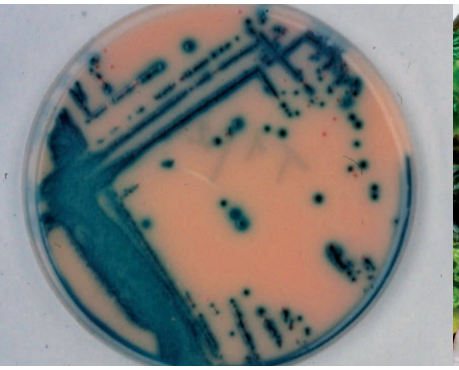
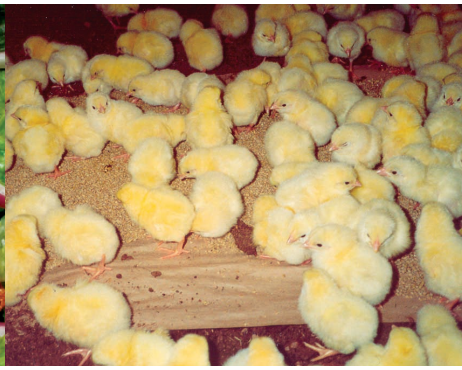
Eläinlääkintä- ja elintarviketutkimuslaitos
National Veterinary and Food Research Institute, Finland

JULKAISU 04/2003 • PUBLICATION 04/2003





SALMONELLA IN BROILER PRODUCTION IN FINLAND
– a Quantitative Risk Assessment

EELA

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- a Quantitative Risk Assessment

ISSN 1458-6878
Julkaisija: Eläinlääkintä- ja
elintarviketutkimuslaitos, EELA
Puh. (09) 393 101 • Fax. (09) 393 1811
Julkaisu 04/2003
Taitto: Adverbi Oy
Kirjapaino: Tammer-Paino Oy, Tampere 2003

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Acknowledgements

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Tekijät	**Riitta Maijala ja Jukka Ranta**
Julkaisun nimi	**Salmonella suomalaisessa broilertuotannossa – kvantitatiivinen riskinarviointi**

Tiivistelmä

Tämän riskinarvioinnin tavoitteina oli kuvata broilertuotannossa salmonellasta aiheutuvaa riskiä kuluttajille sekä arvioida miten kansallisessa salmonellavalvontaohjelmassa käytettävät riskinhallintatoimet vaikuttavat tähän riskiin. Arviointi kattoi koko broilerin tuotantoketjun alkutuotannosta kulutukseen. Tarkastelukohteeksi valittiin vuosi 1999, jolloin salmonellan esiintyvyys teurasbroilereissa oli valvontaohjelman käynnistämisen jälkeisistä vuosista korkein (nk. worst case scenario). Mallin tulosten mukaan vuonna 1999 oli teuraaksi lähetettävien broilerparvien todellinen salmonellaesiintyvyys 0.9-5.8% (95% vaihteluväli), keskiarvon ollessa 91 parvea (kaikkiaan parvia oli 2.939). Arvio todellisesta esiintyvyydestä on korkeampi kuin todettu esiintyvyys (64 parvea), koska mallin avulla arvioidaan myös toteamattomien tartuntojen määrää. Ihmisillä raportoituja broilerin lihan aiheuttamia salmonellatartuntoja olisi ennusteen mukaan ollut 39-82 (95 % vaihteluväli). Vuonna 1999 raportoitiin Kansanterveyslaitoksen tartuntatautirekisteriin yhteensä 566 kotimaista salmonellatartuntaa.

Alkutuotannossa merkittävin riskinhallintatoimi on poistaa tuotannosta ne emoparvet, joissa salmonella on todettu. Ilman tätä toimenpidettä teuraaksi lähetettävien broilerparvien todellinen salmonellaesiintyvyys vaihtelisi arvion mukaan välillä 1.3-17.4% keskiarvon ollessa 145 parvea (vrt. 91 parvea normaalitilanteessa). Tällöin raportoitujen ihmisten salmonellatartuntojen määrä nousisi myös samassa suhteessa eli noin 1.6 kertaisesti. Tällä riskinhallintatoimella on siis selvästi kuluttajan terveyttä suojaava vaikutus jo nykytilanteessa, kun salmonellaa esiintyy vähän. Tutkimuksessa arvioitiin myös kansallisen salmonellavalvontaohjelman toisen merkittävän riskinhallintatoimen, salmonellapositiivisiksi todettujen parvien lihan kuumentamispakon, vaikutusta. Mikäli kuumennusta ei tehtäisi, nousisi broilerin lihan aiheuttamien raportoitujen tartuntojen määrä ihmisillä noin 4.1 kertaiseksi. Tehokkain kuluttajansuoja saavutetaan, kun kumpikin näistä riskinhallintatoimista on käytössä. Ilman niitä ennusteen mukaan ihmisten salmonellatapausten määrä nousisi noin 5.6 kertaiseksi.

Koska Suomen salmonellatilanne on kansainvälisesti ottaen varsin hyvä, arvioitiin mallin avulla myös tilanteita, joissa salmonellan esiintyminen broilertuotannossa selvästi lisääntyisi (esim. rehuepidemian seurauksena). Simuloitaessa tilannetta, jossa yksi isovanhempaisparvi olisi saanut tartunnan muninnan alussa, salmonellan esiintyvyys teuraaksi lähetettävissä broilerparvissa olisi valvontaohjelman voimassa

ollessa 1.2-5.9% (95% vaihteluväli). Tämä tarkoittaisi keskimäärin 95 salmonella-positiivista parvea vuosittain (keskihajonta 36) eli lisäys normaalitilanteeseen olisi varsin vähäinen. Mikäli emoparvia ei tutkittaisi ja positiivisiksi todettuja ei poistettaisi, broilerparvista 2.8-43.1% (95% vaihteluväli) olisi ennusteen mukaan saastunut salmonellalla (keskimäärin 575 parvea, keskihajonta 364). Tämä johtaisi noin 4.7 kertaa suurempaan ihmisten tartuntatapausten määrään. Mikäli sen sijaan poistettaisiin salmonellan kantajiksi todetut emoparvet, mutta positiivisten broilerparvien lihaa ei kuumennettaisi, ihmisten tartuntojen määrä kasvaisi noin 3.4 kertaiseksi. Jos tässä yhden emoparven kuvitteellisessa tartuntatilanteessa ei kumpaakaan näistä riskinhallintatoimista olisi käytössä, ihmisillä raportoitujen salmonellatartuntojen määrä kasvaisi noin 17.8 kertaa nykyistä suuremmaksi.

Mallin avulla simuloitiin myös tilannetta, jossa tartunta tulisi viiteen vanhempaisparveen muninnan alussa eikä näitä toimenpiteitä olisi käytössä. Tällöin ihmisten raportoitujen salmonellatartuntojen määrä kasvaisi noin 7.7. kertaiseksi verrattuna nykyiseen valvontaohjelman mukaiseen tilanteeseen. Nykyisin salmonellaa esiintyy alle prosentissa kaupan olevasta broilerin lihasta. Simuloitaessa tilannetta, jossa salmonellan esiintyvyys puolessa Suomessa myytävästä broilerin lihasta olisi 20-40%, ihmisten salmonellatapausten ennustettu määrä kasvaisi jopa noin 58 kertaiseksi nykytilanteeseen verrattuna.

Mallin avulla voidaan vetää seuraavia johtopäätöksiä:

1. Kansallisessa salmonellavalvontaohjelmassa käytössä oleva pakolliset toimenpiteet vähentävät merkittävästi kotimaisten salmonellatapausten määrää ihmisissä.
2. Valvontaohjelman riskinhallintatoimien vaikutus on selvästi suurempi, jos salmonellaa esiintyisi tuotantoketjussa enemmän kuin nykyisin.
3. Yhdistelemällä eri riskinhallintatoimenpiteitä saadaan aikaan tehokkaampi vaikutus salmonellan torjunnassa kuin yksittäisellä toimenpiteellä.
4. Tuotantoketjun alkupäässä oleva korkea salmonellatartuntataso aiheuttaa suuremman riskin kuluttajalle verrattuna matalampaan tartuntatasoon.
5. Kvantitatiivinen mikrobiologinen riskinarviointi vaatii runsaasti tietoja, aikaa ja resursseja. Parhaimmillaan se voi kuitenkin antaa uuden näkökulman tutkittavaan aiheeseen ja osoittaa aukkoja tiedonkeruussa.

Avainsanat	*Salmonella*, broileri, valvonta, Kansallinen salmonellavalvontaohjelma
Julkaisusarjan nimi ja numero	EELAn julkaisusarja 04/2003 ISSN 1458-6878
Sivuja	100
Kieli	Englanti, tiivistelmä suomi, ruotsi ja englanti
Luottamuksellisuus	Julkinen
Hinta	–
Julkaisun myynti/jakaja	Eläinlääkintä- ja elintarviketutkimuslaitos, EELA Puh. (09) 393 101 • Fax. (09) 393 1811 • tiedotus@eela.fi • www.eela.fi

Resumé

Utgivare	**Forsknings anstalten för veterinär medicin och livsmedel, EELA, Finland**
Författare	**Riitta Maijala & Jukka Ranta**
Verkets titel	**Salmonella i finsk broiler produktion – en kvantitativ riskvärdering**

Beskrivning

Målen för denna riskbedömning var att redogöra för de risker salmonella inom broilerproduktionen medför för konsumenterna samt göra en bedömning av hur den riskhantering som utövas i samband med det nationella programmet för salmonellakontroll påverkar dessa risker. Bedömningen täckte hela produktionskedjan för broiler från primärproduktion till konsumtion. Till föremål för bedömningen valdes året 1999. Under de år som följde på starten för kontrollprogrammet var nämnda år det värsta ifråga om förekomsten av salmonella i slaktbroilrar (ett s.k. worst case scenario). Den reella förekomsten av salmonella hos de broilerflockar som sändes till slakt uppgick 1999 enligt modellens resultat till 0.9-5.8 % (variationsvidd 95%), medeltalet var 91 flockar (totalantalet flockar 2.939). Uppskattningen av den reella förekomsten är högre än den konstaterade förekomsten (64 flockar), eftersom man med hjälp av modellen även uppskattar antalet icke konstaterade smittofall. Enligt prognosen skulle antalet rapporterade fall av salmonella som överförs från broilerkött till människor ha uppgått till 39-82 (variationsvidd 95 %). 1999 rapporterades sammanlagt 566 inhemska fall av salmonellasmitta till folkhälsoinstitutets smittoregister.

Den viktigaste riskhanteringsåtgärden inom primärproduktionen är att avlägsna moderflockar som konstaterats ha salmonella från produktionen. Utan denna åtgärd varierar den reella förekomsten av salmonella hos broilerflockar som sänds till slakt enligt uppskattning mellan 1.3 och 17.4 % med ett medeltal på 145 flockar (jfr 91 flockar i en normal situation). Härvid ökar antalet rapporterade fall av till människor överförd salmonellasmitta i samma proportion, dvs cirka 1.6-faldigt. Den här riskhanteringsåtgärden har sålunda redan i nuvarande situation med låg förekomst av salmonella en klart skyddande effekt med hänsyn till konsumentens hälsa. I samband med undersökningen utvärderades också effekten av den andra centrala riskhanteringsåtgärden som ingår i det nationella programmet för salmonellakontroll, den obligatoriska upphettningen av kött från flockar som konstaterats vara salmonellapositiva. Om denna upphettning inte utförs bedöms antalet rapporterade fall av smitta som överförs från broilerkött till människor öka cirka 4.1-faldigt. Det effektivaste konsumentskyddet uppnås då vardera dessa riskhanteringsåtgärder tillämpas. Enligt prognosen ökar fallen av överföring av salmonella till människor cirka 5.6-faldigt utan dessa åtgärder.

Eftersom salmonellasituationen i Finland internationellt sett är relativt god gjordes det med hjälp av modellen också bedömningar av situationer där förekomsten av salmonella

i broilerproduktionen klart ökar (t.ex. som en följd av en foderepidemi). Vid simulering av en situation där en morförälderflock har blivit smittad i början av värpningen uppgår förekomsten av salmonella i broilerflockar som skall sändas till slakt till 1.2-5.9 % (konfidensintervall 95%) då programmet för salmonellakontroll tillämpas. Det här innebär i genomsnitt 95 salmonellapositiva flockar per år (standardspridning 36), dvs ökningen från en normalsituation vore relativt obetydlig. Om moderflockarna däremot inte undersöks och de som konstaterats vara positiva avlägsnas blir enligt prognosen 2.8-43.1 % (konfidensintervall 95 %) av broilerflockarna salmonellainfekterade (i genomsnitt 575 flockar, standardspridning 364). Det här leder till ett cirka 4.7-faldigt större antal fall av smittade människor. Om däremot moderflockar som konstaterats vara bärare av salmonella avlägsnas, men köttet från broilerflockar som är positiva inte upphettas, så bedöms antalet fall av till människor överförd smitta öka cirka 3.4-faldigt. I en fiktiv situation där ingendera av dessa riskhanteringsåtgärder vidtas för en moderflock bedöms antalet rapporterade fall av överföring av salmonellasmitta till människor öka cirka 17.8-faldigt från nuvarande antal.

Med hjälp av modellen simulerades också en situation där fem föräldraflockar salmonellasmittas i början av värpningen och de nämnda åtgärderna inte vidtas. Härvid ökar antalet rapporterade fall av till människor överförd salmonellasmitta cirka 7.7-faldigt i jämförelse med nuvarande situation med ett fungerande kontrollprogram. För närvarande förekommer det salmonella i under 1 % av det broilerkött som saluförs. Vid simulering av en situation i vilken förekomsten av salmonella uppgår till 20-40 % i hälften av allt broilerkött som saluförs i vårt land visar prognosen för antalet salmonellafall hos människor en upp till cirka 58-faldig ökning jämfört med nuläget.

Med hjälp av modellen kan följande slutsatser dras:

1. De obligatoriska åtgärder som kan användas inom ramen för det nationella programmet för salmonellakontroll minskar avsevärt antalet inhemska fall av salmonella hos människor.
2. Effekten av kontrollprogrammets riskhanteringsåtgärder är klart större om förekomsten av salmonella i produktionskedjan är större än för närvarande.
3. En kombination av olika riskhanteringsåtgärder är ett effektivare medel vid förebyggandet av salmonella än en enskild intervention.
4. En högre salmonella-infektions nivå i början av produktions kedjan förorsakar en klart högre risk för folkhälsan jämfört med en lägre.
5. Kvantitativ mikrobiologisk riskbedömning kräver mycket fakta, tid och resurser. Som bäst kan den dock bidra med nya perspektiv på teman som skall undersökas och peka på luckor i datainsamlingen.

Sökord:	*Salmonella*, broiler, kontroll, Finsk Salmonella kontroll program för broiler
Publikations-seriens namn och nummer	Offentlig handling 04/2003 ISSN 1458-6878
Antal sidor	100
Språk	Engelska, beskrivning svenska, finska och engelska
Publikationen säljs	Forskningsanstalten för veterinärmedicin och livsmedel, EELA, Finland Tel. +358 9 393 101 • Fax. +358 9 393 1811 • tiedotus@eela.fi • www.eela.fi

Description

Publisher National Veterinary and Foor Research Institute, EELA, Finland

Authors Riitta Maijala & Jukka Ranta

Title Salmonella in Broiler Production in Finland – a Quantitative Risk Assessment

Abstract

The goal of this risk assessment was to characterize the risk to consumers from salmonella in broiler production as well as to assess the impact of the interventions used in the Finnish Salmonella Control Program on these risks. The assessment covers the entire broiler production chain, from primary production to consumption. We focused on 1999, when the prevalence of salmonella in broilers sent to slaughter was the highest it had been since the control program was initiated (so-called “worst case scenario”). According to the model, in 1999 the true prevalence of salmonella in broiler flocks sent to slaughter was 0.9-5.8% (95% interval), with a mean of 91 flocks (from a total of 2,939 flocks). This estimate of true prevalence is higher than the reported prevalence (64 flocks), because the model also predicts the number of undetected infections. According to the model, the number of predicted human infections caused by broiler meat would be 39-82 (95% interval). In 1999, 566 domestic infections were reported to the contagious disease register of the National Institute of Public Health.

In primary production, the most significant intervention is to remove from production the breeder flocks which has been positive in salmonella testing. Without this intervention, the true prevalence of salmonella in broiler flocks sent to slaughter would range from 1.3-17.4%, with a mean of 145 flocks (compared to 91 flocks in the normal situation). In this case, the number of reported human infections would increase by the same proportion, about 1.6-fold. This intervention clearly protects public health even in the current situation, where the incidence of salmonella is low. We also estimated the effect of another significant intervention used in the FSCP, compulsory heat-treatment of the meat of salmonella-positive broiler flocks. If heat-treatment were not used, the reported number of human infections caused by broiler meat would increase about 4.1-fold according to this model. The most effective protection is achieved when both interventions are used. Without these, the predicted number of human salmonella cases would increase about 5.6-fold.

Because the salmonella situation in Finland is quite good by international standards, we also used the model to analyze situations where the prevalence of salmonella in broiler production would significantly increase (for example, due to an outbreak caused by contaminated feed). A simulation of a situation where one grandparent flock would have been infected at the beginning of the laying period showed the prevalence of salmonella in the broiler flocks sent to slaughter assuming normal interventions would

be 1.2-5.9% (95% interval). This would mean an average of 95 salmonella-positive flocks per year (sd 36), or in other words only a small increase from the present situation. If breeder flocks were not tested and infected birds were not removed, 2.8-43.1% of broiler flocks (95% interval) would have gotten infected with salmonella (an average of 575 flocks, sd 364). This would lead to about 4.7-fold increase in the number of human cases. If, by contrast, breeder flocks which have been confirmed as salmonella carriers were removed, but positive broiler flock meat was not heat-treated, the number of human infections would increase about 3.4-fold. If neither intervention were used in this fictional scenario where one breeder flock were infected, the reported number of human salmonella infections would increase by about 17.8-fold from the current situation.

With the aid of the model, we also simulated a situation where five parent flocks would be infected at the start of the laying period, and neither of these interventions were in use. In this situation, the reported number of human infections would increase by about 7.7-fold over the current situation under the FSCP. At present, salmonella is present in less than 1% of broiler meat available at retail. In a simulated situation where half of all retail broiler meat would have a salmonella prevalence of 20-40%, the number of reported human infections was predicted to increase by 58-fold compared to the present situation.

Based on the model, however, we can draw the following conclusions:

1. Compulsory interventions used in the FSCP significantly reduce the number of domestic salmonella infections in humans.
2. The effects of the FSCP would be even greater if the prevalence of salmonella in the food production chain were greater than it is today.
3. A combination of different interventions is more effective in preventing salmonella infection than single interventions
4. Higher salmonella infection level early in the production chain clearly causes a greater risk to public health compared to the lower infection level.
5. A quantitative microbiological risk assessment requires large amounts of data, time and resources. At best, however, it can provide a fresh perspective on the topic and reveal important gaps in data.

Key words	*Salmonella*, broiler, control, Finnish Salmonella Control Program
Name and number of Publication	EELA Publication 04/2003 ISSN 1458-6878
Pages	100
Language	English, abstract in English, Swedish and Finnish
Confidentiality	Public
Price	–
Publisher	National Veterinary and Foor Research Institute, EELA, Tel. +358 9 3931 820, Fax. +358 9 3931 740, tiedotus@eela.fi, www.eela.fi

Table of contents

1. Some abbreviations and acronyms

Primary Production Inference Model (PPIM)
The model is for simulating salmonella prevalence in production chain from grandparent flocks to the broiler flocks sent for slaughter. It uses Bayesian probabilistic inference (MCMC sampling / WinBUGS and Matlab).

Secondary Production Simulation Model (SPSM)
The model is for simulating salmonella contamination in production chain from slaughtering and processing to the total number of contaminated servings. It uses Monte Carlo (forward) sampling / @RISK and covers also imported meat.

Consumption Inference Model (CIM)
The model is for joint estimation of the average CFU/g per contaminated servings produced, and the true number of human cases of illness, accounting for under reporting. It uses Bayesian probabilistic inference (MCMC sampling / WinBUGS).

Finnish Salmonella Control Programme (FSCP)
The national salmonella control programme, which was approved by Commission Decision 94/968/EC on December 1994 and started in May 1995. Covering beef, pork and poultry production, it is intended to keep the annual incidence of salmonella below 1%.

MMM
The Ministry of Agriculture and Forestry

MMMELO
The Ministry of Agriculture and Forestry, Food and Health Department (formerly the Veterinary and Food Department, MMMEEO)

EELA
National Veterinary and Food Research Institute

Monte Carlo simulation (MC)
Monte Carlo simulation method of generating random numbers from a defined distribution (i.e. from a model).

Markov chain Monte Carlo Simulation (MCMC)
Monte Carlo simulation based on Markov chain sampling techniques.

Prior distribution
Conditional distribution describing initial uncertainty about an unknown quantity before observing data. ($f(x \mid prior)$).

Posterior distribution
Conditional distribution describing remaining uncertainty about an unknown quantity after observing data. ($f(x \mid data, prior)$).

Marginal distribution
Distribution of one or a few random variables derived from a joint distribution containing a larger number of random variables. ($f(x) = \int f(x, y)dy$).

Bayesian inference, probabilistic inference
Method of inferring probable values of unknown quantities using observed data, i.e. updating prior distributions into posterior distributions.

2. Yhteenveto ja johtopäätökset

2.1. Johdanto

Salmonella on edelleen eräs merkittävimmistä zoonooseista Suomessa ja muualla Euroopassa. Eläintuotannon salmonellatilanne on meillä ollut vuosikymmeniä hyvällä tasolla verrattuna moniin muihin maihin. Siksi Suomelle myönnettiin oikeus Kansallisen salmonellavalvontaohjelman käynnistämiseen sekä sen pohjalta salmonellaa koskevat lisävakuudet Suomen liittyessä Euroopan Unioniin vuonna 1995. Kansallinen salmonellavalvontaohjelma vaatii sekä viranomaisten että elinkeinon harjoittajien aktiivisuutta ja sitoo resursseja. Vuosittain valvontaohjelmassa tutkitaan tuhansia näytteitä, joiden lisäksi omavalvonnan puitteissa tutkitaan kymmeniä tuhansia näytteitä (Seuna 2000). Tämän kaiken työn tarkoituksena on suojella kuluttajaa ja taata, että salmonellan esiintyvyys lihassa ja kananmunissa on alle yksi prosentti kansallisella tasolla.

Kuinka suuri merkitys kuluttajan turvallisuudelle Kansallisella salmonellavalvontaohjelmalla sitten on? Viime vuosien aikana tieteellinen riskinarviointi on noussut erääksi välineeksi arvioitaessa erilaisten riskien suuruutta ja riskinhallintatoimenpiteiden vaikutusta. Riskinarvioinnin avulla voidaan koota tietoja yhteen, arvioida niitä tieteellisesti ja antaa joko kuvaileva tai laskennallinen arvio siitä, kuinka todennäköistä sairastuminen on ja kuinka vakavia seuraukset ovat. Mallien avulla voidaan myös simuloida erilaisia tilanteita sekä riskinhallintavaihtoehtojen vaikutuksia tartunnan leviämisessä.

