of reality (Law et al., 2007). This is certainly true for the development of a simulation model for egg production in Australia. The simulation models described in the P301 risk assessment (FSANZ, 2009) were based on a simple linear supply chain where eggs moved from the farm, to a grading/washing facility, through the retail system, to home and then consumption (Thomas et al., 2006).

This model was extended by EFSA, in collaboration with FSANZ, to evaluate the risk from SE in eggs in Europe. A similar supply chain was used by EFSA for eggs sold through the retail supply-chain for home consumption in Europe (EFSA 2014). A separate model for pooling of eggs in food service was also developed. Both of these models were developed and run using proprietary software. The key differences between the models used in the EFSA assessment and the original Australian Egg Corporation Limited (AECL) model presented in Thomas et al. (2006) include:

1. Temperature Growth Models: The EFSA model uses the Rosso growth rate equation to model the growth of *S.* Enteritidis based on temperature. This equation considers the optimum, minimum, and maximum growth temperatures, while the AECL model originally used a simpler log-transformation approach.
2. Truncation of Poisson Distribution: In the EFSA model, the Poisson distribution for the initial number of SE cells is truncated at one to ensure that there is always at least one cell in a contaminated egg. This was not part of the original AECL model.
3. Adaptation for EU Conditions: The EFSA model adjusted parameters like ambient storage temperatures, storage times, and the prevalence of contaminated eggs to reflect European conditions, which differ from those in Australia. This included adding stages for transport from retail to household and adjusting for the proportion of eggs refrigerated during retail and in household storage.
4. Yolk Mean Time (YMT): The EFSA model continued to use the YMT concept but adjusted the parameters to better fit European data. This included modifications in the linear relationship used to calculate YMT based on temperature.

These adaptations were necessary to ensure the model could accurately assess risks in the European context, considering differences in consumer behaviour, storage conditions, and SE prevalence.

In 2019, a joint paper by ANSES and BfR produced a modified version of the EFSA model (Desvignes et al. 2019). The model was translated into the R programming language. The authors specifically modified several parameters to reflect updated conditions, such as the prevalence of egg contamination and the time-temperature profiles of egg storage. Additionally, a deterministic beta-Poisson dose-response model was used to estimate the risk based on egg cooking methods (lightly cooked, and well-cooked). The risk for uncooked food was not included. The model was made more versatile by considering different scenarios, such as varying storage conditions and consumer cooking habits. The R code provided with the publication has formed the starting point for this QRMA work.

2.2 Scope and modelling approach

SE is a nationally notifiable animal disease in Australia and is not endemic in the national layer flocks. Evidence gathered since the 2018-19 SE in eggs incident (see P1060 SD1) found that SE continues to appear sporadically in layer flocks leading to infrequent cases of human illness. Under the voluntary National Salmonella Enteritidis Response Management

Plan, flocks linked to cases of human illness are likely depopulated to prevent establishment and spread. This fact had implications for development of the current model, as it would not be appropriate to model the national flock using unmodified international risk assessments from countries where SE is endemic. Farm-specific scenarios were further refined to consider only two single farms; a small farm with 1,000 hens and a medium sized farm with 20,000 hens. The incursion of SE into these farms and possible control measures were then evaluated.

Models for large egg layer farms were not considered necessary because large farms are already on voluntary (or in NSW mandatory) schemes. These schemes include SE management strategies similar to those proposed under P1060 including regular environmental monitoring to maintain accreditation.

The primary output of the models is the number of cases for different mitigation scenarios which included the two environmental testing regimes (either once, or four times per production cycle) and storage temperature after egg grading. The baseline is the number of cases of illness before the identification of SE using passive human surveillance.

2.3 Development of the FSANZ model

As part of P1060, FSANZ staff visited layer farms (small, medium and large) in different jurisdictions to understand current industry practices and challenges for egg production. These visits highlighted the complexity of supply-chains and biosecurity challenges for different production systems, e.g. caged, barn and free-range.

In addition, information gathered during investigations related to the 2018-19 SE incidents revealed in detail the movement of eggs, equipment, vehicles and people between different farms and egg grading facilities not previously obtained. Attempting to develop models for the vast array of combinations of farms, in-line and off-line grading facilities and egg supply-chains is impossible for a single risk assessment. This information was also discussed with the FSANZ Scientific Advisory Group for Eggs (SAGE) to determine how to best simulate the Australian situation in the most concise way.