EELAssa on käynnistetty maa- ja metsätalousministeriön pyynnöstä broilereiden, sikojen ja nautojen salmonellatartuntojen riskinarviointityö. Ensimmäisenä näistä on nyt valmistunut broilertuotannon riskinarviointi.

Työn tavoitteena on

1. kuvata minkälainen riski salmonellasta aiheutuu broilertuotannolle ja kuluttajille.
2. arvioida miten valvontaohjelmassa käytettävät interventiot vaikuttavat tähän riskiin.
3. tunnistaa tiedonkeruun ongelmia ja lisätutkimustarpeita.
4. luoda mikrobiologisen riskinarvioinnin käytäntöä Suomessa.

2.2. Kansallinen salmonellavalvontaohjelma

Hyvän salmonellatilanteen vuoksi Suomen liittyessä Euroopan yhteisöön se sai luvan muita tarkempaan maahantuotavan lihan ja kananmunien salmonellavalvontaan. Ehtona oli, että Suomessa järjestetään vähintään saman tasoinen seuranta- ja

valvontaohjelma kotimaiselle tuotannolle. Tätä tarkoitusta varten Suomeen luotiin Kansallinen salmonellavalvontaohjelma. Sen tavoitteena on turvata hyvä salmonellatilanne naudan, sian ja siipikarjan lihan sekä kananmunien tuotannossa ja siten suojella kansanterveyttä. Ohjelman tavoitteena on pitää salmonellan vuotuinen esiintyvyys tuotantoeläimissä ja niistä saatavissa lihassa ja munissa enintään 1 % tasolla. Teurastamoiden ja lihanleikkaamoiden laitoskohtainen tavoite on alle 5 %. Tavoite on toteutunut vuosina 1996-2002 hyvin.

Broilertuotannon osalta Kansallisen valvontaohjelman näytteenottoon kuuluvat isovanhempaisparvet, vanhempaisparvet, hautomot, broilerparvet sekä leikkaamot. Salmonellan löytyminen johtaa aina riskinhallintatoimiin, joiden tavoitteena on katkaista bakteerin leviäminen edelleen tuotantoketjussa. Kansallinen valvontaohjelma on laajempi, kuin mitä nk. EU:n zoonoosidirektiivi (neuvoston direktiivi 92/117/EY) edellyttää. Vastaava salmonellavalvontaohjelma on myös Ruotsissa ja Norjassa ja useat muut EU:n jäsenmaat ovat myös aloittaneet omat valvontaohjelmansa salmonellaesiintyvyyden vähentämiseksi broilertuotannossa.

2.3. Riskinarviointimalli

Tämä riskinarviointimalli on yksinkertaistettu kuvaus siitä, miten salmonellatartunta voi kulkea broilertuotantoketjussa ja päätyä kuluttajalle asti. Riskinarviointimallissa on hyödynnetty vuosien 1996-1999 salmonellavalvontaohjelman tietoja, joita on täydennetty broilerteollisuudelle suunnatulla kyselyllä, salmonella-asiantuntijoiden arvioilla ja sekä kirjallisuudesta ja suomalaisista tilastoista kerätyillä tiedoilla. Mallissa ei ole tehty eroja eri salmonellaserotyyppien välillä, sillä kansallinen salmonellavalvontaohjelmakin käsittelee niitä broilertuotannossa samalla tavalla.

Stokastista riskinarviointia on tehty sekä inferenssiin perustuvien alkutuotantomallin ja lopullisen kulutusmallin että tuotantoketjua kuvaavan simulaatiomallin avulla. Simulaatiomallissa on käytetty hyväksi Monte Carlo menetelmiä, kun taas inferenssiä varten on tarvittu nk. Markovin ketju Monte Carlo -menetelmiä. Inferenssillä tarkoitetaan päättelytehtävää, jossa osa mallin muuttujista on havaittu ja niiden perusteella päätellään todennäköisimmät arvot suoraan havaitsemattomille muuttujille ja parametreille. Inferenssiongelman laskenta on toteutettu WinBUGS ohjelmalla.

Simulaatiomalli on toteutettu @Risk-ohjelman avulla ja se sisältää tuotantoketjun teurastamon ja prosessoinnin osalta. Simuloinnissa seuraavan tuotantovaiheen laskenta perustuu aina edeltävän tuotantovaiheen simuloituun tulokseen ja siten mallin kyky oppia tuotantoprosessin keskeltä saaduista todellisista havainnoista ”taaksepäin” on rajoittunut. Tästä syystä simulointimallia käytettiin teurastamo- ja prosessointivaiheen simulointiin, koska näistä vaiheista ei ole kovin täsmällistä aineistoa josta olisi mahdollista päätellä prosessin havaitsemattomia välitiloja. Simulaatiomallissa on käytetty hyväksi myös inferenssimallista saatuja jakaumia mm. infektoituneiden broilerparvien lukumäärälle (havaitut + havaitsemattomat).

Mallin perusrakenteita ovat säädelleet käytettävissä olevan tiedon lisäksi myös ne riskinhallintatoimenpiteet, joiden vaikutusta mallilla halutaan simuloida. Broilereiden salmonellavalvontaohjelmasta tällaisia interventioita on malliin otettu kaksi: salmonellapositiivisten siitosparvien poistaminen tuotannosta löydöksen jälkeen ja salmonellapositiivisiksi todettujen parvien lihan kuumentaminen.

Valvontaohjelmassa on toki muitakin interventioita, mm. pesu ja desinfektio salmonellapositiivisen löydöksen jälkeen, teuraserän sijoittaminen päivän viimeiseksi ja epidemiologinen selvitys tartuntalähteen löytämiseksi. Näiden interventioiden vaikutuksen kvantitatiivinen arvioiminen on kuitenkin varsin vaikeaa ja ne on siksi

jätetty pois tästä työstä. Siksi myös mallin avulla saadut estimaatit interventioiden vaikutuksesta ovat konservatiivisia. Todennäköisesti valvontaohjelmalla on suurempi vaikutus kuin mitä tässä laskentamallissa saadut tulokset näyttävät.

Interventioiden vaikutuksia on simuloitu nykytilanteessa, jota edustamaan valittiin vuoden 1999 tilanne (skenaario A). Syynä tähän oli se, että vuonna 1999 salmonellaa todettiin eniten broilerteurasparvissa sitten ohjelman käynnistämisen jälkeen ja se edustaa siten nk. ”worst case” -tilannetta. Se oli myös ensimmäinen vuosi, josta saatiin kyselyjen ja tilastojen avulla mallinnuksessa tarvittavia tietoja riittävän kattavasti.

Lisäksi interventioita on tutkittu kolmessa eri skenaariossa. Skenaario B:ssä yksi isovanhempaisparvi ja skenaariossa C viisi vanhempaisparvea saa salmonellatartunnan muninnan alussa. Näiden lisäksi on selvitetty skenaariossa D tilannetta, jossa salmonellan esiintyvyys olisi 20-40% puolessa Suomessa myytävästä broilerinlihasta. Mallissa ei oteta kantaa siihen, johtuisiko tämä tilanne kotimaisen salmonellatilanteen heikkenemisestä vai enemmän salmonellaa sisältävän broilerinlihan maahantuonnista.

Riskinarviointi on tehty Codex alimentariuksen periaatteiden mukaisesti (Codex Alimentarius Comission 2000) ja se jakautuu neljään eri riskinarvioinnin osaan: vaaran tunnistaminen, vaaran kuvaaminen, altistuksen arviointi ja riskin kuvaaminen.

2.3.1. Vaaran tunnistaminen

Jotta riskinarviointi voidaan aloittaa, on tunnistettava vaara (tässä salmonella) yleisellä tasolla. Salmonellan esiintyvyys eläintuotannossa Suomessa on varsin matalalla tasolla moniin Keski-Euroopan maihin verrattuna. Salmonellan esiintymistä broilereissa on seurattu jo ennen Kansallisen valvontaohjelman käynnistymistä. Näyttää siltä, että valvontaohjelmalla on selvästi ollut esiintyvyyttä vähentävä vaikutus: vuosina 1989-1994 salmonellaa todettiin yhtä vuotta lukuunottamatta yli 1% parvissa. Vuoden 1995 käynnistymisponnistelujen jälkeen vain vuonna 1999 on 1%:n taso ylitetty. Yleisin broilerparvista raportoitu serotyyppi on ollut *Salmonella* Infantis.

Suomessa raportoidaan ihmisillä vuosittain noin kolme tuhatta salmonellatapausta, joista suurin osa on ulkomaista alkuperää. Yleisin kotimainen serotyyppi on ollut *Salmonella* Typhimurium. Sen sijaan *Salmonella* Enteritidis on ollut yleisin tyyppi ulkomaisissa tartunnoissa (National Public Health Institute 2002).

Vuosina 1995-2001ei raportoitu yhtään ruokamyrkytysepidemiaa jossa broilerinliha olisi ollut salmonellan aiheuttaja (MMMEEO 2000, Hatakka et al. 2001; Hatakka et al. 2002). Broilerin lihasta peräisin olevien yksittäisten tai raportoimattomien epidemioiden salmonellatartuntojen määrää ei ole arvioitu Suomessa. Tanskassa arvioitiin kotimaisen broilerin aiheuttaneen 2-4% ja maahantuodun siipikarjan lihan 10-14% raportoiduista salmonellatapauksista ihmisillä vuonna 2000. Tuotantorakenteiden erilaisuuden, eri salmonellatasojen yms. syiden vuoksi tanskalaisten arviota ei kuitenkaan voida suoraan soveltaa Suomeen.

2.3.2. Vaaran kuvaaminen

Salmonellabakteeri voi kasvaa 5-46°C:ssa, vaikkakin sen optimikasvulämpötila on 35-37°C. Kasvun minimi vesiaktiivisuustaso on 0.95, mutta solut voivat säilyä kuivassa materiaalissa hengissä pitkään. 9% suolapitoisuus ja pH alle 4.0 tai yli 9.5 estävät salmonellan kasvun. (Jay 2000; Ray 2001).

Salmonellainfektio aiheuttaa harvoin broilereilla oireita. Myös ihmisten salmonellatartunta voi olla oireeton. Ihmisillä salmonella voi kuitenkin melko usein aiheuttaa ruuansulatuskanavan oireita (ripulia, vatsakipua, kuumetta, päänsärkyä ja oksennusta). Ensimmäiset oireet ilmaantuvat yleensä 12-24 tunnin kuluttua tartunnan

saamisesta ja kestävät 3-4 päivää. Näiden perinteisten ruokamyrkytysoireiden lisäksi on erityisesti viime aikoina kiinnitetty huomiota myös salmonellan aiheuttamiin jälkitauteihin (erityisesti nivel- ja silmätulehdukset sekä lisääntynyt pitkän aikavälin kuolleisuus) sekä antimikrobilääkkeille vastustuskykyisten kantojen lisääntymiseen. Reaktiivista niveltulehdusta todetaan 1-15%:lla akuutin salmonelloosin sairastaneista henkilöistä. Niveloireet alkavat yleensä 7-15 päivän kuluttua ruuansulatuskanavan oireiden alkamisesta. Useimmat potilaat paranevat 3-5:ssä kuukaudessa. 16 %:lla näistä tapauksista oireet muuttuvat kuitenkin kroonisiksi (Leirisalo-Repo et al. 1997; Ekman 2000).

Eräs keskeisiä ongelma-alueita mikrobiologisten riskien arvioinnissa on annos-vasteen arviointi, niin myös salmonellan osalta. Useimmat annos-vastekokeet on tehty joko eläimillä tai terveillä nuorilla aikuisilla, joten tuloksia ei suoraan voi verrata normaaliväestön puhumattakaan riskiryhmien annos-vasteiden arvioimiseksi. Yleisesti oletetaan, että vasta annokset 10^7- 10^9 salmonellasolua aiheuttavat sairastumisen. Eräissä ruokamyrkytyksissä on kuitenkin raportoitu sairastumisia jopa annoksilla, jotka ovat alle 10^3 solua. Tässä riskinarviointimallissa on käytetty normaaliväestölle sovitettua beta-Poisson annos-vastemallia (WHO/FAO 2002). Siinä käytettävä arvio tarjoiluhetken salmonellasolupitoisuudesta on saatu laskemalla kulutusta kuvaavassa inferenssimallissa nykytilanteen havaintoaineistoon (1999) perustuva posteriorijakauma.

2.3.3. Altistuksen arviointi

Altistuksen arvioinnissa salmonellan tartuntareittiä on mallinnettu alkutuotannosta kuluttajalle tarjottaviin annoksiin asti. Altistuksen arvioinnista saatu tieto yhdistetään lopulta riskin kuvaamisessa annos-vaste yms. tietojen kanssa riskiestimaatin arvioimiseksi.

Ensimmäisessä mallin osassa (Primary Production Inference Model eli PPIM) on luotu ”probabilistinen salmonellan transmissiomalli” alkutuotannossa. Koska käytettävissä olevasta aineistosta ei käynyt ilmi, mihin emoparviin hautomoista löytyneet salmonellaeristykset liittyvät, perusaineiston muodostivat lintuparvista saadut vuosittaiset tilastot. Broilerparvet voivat saada salmonellatartunnan joko vanhempaisparvista muninnan tai haudonnan kautta (nk. vertikaalinen tartuntareitti) tai parven saavuttua tuotantotilalle esimerkiksi rehun, ihmisten tai haittaeläinten välityksellä (nk. horisontaalinen tartuntareitti). Rehuperäinen altistus sisältyy horisontaalisen tartunnan malliparametriin, sillä parvikohtaisia rehutietoja tai raportteja rehujen aiheuttamista salmonellaepidemioista broilertuotannossa ei ollut käytettävissä. Lisäksi käytettiin hyväksi elinkeinolta saatuja tietoja kanaloiden määrästä. Mallissa otettiin huomioon myös se, että kasvattamoissa ja kanaloissa voi vuoden aikana olla useampikin parvi peräkkäin. Asiantuntijoiden arvioita käytettiin hyväksi menetelmän herkkyyden, horisontaalitartunnan todennäköisyyden, hautomon aiheuttaman ristikontaminaatiovaikutuksen sekä infektion säilyvyystodennäköisyyksien nk. priorijakaumien arvioinnissa. Inferenssimallin avulla näistä ja käytettävissä olevista tiedoista muodostettiin nk. posteriorijakaumia kuvaamaan mallin mukaista tietämystä todellisesta tilanteesta.

Altistuksen arviointi jatkuu toisessa mallin osassa (Secondary Production Simulation Model eli SPSM), jossa voidaan simuloida yleisellä tasolla salmonellatartunnan kulkua läpi teurastamo-, leikkaamo- ja jalostusvaiheiden. Mallissa on huomioitu kansallisen salmonellavalvontaohjelman tietojen lisäksi elinkeinolta saatuja tietoja mm. teurasparvien koosta sekä broilerien teuraspainosta, tuontilihan ja lihatuotteiden määrästä, Kansanterveyslaitoksen Finravinto 97 (National Public Health Institute 1998) tutkimuksen perusteella arvioidusta keskimääräisestä annoskoosta sekä ensi-

saapumispaikkojen tilastoista. Asiantuntijoiden arvioiden perusteella on lisäksi saatu syöttötiedot parven sisäiselle salmonellan esiintyvyydelle, kuumennuskäsittelyn vaikutukselle, teurastus- ja leikkaamovaiheen ristikontaminaation todennäköisyydelle, kuumennetun ja raa'an lihan väliselle ristikontaminaatiolle sekä sille, kuinka paljon salmonellaa on positiiviseksi todetussa tuontierässä.

Vaikka riskinarviointimalli pyrkii kuvaamaan vain yleisellä tasolla salmonellatartuntaa, siinä on silti monia sellaisia kohtia, joiden osalta arvioinnin kuluessa on turvauduttu asiantuntijoiden arvioihin. Asiantuntijoiden käyttäminen puuttuvien tietojen lähteenä on yleistä mikrobiologisessa riskinarvioinnissa. On mahdollista, että asiantuntijoiden arviot osuvat harhaan, mutta toisaalta nykytekniikan antama mahdollisuus käyttää todennäköisyysjakaumia keskimääräisen arvion sijasta helpottaa jonkin verran tätä kysymystä – vaikkakin menetelmät tuovat mukanaan uudenlaisia haasteita.

Inferenssi- ja simulointimallin tuloksia voidaan verrata alkutuotannon osalta tarkastelemalla salmonellapositiivisten broilerkasvatuserien todennäköisyysjakaumaa esim. vuodelta 1999. Mallia voidaan myös validoida vertaamalla saatua todennäköisyysjakaumaa salmonellan esiintyvyydelle lihassa ja mikrobiologisten tutkimusten antamia tuloksia. Tulokset sopivat melko hyvin yhteen, joten voidaan olettaa, että malli kuvastaa kohtuullisen hyvin tilannetta tuotantoketjun tähän vaiheeseen asti. Ennusteen 90% todennäköisyysväli salmonellaprevalenssille kotimaisessa broilerinlihassa vuoden 1999 tilanteen perusteella oli [0,07 %-0,43 %], keskiarvo 0.21 % ja moodi 0.17 %.

2.3.4. Riskin kuvaaminen

Syöntitilanteen salmonellasolujen määrä riippuu salmonellan esiintymistiheydestä, salmonellasolujen määrästä lihassa, kypsennysasteesta sekä ristikontaminaation mahdollisuudesta keittiössä. Siksi sen arvioiminen on vaikeaa. Kolmannessa riskinarviointimallin osassa (Consumption Inference Model eli CIM) hyödynnettiin siksi inferenssimallia, joka perustuu arvioituun broilerperäiseen tapausmäärään havaintovuoden tilastoitujen ihmistapausten perusteella (MMM 2000). Tästä, sekä SPSM-mallissa simuloidusta annosten määrästä laskettiin annetulla annosvastemallilla posteriorijakauma pesäkettä muodostavien yksikköjen (PMY/g) yleistasolle per gramma (Colony Forming Units, CFU/g), huomioimalla samalla myös tapausten aliraportointi. Saatu jakauma keskimääräisestä pesäkettä muodostavien yksikköjen määrästä oli lähtökohtana simuloitaessa ennustejakaumia ihmistapausten määrästä nykytilanteessa ja skenaarioissa. Näin annosvastemalli kalibroitiin havaintovuoden tietojen perusteella, eikä syöntihetken solumäärälle tarvinnut antaa suoraa epävarmuusjakaumaa, joka johtaisi suuren epävarmuutensa vuoksi helposti ylileveään tapausennusteeseen.

Yhdistämällä näin kaikki kolme mallin osaa (PPIM, SPSM ja CIM) saadaan todennäköisyysjakauma sille, kuinka monta suomalaista vuosittain sairastuu broilerin lihasta peräisin olevasta salmonellatartunnasta (Kuva 1). Koska mallin tavoitteena on tutkia kansallisen salmonellavalvontaohjelman vaikutusta kuluttajien riskiin ja vertailtavien skenaarioiden sijoituspaikka on siten alkutuotanto tai teurastamo, ei mallin tarkentamista tuotantoketjun loppuosan kohdalta ole katsottu mainitun tavoitteen kannalta erityisen tarpeelliseksi. On kuitenkin huomattava, että tarkasteltaessa mallin tuottamia arvioita kuluttajan riskistä sairastua broilerinlihan salmonellatartunnasta, niitä on pidettävä vain suuntaa-antavina. Ennusteen 95 % todennäköisyysväli broilerinlihan aiheuttamien tilastoitujen kotimaisten sairastapausten määrälle Suomessa vuoden 1999 aineiston perusteella oli [39,82], keskiarvo 59 ja moodi 58.

2.4. Riskinhallintatoimien vaikutus

2.4.1. Vaikutus broilerparvien tartuntatasoon

Luodun salmonella/broilermallin avulla tutkittiin seuraavaksi Kansallisessa salmonellavalvontaohjelmassa olevien riskinhallintatoimien eli interventioiden vaikutusta tartuntaketjun katkaisemisessa. Alkutuotannossa tutkittava interventio oli salmonellapositiiviseksi todetun emoparven poistaminen tuotannosta. Mallissa simuloitiin nk. nykytilannetta vuoden 1999 tasolla (skenaario A) sekä kuvitteellista tilannetta B, jossa yksi isovanhempaisparvi on saanut tartunnan sen munintakauden alussa. Nykyisessä tilanteessa teuraaksi lähetettävien broilerparvien todellisen salmonellaesiintyvyyden vaihteluväli (95%) on mallin mukaan 0.9-5.8% keskiarvon ollessa 91 parvea 2939:stä parvesta. Tämä arvio on luonnollisesti korkeampi kuin on todettu salmonellan esiintyvyys broilerparvissa. Vuonna 1999 raportoitiin 64:ssä teurasparvessa salmonellatartunta (2.2%), mikä oli korkein esiintyvyys, jota käynnistymisvuoden 1995 jälkeen on todettu. Ilman positiiviseksi todetun emoparven poistoa broilerparvien salmonellaesiintyyvys vaihtelisi arvion mukaan välillä 1.3-17.4% keskiarvon ollessa 145 parvea. Simuloitaessa tilannetta, jossa yksi isovanhempaisparvi olisi saanut tartunnan muninnan alussa (skenaario B), broilerparvien salmonellaprevalenssin vaihteluväli positiivisia parvia poistettaessa olisi 1.2-5.9% ja ilman poistoa 2.8-43.1%.

Näin mallin avulla voidaan todeta se, mikä jo kokemusperäisestikin on pitkään tiedetty: infektoituneiden siitosparvien poistaminen vähentää huomattavasti broilerparvien tartuntariskiä. Mallin avulla voidaan kuitenkin saada tälle vaikutukselle suuruusluokka, jonka perusteella voidaan tarkastella tämän toimenpiteen vaikutusta sekä ihmisten sairastumisriskiin että tarvittaessa myös sen taloudellisia seurauksia.

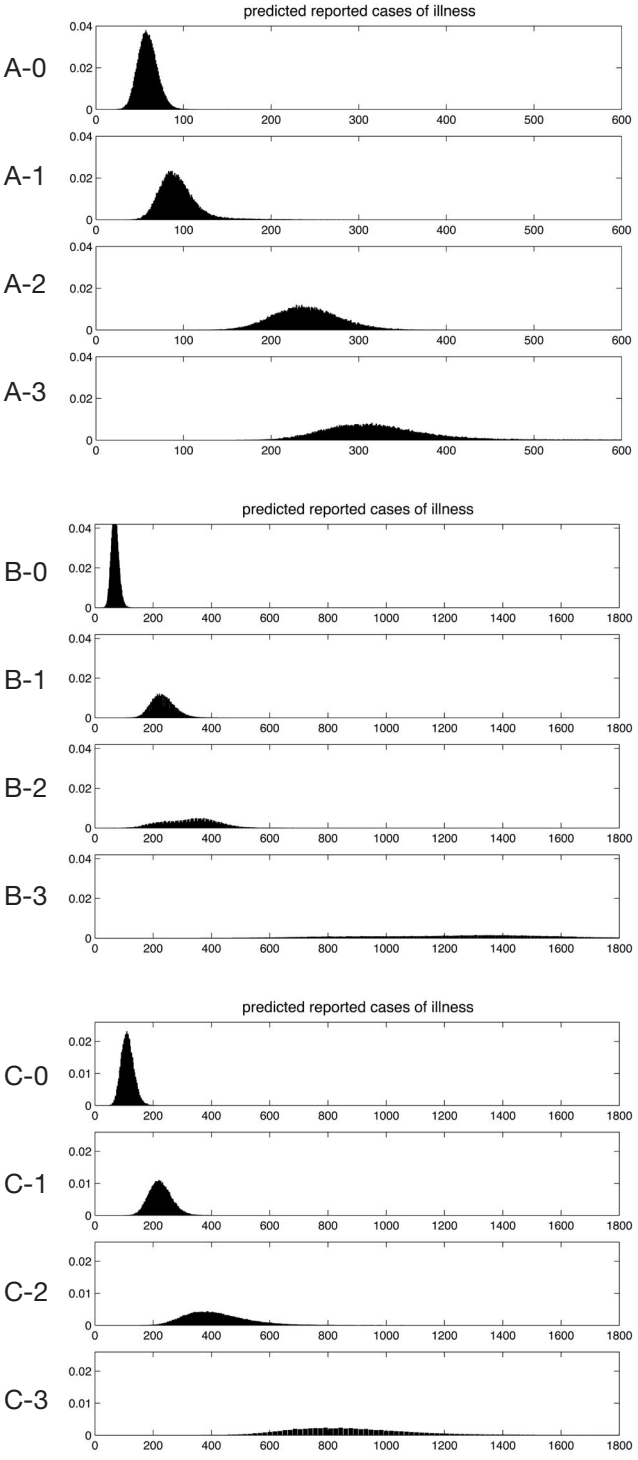
Valvontaohjelman tilastojen perusteella näyttää siltä, että broilereiden salmonellatilanne oli vuosina 1996-1998 parempi kuin vuonna 1999. Kun huomioon otetaan ulostenäytteiden mikrobiologisen analyysimenetelmän herkkyyden parantuminen vuonna 1999, vuosien välillä oleva ero pienenee ja näyttää siltä, että todellinen salmonellan esiintyvyys on pysynyt käytännössä lähes samalla tasolla vaihdellen vuosina 1996-1999 seuraavasti: 2.3%, 1.9%, 1.9% ja 2.9%. Menetelmän herkkyyden parantaminen on lisännyt kuluttajan turvallisuutta, koska näin on pystytty poistamaan enemmän salmonellapositiivisia broilerparvia elintarvikeketjusta.

2.4.2. Vaikutus ihmisten tartuntatapausten määrään

Mallin avulla simuloitiin myös riskinhallintatoimien vaikutusta ihmisten salmonellatapausten määriin. Nykytilanteen (skenaario A) lisäksi tutkittiin tuotantoketjun interventioita skenaarioissa B (isovanhempaisparvessa muninnan alkaessa tartunta) ja C (viidessä vanhempaisparvessa tartunta muninnan alkaessa). Tutkittavina oli sekä salmonellapositiiviseksi todetun emoparven poiston että salmonellapositiiviseksi todetun parven lihan kuumentamisen vaikutus ihmistapausten määrään. Skenaarioiden laskenta perustui mallissa annosmäärän skenaariojakauman ja annosmäärän perustilannetta kuvaavan posteriorijakauman yhdistämiseen (stochastic coupling), joka tehtiin Matlab-ohjelman avulla.

Interventioilla oli selvästi kuluttajan terveyttä suojaava vaikutus jo nykyisessä, matalassa salmonellan esiintyvyystasossa (skenaario A). Mikäli positiiviseksi todettua emoparvea ei poistettaisi tuotannosta, nousisi ihmisten raportoitujen salmonellatapausten odotettu määrä noin 1.6 kertaisesti (Kuva 1). Mikäli salmonellapositiiviseksi todettujen parvien lihaa ei kuumennettaisi, nousisi broilerin lihan aiheuttamien raportoitujen ihmistapausten odotettu määrä noin 4.1 kertaiseksi (A-2). Mikäli kumpaakaan näistä interventioista ei olisi käytössä, odotettujen tapausten määrä nousisi noin 5.6 kertaiseksi (A-3).

Arvioitaessa interventioiden vaikutusta korkeammassa salmonellatasossa niiden vaikutus lisääntyi. Mikäli yksi isovanhempaisparvi olisi infektoitunut muninnan alussa (skenaario B) eikä salmonellapositiivisia emoparvia poistettaisi eikä positiivisten parvien lihaa kuumennettaisi, odotettavissa oleva raportoitujen tapausten määrä ihmisillä kasvaisi noin 17.8 kertaisesti verrattuna tilanteeseen, jossa molemmat riskinhallintatoimet olisivat käytössä (B-3). Pelkkä kuumakäsittelyn käyttäminen johtaisi tässä skenaariossa noin 4.7 kertaiseen odotettuun tapausmäärään (B-2). Vastaavasti pelkkä positiivisten emoparvien poistaminen johtaisi noin 3.4 kertaiseen odotettuun tapausmäärään (B-1).



Kuva 1.
Ennustejakaumat tilastoitujen kotimaisten broilerin lihasta välittyneiden salmonellatapausten määrille nykytilanteessa perustuen vuoden 1999 tietoihin.

Skenaario A:
0. valvontaohjelma käytössä,
1. ilman todettujen positiivisten emoparvien poistamista,
2. ilman todettujen positiivisten broilerparvien kuumakäsittelyä,
3. ilman kumpaakaan interventiota.

Skenaario B:
0. valvontaohjelma käytössä,
1. ilman kuumakäsittelyä,
2. ilman positiivisten emoparvien poistamista,
3. ilman kumpaakaan interventiota.

Skenaario C:
0. valvontaohjelma käytössä,
1. ilman todettujen positiivisten emoparvien poistamista,
2. ilman kuumakäsittelyä,
3. ilman kumpaakaan interventiota.

Jos viisi vanhempaisparvea saisi tartunnan muninnan alussa (skenaario C) eikä em. interventioita käytettäisi, ihmistapausten odotettu määrä kasvaisi noin 7.7. kertaisesti verrattuna tilanteeseen jossa molemmat interventiot ovat käytössä (C-3). Pelkkä kuumakäsittely johtaisi tässä skenaariossa noin 2.0 kertaiseen odotettuun tapausmäärään (C-1), ja pelkkä positiivisten emoparvien poistaminen noin 3.7 kertaiseen (C-2).

Tuotantoketjussa käytettävissä olevien riskinhallintatoimien lisäksi mallilla simuloitiin skenaariossa D tilannetta, jossa salmonellan esiintyvyys olisi puolessa Suomessa kaupan olevasta broilerin lihasta 20-40%. Tällaisessa tilanteessa ihmistapausten odotettu määrä kasvaisi jopa noin 58 kertaiseksi.

2.5. Mallin keskeiset oletukset

Koska malli on yksinkertaistettu kuvaus todellisuudesta, tätä mallia rakennettaessa tehtiin useita oletuksia. Ne on esitetty kunkin luvun kohdalla tarkemmin.

Mallin keskeisemmät oletukset olivat:

1. Salmonellatartunnan kulkeutuminen broilereiden tuotantoketjussa tai taudinaiheuttamiskyky ei riipu sero- tai faagityypistä.
2. Koska mallin avulla simuloidut toimenpidevaihtoehdot kohdistuvat kotimaiseen tuotantoon, tuontilihaan vaikuttavia toimenpidemahdollisuuksia ei tarvinnut huomioida mallissa.
3. Tarjoiltavassa ruoka-annoksessa olevien salmonellasolujen määrä syöntihetkellä ei riipu siitä, kuinka monessa annoksessa salmonellaa esiintyy. Eli vaikka prevalenssi simulaatioissa nousisi, ei solumäärä syöntihetken annoksessa kasvaisi.
4. Broilerannoksien valmistus ja tarjoilu keittiössä voitiin jättää mallintamatta mallintamalla suoraan syöntihetken solumäärää annoksien ja ihmistapausten määrän perusteella.
5. Broilerin lihan aiheuttamien salmonellatartuntojen määrä ihmisissä voidaan karkeasti arvioida vertailemalla broilereista, broilerin lihasta ja ihmisistä eristettyjen salmonellakantojen sero- ja faagityyppejä.
6. Kaikki raportoidut ihmisten tapaukset ovat tautitapauksia. Saatu riskiestimaatti kohdistuu koko suomalaiseen väestöön, ei vain riskiryhmiin.

Valitettavasti kaikkiin mallin kannalta olennaisiin kysymyksiin ei tilasto- tai tutkimustietoa ollut saatavilla. Sen vuoksi mallissa jouduttiin käyttämään asiantuntija-arvioita. Inferenssimalleissa (Markovin ketju Monte Carlo menetelmä) keskeisimmät asiantuntija-arviot annettiin seuraaville parametreille: horisontaalisen tartunnan todennäköisyys broiler parvissa, todennäköisyys tartunnan jatkumisesta broilerparvessa kahden näytteenottokerran välillä ja hautomon ristikontaminaation vaikutus vertikaaliseen tartunnan todennäköisyyteen. Näiden lisäksi @Riskillä tehdyssä Monte Carlo-malliosuudessa käytettiin seuraavia asiantuntija-arvioita: parven sisäinen salmonellan esiintyvyys, teurastuksen aikaisen tartunnan leviämistodennäköisyys, ristikontaminaation suuruus ja salmonellan esiintyvyys maahantuodussa lihassa.

2.6. Johtopäätökset

Tämän matemaattisen riskinarviointimallin avulla voidaan broilertuotannon salmonellavalvontaohjelman vaikutusta arvioida niin eläinten kuin ihmistenkin tartuntatodennäköisyyksien osalta. Mallin vahvin alue on alkutuotanto, sillä kansallinen salmonellavalvontaohjelma antaa esiintymistietoja erityisesti tästä tuotantovaiheesta. Mitä lähemmäs kuluttajaa mallissa tullaan, sitä enemmän mallin osatekijät perustuvat asiantuntijoiden arviointeihin. Mallin avulla voidaan kuitenkin tutkia muutamien riskinhallintatoimien vaikutuksia riskiin ja siten arvioida sitä merkitystä, joka tällä valvontaohjelmalla on Suomessa.

Riskinarviointimallien käyttäminen päätöksenteon apuvälineenä on haaste niin arviointeja tekeville tahoille kuin niiden tulosten käyttäjillekin. Oleellista kuitenkin on, että tämän mallin tulosten perusteella voidaan arvioida, miten viranomaisten ja elinkeinon ponnistelut salmonellan kurissapitämiseksi vaikuttavat kuluttajan terveyteen ja näin saada tehdyn työn merkityksestä parempi kuva. Esiin kohonneitta tutkimustarpeita voidaan myös käyttää hyödyksi uusia tutkimussuunnitelmia laadittaessa. Mallin tulosten luotettavuutta ja tarkkuutta voitaisiin kehittää, mikäli elinkeinon laajat tutkimukset olisivat käytettävissä myös kansallisella tasolla tällaiseen työhön. Salmonellavalvonnan riskinarviointimallia voidaan käyttää hyväksi myös suunniteltaessa muita vastaavia seuranta- tai valvontaohjelmia broilertuotannossa.

Vaikka osa puuttuvista tiedoista voidaan kerätä kehittämällä kansallisen salmonellavalvontaohjelman tiedonkeruuta, arviointityön kuluessa todettiin myös keskeisiä tutkimustarpeita:

1. Salmonellatartunnan riskitekijöiden tunnistaminen ja niiden todennäköisyyksien arvioiminen broilertuotantoketjussa.
2. Eri tutkimusmatriisien vaikutus salmonellatestausmenetelmän herkkyyteen.
3. Teurastuksen ja leikkuun vaikutus salmonellatartunnan leviämiseen kun salmonellaesiintyvyys on matala.
4. Lämpötilan, ajan ja ristiinsaastumisen merkitys salmonellapitoisuuksille broilerruokien valmistuksen yhteydessä.

Malliin sisältyy epävarmuuksia ja olettamuksia, jotka tässä raportissa on esitelty. Sen avulla voidaan kuitenkin vetää seuraavia johtopäätöksiä:

1. Kansallisessa salmonellavalvontaohjelmassa käytössä olevat pakolliset toimenpiteet vähentävät merkittävästi kotimaisten salmonellatapausten määrää ihmisissä.
2. Valvontaohjelman riskinhallintatoimien vaikutus on selvästi suurempi, jos salmonellaa esiintyy enemmän tuotantoketjussa kuin nykyisin.
3. Yhdistelemällä eri riskinhallintatoimenpiteitä saadaan aikaan tehokkaampi vaikutus salmonellan torjunnassa kuin yksittäisellä toimenpiteellä.
4. Tuotantoketjun alkupäässä oleva korkea salmonellatartuntataso aiheuttaa suuremman riskin kuluttajalle verrattuna matalampaan tasoon.
5. Kvantitatiivinen mikrobiologinen riskinarvionti vaatii runsaasti tietoja, aikaa ja resursseja. Parhaimmillaan se voi kuitenkin antaa uuden näkökulman tutkittavaan aiheeseen ja osoittaa aukkoja tiedonkeruussa.

3. Summary and conclusions

3.1. Introduction

Salmonella is still one of the most significant zoonoses in Finland and elsewhere in Europe. Compared to many other countries, Finland has for many decades had excellent salmonella situation in animal production. The country was therefore granted the right to initiate its own Salmonella Control Program, and received additional guarantees regarding salmonella protection when it joined the European Union in 1995. The Finnish Salmonella Control Program (FSCP) demands the active participation of both government officials as well as producers of food products both in terms of time and resources. Every year, thousands of samples are analyzed under the FSCP, and another tens of thousands analyzed as part of industry surveillance programs (Seuna 2000). The purpose of all of this surveillance is to protect consumers and ensure that the level of salmonella in meat and eggs remains under 1% at the national level.

How significant for consumer safety is the national Salmonella Control Program? In the past few years, scientific risk assessments have become an important tool to estimate the magnitude of different risks and the effects of different interventions on controlling these risks. With the help of risk assessments, we can gather the necessary information together, assess this information scientifically and make either a qualitative or a quantitative assessment of the likelihood of illness, as well as of the severity of the consequences. With the help of these models, we can also simulate different situations as well as the effects of different risk management interventions designed to stop the spread of disease.

Based on the request by Ministry of Agriculture and Forestry, the National Veterinary and Food Research Institute has initiated risk assessments assessing the risk of salmonella infection from broilers, pigs and cattle. This one on broiler production is the first to be completed.

The objectives of this risk assessment are:

1. To describe the risks salmonella might cause to the broiler production and to consumers.
2. To estimate how the interventions used in the control program affect these risks.
3. To identify problems in collecting data and needs for further research.
4. To initiate the use of microbiological risk assessments in Finland.

3.2. The Finnish Salmonella Control Program (FSCP)

As a result of the low incidence of salmonella, when Finland joined the European Union it was given permission to place stricter salmonella controls on imported meat and eggs, with the provision that equal or stricter surveillance be applied to domestically-produced products. In order to carry out this salmonella control, the FSCP was initiated. Its aim is to maintain a low incidence of salmonella in beef, pork, poultry, as well as egg production, thus safeguarding public health. The aim is to keep the national prevalence of salmonella in production animals, and in the meat and eggs which come from these animals, under 1%, and the prevalence at individual abattoirs or cutting plants below 5%. These objectives were well met in 1996-2002.

In terms of broiler production, the FSCP collects samples from grandparent flocks, parent flocks, hatcheries, broiler flocks, and cutting plants. Detection of salmonella always leads to risk control measures, whose aim is to prevent the spread of bacteria in the food production chain. The FSCP is broader than what is required in the EU's zoonosis directive (Council Directive 92/117/EEC). There are similar salmonella control programs in both Sweden and Norway, and several EU member countries have also initiated their own programs to reduce the prevalence of salmonella in broiler production.

3.3. Risk Assessment Model

This risk assessment model is a simplified picture of how a salmonella infection might be transmitted through the broiler production chain and end up in consumption. This risk assessment model has made use of FSCP data from 1996-99; these data have been supplemented by a questionnaire sent to the broiler industry, expert opinions from salmonella experts and information obtained from scientific literature as well as other statistics collected in Finland. The model does not differentiate between different salmonella serotypes, as the FSCP treats all of them in broiler production in the same way.

Stochastic models have been used in the risk assessment for both inference modelling and direct simulations. In the simulation models we have used Monte Carlo methods, while for inferences we needed the so-called Markov chain of Monte Carlo techniques. By inference we mean a deductive operation, where some of the variables in the model have been observed and on the basis of these we deduce the most probable values for the variables and parameters which cannot be directly observed. This probabilistic inference was implemented using WinBUGS software.

The model simulations were carried out with @Risk software, and these cover the production chain at slaughter and processing. In the simulations, values for the next production stage are always based on the results of the simulations of the previous stage and thus the model has only a limited ability to learn "backwards" from the actual values obtained in the middle of the production process. For this reason, the ("forward") simulation concerns only the slaughter and processing stage, because there were little exact data on these stages from which we could have learnt values for the intermediate states of the process. The simulation model has also made use of distributions produced by the inference models, including the number of infected broiler flocks (detected and undetected).

The model's basic structure has been determined not only by the availability of information, but also by the interventions whose effects the model seeks to simulate.

For this model, we took two interventions used in the FSCP: 1) eliminating breeder flocks from production who have tested positive for salmonella and 2) heat-treating the meat of positive flocks.

There are of course other interventions included in the FSCP, including cleaning and disinfecting infected poultry houses after a positive test flock, slaughtering salmonella-positive flocks last on a given workday, and epidemiological investigations to identify the source of infection. However, it is extremely difficult to quantify the effects of these interventions, so they have been left out of this risk assessment. For this reason, the model's estimates of the effects of interventions of FSCP are conservative. In all likelihood, the control program has a greater effect than what the figures produced here would indicate.

The effects of interventions were simulated for the present situation, drawing on data from 1999 (scenario A). We chose this year because 1999 had the highest rates of detected salmonella in broiler flocks since the inception of the FSCP and thus represents a "worst case" scenario. It was also the first year for which we were able to gather sufficient data for the model, with the help of questionnaires and other statistics.

In addition, we studied interventions in three other scenarios. In scenario B one grandparent flock and in scenario C five parent flocks were modelled to be infected at the beginning of the laying phase. In scenario D we modelled a situation where the incidence of salmonella would be 20-40% in half the broiler meat sold in Finland. The model does not consider whether this would be the result of a weakening of the domestic situation or an increase in the salmonella levels of imported broiler meat.

This risk assessment is based on the principles of the Codex Alimentarius Commission (Codex Alimentarius Commission 2000) and is divided into four parts: hazard identification; hazard characterization, exposure assessment and risk characterization.

3.3.1 Hazard identification

In order to begin a risk assessment, it is necessary to identify a hazard (in this case, salmonella) on a general level. The incidence of salmonella in animal production in Finland is low when compared to that in many other Central European countries. The incidence of salmonella in broilers was monitored even before the initiation of the FSCP, and it seems that the national control program has clearly reduced the incidence of salmonella: in 1989-94, with the exception of one year all years had levels above 1% of flocks. Since 1995 when the FSCP was started, however, this level was exceeded only once, in 1999. The most common reported serotype in broiler flocks is *Salmonella* Infantis.

In Finland, there are annually about 3,000 reported cases of salmonellosis in humans, of which the majority of infections are acquired abroad. The most common domestic serotype has been *Salmonella* Typhimurium, whereas the most common serotype in the infections acquired abroad has been *Salmonella* Enteritidis (National Public Health Institute 2002).

In 1995-2001, none of the human salmonella outbreaks were reported to have been caused by broiler meat (MMMEEO 2001, Hatakka et al. 2001, Hatakka et al. 2002), and there have not been estimates of the number of individual or unreported salmonella infections caused by broiler meat in Finland. In Danish estimates, domestic broilers were responsible for 2-4% of human infections, whereas imported poultry was the source in 10-14% of cases in 2000. Due to differences in production structures, differing levels of salmonella and other reasons, these Danish figures are not directly applicable to Finland.

3.3.2. Hazard characterization

Salmonella bacteria can grow in temperatures of 5-46°C, although the optimal temperature is 35-37°C. The minimum water activity is 0.95, but cells can survive long periods in dry material. 9% NaCl prohibits the growth of salmonella, as well as a pH outside the range of 4.0-9.5 (Jay 2000; Ray 2001).

A salmonella infection rarely causes symptoms in broilers. Similarly, human infections can also be symptom-free. In humans, however, salmonella usually causes gastrointestinal symptoms (diarrhea, stomach ache, fever, headache and vomiting). The first symptoms usually appear within 12-24 hours after infection and last 3-4 days. In addition to these typical symptoms of food poisoning, much attention has recently been paid to salmonella-induced secondary infections (especially joint and eye inflammations and higher mortality rates in the long term) as well as to the increase of salmonella strains resistant to antimicrobial drugs. Reactive arthritis is observed in 1-15% of patients with acute salmonellosis. Symptoms usually appear 7-15 days after the beginning of gastrointestinal symptoms, and most patient recover in 3-5 months. In 16% of these patients, however, the disease becomes chronic (Leirisalo-Repo et al. 1997; Ekman 2000).

One problematic area in microbiological risk assessment is determining the dose-response, as is also the case with salmonella. Most dose-response experiments have been done either on animals or with healthy young adults, so these results cannot be directly compared to the normal population, to say nothing of susceptible populations. It is generally believed that doses as high as 10^7-10^9 cells/g are needed to cause salmonellosis. Data from outbreaks of salmonellosis, however, have indicated that in some cases even doses under 10^3 cells can cause infection. In this risk assessment, we have used the beta-Poisson dose-response model which is adapted for the normal population (WHO/FAO 2002). The estimated (mean) level of contamination at the time of serving was generated by calculating the posterior distribution in the CIM model, based on data from 1999.

3.3.3. Exposure assessment

In order to assess the risk of exposure, we modelled transmission from the beginning of production right up to the serving which ends up on a consumer's plate. Finally, information derived from the exposure assessment is combined with information about the dose-response to produce a general estimate of the risk of infection.

In the first part of the model, the Primary Production Inference Model (PPIM), we created a probabilistic transmission model of salmonella in the primary production chain. Since we had no data available linking salmonella infections detected at the slaughter house to a specific parent flock, we gathered our basic data from annual statistics covering all flocks. Broiler flocks can be infected either by the parent flocks through eggs or hatching (so-called vertical transmission) or from factors in the production facility, such as feed, humans, or pests (so-called horizontal transmission). We considered horizontal transmission as a single parameter describing all horizontal transmissions, since information on a specific flock's feed or reports of salmonella epidemics in broiler production traced to contaminated feed were not available. In addition, we used information provided by industry on the number of poultry farms. In the model, we also took into account the fact that in a given calendar year, breeding and poultry farms might have several different flocks in succession, rather than just one flock for the whole year. For the prior distributions, expert opinions were used to determine the sensitivity of the salmonella testing method, the chance of horizontal infection, the chance of vertical infection and the

effect of cross-contamination in hatcheries, as well as the likelihood that an ongoing infection would persist. From these prior distributions and the data available to us, the PPIM enables us to compute posterior probability distributions, which give us an estimate of the true prevalence of the disease.