The FSANZ 2024 model builds upon the EFSA (2014) model, incorporating several key modifications and additional components to answer the P1060 risk assessment questions. While both models aim to estimate the risk of SE-related illness from egg consumption, the FSANZ model allows investigation of interventions such as environmental testing and passive human surveillance. Below is a comparison highlighting the key differences and assumptions between the two models (Table 1).

Table 1: Comparison between the EFSA 2014 Model and the FSANZ 2024 Model

Component	EFSA (2014) Model	FSANZ P1060 Model
Model Objectives and Scope	The focus is on the public health risk posed by Salmonella in the consumption and handling of table eggs and considers the public health risk from of changes to shelf-life dates. Models are developed for the consumption of eggs in the household only and pooling of eggs for both household and food service/institutional settings.	Focusses on estimating the number of illnesses from SE-positive eggs produced by a single small or medium-sized farm, and allows for investigation of interventions such as environmental monitoring, passive human surveillance, and temperature control in different parts of the supply chain.

Component	EFSA (2014) Model	FSANZ P1060 Model
Consumption	For the household egg model each person consumes a single egg. The household and food service/institutional egg pooling models uses different pool sizes.	The inclusion of passive human surveillance into the model required a more realistic consideration of egg consumption events. This is achieved by considering the number of people consuming a food containing SE-contaminated eggs in either the home or food service settings.
Dose-Response Modelling	Calculates the dose of SE based on initial contamination and reduction factors during cooking. The pooling model applies to an average pool concentration of SE cells.	Uses the same beta-Poisson model where parameters alpha and beta are drawn from a multivariate normal distribution, which introduces correlation and variability. The dose-response model is applied to each individual consumption in a simulated outbreak, rather than the average dose.
Supply Chain Pathways and Stages	Two linear supply-chain models for the household (10 stages) and the catering/food service and institutional (8 stages) were developed	A non-linear supply chain which allows for the movement of eggs between different entities is used. The final points of preparation and consumption are the household and food service settings.
Environmental Monitoring and Surveillance	Does not include environmental testing or passive human surveillance to identify SE-positive farms.	Integrates environmental testing with regular 13-week testing intervals or a single test per production cycle (at peak of production) to detect SE in the farm environment. Introduces passive human surveillance with two stop rules to identify and respond to multiple notified cases of illness or outbreaks. Models the effect of timely intervention (e.g., recalls) based on the detection of SE-positive eggs and the effectiveness of surveillance measures.
Illness and Outbreak Simulation	Focuses on the probability of illness per serving for raw, lightly and well-cooked eggs. The household egg model assumes that a single person consumes one egg. The pooling model appears to use an average dose for dose response modelling. A single SE-positive egg contaminates each pool.	Simulates illness at the individual level for each serving, allowing for the estimation of the number of illnesses from a single SE-contaminated egg. Eggs may be consumed by an individual as an egg meal or as an ingredient in both the home or food service settings. Introduces outbreak detection mechanisms based on notified case counts and reporting of genomic data to health departments to initiate epidemiological investigations. Health care seeking behaviour including doctor visits, stool testing, and reporting to surveillance systems. Simulates outbreak response including traceback investigations.

Component	EFSA (2014) Model	FSANZ P1060 Model
Response to Surveillance and Intervention	Out of scope.	Includes a detailed response mechanism, where detection of SE through environmental testing triggers interventions such as recalls and flock depopulation. Models timing and effectiveness of these interventions, assessing their impact on the overall burden of illness.
Outputs and Risk Metrics	Outputs include number of illnesses per million servings for different cooking methods and relative risk when considering shelf-life scenarios.	Outputs a wide range of metrics, including number of SE-positive eggs, actual illnesses, notified illnesses, outbreak events, and effectiveness of interventions. Generates time series data for illness cases and the timeline of outbreak detection and response, providing a more dynamic view of SE risk management.

The FSANZ model extends on the EFSA (2014) model by adding additional components and complexity to the modelling of SE risks in eggs. It introduces new components such as environmental testing, passive human surveillance to initiate public health response, non-linear supply chains, all of which contribute to a more comprehensive assessment of SE-related risks and the effectiveness of public health interventions.

2.4 Conceptual models

The schematic representation of the EFSA household and catering/food service and institutional setting models are presented below. Assumptions regarding the temperatures and times which eggs experience in each stage are the same for both models until retail for the household or Catering/food service and institutional settings.

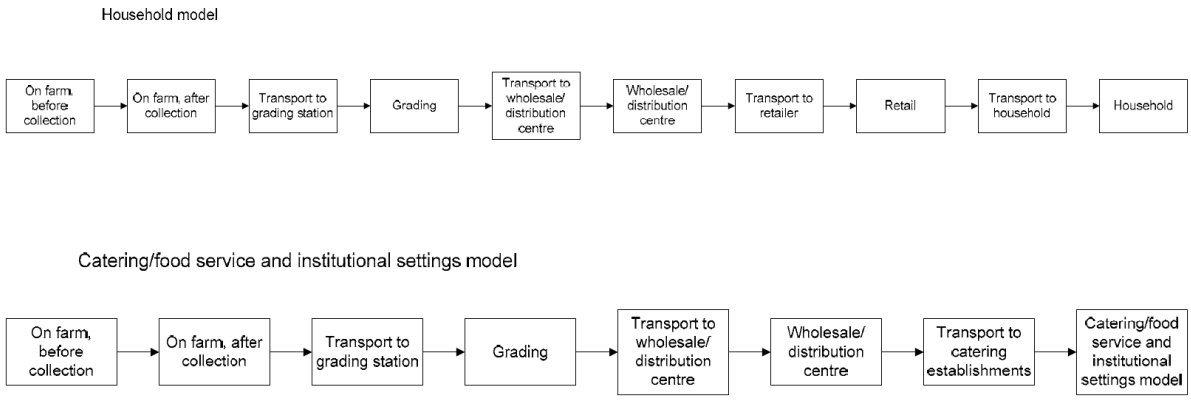

Figure 2: Schematic representation of the models developed for EFSA (2014)

As part of the risk analysis process, FSANZ created a simplified flow diagram for the production and movement of eggs through supply-chains and their subsequent preparation and consumption was developed (Figure 2). This supply-chain incorporates many of the EFSA model stages and includes a new stage “Direct sale” which represents eggs sold directly from the farm. Conceptually this may be from the ‘farm gate’, farm shops or via farmers markets. This supply-chain is non-linear as it provides for additional options not included in the EFSA model, notable the purchase of eggs from retailers for use in a food service setting. Evidence gathered by FSANZ has highlighted that this is a valid scenario.

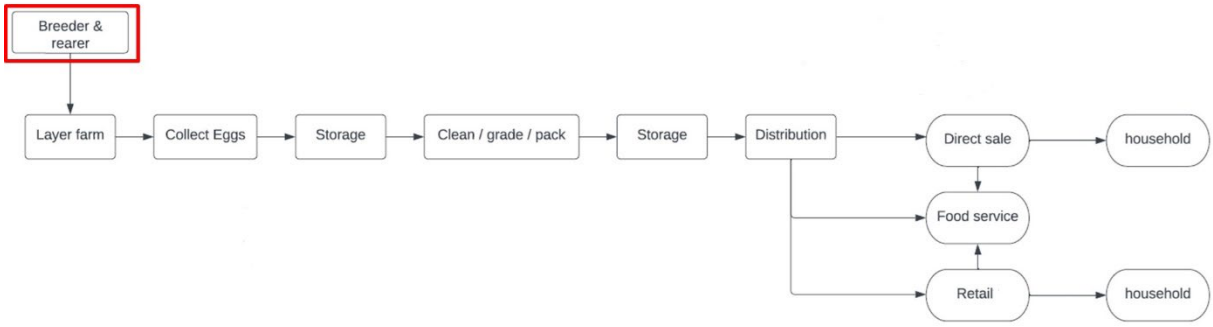

Figure 3: Schematic representation of the supply-chain considered for P1060.

For the model development the non-linearity is dealt with by defining the five distinct linear pathways (Figure 4).