Estimating the risk of exposure continues in the second part of the model, the Secondary Production Simulation Model (SPSM), where we can simulate on a general level the transmission of infection through the slaughterhouse, cutting plant and distribution to retail outlet. In this model, we use information from a variety of sources: the FSCP; industry, from whom we obtained information on the size of flocks sent to slaughter, the meat weight of a broiler carcass, and the amount of imported meat and meat products; first destination center data and the National Public Health Institute, whose FINN DIET 1997 survey (National Public Health Institute 1998) provides information on the size of an average serving. In addition, we have used expert opinions to determine input data on the prevalence of salmonella within a specific flock, the effects of heat treatment, the chance of cross-contamination at the slaughterhouse and cutting plants, the chance of cross-contamination between raw and heat-treated meat, and the amount of salmonella-positive meat imported from abroad.

Although the risk assessment model attempts to characterize the risk of salmonella infection on a general level, it nevertheless contains many points for which we have had to resort to expert opinions. Indeed, it is common practice in microbiological risk assessment to seek such expert opinion to fill in blanks in the data. It is of course possible that these expert opinions could be wide off the mark, but fortunately modern technology gives us the possibility to use probability distributions instead of averages, so the potential for error is not as great – although these methods bring along new kind of challenges.

We can compare the results of the inference and simulation models, concerning the primary production, by comparing the predicted distributions of salmonella-positive broiler meat to statistics, for example from 1999. We can also validate the model by comparing the predicted distribution of the salmonella prevalence in meat and the results of microbiological experiments. These results are in agreement, allowing us to conclude that the model provides a reasonably accurate picture of the production chain up to this stage. Based on these 1999 statistics, the 90% probability interval for salmonella prevalence in domestic broiler meat was 0.07%-0.43%, with a mean value of 0.21% and mode 0.17%.

3.3.4 Risk characterization

The number of salmonella cells consumed is difficult to estimate, since it depends on the frequency of salmonella contamination, the number of salmonella cells in meat, the temperature to which it has been heated, and the chance of cross-contamination in the kitchen. Therefore, in the third part of the risk assessment model, the Consumption Inference Model (CIM), we made use of an inference model based on an estimate of the number of reported human salmonella cases due to broilers generated from statistics on the total number of reported human salmonella cases in a given year (MMM 2000). Using this estimate as well as the number of contaminated servings calculated in the SPSM, we then used a selected dose-response model to calculate a posterior distribution for the mean number of colony forming units per gram, also taking into consideration the under-reporting of cases. This posterior distribution for the mean number of colony forming units is then used in the final part of the simulation model (CIM), in order to produce a prediction of the number of reported human cases. In this way, the dose-response model is calibrated on the basis of known information from a specific year, and it was not necessary to specify

an independent probability distribution for the mean number of colony forming units at time of consumption, which, because of its wide uncertainty, would lead to unrealistically wide predictions of salmonella infections.

By combining all three parts of the model (PPIM, SPSM and CIM) we can generate a probability distribution of how many Finns contract salmonella from broiler meat each year (Figure 1). Because the objective of the model is to study the effects the FSCP has had on consumer risk and the different scenarios are thus located in the primary production or the slaughter house, we have not - in light of the stated objective - considered it particularly necessary to extend the model to describe the end of the production chain. It is worth noting, however, that these estimates of the consumer's risk of contracting salmonella from broiler meat give only a general picture of the situation. Based on the 1999 data, the 95% prediction interval for the reported domestic broiler-borne human salmonella cases in Finland was [39,82], with a mean value of 59 and mode 58.

3.4. The Effects of Interventions

3.4.1 Effects on Infections in Broiler Flocks

Using this model of salmonella infections in broilers, we then analyzed the effects of the risk management measures or interventions taken under the FSCP to break the infection chain. In primary production, we examined the effects of slaughtering breeder flocks which had tested positive for salmonella. The model simulated the so-called present situation, using statistics from 1999 (scenario A), as well as a fictional scenario B, where one grandparent flock was infected at the beginning of the laying phase. Based on this 1999 data, the 95% prediction interval given by the model for the true incidence of salmonella infection in broiler flocks sent to slaughter was 0.9-5.8% with the mean being 91 out of 2,939 flocks. Naturally, this figure is higher than the prevalence of salmonella actually detected in broiler flocks. In 1999, there were reports of salmonella infection in 64 flocks sent to slaughter (2.2%), which was the highest prevalence detected since the FSCP's initial year of 1995. According to the estimate, without the removal of the positive breeder flocks the prevalence of salmonella would vary between 1.3-17.4%, with a mean of 145 flocks. In a simulated scenario where one grandparent flock would have been infected at the beginning of the laying phase (scenario B), with intervention the prevalence of salmonella in broiler flocks would have been 1.2-5.9%; without intervention it would have been 2.8%-43.1%.

On the basis of these models we can thus conclude what we have already long known from experience: removing infected breeding flocks greatly reduces the risk of infection in broiler flocks. With the help of the model, however, we can also determine the magnitude of the effect of this intervention, allowing us further to examine the effects it has on the risk of human infection, and if necessary, also its economic consequences.

FSCP statistics show that the salmonella situation in 1996-98 was better than in 1999. However, if we also take into account the fact that the sensitivity of the microbiological testing of faecal samples improved in 1999, the differences appear smaller, so that it seems that the actual prevalence has remained practically on the same level in 1996-99, with prevalences of 2.3%, 1.9%, 1.9% and 2.9% respectively. This improved sensitivity of testing has further improved consumer safety, as it is now possible to remove more salmonella-positive broiler flocks from the production chain.

3.4.2 Effects on the Number of Human Infections

Using the model, we also simulated the effects of interventions on the number of salmonella infections in humans. In addition to the present situation (scenario A), we also studied interventions in the production chains in scenarios B (grandparent flocks infected at the start of the laying period) and C (five parent flocks infected at the start of the laying period). We investigated both the effects of removing infected breeder flocks and of heat-treating infected meat on the number of human infections. In the model, the calculation of the scenario predictions was based on stochastic coupling of the scenario distribution and the posterior distribution of the number of contaminated servings using Matlab.

Interventions quite clearly protected consumer health even in the first scenario (A), which modelled the present low incidence of salmonella. If positive breeder flocks were not removed from production, we could expect the number of reported human salmonella infections to increase about 1.6-fold (Figure 1). If infected broiler meat were not heat treated, the number of reported human cases could be expected to increase 4.1-fold (A-2). If neither of these interventions were used, the number of anticipated cases would increase by 5.6-fold (A-3).

If we examine the effects of these interventions at high levels of salmonella infection, their effect increases. If one grandparent flock were infected at the beginning of the laying period (scenario B) and the positive breeder flocks were not removed, nor was the meat heat-treated, the anticipated number of reported cases in humans would increase 17.8-fold (B-3) compared to the use of both interventions. Heat treatment alone in this scenario would lead to a 4.7-fold increase in the number of anticipated cases (B-2). Similarly, removal of the infected breeder flocks alone would lead to a 3.4-fold increase in the number of anticipated cases (B-1).

If five parent flocks were infected at the start of the laying phase (scenario C), and no interventions were used, the anticipated number of human infections would increase 7.7-fold (C-3) compared to a situation where both interventions were used. In this scenario, heat treatment alone would lead to a 2.0-fold increase in the number of anticipated infections (C-1), and removal of the infected breeder flocks alone to a 3.7-fold increase (C-2).

In addition to these interventions in the production chain, we also used the model to simulate a fourth scenario (D), where the prevalence of salmonella in half the retail broiler meat is 20-40%. In this case, the anticipated number of human infections increases up to 58-fold (Figure 38).

3.5 Main assumptions

Many assumptions needed to be made during the construction of the model of salmonella in broiler production. They are presented in each section of this report.

The main assumptions in this work include:

1. No differences exist between the different salmonella serotypes either in the transmission of infection in broiler production or in the pathogeneticity.
2. Since the FSCP interventions studied by the model are focused on domestic production, the interventions on broiler meat entering Finland were not taken into account.
3. The number of salmonella cells in a contaminated serving is independent of the prevalence of salmonella in the population of servings, e.g. if prevalence increases the number of cells per serving does not change.
4. The preparation and consumption of broiler meat in kitchens was not modelled but included in the overall inference model for estimating salmonella contamination levels at the time of consumption.

5. The salmonella isolates reported in humans that are common to those of broilers and broiler meat can be used as a crude estimate of the reported broiler borne salmonella infections in humans.
6. All the reported salmonella infections in humans are cases of illness. The estimation covers the total population, i.e. no risk groups are specially assessed.

Unfortunately, not all of the data needed were available and expert opinions had to be used. The expert opinions were given on the following parameters and used as prior distributions in the inference models: chance of horizontal infection in broiler

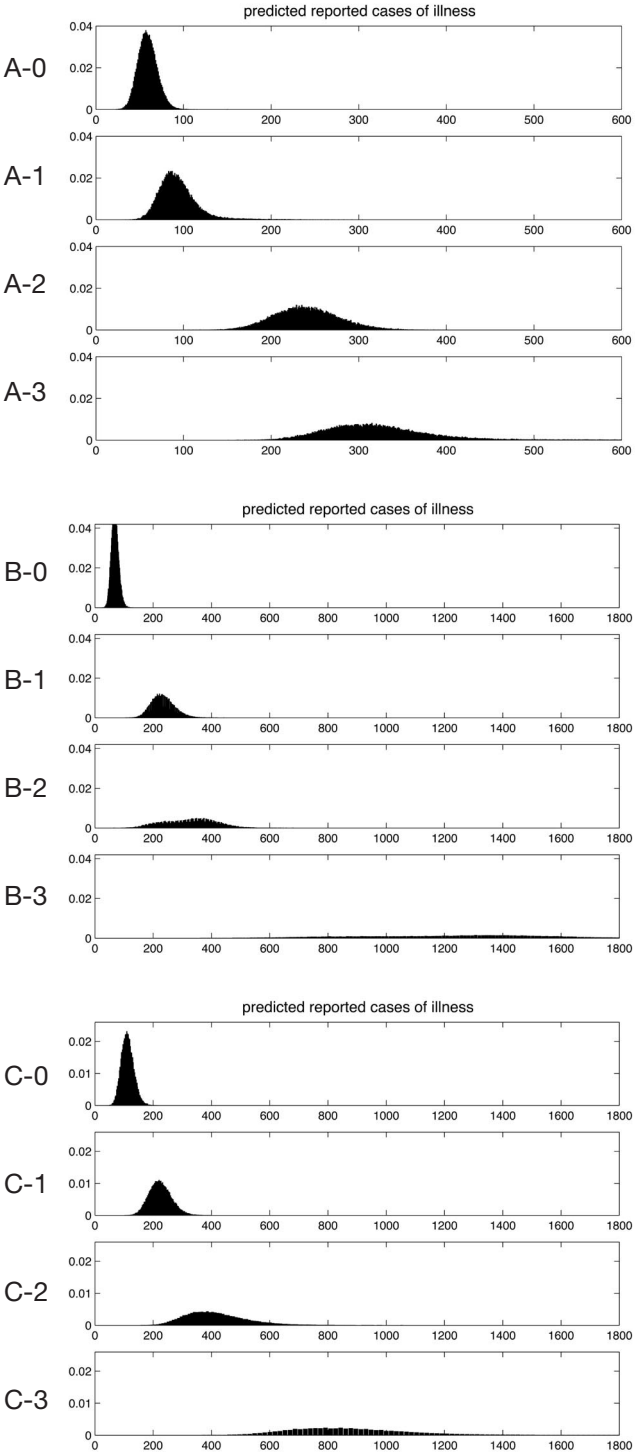


Figure 1.
Based on 1999 statistics, the predicted number of domestic reported infections caused by broiler meat in the present situation.

Scenario A:
0. with interventions;
1. without removal of positive breeder flocks;
2. without heat-treatment of positive broiler flocks;
3. without either intervention.

Scenario B:
0. with interventions;
1. without heat-treatment;
2. without removal of positive breeder flocks;
3: without either intervention.

Scenario C:
0. with interventions;
1. without removal of positive breeder flocks;
2. without heat-treatment;
3. without either intervention.

flocks, chance of ongoing infection to persist in the flock between two consecutive sampling times, and the parameter controlling the cross contamination effect of the hatcheries in the chance of vertical infection. In addition, the following expert opinions were used in 'forward' Monte Carlo modelling by @Risk: within flock prevalence, cross-contamination during the processing and proportion of contaminated meat imported to Finland.

3.6. Conclusions

With the aid of this quantitative risk assessment model, we can estimate the effects of the FSCP for broiler production, both for animals and for humans, on the risk of infection. The model's strongest part is primary production, since the national control program provides prevalence data on this stage of production. The closer to the consumer we get in the model, the more we have needed to include expert opinions. The model does, however, allow us to study the effects of some interventions and thus estimate the impact of the FSCP in Finland.

Using the results of risk assessments as a basis for decision-making is a challenge both for those doing the assessments as well as for those using the results. The important point, however, is that this model allows us to estimate how government and industry efforts to control salmonella affect public health, and thus get a better picture of the work that has been done. We can also use the gaps in data identified in the development and use of the model as spurs for further research. We could further improve the model's reliability and accuracy if we had access on the national level to the industry's own wide-ranging research projects. We can also make use of this salmonella risk assessment by applying it to other surveillance and control programs in broiler production.

Although some of the data gaps could be solved by changing the data collection system of FSCP, some research needs were also identified during this work:

1. The effect of main risk factors for salmonella infection in broiler production.
2. The sensitivity of salmonella analysis method for various matrices.
3. The effect of slaughtering and cutting on contamination level of broiler meat under low prevalence of salmonella.
4. The effect of temperature, time and cross-contamination on the survival of salmonella cells during preparation of broiler meat.

The model contains uncertainties and hypotheses which are discussed in this report. Based on the model, however, we can draw the following conclusions:

1. Interventions used in the FSCP significantly reduce the number of domestic salmonella infections in humans.
2. The effects of the FSCP would be even greater if the prevalence of salmonella in the food production chain were greater than it is today.
3. A combination of different interventions is more effective in preventing salmonella infection than single interventions.
4. Higher salmonella infection level early in the production chain clearly causes a greater risk to public health compared to the lower infection level.
5. A quantitative microbiological risk assessment requires large amounts of data, time and resources. At best, however, it can provide a fresh perspective on the topic and reveal important gaps in data.

4. Introduction

Salmonellosis is a disease caused by the *Salmonella enterica* bacterium, which originates from animal or human faeces. In most cases bacteria are transmitted to humans via contaminated foodstuffs. Common symptoms include fever lasting a few days and diarrhea. Acute salmonellosis leads to so-called reactive arthritis in 1% to 15% of patients, with onset typically occurring from seven to 14 days after the beginning of gastrointestinal symptoms. The excretion of salmonella in faeces usually ceases in about a month; however, a small number of those infected become chronic asymptomatic salmonella carriers. Only very few salmonella serotypes can cause severe disease in animals, including *Salmonella* Gallinarum/Pullorum in poultry or *Salmonella* Dublin in cattle (Miller et al. 1995; Humphrey 2000; Ekman 2000; Poppe 2000).

When Finland joined the European Union in 1995 its extraordinarily good salmonella situation in animal production was acknowledged, so it was granted special permission to run its own quite strict procedures for controlling salmonella infections in meat and egg production. This EU-approved programme is called the Finnish Salmonella Control Program (FSCP) (MMMEEO 1999). In practice, this programme also allows Finland to demand the same level of safety in certain products entering the country from abroad.

The good salmonella situation in Finland has a long history, extending back to the 1960s. The control system is organized co-operatively, through both voluntary industry mechanisms and mandatory rules and regulations. For example, for over 40 years a Feedingstuff Act has been in force to detect salmonella in feedstuffs. Furthermore, competitive exclusion is regularly used to prevent the salmonella contamination of broiler flocks (Nurmi & Rantala 1973; Seuna et al. 1978; Schneitz 1993). As a result of these tight domestic production control and negligible imports, the salmonella situation was good when Finland joined the EU, and in international terms has indeed remained extremely good since then, as a result of the serious commitment of farms and production plants. However, the salmonella risk to consumers has never been assessed scientifically.

Models of salmonella transmission throughout the production chain can be valuable tools for decision-makers. WHO/FAO have recently published an international risk assessment on salmonella in broiler production. One of the key findings was that a reduction in the prevalence of salmonella-contaminated chicken was associated with a reduction in the risk of human illness. A one-to-one relationship was estimated, i.e. a 50% reduction in the prevalence of contaminated poultry (20% to 10%) produced a 50% reduction in the expected risk of illness per serving. Moreover, the study also estimated that a decrease in the level of contamination, i.e. the numbers of salmonella bacteria in chickens, would lower the risk of human illness even more (there was a greater than a one-to-one relationship between lower salmonella levels

and human risk). However, because the WHO/FAO model was not conducted for a specific region or country, it is not possible to compare the effects of intervention measures (WHO/FAO 2002). Therefore, a national risk assessment model was needed in order to study the effects of risk management measures applied in Finland.

4.1. Project history

In 1998, the Ministry of Agriculture and Forestry asked the National Veterinary and Food Research Institute (EELA) to assess the risk caused by salmonella in foods of animal origin. However, due to a lack of resources and also a relatively new approach to microbiological risk assessment procedures for microbiological hazards in Finland, it took many years for this first part of the project to be completed. Similarly, work on beef and pork production is in progress. In 1999, EELA established a resource group for salmonella risk assessment, which gathered data and discussed the approach. In summer 2000, a joint risk assessment team of EELA and the Rolf Nevanlinna Institute of the University of Helsinki started to create a mathematical model for assessing the risk of salmonella in the broiler production chain. Parts of the model as well as general outlines have been presented and discussed at several international meetings, in scientific articles and in domestic circles. Our model uses the principles of the Codex Alimentarius Commission on microbiological risk assessment (Codex Alimentarius Commission 2000), mainly using data from 1999.

4.2. Objectives

The objectives of this risk assessment on salmonella in broiler production were:

1. To create a basic model of salmonella transmission from broiler grandparents to consumers in Finland.
2. Using this model, to assess the effect of the FSCP on broiler flocks and on public health.
3. To identify gaps in data, thereby providing a guide for future research and data collection efforts concerning salmonella and other necessary relevant information.
4. To create a practical format for other microbiological risk assessments.

5. Background information

5.1. Broiler Production in Finland

Agriculture is practised all over Finland even though the country lies between 60 and 70 degrees North. Farming is successful because the Gulf Stream keeps temperatures 3-4°C higher than in other areas at the same latitude. The Finnish climate is unpredictable, however. In southern Finland, the ground is covered with snow for 3-4 months and in northern Finland for 7 months. However, this harsh climate can also have a positive impact: frozen soil and sub-zero temperatures keep many plant and animal diseases under control.

Most of Finland's agricultural production takes place on family farms. Compared with other EU Member States, Finnish livestock farms are relatively small. In 1998, the average poultry farm had 2,750 hens or 27,814 broilers (MTTL 2000). The number of grandparent birds entering Finland from Scotland increased from 17,705 in 1996 to 25,938 in 1999. In 1996-99, annual imports from Sweden of the hatching eggs of broilers varied between 15,000-755,280. Since then there have been further increases: in 2002, 31,450 broiler grandparent chickens entered from Scotland and 1,589,962 hatching eggs from Sweden (ETT 2003).

Poultry meat production has increased considerably in the last few years, whereas egg production is struggling with overproduction. In 1995-2000, the number of commercial egg producing farms decreased from 1,893 to 832, while the number of poultry meat producing farms increased by 45, to a total of 391 farms in 2000. Most of these farms are located in the western part of Finland. In 1999, there were 53 broiler breeding holdings and 206 broiler holdings (Figure 2). Broiler meat consumption increased from 38.9 million kg in 1995 to 60.1 million kg in 2000, out of which 1.3-3.2% originates from EU or third countries (Figure 3). Most of the broiler meat produced is consumed domestically, only 0.4-3.1% of broiler production was exported in 1995-2000 (Suomen Gallup Elintarviketieto Oy 2001).

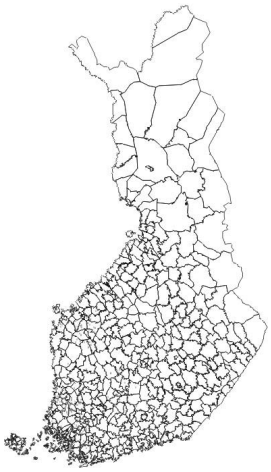


Figure 2.
The location of broiler farms in Finland in 1999 (TIKE 2001).

Figure 3.
The production, consumption, import and export of broiler meat in Finland in 1995-2000 (Suomen Gallup Elintarviketieto Oy 2001).

5.2. The Finnish Salmonella Control Program for broilers

In the EU, zoonoosis directive 92/117/EEC (Council Directive 92/117/EEC) includes the surveillance of salmonella in poultry breeder production. When Finland joined the European Union, the extraordinarily good salmonella situation in animal husbandry was acknowledged, and the EU granted Finland the so-called Finnish Salmonella Control Program (FSCP). This program allows Finland to place demands on salmonella surveillance in addition to those measures laid out in the zoonosis Directive. Covering beef, pork and poultry production, this EU-approved program in practice allows Finland to demand the same level of salmonella protection in a variety of imported products, i.e. so-called additional guarantees. Therefore, the FSCP is based on measures concerning both domestic salmonella contamination, including primary production, abattoirs and meat cutting plants, as well as on measures concerning other Members States of EU and third countries.

The objective of FSCP is to keep the national prevalence of salmonella under 1% and the prevalence at individual abattoirs or cutting plants below 5%. The program covers all salmonella serotypes, not just *Salmonella* Enteritidis and *Salmonella* Typhimurium as is common in many other European countries (Commission Decision 94/968/EC; Commission Decision 95/160/EC; Commission Decision 95/161/EC; MMMEEO 2000; European Commission 2001). Until 2003, only the ISO 6579:1993 method and NMKL method No. 71:1991 were approved for use in FSCP (NMKL 1991; ISO 1993; MMMEEO 1994; Seuna 2000).

The FSCP's control of salmonella in poultry meat is based on control of flocks. Faecal, environmental and occasionally also organ samples are taken from breeding flocks, hatcheries and production flocks. Flocks intended for slaughter are sampled 1-2 weeks before slaughter; the results of these examinations must be available before the birds are sent to slaughter (Table 1,Table 2). If salmonella is detected

in a breeding flock, the positive flock is put under official restrictions and official sampling is carried out according to Dir. 92/117/EEC to confirm the infection. If the infection is confirmed, restrictions are not lifted until the salmonella positive flock has been slaughtered or killed, and cleaning and disinfecting measures have been completed. Meat originating from salmonella-positive flocks has to be heat-treated. Production farms are freed from restrictions only after it has been established that there is no longer salmonella on the farm (MMMEEO 1994; MMM 23/EEO/2001).

Further control of fresh poultry meat is carried out at poultry meat cutting plants (MMM 20/EEO/2001). Such control covers the meat of hens, turkey, guinea-fowl, duck and geese. Sampling is done randomly during operation and is carried out at least once a week. A sample consists of 25 grams of crushed meat taken from the cleaning tool of a conveyor belt, from tables or a similar point. Each poultry production line is sampled separately. If salmonella is detected in one sample, an additional 59 samples must be taken at the cutting plant in order to determine how widely salmonella has spread.