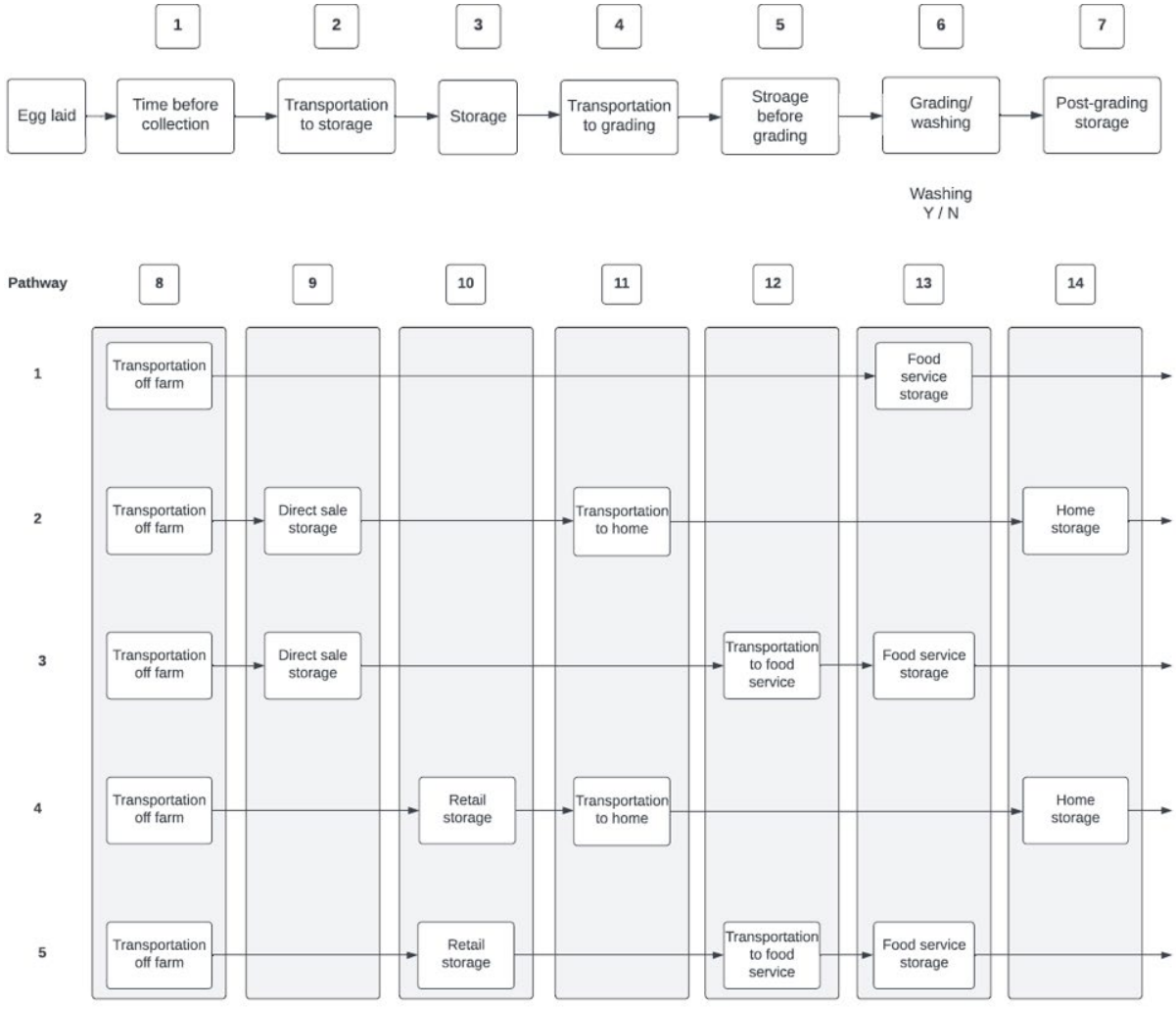

Figure 4: The 14 stages of the P1060 egg supply chain.

Within FSANZ's model (Figure 4), each laid egg is subjected to pathway stages 1-7. The temperature and time for each stage is individually simulated. At stage 6, the effects of washing can also be simulated or ignored. Stages 8-14 are dependent on the supply chain pathway assigned to each individual egg:

- Pathway 1 represents food service distribution without any intermediate storage and is composed of stages 8 and 13.
- Pathway 2 represents a home consumer directly purchasing from the farm, such as from the farm gate, and is composed of stages 8, 9, 11, and 14
- Pathway 3 represents food service distribution via one intermediate storage stage and is composed of stages 8, 9, 12, and 13
- Pathway 4 represents a home consumer purchasing from a retail business, such as a supermarket, and is composed of stages 8, 10, 11, and 14
- Pathway 5 represents food service distribution via a retail intermediate and is composed of stages 8, 10, 12, and 13

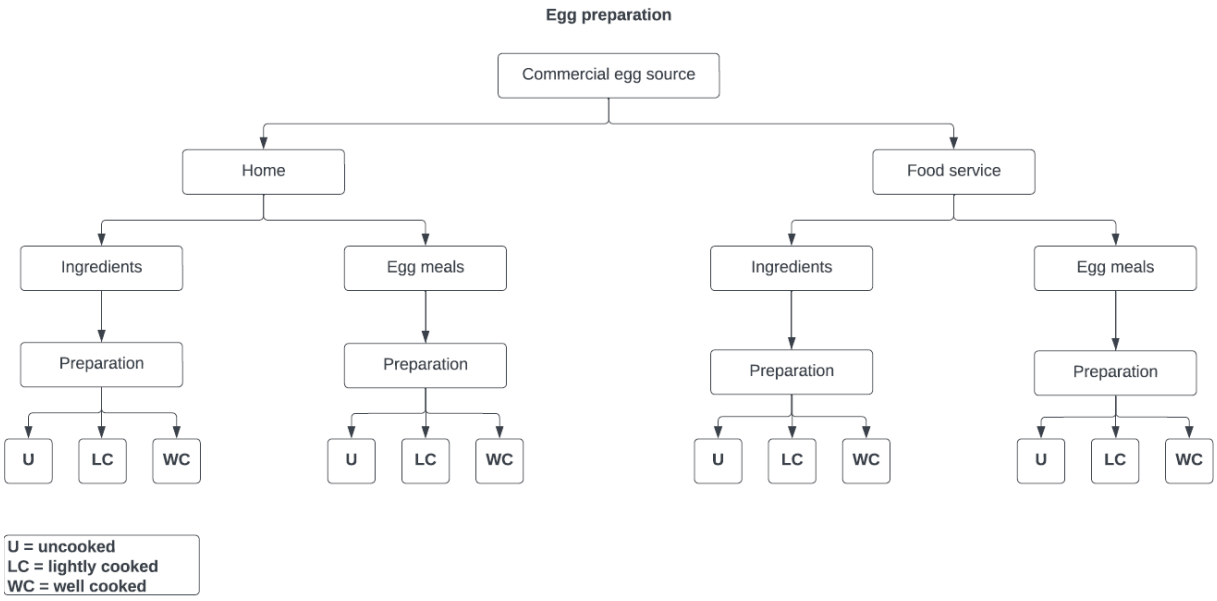

Figure 5: Flowchart of the preparation of foods containing egg in the home and food service settings

The cooking preparation of each egg (Figure 5) is individually simulated within the FSANZ model. There are two possible consumption destinations for each egg. Firstly, an egg could be an ingredient in a meal where the egg is split up into multiple servings. Secondly, the egg could represent a single serving and be constituted as an egg meal. From here there are three alternatives for how the egg can be prepared for consumption. These are uncooked, lightly cooked or well cooked. The effects of egg preparation are described further below.

3. High level walk through of the Base Model

Key steps and assumptions in the model:

The base model assumes that there is no SE testing of the layer environment to determine the presence of SE in the layer flock. Under this case, the only way that a farm would be identified would be from cases of human illness following the consumption of contaminated eggs.

3.1 Introduction of SE into the layer environment

SE contamination enters the environment at a randomly determined time during the egg-laying cycle (from a hen's age of 16-80 weeks). This is modelled by drawing a date from a uniform distribution for the entry time of SE.

3.2 Daily egg production

Egg production follows a logistic growth curve with some added noise. The model also introduces random noise to the egg production function to account for day-to-day variations in egg production that are not captured by the logistic function alone. This stochastic element ensures that the model reflects the inherent variability in biological processes.