According to the FSCP-based additional guarantees, Finland may require poultry meat and eggs, as well as live poultry, to be analyzed for salmonella before entering Finland, or require that these originate from a country with a similar salmonella control program. Proof of a negative test result has to accompany the load. Only some raw materials entering processing plants which will be used as inputs in products undergoing heat treatment are exempt from this rule. Food stuffs of animal origin

Table 1.
The FSCP sampling frame of broilers in general and after the detection of salmonella.

Production level	Time of sampling	Type of sample	No of samples
Breeder pullets Official sampling once a year	At arrival to rearing house	Swabs or bottom papers of transport boxes	10 papers or 10 swabs pooled into 2 samples
	At 4 wk of age	Faecal samples	According to table 2, pooling 10 subsamples into one sample
	2 wk before transfer to laying house	Faecal samples	According to table 2, pooling 10 subsamples into one sample
Breeder layers Official sampling once a year	Sampling every eight weeks, last one 1-2 weeks before slaughter	Faecal samples	According to table 2, pooling 10 subsamples into one sample
Breeder flocks additional official sampling	After detection of salmonella in faecal samples taken by owner	Faecal samples	According to table 2, pooling 10 subsamples into one sample
Breeder flocks additional official sampling	After detection of salmonella in faecal samples taken by owner if S. Typhimurium or S. Enteritidis is suspected	Organ samples (liver + ovaries and intestines)	According to table 2, pooling 5 subsamples into one sample
Breeder houses additional official sampling	After cleaning and desinfecting of a house where positive flock was	Surface samples	Decided by official veterinarian
Hatcheries Official sampling every eight weeks	Sampling chickens from every breeder flock every two weeks	Meconium or bottom papers of transport boxes	Meconium form 250 chickens or papers from 5 boxes pooled into one sample
	Regular sampling	Surface swabs	Decided by official veterinarian
Hatcheries additional official sampling	After detection of salmonella	Surface swabs	Decided by official veterinarian
Hatcheries additional official sampling	After cleaning and desinfecting due to salmonella detection	Surface swabs	Decided by official veterinarian
Suspected flocks	After detection of salmonella in the hatchery	Faecal samples or organ samples (if SE or ST suspected)	Decided by official veterinarian
Broiler flocks Official sampling once a year	1-2 weeks before slaughter	Faecal samples	According to table 2, pooling 5 subsamples into one sample
Broiler flocks additional official sampling	After cleaning and desinfecting due to salmonella detection	Surface swabs	Decided by official veterinarian

Table 2.
The number of subsamples depending on the flock size (MMMEEO 1994).

No. of birds	No. of subsamples
1-24	As many as birds, maximum 20
25-29	20
30-39	25
40-49	30
50-59	35
60-89	40
90-199	50
200-499	55
500 or more	60

delivered from other member states of the EU are checked at their first destination in Finland for certificates of salmonella examination. If salmonella is detected, the lot must be returned to the country of origin or destroyed. In the case of lots entering from a third country, a veterinary border inspection must be performed at the border. If salmonella is detected, the lot is returned or rejected. Costs are almost fully carried by industry, though government officials are responsible for inspection, analysis of suspected cases on the farm, and follow-up of the situation based on notifications from municipal food control laboratories, municipal, and provincial veterinarians.

5.2.1. Other measures to combat salmonella

In addition to the FSCP, other measures have also been taken to control salmonella in the food production chain. All imported, marketed and manufactured feed materials and compound feeds are under the control of the Plant Production Inspection Centre or, in the case of imported and certain domestically-manufactured feedingstuffs of animal origin, under the control of the Food and Health Department of the Ministry of Agriculture and Forestry. Controlling frequency varies depending on the estimated risk of salmonella. In import control, every consignment of feedingstuffs with a risk for salmonella is sampled and investigated regularly by the official control. Feed materials of both plant and animal origin are examined for salmonella. In marketing control, every batch of feed materials from EU countries is sampled and investigated regularly by the official control or by the self control systems of the producers regulated by the legislation. Official control includes random sampling except in the case of feedingstuffs of plant origin, where every consignment with a salmonella risk is sampled for analysis (MMMEEO 2000).

In Finland the control and handling of foodstuffs is mainly based on three acts: the Act on the Hygiene of Foodstuffs of Animal Origin (Hygiene Act, 763/1994); the Food Act (361/1995); and the Health Protection Act (763/1994). These Acts, as well as the Decrees based on them, also deal with zoonotic agents in foodstuffs. The purpose of the Hygiene Act is to secure the quality of foodstuffs of animal origin and to prevent the spread of infection from animals to humans via foodstuffs. The Act regulates the handling of foodstuffs of animal origin, quality requirements for food hygiene, and control and inspection before foodstuffs are sold in retail outlets. Detailed provisions and recommendations for these activities and requirements involved are laid down in the Decisions and Decrees of the Ministry of Agriculture and Forestry, issued on the basis of the Hygiene Act. For example, instructions about individual zoonotic agents are given in the rules on meat inspection laid down in the Decision on meat hygiene (16/EEO/2001).

In addition, industry takes voluntary measures in order to decrease the contamination level of salmonella, including, for example, the use of competitive exclusion for all broiler flocks as well as voluntary sampling.

5.3. Modelling of health risks in a production chain

When any biological system is modelled, a first consideration is choosing the level of description. If quantitative results are required, this choice is closely related to the quality of available data. Often, a quantitative risk assessment of a large and convoluted system combines both expert opinions and data sources. These two sources of information can be treated coherently in a probabilistic framework of analysis which takes into account all the uncertainties involved.

A hierarchical model consists of conditional probability distributions organized in the shape of a tree. Each node in the tree denotes a random variable, and the variables are related according to the tree structure. The conditional distribution of each ”child variable” depends on the random (uncertain) values of its ”parent variables”. This hierarchy provides a useful and intuitive description of many phenomena, e.g. production processes, and can be straightforwardly implemented as a simulation algorithm once all the ”parents” and ”children” in the tree have been specified. When completed, it can also be called an expert system, or a belief network.

Some of the variables in the model are drawn from data, whereas some are unknown, i.e. unobserved. Probabilistic inference means constructing probability distributions of the unknown variables, given the known variables within a specified model. In other words, we can make inferences about some things we have not directly observed based on observations we have been able to make. An unobserved variable might be, for example, the future number of salmonella positive flocks, or it can be the current true number of salmonella positive flocks. Since neither of these can be observed directly or known accurately, there remains uncertainty about them; a probability distribution aims to summarize this uncertainty.

In Bayesian analysis, a probability denotes (subjective) uncertainty, which means that the probabilities are always conditional on a given piece of information. There are different sources of uncertainty, however: there are uncertainties about our knowledge, as well as uncertainties about biological and physical processes. Finally, in all situations, a probability model describes and summarizes our total uncertainty about the quantities in question. In this way, probability theory works as extended logic where probabilities of one (100%) and zero (0%) mean full certainty (true/false).

When no variables in the hierarchical model are fixed as data points, the probabilities describe our a priori uncertainty. This prior uncertainty can be visualized as a distribution, or as a chain of distributions describing the entire biological/physical system of interest. Thus, each distribution depends on the random result of a previous distribution in the chain description. The resulting joint distribution may not have an easy analytical solution, but it can always be visualised using sufficiently large random samples drawn successively from the chain of distributions. This is the conventional Monte Carlo approach. Typically, this approach requires that each of the conditional distributions in the chain is a known standard probability density from which we can obtain random numbers, for example by using @RISK or some other tools. If the distributions involved are not among the list of known probability densities, it is still possible to visualize them with numerical sampling techniques, but one may need to do some programming first. Generally, it is sufficient if the densities can be written up to the normalizing constant, or if the full conditional densities can be solved. In such cases sampling is based on various versions of Markov chain Monte Carlo techniques (MCMC), all of which require more specialized algorithms and tools which are not available in basic spreadsheet software. Such techniques become especially useful if some model variables are observed as data points. We can then compute a conditional distribution (a so-called posterior distribution) of

the remaining unknown variables, given the observed values of the other variables. This is probabilistic inference in operation, and as such is a form of empirical science: learning from observations. Before a posterior distribution can be computed, we still need to define prior probability densities – in other words, the full hierarchical model. These priors can be based on past experience, or they can be elicited by interviewing a group of experts. Typically, many Monte Carlo models in risk analysis are based on the study of prior probabilities only. We were able to extend the analysis towards actual probabilistic inference by utilizing observed data from various points of the production chain simultaneously with the priors drawn from expert opinion.

Computing posterior probability distributions is usually not straightforward, so specialized algorithms are needed. WinBUGS software was used for computing the model of the primary production chain as well as the model of reported human infections. The results of these analyses could be further used as inputs in a more straightforward simulation of the production chain, which we did using either Matlab or @RISK software.

For more information about the software, numerical methods and modelling typically used in Finnish universities, see the report of the Centre for Scientific Computation (2000), available at http://www.csc.fi/raportit/mallinnus/. For more information about expert systems, Bayesian analysis and modelling see e.g. the books by Congdon (2001), Cowell et al. (1999), French & Smith (1997), Gelman et al. (1995), and Robert & Casella (1999).

6. Risk assessment on salmonella in the broiler production chain

This risk assessment on salmonella in broiler production was done following the principles of the Codex alimentarius commission (Codex Alimentarius Commission 2000). Therefore, our risk assessment process was divided into four parts:

1. Hazard identification
2. Hazard characterization
3. Exposure assessment
4. Risk characterization

The modelling focuses on broiler production in Finland. No distinctions were made between either the different serotypes or antibiotic resistance, since the preliminary report of a WHO working group doing a risk assessment on salmonella in broilers has concluded that the outbreak data did not produce any evidence to support the hypothesis that Salmonella Enteritidis has a higher likelihood of causing illness and that the epidemiological data does not offer any evidence to conclude that different serotypes (non-typhoide) are more or less pathogenic than others (Fazil et. al. 2000). In the FSCP, all serotypes are covered.

Since no clear connections between the particular feed lots and infections in broiler flocks were reported, the link between feed and animals was not modelled. Feed was included in the general ”horizontal” risk, which was estimated as a posterior distribution.

The modelling has been performed in three parts: (1) Primary Production Inference Model (PPIM); (2) Secondary Production Simulation Model (SPSM); and (3) Consumption Inference Model (CIM). These three models were specified using the available data which represents our best understanding of the behaviour of salmonella in the broiler production chain (Figure 4). The annual results refer to the years 1996-1999.

In the PPIM, we described the primary production chain and the computation was performed using WinBUGS software. We also computed the posterior joint distribution of all the unknown variables and parameters (50,000 MCMC iterations with a burn-in period of 500). As a result, we obtained the marginal posterior distributions of the unknown quantities and model parameters of interest, which could be used further in the subsequent modules. In the SPSM, the secondary production chain was modelled using @RISK, software (Palisades Corporation) by forward Monte Carlo sampling (50,000 iterations). Thereafter, the results of the SPSM and the PPIM were used together with the results of the Consumption Inference Model (CIM) to compute the predictive distributions of human infections of salmonella due to broilers (50,000 MCMC iterations). The results are expressed as probability distributions rather than

as point estimates. These distributions reflect the current state of uncertainty about particular variables based on the available evidence.

At the end of the risk assessment, we obtain baseline estimates of the number of human salmonella infections caused annually by broiler meat in Finland. These results reflect the information and uncertainties about primary production, secondary production, consumption patterns, under-reporting and the dose-response relationship (Section 3). In addition, we studied the effect of some risk management options in four different scenarios: (A) for the current situation, (B) with one grandparent flock infected, (C) with five parent flocks infected and (D) with half the retail broiler meat replaced by 20-40% contaminated meat.

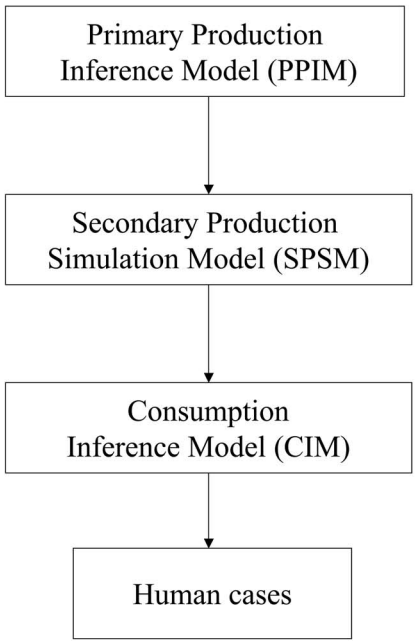


Figure 4.
The basic structure of the risk assessment model of salmonella in the broiler production chain.

6.1. Hazard identification

Salmonellae are Gram-negative, facultative anaerobe, motile rodshaped bacteria, belonging to the genus *Enterobacteriaceae*. They are widely distributed in nature, with humans and animals being their primary reservoirs. At least 2,400 different serovars of salmonella are known and have been placed in two species, *S. enterica* and *S. bongori* (Jay 2000; Popoff et al. 1996). *S. enterica* is divided into six *S. enterica* subspecies: *enterica, salamae, arizonae, diarizonae, houtenae* and *indica* (Popoff & Le Minor 1997). Serotyping of salmonella is done by identifying the O- and H- antigens (phase 1 and 2) in order to name the serovar. Names for salmonella serovars are only maintained for the subspecies enterica serovars, which account for more than 99.5% of isolated salmonella strains.

Salmonella may cause enteritis or a general infection in animals and humans. Most serovars are not species specific. All mammals, birds and reptiles may act as carriers of salmonella without symptoms. For epidemiological purposes, serotypes can be divided into three groups: (1) those that infect humans only, *S.* Typhi, *S.* Paratyphi A and *S.* Paratyphi C. These cause typhoid and paratyphoid fevers, which are the most severe of all the diseases caused by salmonella in humans; (2) those that only infect specific animals, such as *S.* Gallinarum/ Pullorum, which causes diarrhea in poultry, *S.* Abortus equi, which causes abortions in horses, *S.* Abortus ovis, which

causes abortions in sheep and *S.* Choleraesuis, which causes disease in swine; (3) unadapted serovars with no host preference. These are pathogenic for humans and sometimes also for animals, and include most food-borne serovars (Jay 2000). In this risk assessment, we only discuss salmonella belonging to group 3.

In the European Union, *S.* Enteritidis is the most prevalent serotype isolated from humans (26-87% of isolations in different MS's), followed by *S.* Typhimurium. By contrast, in the USA in 1996-1997, S. Typhimurium accounted for 27-29% of salmonella isolations, while *S.* Enteritidis was isolated in 16-17% of cases (Jay 2000; European Commission 2001).

An infected animal sheds salmonella in the faeces, thus enabling the bacteria to spread in the environment. The duration of salmonella shedding depends on the animal species and the serovar, though the infection might persist in the animal for the rest of its life. Some serotypes, especially *Salmonella* Enteritidis and *Salmonella* Typhimurium, may be transmitted via eggs. Although the usual transmission route of salmonella to humans is faecal-oral via foodstuffs, infections can also be transmitted from person to person, especially due to a lack of attention to proper hand washing or from other sources (Miller et al. 1995).

Finland, Sweden and Norway have traditionally fought against salmonella with strict measures, resulting in a good situation compared to many other European countries (Figure 5). Even before 1995, a control program for salmonella in broilers existed in Finland. However, the initiation of FSCP clearly increased the numbers of samples taken. In 1996-2001, the number of salmonella positive flocks sent to slaughter has remained under 1%, as stated in the FSCP (Figure 6). The only exception was 1999, when the detected salmonella prevalence was 2.2% (Seuna 2000). The most common serotypes isolated from broiler flocks in 1996-1999 was *S.* Infantis, which accounted for 88% of isolations (Table 3).

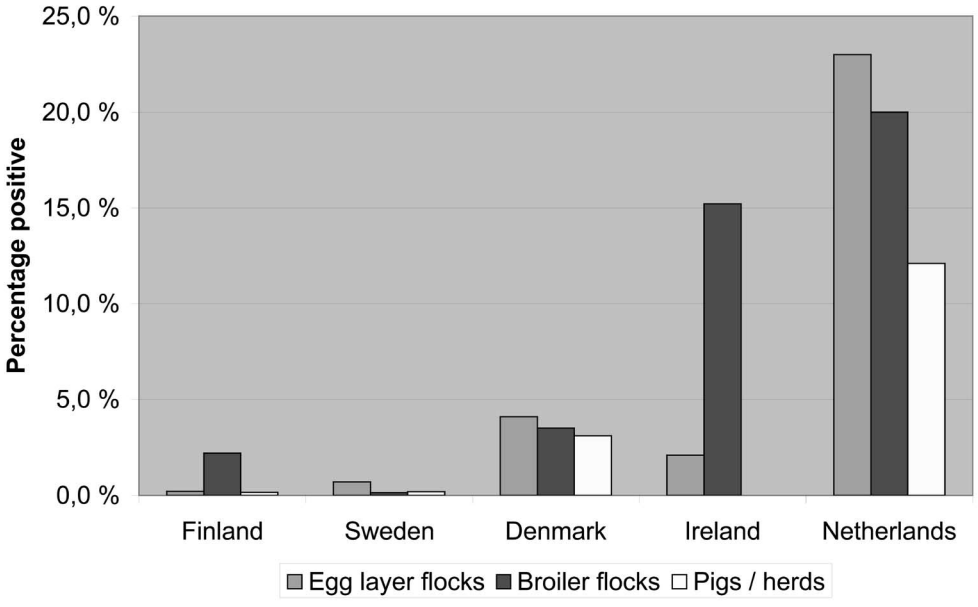


Figure 5.
The reported prevalence of salmonella infections in broilers, egg layers and pigs in some European countries in 1999. Data from Irish pigs is missing (European Commission 2001).

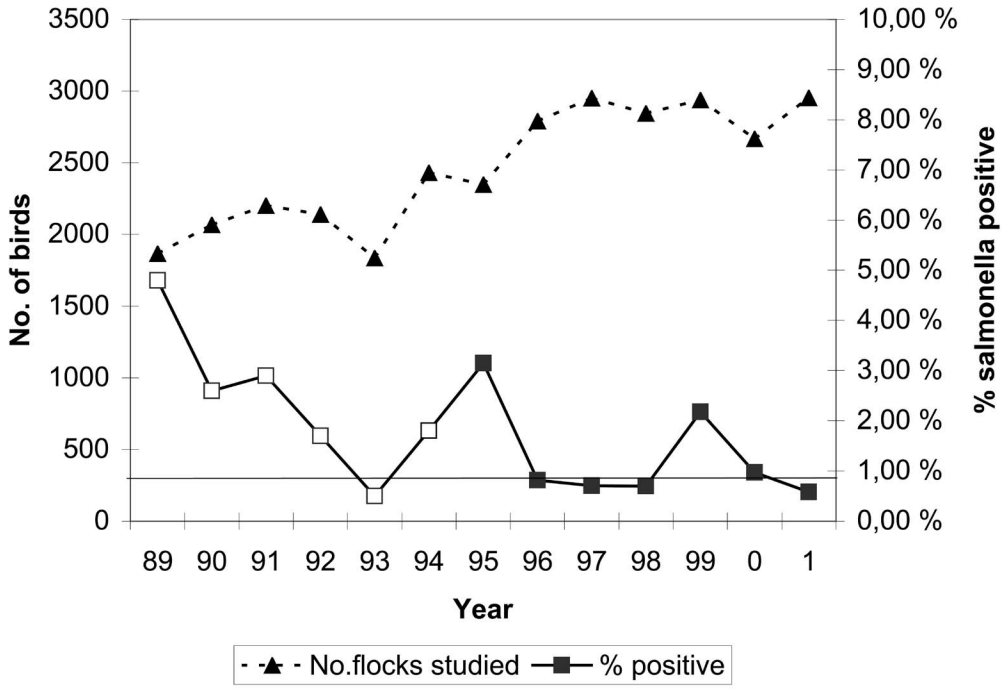


Figure 6.
The percentage of salmonella positive broiler flocks sent to slaughter in Finland in 1989-2001 before (white squares) and after the implementation of the FSCP (black squares) (EELA).

Table 3.
Serotypes isolated from broiler flocks in 1996-1999 (Seuna 2000).

Serovar	No. of salmonella positive flocks			
	1996	1997	1998	1999
Anatum	4	5	2	2
Infantis	10	9	15	56
Isangi	4	0	1	0
Livingstone	0	5	0	5*
Montevideo	0	0	1	0
Thompson	3	0	1	0
Salmonella ssp.	2	2	0	0
Tennessee	0	0	0	2
Total	23	21	20	64

*** Salmonella Infantis was also isolated in one flock**

Due to the good domestic salmonella situation, the majority of human infections (80-90%) are contracted abroad at the most popular tourist resorts visited by Finns. In 1995-1999, the number of all salmonella infections (both domestic and acquired abroad) has fluctuated only slightly: there has been an average of 3,000 infections reported per year, as compared to approximately 4,600 infections reported per year in 1990-1994. The most common serotype isolated in domestic infections has been *S.* Typhimurium, whereas *S.* Enteritidis has dominated in cases infected abroad (National Public Health Institute 2000) (Table 4).

In Finland, occupational salmonella control for food industry and hospital workers annually includes over 50,000 samples. In 1982-1996, almost 808,000 faecal samples were studied for this purpose, usually obtained from clinically symptomless persons.

In the annual testing of these workers, on average 0.11% (range 0.06-0.20%) have been infected with salmonella. New workers had about the same infection rates, 0.12 % (range 0.07-0.21%), whereas 3.1% (range 2.16-3.73%) of those who had vacationed outside the Nordic countries were infected (Siitonen 2001, personal communication).

In general, eggs, poultry meat and meat products are regarded as the most common food vehicles of salmonellosis to humans (Jay 1996). For example, in the Netherlands chickens contributed to 20-22% of the occurrences of human salmonellosis in the period 1994-1998 (KvW & RIVM 2002). In Denmark, broilers were the major source of human infections in the late 1980s; since then, pork and eggs have been the main sources (Ministry of Food, Agriculture and Fisheries 2000). In Denmark, domestic broilers were responsible for 2-4% of cases of human salmonellosis, whereas imported poultry was estimated to be the source in 10-14% of cases in 2000 (Ministry of Food, Agriculture and Fisheries 2001). In Finland, in 1995-2001, none of the human salmonella outbreaks were reported to have been caused by broiler meat (MMMEEO 2001, Hatakka et al. 2001, Hatakka et al. 2002).

Table 4.
Reported human infections of salmonella in Finland 1995-1999.
(National Public Health Institute 2000).

	1995	1996	1997	1998	1999	2000	2001
Domestic origin	1059	469	799	436	566	314	364
Foreign origin	2076	2118	1823	1949	1740	2101	2226
Origin not known	161	145	263	349	495	209	144
Total	3296	2732	2885	2734	2801	2624	2734

6.2. Hazard characterization

6.2.1. Microbe

Salmonella can grow in temperatures of 5-46°C, although the optimal temperature is 35-37°C. The minimum water activity for growth is 0.95, but cells can survive long periods in dry material. 9% NaCl prohibits the growth of salmonella, as well as a pH outside the range of 4.0-9.5 (Jay 2000; Ray 2001). Salmonella is destroyed at temperatures above 70°C, though even this is affected by the matrix, especially by humidity: sometimes even temperatures over 100°C are needed to destroy salmonella in dry feedstuffs (MMMEEO 2001). There are variations in the abilities of different strains and serotypes to survive in the environment, e.g. in dry heat or at non-optimal pH (Jay 2000).