The logistic egg production function in the FSANZ model is designed to represent the typical curve of egg production for a flock, which starts slowly, increases to a peak, and then gradually declines as the flock ages. The function is defined as follows:

$$E(t) = a \cdot \left(1 + e^{-c \cdot (t - t_0)}\right)^{-d} \cdot e^{-x \cdot (t - t_0)}$$

Where:

- t is the time (in weeks) since the flock started laying eggs.
- t_0 is the time (in weeks) at which the flock begins laying eggs, set at 16 weeks of age.
- a is a scaling parameter that adjusts the peak production level.
- c controls the steepness of the curve during the initial rise in egg production.
- d affects the shape of the curve as it approaches its peak.
- x controls the rate of decline in egg production after the peak.

3.3 Prevalence of SE positive eggs

The 'rate' of SE contaminated eggs laid by infected hens is taken from the EFSA model, namely a Gamma distribution with an alpha shape parameter of 9.523319 and beta rate parameter of 1/0.00035828 (inverse scale). The gamma distribution reflects the variability in the probability of an egg being SE-positive based on prior knowledge and data.

The FSANZ base model considers the rate of lay of SE-positive eggs produced from a single small or medium-sized farm. By contrast, the EFSA model simulates eggs from a randomly selected SE-positive European egg farm. The calculation of EU egg prevalence combines the prevalence of SE-positive layer flocks in the EU and the prevalence of SE-infected hens within a flock and the 'rate' of SE contaminated eggs laid by infected hens. The FSANZ models differs because the prevalence of SE-positive layer flocks in Australia is not currently known.

From the evidence collected by FSANZ (see SD1) it was not considered appropriate to assign a flock prevalence, as the discovery of SE-positive farms appears to be infrequent and sporadic. Further, information gathered during veterinary investigations, especially the serology of infected chickens highlighted the dynamic nature of SE infection in flocks. A within-flock prevalence would be expected to change as the infection spread within a flock. To account for this we used the findings of Thomas *et al*. (2009), which simulated the time course of colonisation of hens in a flock after the introduction of SE. For a 20,000 bird flock the median time for infection was between 40 and 50 days. We have used a delay between the introduction of SE into the layer environment and the production of SE-positive eggs of 42 days. This assumption means that the within flock prevalence before 42 days post-introduction is zero and all birds are considered infected after this time.

3.4 Number of SE cells in the egg at lay

At the point of lay, the number of SE cells within an SE-positive egg is determined as a random number generated from a truncated Poisson distribution. The use of a truncated Poisson distribution ensures biologically meaningful, non-negative values for SE cells. The distribution uses the following arguments:

- lambda = 7: The mean (rate) parameter of the Poisson distribution. This represents the expected value before truncation.
- a = 0: The lower bound of truncation. Values below this are excluded.
- b = Inf: The upper bound of truncation. Values above this are excluded. Since this is set to infinity, there is no upper truncation.

3.5 Assigning distribution pathway

Each egg's distribution pathway (as shown in Figure 1) is assigned using a multinomial distribution for probabilistic determination. The input probabilities are indicative and can be changed to model specific scenarios. Five different pathways of distribution are assigned, ensuring each egg has a primary pathway (direct sale, food service, retail) and a secondary sub-pathway (household or food service), if applicable.

3.6 SE growth through various supply chains

The SE growth rate in the FSANZ model is modelled using a combination of temperature-dependent growth kinetics and time-based progression through different stages of the supply chain. The growth rate model is designed to capture the complex interactions between temperature, time, and the biological characteristics of SE as it moves from farm to fork.

3.6.1 Temperature-dependent growth rate

The growth rate of SE is highly dependent on the temperature at which eggs are stored and handled throughout the supply chain. The FSANZ model uses the following key components to model the SE growth rate:

3.6.1.1 Rosso equation

The Rosso equation describes the non-linear relationship between temperature and SE growth. It adjusts the growth rate based on how close the current temperature is to the optimal temperature for SE growth. The function is defined as:

$$\gamma(T) = \frac{(T - T_{\max}) \cdot (T - T_{\min})^2}{(T_{\text{opt}} - T_{\min}) \cdot [(T_{\text{opt}} - T_{\min}) \cdot (T - T_{\text{opt}}) - (T_{\text{opt}} - T_{\max}) \cdot (T_{\text{opt}} + T_{\min} - 2T)]}$$

- $T_{\min}$: Minimum temperature for SE growth.
- T_{opt}: Optimal temperature for SE growth.
- $T_{\max}$: Maximum temperature for SE growth.

The values of $\gamma(T)$ has the value of zero for temperatures below T_{min} and greater than T_{max}. The growth rate is calculated as:

$$k = k_{opt} \times \gamma(T)$$

This function ensures that SE grows most rapidly at optimal temperatures and that growth slows down or stops at temperatures outside the optimal range.

3.6.1.2 Cooling rate

The internal temperature of an egg, T(t): is modelled using Newton's Law of Cooling:

Where:

$$T(t) = T_s + (T_i - T_s) \cdot e^{-k_{rs} \cdot t}$$

- T(t) is the temperature at time (t).
- T_s is the steady-state or surrounding temperature.
- T_i is the initial temperature.
- k_{rs} is the decay rate constant.
- t represents time.

This equation describes how an egg's temperature (T) changes over time (t) as it approaches the surrounding temperature (T_s). The cooling rate equation is applied in the model at each stage shown in Figure 1.

3.7 Cumulative growth (ft) and yolk mean time (YMT)

The cumulative effect of temperature over time on SE growth is modelled using an integrated approach that sums the effects of temperature across all time points:

$$f_t = \sum_{i=1}^{t} \frac{1}{10^{a+b \cdot T_i + \text{YMT.mse}} \cdot 24}$$

Here, *ft* represents the cumulative time effect, where the summation is performed over each hour of exposure at different temperatures. This cumulative effect determines the potential for SE growth over a given period. The YMT variable is introduced as YMT.mse. This variable is generated from a normal (Gaussian) distribution.

3.8 Growth kinetics adjusted for time (NCD)

The moment that SE growth becomes possible a number of ten-fold increase (NCD) is calculated for each egg:

$$NCD = \sum(\text{ft} \geq 1) \cdot \gamma(T) \cdot k_{\text{opt}}$$

- k_{opt}: Optimal growth rate of SE, modeled as a normal distribution to introduce variability.

The NCD represents the overall growth of SE (in log10 CFU/g per hour) as it progresses through different stages of the supply chain. NCD considers both cumulative growth (ft) and temperature-modulated growth (γ(T)).

3.9 Threshold for breakdown (TRMV) and stage of SE growth

Cumulative growth (ft) is monitored by TRMV to output when ft >= 1. This point in time represents when the deterioration of the yolk membrane is observed. At this point, the stage (from Figure 1) where the threshold is reached is assigned as the beginning of SE growth.

3.10 SE cells at preparation

The number of SE cells within an egg after traveling through its distribution pathway is calculated considering the potential growth (described above) and an upper bound. The SE cells at the time of preparation (SE_{prep}) can be shown as:

$$SE_{\text{prep}} = \min(SE_{\text{lay}} \cdot G, U)$$

Where:

$$G = 10^{\text{NCD}} \qquad U = 10^{\text{PERT value}}$$

- G is the growth factor adjustment (based on the NCD value).
- U limits the maximum SE count based on a PERT distribution.

3.11 Preparation effects

The food type (ingredient or meal) is assigned using a binomial distribution where the probability is dependent on the pathway destination for the egg (food service or home). A multinomial distribution is used to determine the preparation effect (uncooked, lightly cooked or well cooked) based on whether the food type is an ingredient or an egg meal. The number of servings is determined by the food type and the pathway designation using a truncated Poisson distribution.

The preparation of eggs (uncooked, lightly cooked, well cooked) has specific effects on SE survival:

- Uncooked eggs are assumed to have no reduction in SE cells
- Lightly cooked eggs have a reduction in SE cells based on a log-normal distribution

$$SE_{lightly\ cooked} = SE_{preparation} \times 10^{-Normal(2,0.5)}$$

- Well cooked eggs do not cause illness as all SE cells are assumed to be destroyed through cooking.