Scientists are continuing to unravel the virulence mechanisms of salmonella. Although enterotoxin and a cytotoxin have been identified in pathogenic salmonella, they seem to play only a minimal (if any) role in the gastroenteritis syndrome (Jay 2000). Virulent strains of *S. enterica* initiate infection in non-phagoscytic cells by attaching to the intestinal mucosa. This is followed by the penetration of the intestinal mucosa, thus invading the M cells of Peyer's patches.

6.2.2. Poultry hosts

In animals, the infective dose depends on the animal's immunostatus; especially newborns, the young and stressed are more likely to become infected. A few salmonella bacteria are enough to infect a young chick, especially if the normal gut

flora has not yet developed. Animals experience stress from transport, changes in the environment and the mixing of different animal groups, all of which cause immunocompromising effects.

6.2.3. Human host

Infections in humans with the non-human adapted *Salmonella sp.* are characterized by febrile gastroenteritis, i.e. diarrhea, stomach ache, fever (up to 40°C), headache, nausea, vomiting and malaise. The first symptoms appear after 12-24 h (range 5-72 h) and continue for about 3-4 days (range 2-7 days) (Baird-Parker 1990; Flowers 1988; European Commission 2000).

In addition to causing morbidity with gastrointestinal symptoms, patients can have a variety of extraintestinal symptoms. In approximately 5% of cases, sequellae arise (e.g. septicemia, endocarditis, multiple abscesses, polyarthritis, osteomyleitis) (European Commission 2000). One of these complications is arthritis, which can be either septic or sterile (reactive). Septic arthritis is rare, but reactive arthritis (ReA) is observed in 1-15% of patients with acute salmonellosis. The onset typically occurs from 7 to 15 days after the beginning of gastrointestinal symptoms and most patients recover in 3-5 months. Nevertheless, many patients continue to have mild joint symptoms after the acute phase of ReA; in 16% of patients the disease becomes chronic, mainly in those who are HLA-B27-positive (Leirisalo-Repo et al. 1997; Ekman 2000, Hannu et al. 2002). Furthermore, there is new evidence for increased relative mortality within one year after salmonella infection (Helms et al. 2003).

6.2.3.1. Dose-response

Studies with volunteers have demonstrated that the larger the inoculum size, the greater the attack rate. Generally, 10^7- 10^9 cells/g are needed to cause salmonellosis in healthy adults (Jay 1996). However, data from outbreaks of salmonellosis have indicated that sometimes even low doses of salmonella (even below 10^3) are also able to cause gastroenteritis (Table 5). In data from 33 outbreaks, the Log CFU dose varied between 1.23 and 9.90 (WHO/FAO 2002).

In particular, immunosuppression or a lack of stomach acidity have been used to explain the susceptibility of newborns, infants, the elderly, and immunocompromised individuals (Miller et al. 1995). Given the data on salmonella outbreaks in the WHO/FAO risk assessment (WHO/FAO 2002) there was insufficient evidence to conclude that ”susceptible” individuals have a higher probability of illness compared to the ”normal” population. Therefore, in this risk assessment, no difference is made according to the susceptibility of the target population, i.e. all calculations are done for the total population. It should not be forgotten, however, that the severity of illness may be higher in susceptible individuals, thereby increasing the risk (risk is a combination of probability and severity).

In addition, some suggestions have been presented about the excess mortality associated with drug-resistant *Salmonella* Typhimurium (Helms et al. 2002). Patients with pansusceptible *S.* Typhimurium infections were 2.3 times more likely to die two years after infection than persons in the general Danish population. The likelihood was bigger with multiresistant strains: with quinolone-resistant strains the mortality rate was 10.3 times higher than the general population.

It has been suggested that a high fat or protein content in food lowers the infective dose, due to the protection of salmonella from gastric acidity. Some outbreaks, e.g. caused by chocolate, have been reported with a low infection level (Fontaine et al. 1980; Blaser & Newman 1982; Kapperud et al. 1990).

Table 5.
Human infectious doses of *Salmonella* spp. (D'Aoust 2000)

Food	Serovar	Infectious dose (cells)
Eggnog	S. meleagridis	$10^6 – 10^7$
	S. anatum	$10^5 – 10^7$
Goat cheese	S. zanzibar	$10^5 – 10^{11}$
Carmine dye	S. cubana	10^4
Imitation ice cream	S. typhimurium	10^4
Chocolate	S. eastbourne	10^2
Hamburger	S. newport	$10^1 – 10^2$
Cheddar cheese	S. heidelberg	10^2
Chocolate	S. napoli	$10^1 – 10^2$
Cheddar cheese	S. typhimurium	$10^0 – 10^1$
Chocolate	S. typhimurium	$<10^1$
Paprika potato chips	S. saintpaul	$<4.5 * 10^1$
	S. javiana	
	S. rubislaw	

Unfortunately, data for dose-response in humans is difficult to obtain for ethical and practical reasons. Therefore, not surprisingly, there is no consensus on which dose-response model is most applicable to modelling the salmonella dose-response. Holcomb et al. (1999) compared six dose-response models with the maximum likelihood method for use with food-borne pathogens, including *Salmonella* typhosa. They concluded that there was especially a need to predict infection at low doses.

In a microbiological risk assessment on food, the WHO studied five dose-response models in detail, concluding that at present a single model of the relationship between dose and response cannot be said to be vastly superior to any other model (WHO 2000).

6.3. Exposure assessment

The occurrence of contamination at the time of consumption depends on the previous steps of the production chain. Therefore, we modelled the whole production chain, starting from the grandparent chickens up to consumers. Since the FSCP data cover only primary production and cutting plants, the exposure model was divided into two parts: the Primary Production Inference Model (PPIM) and the Secondary Production Simulation Model (SPSM) (Figure 7). First, a probabilistic transmission model of salmonella in the primary production chain was created and computed using WinBUGS software (PPIM). This model utilized data covering the entire primary production chain for computing a joint posterior distribution of unknown parameters. The secondary production chain up to the meat produced was modelled using @Risk software (SPSM). This model utilized the joint posterior distribution (PPIM) as an input distribution in order to compute simulations of the stages of the secondary production chain. The combination of exposure to dose-response information was done in the Consumption Inference Model (CIM), as described in risk characterization (Section 6.4.).

6.3.1. Primary Production Inference Model (PPIM)

6.3.1.1. Summary of the Primary Production Inference Model (PPIM)

The Primary Production Inference Model (PPIM) estimates the true annual production of salmonella-positive broiler flocks sent to slaughter (Figure 7). A probability model of salmonella transmission in the primary broiler production chain was described in grandparent, parent and production broiler flocks at the flock level, based on available data on detected positive flocks in the FSCP as well as on expert opinion. The estimation, i.e. probabilistic inference, was conducted by computing the joint posterior probability distribution using WinBUGS software. The resulting probability distribution, then, represents the uncertainty about the model parameters and other unknown variables, e.g. the true number of infected broiler flocks.

The core of the salmonella transmission model was a conditional probability model for the natural course of infection (Ranta & Maijala 2002).This conditional probability -- that a flock is truly infected at some visit (i.e. testing time) given its true infection status at the previous visit -- was specified by the chance of horizontal (new) infection and the chance of prevailing infection. Because the underlying true status is uncertain if the test is negative, this model structure can also be called a Hidden Markov Model (HMM). Uncertainty concerning the numbers of broiler flocks raised in a given poultry farm was accounted for by modelling the unknown temporal shifts (permutations in calendar time) of different flock-specific HMMs by assuming that all possible shifts are equally probable.

The apparent prevalence of salmonella in broiler flocks sent to slaughter has been below 1% except in 1995 and 1999 (Seuna 2000). With this model, however, we could obtain an estimate of the true prevalence. According to the PPIM, the estimated mean true prevalences of salmonella in broiler flocks sent to slaughter were 2.3%, 1.9%, 1.9% and 2.9% in 1996-1999, respectively. This would imply that the increase of test sensitivity in 1999 was not the only reason for the higher number of positive broiler flocks detected. The effect of increased sensitivity can be seen as a decrease in uncertainty by looking at the width of the distributions.

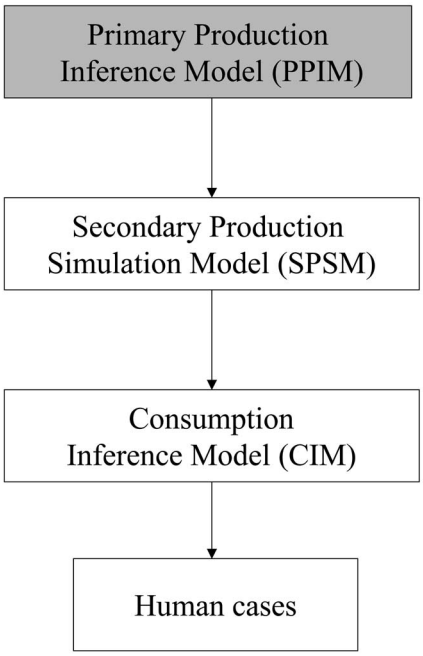


Figure 7.
The Primary Production Inference Model (PPIM) in the whole risk assessment model.

6.3.1.2. Inputs and Parameters of the Primary Production Inference Model (PPIM)

The PPIM covered three production levels: grandparent, parent and broiler flocks (Figure 8). The data variables used for modelling were obtained from the FSCP. In addition, experts in the resource group were used to elicit prior distributions on quantities where only a limited amount of information was available (Table 6).

Even if the PPIM only coarsely describes salmonella transmission in primary broiler production, data were not available for all variables in the production chain. Fortunately, by using inferences from other data and assumptions within PPIM, it was possible to obtain estimates for vertical and horizontal transmission. This was based on computing the joint posterior distribution of all unknown model quantities, conditionalized on all data values and expert opinions expressed as prior distributions of unknown parameters. In the model, the horizontal chance of infection describes all routes of infection which are not vertical transmissions. It is well known that feeding stuffs can be an important source of infection but there have been no reports of feed-borne infections in Finnish broiler production. In particular, there are no data available on both feed and faecal test results from the same flock.

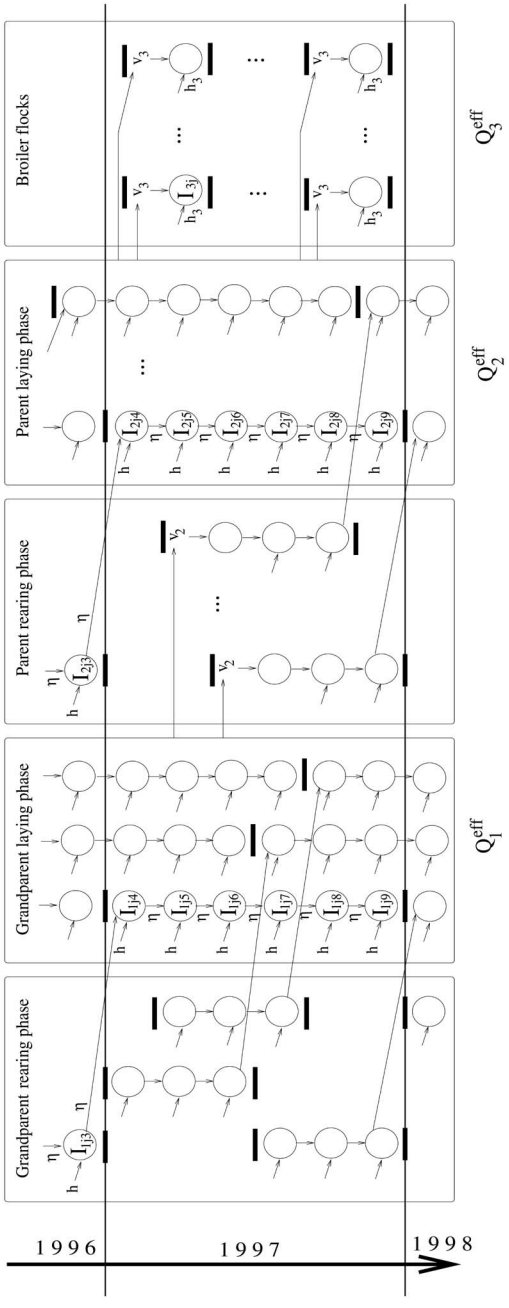


Figure 8.
Schematic presentation of the conditional probabilities defined in the PPIM. Nodes denote underlying infection states of flocks at different visits. Different flocks are separated by bars. Arrows denote either the chance of vertical (v_2,v_3) or horizontal transmission (h,h_3), or temporal dependency (η). Calendar time is indicated for three years. Reproduced from Ranta & Maijala (2002). See also Table 11.

Table 6.
Input variables and model parameters used in the Primary Production Inference Model.

Code	Data variable	Source of information
n_1,n_2	Number of granparent and parent houses for layers per year.	Inquery for broiler companies and the Associaton of boiler producers.
n_3	Number of broiler slaughter flocks per year.	FSCP 1996-1999
d_1,d_2	Apparent annual number of salmonella positive grandparent and parent flocks, i.e. positive testing times.	FSCP 1996-1999.
d_3	Apparent annual number of salmonella positive broiler flocks.	FSCP 1996-1999.
Code	Model parameter	Source of information
p	Sensitivity of salmonella testing method.	Prior distribution elicited from expert opinion.
-	Spesificity of salmonella testing method.	Expert opinion.
h	Chance of horizontal infection between two consecutive samplings in breeder flocks.	Prior distribution elicited from expert opinion.
h_3	Chance of horizontal infection before sampling in broiler flocks.	Prior distribution elicited from expert opinion.
θ	Parameter for the effect of cross contamination in the model of the chance of vertical transmission in the hatchery.	Prior distribution elicited from expert opinion.
η	Chance of ongoing infection to prevail in a grandparent or parent flock between two consecutive samplings.	Prior distribution elicited from expert opinion.

Data variables

Data on the number of flock houses n_1, n_2 and flocks n_3 were collected from the annual statistics of the FSCP or by inquiry of the five main broiler producing companies in Finland. Since the first year of FSCP implementation was not complete (since it started on 1 May 1995), these data were not used.

The sampling scheme of the grandparent and parent flocks is on average based on nine faecal samplings during the entire lifetime of a flock. Three of these nine samplings are done during the pullet phase. During the laying period of breeders, pooled samples are taken every eight weeks before the flock is slaughtered, resulting in six samplings per year. In order to simplify, the number of laying flocks was regarded to be the same as the number of pullet flocks and infection acquired at pullet age could therefore be transmitted to the following layer flock in time. Furthermore, the transmission of salmonella infection to the next generation can only happen during the laying phase since eggs are not produced by pullets. This assumption was implemented in the model of vertical transmission.

All flocks are not born exactly at the beginning of the year and houses are kept empty for short periods between the change of flocks. At any given point, there are many flocks of different ages and thus the lifetimes of most breeder flocks fall partly within two consecutive years. This was taken into account in the model by equal probabilities for each possible temporal shift (permutations in calendar time) of flock lifetimes with respect to the reported data concerning the calendar year. This model reflects uncertainty about the true number of different flocks falling partially within the same annual records. Hence, there are an uncertain number of Hidden Markov Models, because each HMM describes exactly one flock lifetime history, but we do not know how many different flock lifetimes actually contributed to the available annual data.

Table 7.
The annual data used for the Primary Production Inference Model.

Code	Explanation	1995	1996	1997	1998	1999
n_1	No. of laying grandparent houses.	3	3	3	3	3
d_1	Apparent No. Of positive grandparent flocks. (i.e. number of positive testing results).	0	0	0	0	0
n_2	No. of laying parent houses.	54	54	53	53	53
d_2	Apparent No. of positive parent flocks. (i.e. number of positive testing results).	0	1[2]	0	0	1[1]
–	No. Of positive / No. of samples of hatcheries studied.	3/1129*	0/1688	13/1371 (0.9%)	2/1113 (0.2 %)	5/996 (0.5%)
n_3	No. of production broiler flocks.	2350	2793	2951	2846	2939
d_3	Apparent No. of positive broiler flocks.	74	23	21	20	64

1 The second sampling during the flock life time (pullet).
2 The fourth sampling during the flock life time i.e. the first sampling at the laying house

Model parameters

Flock sensitivity (p)

For salmonella detection, the FSCP allows only the use of ISO 6579:1993 or NMKL 71:1991 methods (ISO 1993; NMKL 1991). In 1996-98, pre-enrichment was not used for faecal poultry samples, which had been a general practice before. Since 1999, pre-enrichment has been included and a sample size of 1 g was used instead of a loopful of faeces (taken by a loop of 10 ml). However, there is only a limited amount of information published on the sensitivity of these methods, either with or without pre-enrichment in poultry faecal samples. Voogt et al. (2001) obtained a sensitivity of 56% (61/108) for the method used for faecal samples from infected broiler flocks (n=892) with pre-enrichment after a 24-hour incubation period. However, as selective enrichment they used Rappaport-Vassiliadis broth (RV) with a high magnesium chloride concentration (18.7 g/L, anhydrous), which has been reported to inhibit the growth of salmonella (Peterz et al. 1989; Maijala et al. 1992). A concentration of 13.6 g/L (anhydrous) is adopted in the ISO 6579 [17]. In a 1996 collaborative study organized by the community reference laboratory for salmonella (CRLS), the overall sensitivity (17 laboratories) to detect 120 CFU/g *Salmonella* Typhimurium from a 1 g sample with pre-enrichment was 85% (218/255) (Voogt et al. 1997).

In addition to published information, information on poultry faecal samples was available to the experts and was also used as a basis for the prior distributions chosen for the model. A graduate thesis by Siiskonen (2000) showed that without pre-enrichment test sensitivity was 23%, but with pre-enrichment it was 92%. In another study with five salmonella-positive poultry flocks (3 of these broiler flocks), sensitivity without pre-enrichment was 0.30 and with pre-enrichment 0.74 (Pelkonen, personal communication).

In the model, the distributions for flock sensitivity of the isolation methods were given as Uniform (0.3,0.5) and Uniform (0.65,0.85) for 1996-1998 and 1999, respectively (Figure 9). Since all suspected strains are verified by serotyping in the reference laboratory, the specificity was estimated to be virtually 100%.

Chance of horizontal infection (h and h_3)

Salmonella can be transmitted to a flock either vertically from breeding animals and/or horizontally from, for example, the environment, personnel or feeding stuffs. The transmission of salmonella could be modelled if the effect of these various

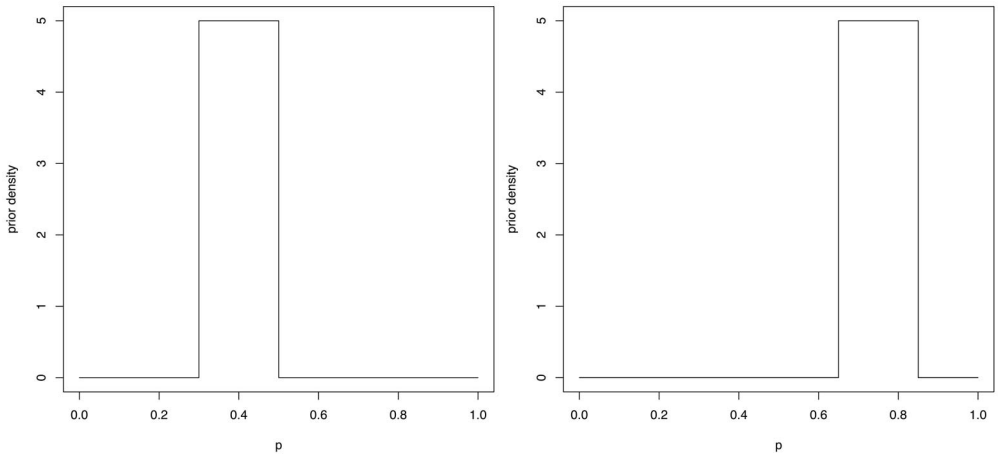


Figure 9.
Prior distributions of the sensitivity of the salmonella testing method used (p) in 1996-1998 (left) and 1999 (right) in the PPIM.

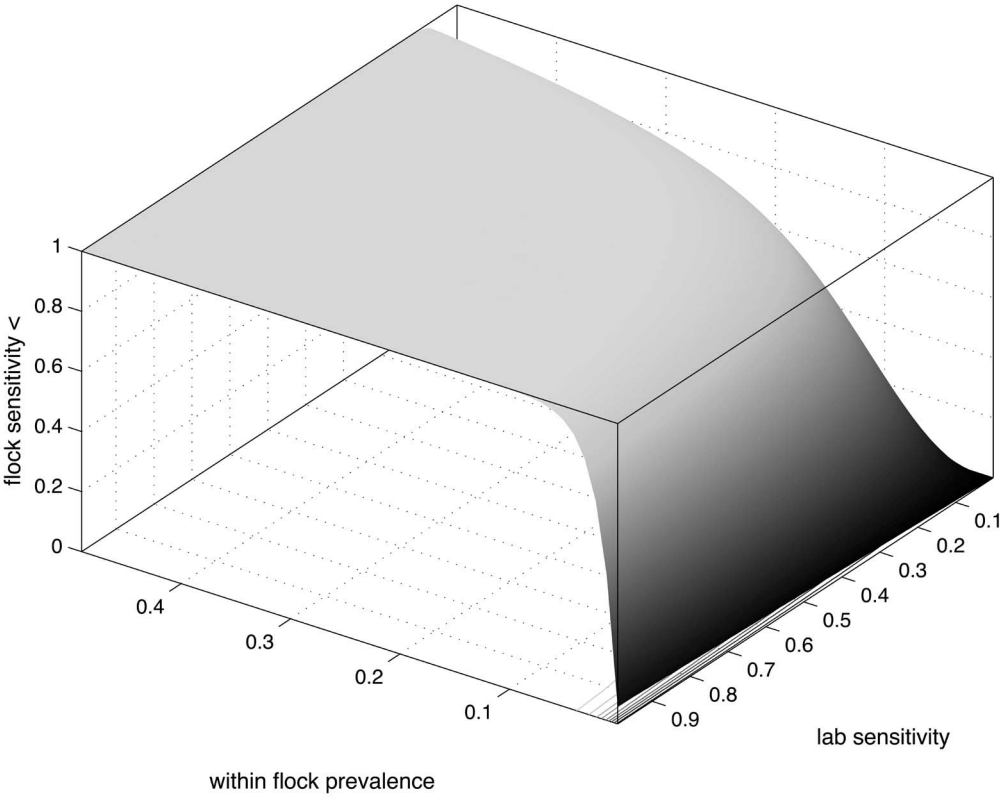


Figure 10.
Upper bound of flock sensitivity as a function of within-flock prevalence and lab sensitivity (assuming 6 pooled samples, each containing 10 individual subsamples). See section: Mathematics of the PPIM.

routes were known. Unfortunately, no such official data exist in Finland. For some data available in other countries, the risk factors can be examined (Angen et al. 1996; Chriél et al. 1999; Rose et al. 1999; Skov et al. 1999), but it is difficult to know how well these various factors apply to the situation in Finland, with its low salmonella prevalence.