3.12 Dose-response relationship

The probability of illness from consuming SE-contaminated eggs follows a Beta-Poisson model, where α and β parameters for each individual are drawn from a multivariate normal distribution. The parameters introduce correlation and variability into the illness probability, which assumes that individual susceptibility to SE infection varies. The probability of illness equation can be shown as:

$$p_{ill} = 1 + \left(\frac{Dose}{10^{(\log_{10} \beta)}} \right)^{-10^{\log_{10} \alpha}}$$

Here, dose is the number of SE cells the individual consumed. The model parameters for $log_{10}\alpha$ = -0.871 and $log_{10}\beta$ = 1.727 are drawn from a variance-covariance matrix:

$$\begin{pmatrix} 0.008035438 & 0.01801451 \\ 0.018014510 & 0.05149408 \end{pmatrix}$$

Whether an individual gets ill is determined using a binomial random variable based on the calculated illness probability. For eggs that are destined for multiple servings, illness outcome is individually modelled for each serving.

3.13 Illness severity and duration

The pathway from illness to reporting is modelled in the context of a public health surveillance system using probabilities informed by the National Centre for Epidemiology and Population Health (NCEPH) Working Paper 52 (Hall et al., 2006). Cases of illness are simulated through various public health steps (e.g. visiting a doctor, stool testing, reporting) and calculates the probabilities at each stage.

Illnesses are first distributed into six severity groups based on predefined probabilities and drawn from a multinomial distribution. At each key public health step a truncated normal distribution is drawn from, with different severity groups having different means and standard deviations, reflecting varying likelihoods of success. The underreporting factor for each illness severity group is also simulated. This helps estimate the true community burden of illness. The model combines the probabilities across all steps to output whether an individual's illness is notified or not.

3.14 Passive human surveillance rules

The model uses specific rules to define when a public health investigation is initiated:

- **Rule 1:** An outbreak is identified if three unrelated cases within a production cycle are linked by Whole Genome Sequencing (WGS).
- **Rule 2:** An outbreak is also identified if two or more cases are notified and epidemiologically linked.

The time required for epidemiological investigation, response, and recall is fixed (e.g., 21 days for WGS clustering, 30 days for epidemiological investigation). Traceback investigations are also assumed to always be successful in the model.

4. Modelling implementation of environmental testing

4.1 The base model environmental testing

The base model discussed above in Section 3, which represents the current situation in Australia, is maintained here. Periodical environmental testing on-farm is added to the model to simulate its effect on reducing foodborne illness.

4.2 Single test per production cycle

The first environmental testing scenario is for a single test per production cycle at the date of a flock's peak production, which is approximately 9 weeks into their laying cycle. Peak production is a time where SE shedding, for an SE-positive flock, is high. If this environmental test is positive for SE, 10 days is added to the flock's egg laying cycle until the farm has production stopped. This time accounts for the days between sample collection, laboratory testing, reporting, and action taken by the regulator to initiate a recall. Environmental test results are assumed to be accurate, and the response time to positive tests is fixed.

4.3 Regular 13-week testing

Regular environmental monitoring occurs every 13 weeks, which fits within the 12-15 week schedule applied by SE monitoring schemes already in place domestically and internationally. Similarly to the annual testing scenario, if one of the environmental tests is positive for SE, 10 days is added to the flock's egg laying cycle until the farm has production stopped.

5. Modelling implementation of temperature control

5.1 The base model for temperature control

The base model discussed above in Section 3, which represents the current situation in Australia, is maintained here. Transport and storage temperatures are changed to reflect alternative storage temperature scenarios including refrigeration or ambient temperatures from transportation after grading.

5.2 Temperature control scenarios

For modelling through-chain refrigeration, the probability of refrigeration is set to 1 for distribution stages from transportation after grading to home/food service storage. For scenario-based modelling, the probability for individual stages can be set at different values. In the through-chain refrigeration scenario the temperature ranges for each stage are set as:

- Minimum = 2°C
- Mode = 5°C
- Maximum = 8°C

Whereas without through-chain refrigeration the temperature ranges are set at ambient levels with some variability between stages:

- Minimum = 12°C or 18°C
- Mode = 15°C or 22°C
- Maximum = 18°C or 25°C

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