The only data which could have been used was the difference between serotypes isolated from breeders and production flock. The only serotype isolated from a breeder flock in 1996-1999 is *S.* Infantis. The assumption that all *S.* Infantis contamination would be vertically-acquired, while all others would be acquired horizontally, would give a result as below (Table 8). However, since S. Infantis is also common in other animal species, it is probably also acquired horizontally, e.g. via feed. Therefore, this information was not used in the model.

Some prior information was obtained from experts, namely, that the chance of horizontal infection in broiler flocks (h_3) during their lifetime is the same or higher compared to that of breeder flocks (h) between two visits. The prior distribution of h_3 was then specified conditionally, given h. The prior distribution of h was uniform over the range [0,1] and the conditional density of h_3 was uniform over [h,1] (Figure 11, Figure 12).

Table 8.
The Serotypes isolated from production broiler flocks according to FSCP and their share from the whole (Seuna 2000).

Year	1996	1997	1998	1999
Anatum	4	5	2	2
Infantis	10	9	15	56
Isangi	4	0	1	0
Livingstone	0	5	0	5*
Montevideo	0	0	1	0
Salmonella ssp.	2	2	0	0
Tennessee	0	0	0	2
Thompson	3	0	1	0
Typhimurium	0	0	0	0
Yhteensä/total	23	21	20	64
Vertical transmission	0,43	0,43	0,75	0,88
Horizontal transmission	0,57	0,57	0,25	0,13

* Both S. Livingstone and S. Infantis isolated in one broiler flock

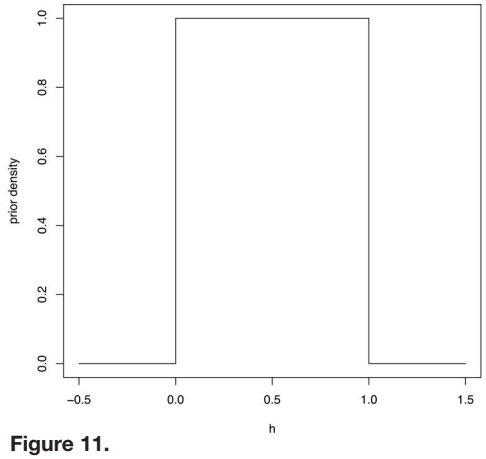


Figure 11.
Prior distribution of the chance of horizontal infection between two consecutive sampling times in breeder flocks (h) in the PPIM.

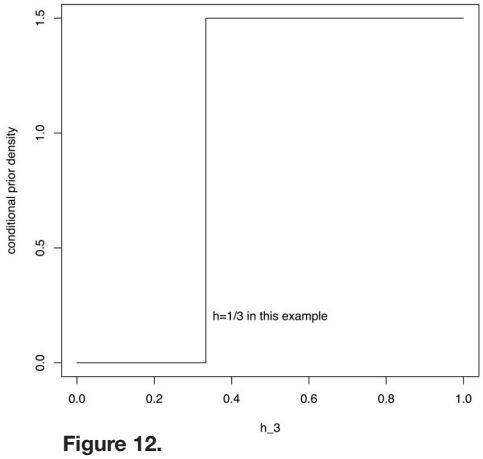
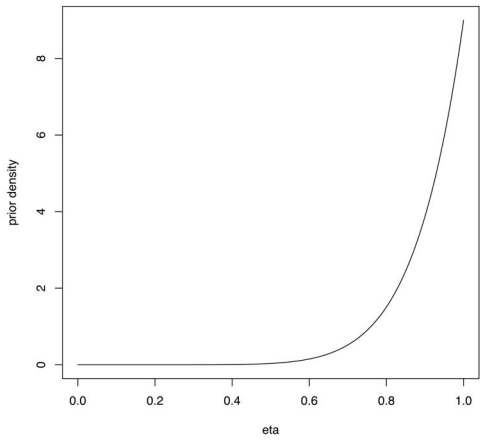


Figure 12.
Conditional prior distribution used for the chance (h_3) of horizontal infection in a broiler flock before sampling time in the PPIM.

Chance of ongoing infection to persist between two consecutive visits (η)

Once a flock is infected, the infection is likely to persist if no intervention is taken. Parameter η accounts for the natural duration of salmonella in such a situation. Since the model was defined stepwise according to the testing scheme (i.e. regular visits), this parameter represents the conditional probability that a salmonella infection would last at least from one visit to the next, given that the flock was infected at the time of the previous visit. According to expert knowledge, this probability is high if interventions are not taken. This knowledge is included in the form of the prior distribution of η (Figure 13).

Figure 13.
Prior distribution of the chance (η) that an ongoing infection will persist in the flock between two consecutive sampling times in the PPIM.



The effect of cross-contamination in the hatcheries (θ)

The probability of vertical transmission is defined to depend on the effective true prevalence of salmonella in the parent generation during the laying period. The functional form of this dependency had to be chosen to represent the plausible assumptions. We assumed that the probability of vertical transmission must always be at least as large as this prevalence. Different functional forms are shown in Figure 15. These simple functions are determined by a single parameter, θ, which controls the slope of the function. Results from hatcheries were used as basic information for experts in order to elicit the prior distribution for the cross-contamination parameter in hatcheries (θ), for a given function of the probability of vertical transmission (Figure 14). A summary of the conditional distributions elicited by expert opinion and their basic assumptions is presented in Table 9.

Figure 14.
Prior distribution of the parameter (θ) for the cross-contamination effect in the model of vertical transmission.

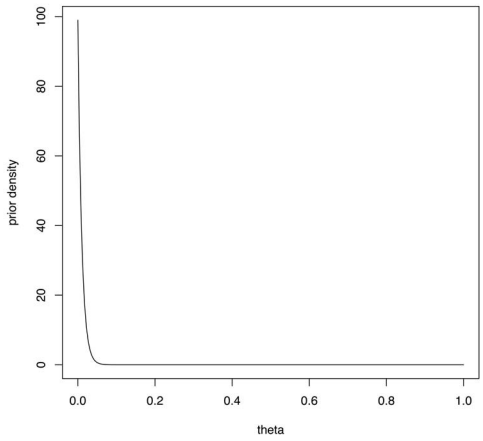


Figure 15.
Chance of vertical transmission as a function of effective salmonella (flock) prevalence during the laying period. Lower bound of the simple model and the polynomial model (solid line), upper bound of the polynomial model (dashed line), and lower bound of the exponential model (dot-dashed line). Reproduced from Ranta & Maijala (2002).

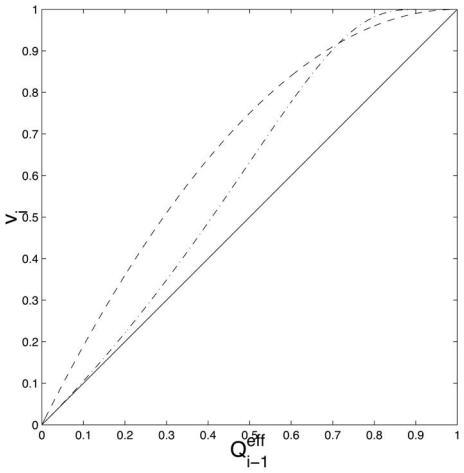


Table 9.
The prior distributions of model parameters in the PPIM, based on expert opinions and their basic assumptions.

Code	Parameter	Distribution/value	Basic assumptions
p	Sensitivity of salmonella testing method used.	In 1999 U(0.65,0.85). In 1996-98 U(0.3-0.5)	The inclusion of pre-enrichment had a clear improving effect on sensitivity. The change at 1.5.1999 affected on the results of the whole year.
-	Spesificity of salmonella analysis.	100 %	The test is 100 % specific i.e. no false positive exist in the statistics.
h	Chance of horizontal infection between two consecutive sampling times in breeder flocks.	Uniform (0,1)	No reliable data exists.
h_3	Chance of horizontal infection before sampling in broiler flocks.	Uniform (h,1)	Since the safety measures are higher in breeder than production flocks, h_3 was estimated to be at least equal or higher than h.
θ	Parameter describing the effect of cross contamination in the model of the chance of vertical transmission in hatchery.	Beta (1,99)	Usually the eggs from one-two-three flocks are pooled together in a hatchery. Therefore, the changes of cross contamination from a positive flock to a negative one were estimated to be relatively small.
η	Chance of ongoing infection to prevail in the grandparent and parent flocks between two consecutive samplings times.	Beta (9,1)	If a flock becomes infected by salmonella, it is difficult to cure. Therefore, a high prior probability was assigned for the event that an infection remains in an infected flock.

6.2.1.3. Outputs of the Primary Production Inference Model

After computing the PPIM, posterior probability distributions for different parameters can be obtained (Table 10) for various years. In general, very little difference can be seen between the estimated true prevalences (Q_3^{eff}) for broiler flocks and therefore it seems that the situation has been relatively stable over these years. The prevalence Q_3^{eff} was defined as the ratio (x_3 / n_3) of the number of infected broiler flocks and the total number of broiler flocks.

The PPIM ends at the stage where broiler birds are sent to slaughter. At this point, we have an annual data set of detected salmonella-positive broiler flocks 1-2 weeks before slaughter. Based on all the data and prior distributions in the PPIM, posterior distributions for the true annual incidence in broiler flocks can be obtained (Figure 16). According to the model, the mean true prevalences of salmonella in broiler flocks sent to slaughter were 2.3%, 1.9%, 1.9% and 2.9% in 1996-1999, respectively. This would imply that the increase of sensitivity in 1999 was not the only reason for the higher number of positive broiler flocks detected. The effect of increased sensitivity can be seen in the width of the distributions.

Table 10.
Marginal posterior probability distributions summarized by their means and standard deviations. In 1996-1998, [a,b]=[0.3,0.5], in 1999 [a,b]=[0.65,0.85].

	Year 1996		Year 1997		Year 1998		Year 1999		Prior
Quantity	Mean	Std	Mean	Std	Mean	Std	Mean	Std	
p	0.39	0.06	0.39	0.06	0.39	0.06	0.75	0.06	Uniform(a,b)
h	0.003	0.002	0.002	0.002	0.002	0.002	0.003	0.002	Uniform(0,1)
h_3	0.012	0.006	0.016	0.007	0.016	0.007	0.023	0.008	Uniform(h,1)
η	0.89	0.097	0.89	0.098	0.89	0.097	0.89	0.101	Beta(9,1)
θ	0.005	0.005	0.008	0.009	0.008	0.009	0.008	0.008	Beta(1,99)
v_2	0.006	0.024	0.004	0.019	0.003	0.017	0.004	0.016	-
v_3	0.012	0.005	0.004	0.006	0.004	0.006	0.007	0.008	-
x_3	64.5	14.0	57.3	13.1	55.3	13.0	86.7	8.7	-
Q_3^{eff}	0.02	0.005	0.02	0.005	0.02	0.005	0.03	0.003	-

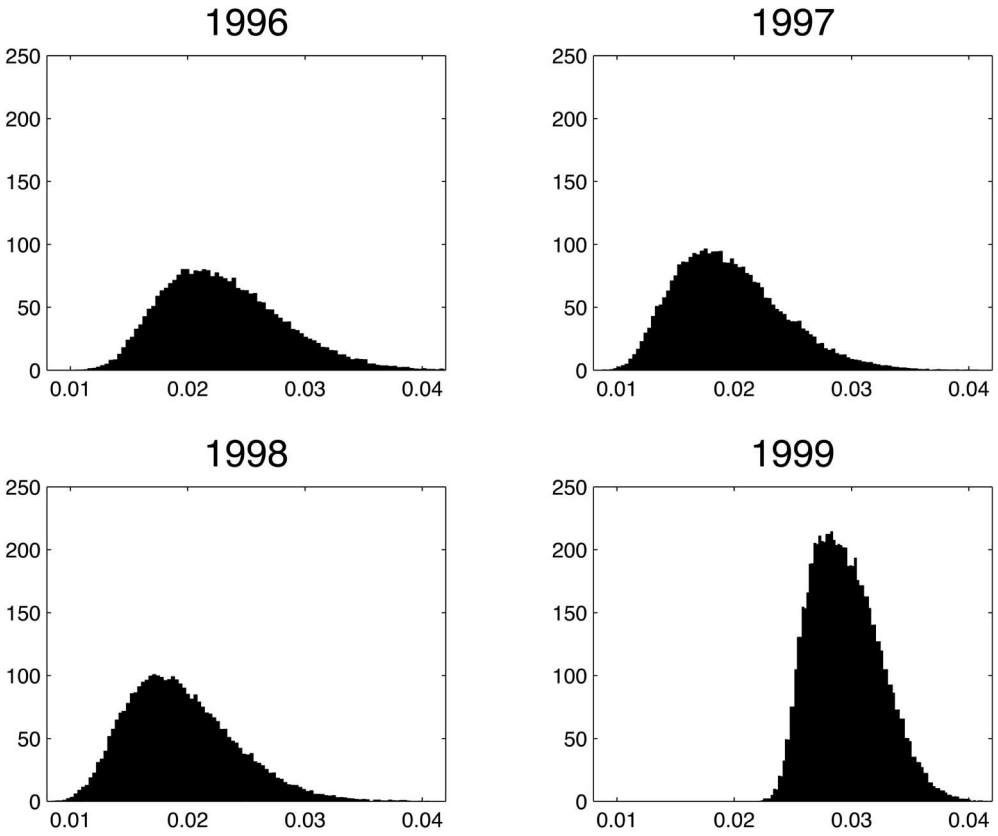


Figure 16.
Posterior distribution of true flock prevalence in broiler flocks for different years, taking into account the data originating from different years as well as the change of the microbiological analysis method in 1999.

6.3.1.4. Model Validation and Sensitivity Analysis

Posterior distributions may be sensitive to the choice of prior distributions for some parameters. The results of sensitivity analysis were reported in Ranta & Maijala (2002). The predictions were sensitive to the prior distribution of η. When the default prior was replaced by a prior distribution closely centred on 0.5, Beta(100,100), large

outbreaks did not occur. This shows that the effect of intervention is the larger the more persistent the infection in a flock. By contrast, if the chance η that an ongoing infection will persist between two visits is small, the effect of the intervention will diminish. However, with small η the chances of large outbreaks would also be small, regardless of whether intervention is adopted or not. As long as there are no data on the persistence of infection within flocks we need to rely on expert knowledge. The predictions were also sensitive to the prior of θ. When the prior Beta (1,99), mean 0.01, was replaced with Beta (1,4), mean 0.2, this resulted in a higher predictive probability of large outbreaks. In general, this is due to the sensitivity to the submodel specification of vertical transmission. Under any initial salmonella prevalence scenario in the grandparent flock population, the resulting predictions will depend on the assumed chance of vertical transmissions between flock generations in that situation. However, under the current low prevalence situation there were no empirical data to validate any particular model for v. applicable to the entire range of prevalences, especially for the high values. Therefore, worst case and best case scenarios should be compared if predictions with very high initial prevalence are needed.

6.3.1.5. Limitations of the Primary Production Inference Model

There are five main producers of broiler hatching eggs in Finland, all using Ross broiler breeders. The number of laying breeder flocks varies from 2 to 16 in different producers. The model does not take into account either the variable numbers of flocks per company or sizes of the breeder flocks. However, since the FSCP results are collected annually at the national level and no information on the sampling of a producer is collected in the central database (except when salmonella is detected), we did not think it necessary to define a submodel for each producer. The results from hatcheries obtained in the FSCP were not used in the model since they could not be traced back to the actual flocks of the next nor of the previous generation. Actually, the “flock-specific” faecal test results were not truly flock-specific, but rather flock-house specific. This uncertainty was taken into account via the assumption of a small number of possible temporal configurations for consecutive flocks in a flock house during a year. The results from hatcheries may be linked to any of the parent flocks and to any of the flocks in the next generation, which is an obstacle for a flock-specific model. Either more specific hatchery data are needed, or the model should be made more complex. Without specific data, it remains questionable if such a more complex model could provide useful results, or if the associated posterior distribution would even be computable.

Egg production by a breeder flock starts gradually. In general, a grandparent flock only produces eggs which are good enough for hatching 30-34 weeks per year and a parent flock 33-42 weeks (based on inquiry of broiler producers). However, flocks are sampled over their whole lifetime and FSCP statistics do not follow whether eggs are taken for hatching or not. Therefore, in the model, we assumed continuous production of eggs. This is not likely to be a severe problem since only the cumulative effective prevalence (proportion of visits at which the flocks were truly infected among all visits in all breeding flocks, during their laying period) is taken into the model of vertical infection pressure for the next generation.

The model of the chance of vertical transmission relies on information about the current situation, with low salmonella prevalence. It was not possible to estimate what this chance would be under considerably higher prevalence. Therefore, care should be taken when extrapolating the model to describe situations with considerably higher prevalence.

6.3.1.6. Mathematics of the Primary Production Inference Model

The PPIM is a joint probability distribution of all unknown variables and parameters. Given some observed values, we can compute the conditional distribution of the remaining unknown quantities, including e.g. predicted (replicate) values. The joint model is specified by the prior distributions and the chain of conditional distributions leading from parameters to data (Table 11).

Table 11.
A short summary of the conditional distributions used in the PPIM.

Quantity	Depends on	Conditional distribution, or function
p	Prior (in 1999)	Uniform{0.65,0.85}
p	Prior (before 1999)	Uniform{0.3,0.5}
η	Prior	Beta{9,1}
θ	Prior	Beta{1,99}
h	Prior	Uniform{0,1}
h_3	h	Uniform{h,1}
I_{1j1}	h	Bernoulli{h}
I_{1jt}	$I_{1j,t-1}$ = 0, h $I_{1j,t-1}$ = 1, h,η	Bernoulli{h} Bernoulli{1-(1-h)(1-η)}
Q_1^{eff}	I_{1jt} 4< t<9	(Σ I_{1jt}) / (No. of grandparent flock tests during laying period)
v_2	θ , Q_1^{eff}	Q_1^{eff} + θ (1-Q_1^{eff})
I_{2j1}	v_2	Bernoulli{v_2}
I_{2jt}	$I_{2j,t-1}$ = 0, h $I_{2j,t-1}$ = 1, h, η	Bernoulli{h} Bernoulli{1-(1-h)(1-η)}
Q_2^{eff}	I_{2jt} 4< t<9	(Σ I_{2jt}) / (No. of parent flock tests during laying period)
v_3	θ , Q_2^{eff}	Q_2^{eff} + θ (1-Q_2^{eff})
x_3	v_3, h_3, n_3	Binomial{n_3,1-(1-v_3)(1-h_3)}
d_3	p, x_3	Binomial{x_3,p}
Q_3^{eff}	x_3, n_3	x_3 / n_3
w_j	Prior of temporal shift of flock j.	Categorical{1/6,1/6,1/6,1/6,1/6,1/6}

Each of the quantities (parameters and variables) of the PPIM and their associated conditional distributions are summarized in Table 11. Also, some quantities defined by deterministic functions are listed because they appear as parameters of conditional distributions in the hierarchical model. In grandparent and parent flocks the true underlying infection status at each of the testing times is denoted by a state variable I_{ijt} which is either one or zero corresponding to the two states "infected" and "not infected". The probability model for the observed number of positive grandparent and parent laying flocks is a product of probabilities which depend on the state variables of the flock in question. For example, the probability that flock j in population i is detected (and terminated after that) at testing time t is

$$(1-pI_{ij1})(1-pI_{ij2})(1-pI_{ij3})\times\ldots\times(1-pI_{ij,t-1})p\ .$$

When the posterior distribution is computed, it is known which flocks were detected and at which testing times, because this information is given as data. Therefore, the exact formula depends on the actual data. This corresponds to the so-called likelihood

function in statistical jargon. When posterior predictive distributions are computed, another set of state variables for the whole primary production chain needs to be defined. These are called replicate variables, and the predictive distribution is in fact a simulated replicate process, conditionalized on the posterior distribution of the (hyper) parameters π, η, θ, h, and h_3. Mathematically, the posterior distribution is a conditional density $\pi(\bullet \mid \bullet)$ of the form

$$\pi(p,\eta,\theta,h,h_3,x_3,I_{ijt};i=1,2;j=1,...,j_i;t=1,...,9 \mid data),$$

where "data" denotes all the observed (fixed) values of variables. In short, if all the unknown parameters and variables on the left hand side of the condition sign ("|") are denoted by χ, and the replicate variables by χ^{rep}, then the posterior predictive distribution is of the form

$$\pi(\chi^{rep} \mid data) = \int_{\aleph} \pi(\chi^{rep} \mid \chi)\pi(\chi \mid data)d\chi ,$$

where $\aleph$ denotes the set of all possible values the unknown parameters and variables χ can take. Both the posterior predictive distribution and the posterior distribution $\pi(\chi \mid data)$ require numerical integration methods, such as MCMC (Markov chain Monte Carlo). Finally, the model accounts for the unknown timing of the lifespan of individual flocks within a calendar year. There may be several different flocks (i.e. different Markov processes) during a year. Each of the possible alternatives was given equal prior probability. Due to the discrete time Markov chain model, there were only 6 possible alternatives in the case of (at most) two consecutive flocks in the same flock house during a year. Each alternative corresponds to one configuration of the likelihood function, and the different configurations were coded in the model (i.e. as logical expressions in the WinBUGS code).

Flock sensitivity (p)

Overall flock sensitivity depends on the laboratory sensitivity of the testing method, the within-flock prevalence, and the number of individual samples collected. Prior distribution of flock sensitivity was elicited directly from expert opinion (resulting simply into a uniform distribution), but it could also be modelled as follows, assuming that the sample size is much smaller than the flock size. Let p_{lab} denote the laboratory sensitivity of the test, p_w the within flock prevalence, and n the number of individual samples. Then, the upper boundary can be derived as a function of p_{lab}, p_w and n:

$$P(+ \mid p_{lab}, p_w, n) = \sum_{x=0}^{n} (1-(1-p_{lab})^x) \binom{n}{x} p_w^x (1-p_w)^{n-x}$$

$$= 1 - \sum_{x=0}^{n} \binom{n}{x} ((1-p_{lab})p_w)^x (1-(1-p_{lab})p_w)^{n-x} \left(\frac{1-p_w}{1-(1-p_{lab})p_w} \right)^{n-x}$$

$$\leq 1 - \sum_{x=0}^{n} \binom{n}{x} ((1-p_{lab})p_w)^x (1-(1-p_{lab})p_w)^{n-x} \left(\frac{1-p_w}{1-(1-p_{lab})p_w} \right)^{n}$$

$$= 1 - \left(\frac{1-p_w}{1-(1-p_{lab})p_w} \right)^{n}$$

Uncertainty about flock sensitivity could then be quantified by addressing the uncertainty concerning p_{lab}, p_w and n. The number of individual samples is known to be n=10, and these are pooled together to conduct a single test. Thus p_{lab} describes the probability that a single truly positive individual sample leads to a positive test result. When many pooled tests are done, the overall flock sensitivity becomes (Figure 10)

$$p_{fsens} = 1 - (1 - P(+ \mid p_{lab}, p_w, n))^K \ ,$$

where K is the number of pooled tests. Combining this formulation explicitly with the PPIM could lead to a more realistic estimate of true prevalence. The current vague uniform prior on flock sensitivity may be an underestimate, but this remains a topic for further research.

6.3.2. Secondary Production Simulation Model (SPSM)

6.3.2.1. Summary of the Secondary Production Simulation Model (SPSM)

A simulation model was constructed in order to describe the secondary production chain after primary production up to the consumers (Figure 17). The results of the PPIM (marginal posterior distributions) were used as input distributions, i.e. prior distributions, for the simulations. In this way, we can exploit the inference results concerning the true number of infected flocks and the sensitivity of the testing method. For other parameters and variables not included in the PPIM, expert opinions and other data sources were used to derive an input distribution, i.e. a prior distribution for the Monte Carlo simulations. The PPIM only concerns primary production, and its results are only exploited as input distributions in the SPSM. The consumption module is also separate from the SPSM. There are very little data concerning consumption and hence the uncertainties are dealt with using the Consumption Inference Model (CIM), which utilizes records of reported human infections. Hence, the SPSM is a simple ”forward simulation model” which does not allow inference, i.e. probabilistic learning ”backwards”. The SPSM is only used for transforming the output of the PPIM into the number of contaminated servings, which is the input for the CIM. Although the SPSM was originally constructed to cover primary production

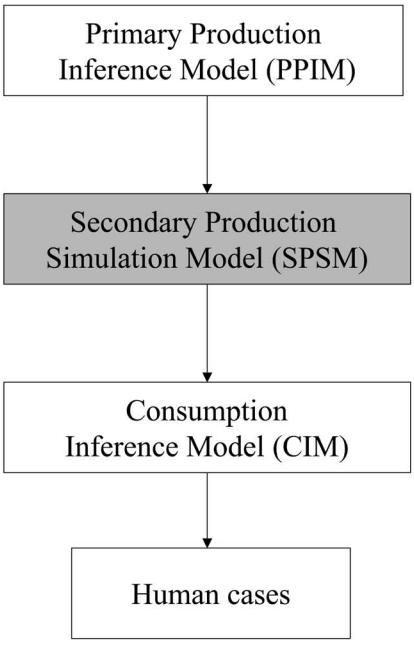


Figure 17.
The Secondary Production Simulation Model (SPSM) in the whole risk assessment model.

to the resulting human infections, it is not used alone as such, but in combination with the PPIM and the CIM. The predictive distribution (from SPSM) of the proportion of salmonella contaminated meat in the total volume of broiler meat was computed. In the simulation (20,000 Monte Carlo iterations) based on the situation in 1999, the mean was 0.21% and the mode was 0.17%. The 90% probability interval was [0.07% - 0.43%].

6.3.2.2. Inputs and parameters of the Secondary Production Simulation Model

The data used for SPSM were obtained from the FSCP, official statistics and the PPIM. In addition, we also elicited prior distributions from expert opinions of the resource group on model quantities where only limited or no information was available (Table 12). Data variables denote all those variables for which numerical data records exist, or for which observations could be made. These records can be used to specify the probability distribution for a simulation model describing uncertainty over the possible true values of that variable. In some situations these variables can also be fixed numbers. Model parameters denote abstract quantities for which observations are not possible, so expert opinions were used to quantify these. A summary of the distributions and values used in the SPSM (Figure 18) are presented in Table 12.

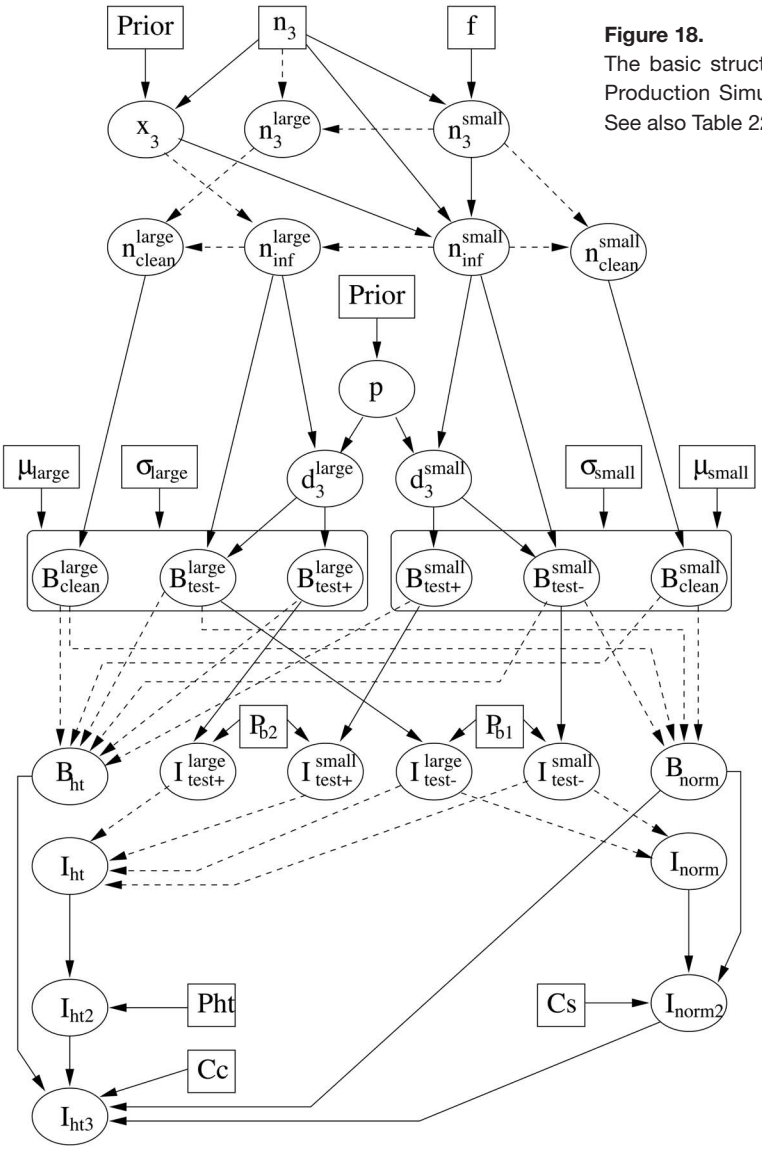


Figure 18.
The basic structure of the Secondary Production Simulation Model (SPSM). See also Table 22.

Table 12.
The inputs used in the Secondary Production Simulation Model. The parts covered by the PPIM or the CIM are shaded. These parts do not reproduce the same computation results of the inference modules, but could be used for Monte Carlo simulations where appropriate.

Code	Data variable	Source of information
n_1, n_2	Number of grandparent and parent houses for layers per year	Inquery for broiler companies and the Associaton of boiler producers
n_3	Number of broiler slaughter flocks per year	FSCP 1996-1999
T	Number of testing times of breeder flocks	FSCP 1996-1999
Mw	Meat Weight of a broiler carcase	Inquery for broiler companies
MRimp	Amount (kg) of imported raw meat	Food and farm facts Ltd
MPRimp	Amount (kg) of imported meat products	Food and farm facts Ltd
u	Percentage of raw meat (domestic or imported) used for making processed meat products.	Expert opinion about the amount of meat sold as raw meat versus the amount sold as meat products.
ssize	Size of a portion eaten.	The 1997 dietary survey of Finnish adults, National Public Health Institute
cfu	Colony forming units / gram at the time of consumption.	Consumption Inference Model
ncobs	Number of reported human cases attributable to broiler born salmonella.	Expert opinion & Zoonoses report.
Code	Model parameter	Source of information
p	Sensitivity of salmonella testing method.	Expert opinion.
-	Spesificity of salmonella testing method.	Expert opinion.
h	Chance of horizontal infection between the samplings in breeder flocks.	Primary Production Inference Model.
h_3	Chance of horizontal infection before sampling.	Primary Production Inference Model.
θ	Parameter describing the cross contamination effect in the hatchery (vertical infection model).	Primary Production Inference Model.
η	Chance of ongoing infection to prevail in a flock between two consecutive samplings.	Primary Production Inference Model.
f	Expected proportion of "small" flocks.	Expert opinion & total production volume from Food and farm facts Ltd
μ_{small}	Expected flock size of a "small" flock.	Expert opinion & total production volume from Food and farm facts Ltd
μ_{large}	Expected flock size of a "large" flock.	Expert opinion & total production volume from Food and farm facts Ltd
σ_{small}	Expected standard deviation of "small" flock sizes.	Expert opinion & total production volume from Food and farm facts Ltd
σ_{large}	Expected standard deviation of "large" flock sizes.	Expert opinion & total production volume from Food and farm facts Ltd
P_{b1}	Expected prevalence of salmonella infection within an infected flock which has been tested negative	Expert opinion
P_{b2}	Expected prevalence of salmonella infection within an infected flock which has been tested positive	Expert opinion
P_{ht}	Probability that an infected carcase remains infected after heat treatment	Expert opinion
Cs	Parameter for the model of increment of infection prevalence due to secondary infections during the slaughter and cutting processes	Expert opinion
Cc	Parameter describing cross contamination effect from non-heat treated carcases to heat treated carcases after heat treatment	Expert opinion
Pir	Expected % of positive lots in imported raw meat.	Inquiry for first destination stations in Finland, expert opinion
Pip	Expected % of positive lots in imported meat products.	Inquiry for first destination stations in Finland, expert opinion
Pl	Expected % of positive meat within a positive lot.	Expert opinion.
α,β	Parameters of the dose-response model.	WHO/FAO report (2002).
Psel	Chance for each infected human to become selected as a reported case.	Expert opinion.

Data variables

Data from Food and Farm Facts, Ltd on the slaughter, export and import of broiler meat was used (Table 13,Table 14). In addition, data obtained from broiler companies on the meat weight of broiler carcasses were available (Table 15).

Broiler meat of foreign origin (MRimp, MPRimp)

Information on the amount of foreign meat was obtained from Food and Farm Facts, Ltd. Results from the first destination centres were collected with an enquiry

(Table 16). However, not all the centres answered the questionnaire and therefore the information was used as the basis for expert opinion.

Table 13.
The amount of broiler meat slaughtered, exported and consumed annually in Finland (Suomen Gallup Elintarviketieto Oy).

Year	Slaughter (million kg)	Export (million kg)	Consumption (million kg)	Consumption (kg/ person)
1995	38,22	0,33	38,94	7,5
1996	44,93	0,21	44,65	8,6
1997	48,41	0,97	48,86	9,4
1998	55,98	0,84	55,48	10,7
1999	60,79	1,81	58,48	11,2

Table 14.
The amount (million kg) of broiler meat and meat products entering Finland in 1995-1999 (Suomen Gallup Elintarviketieto Oy 2000).

Year	Raw meat	Meat products	Total
1995	0,84	0,3	1,15
1996	0,37	0,24	0,61
1997	0,34	0,55	0,89
1998	0,36	0,69	1,05
1999	0,59	0,85	1,44

Table 15.
Part of the data used for the Secondary Production Simulation Model.

Code	Name of data	Smallest value	Average value	Highest value
Mw	Meat Weight of a broiler carcase	1020 g	1280 g	1520 g
MRimp	Amount (kg) of imported raw meat	340.000 kg		840.000 kg
MPRimp	Amount (kg) of imported meat products	240.000 kg		850.000 kg

Table 16.
Information obtained from an inquiry sent to first destination centres in Finland in 1999.

	Studied	Positive	% positive
Imported poultry meat	440 000 kg	6 000 kg	0.4%
Imported poultry meat	71 lots	5 lots	7.9%

Use of broiler meat (u)

The use, as percentage (u), of the slaughtered broiler raw meat used for making (heat-treated) meat products was based on the information in Table 17. Cross-contamination in the consumer's kitchen can be an important factor in transmitting salmonella from broilers to foodstuffs which are not heat-treated (such as salad). However, there is very little quantitative information on the behaviour of consumers.

Table 17.
Estimates of the shares of raw broiler meat, frozen broiler meat and heat-treated products sold in Finland.

Year	Raw broiler meat		Frozen broiler meat		Heat treated meat	
	Million kg	%	Million kg	%	Million kg	%
1999	42	72	1	2	15	26
1998	39	71	1	2	15	27
1997	34	69	1	2	14	29
1996	30	67	1	2	14	31
1995	25	64	1	3	13	33

Since the forward sampling technique used in @Risk modelling gives an estimate of the salmonella prevalence in meat at cutting plant as an output, this information was not used as an input in the model, but as a validation point (Table 20).

Slaughterhouses also provided information on the percentage of condemnation during slaughtering as well as on the meat weight of a broiler carcass. Since the condemnation percentage was so small compared to the variability in the other numbers, it was not taken into account in the model.

Model parameters

Expected within-flock prevalence (P_{b1}, P_{b2})

Since the sampling of broiler flocks is done by taking 60 samples and pooling them into 6 samples (each 10 subsamples), there are no bird-specific data for estimating the prevalence of salmonella in a flock tested positive for salmonella. Furthermore, there are no data on the prevalence of salmonella within a flock which has tested negative but yet would be truly infected.

Experts provided an opinion on the within-flock prevalence of salmonella in a truly infected but test negative broiler flock. This opinion was partly affected by the fact that all broiler flocks are treated with the competitive exclusion method when they arrive at the production unit from the hatchery. We chose 30% as the expected prevalence of salmonella within a flock which has tested positive. However, there is a dataset available on the numbers of positive pooled samples out of all pooled samples; it is a topic for further research whether these data could be used for estimating the within-flock prevalence. For the flocks which tested negative, yet are truly infected, we chose 3% as the expected prevalence.

Table 18.
The share of the number of positive samples in broiler flocks where salmonella was detected in 1998 and 1999 (source: industry inquiry). Six samples, each consisting of 10 subsamples, are taken.

No. of positive samples/ positive flocks	1998	1999	Total	Share in 1998	Share in 1999
1	6	28	34	46 %	43 %
2	5	8	13	38 %	12 %
3	0	2	2	0 %	3 %
4	0	6	6	0 %	9 %
5	2	12	14	15 %	18 %
6	0	9	9	0 %	14 %
All flocks	13	65	78	100 %	100 %

Cross-contamination during processing (Cs, Cc)

When a flock is infected, only some proportion of the birds in that flock are infected. Therefore, one contaminated carcass can infect other carcasses within the same flock or within another, initially clean flock. There are no Finnish data available on the effect of cross-contamination in slaughtering and cutting. Therefore, these two processing steps were pooled together and the experts were asked how many other carcasses one infected bird would cross-contaminate. However, for simulations, it is necessary to specify how many of the initially clean birds would be expected to be infected in each possible situation with a different initial infection prevalence. Therefore, a parametric function (with parameter Cs) was specified describing the probability for each initially clean bird to be infected, depending on the initial infection prevalence before slaughter. Moreover, all these effects need to be specified using annual total quantities. In order to help this, a graph showing the effects of various parameter values was presented to the experts (Figure 19).

A similar approach, i.e. the same mathematical function with a different parameter (Cc), was used to estimate cross-contamination from non-heat treated salmonella positive carcasses to heat-treated carcasses (Cc). The experts regarded that the probability p_{ht} that an infected carcass remains infected after heat treatment was $p_{ht} = 0.0$.

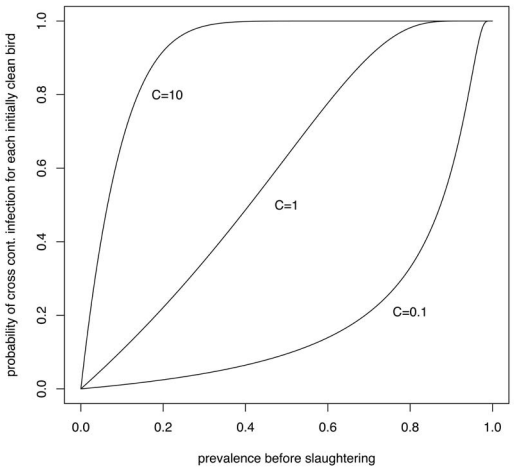


Figure 19.
The effect of various parameter values (C=10, 1, 0.1) on the expected percentage of cross-contaminated salmonella-positive carcasses among initially clean carcasses in slaughtering and cutting annually.

Expected flock sizes and standard deviations for small and large flocks (μ_{small}, μ_{large}, σ_{small}, σ_{large})

The broiler industry has been growing quickly; we may well assume that the number of producers has stayed almost the same, so the increase in production has been due to an increase in flock sizes. In the model, flocks were divided crudely into ”small” and ”large” (Figure 20), and the size distributions as well as the ratio of small to large flocks were adjusted to produce a distribution for a total production amount comparable to the known total amount of broiler meat produced in that particular year (Table 13). The width of the distribution reflects what total amounts might occur in a similar situation purely due to random changes in flock sizes and proportions of large and small flocks. This part of the model could be refined by using actual flock size data for each of the 2,939 flocks, but such data were not available to us. However, flock size information would become important if the infection probability of a flock were modelled to depend on flock size. Currently, this was not possible, so the infection probability is the same for every flock; flock size only affects the total production, which should closely match the known data point. Therefore, exact sizes of individual flocks are not very important in this model – the total amount produced is.

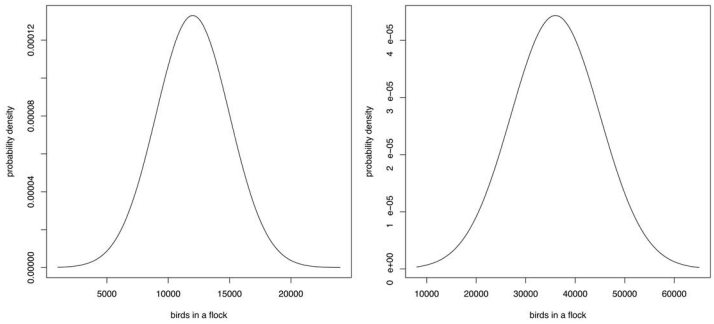


Figure 20.
Two normal distributions of the number of birds in a small (left) and in a large (right) broiler flock.

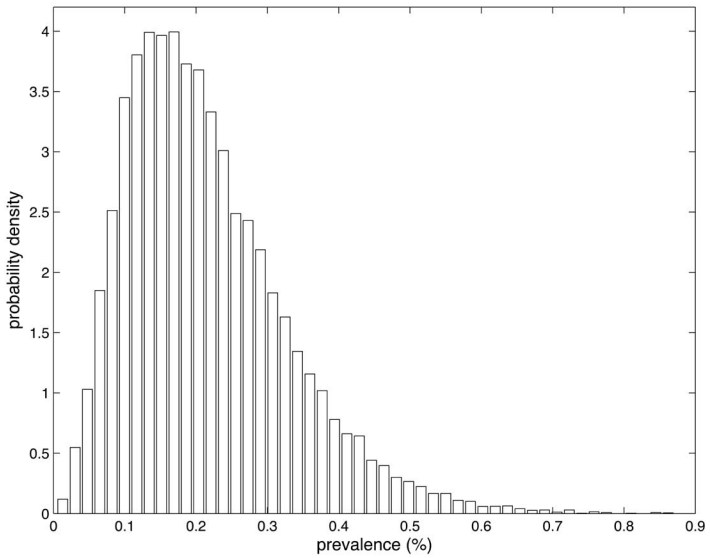
Expected proportion of contaminated meat entering Finland (p_{ir} , p_{ip} ,p_l)

Expert opinions were used to assess uncertainty about the expected proportion of contaminated lots of raw meat p_{ir} and processed meat p_{ip} and the expected proportion of contamination p_l within such lots. Uniform distributions were chosen to represent such uncertainty over a range of values.

Table 19.
Distributions and values based on expert opinion and industry inquiry used in the SPSM, and their basic assumptions.

Code	Parameter	Distribution/value	Basic assumptions
μ_{small}	Expected number of birds in a ”small” broiler flock	12000	Based on the inquiry for industry and the statistic of the total produced broiler meat, the division of the flocks to small and large was made for year 1999.
μ_{large}	Expected number of birds in a ”large” broiler flock	36000	Based on the inquiry for industry and the statistic of the total produced broiler meat, the division of the flocks to small and large was made for 1999.
σ_{small}	Expected standard deviation of the number of birds in a ”small” flock.	3000	Based on the inquiry for industry and the statistic of the total produced broiler meat, the division of the flocks to small and large was made for 1999.
σ_{large}	Expected standard deviation of the number of birds in a ”large” flock.	9000	Based on the inquiry for industry and the statistic of the total produced broiler meat, the division of the flocks to small and large was made for 1999.
f	Expected proportion of ”small” flocks.	0.825	Based on the inquiry for industry and the statistic of the total produced broiler meat, the division of the flocks to small and large was made for 1999.
u	Percentage of raw meat (domestic or imported) used for making processed meat products.	26 %	Expert opinion
P_{b1}	Expected prevalence of salmonella infection within an infected flock which has been tested negative	3 %	The infection passess through the flock and not all the birds are infected at the same time. The detection level of the method used is regarded to be rather good. The concrete number of infected birds has binomial distribution Bin(Pb1,N) where N is the number of birds in those flocks not detected, yet infected.
P_{b2}	Expected prevalence of salmonella within an infected flock which has been tested positive	30 %	The concrete number of infected birds has binomial distribution Bin(Pb2,N) where N is the number of birds in the detected positive flocks.
Cs	Parameter in the model of secondary infections during the slaughter and cutting processes	10	The probability of spreading infection increases dramatically after the initial infection prevalence is over 5% in carcases. After that, the slaughterhouses have difficulties in handling all the meat intended for heat-treatment. The probability of secondary infection is defined as a function of initial prevalence. Parameter Cs defines the slope of the chosen function. (See Figure 17).
Cc	Parameter in the model of Cross contamination from non-heat treated carcases to heat treated carcases after heat treatment	0.05	This parameter value corresponds to the chosen function similarly as with parameter Cs. (See Figure 17)
P_{ht}	Probability that an infected carcase remains infected after heat treatment	0	Since there were no previous knowledge of lots stayed infected in the heating process, it was assumed to be hundred percent effective
P_{ir}	% of positive lots in imported raw meat	Uniform (0.05,0.3)	Based on the information achieved from the inquiry for first destination services and other,non official information
P_{ip}	% of positive lots in imported meat products	Uniform (0,0.05)	Based on the information achieved from the inquiry for first destination services and other,non official information
P_l	% of positives within a positive lot	Uniform(0.3,0.6)	Expert opinion

Figure 21.
Predictive distribution (from SPSM) of the prevalence of salmonella in Finnish broiler meat based on data from 1999. Mean 0.21%, mode 0.17%. 95% probability interval [0.05%,0.49%]. (20,000 Monte Carlo iterations).



6.3.2.3. Outputs of the Secondary Production Simulation Model

The SPSM provides simulations of the amount of contaminated meat and the total amount of meat, including both domestic (Figure 21) production and meat entering Finland. These predictive distributions can then be further used as prior distributions in the CIM.

In order to make more accurate predictions, one would need to collect more data about consumers and the final doses of salmonella in broiler meat at the time of consumption. In addition, more data would be needed about secondary infections and cross-contamination effects at slaughterhouses and during processing. However, these are difficult or impossible to obtain because, ideally, prospective observations of the natural course of undetected salmonella contamination would be needed.

6.3.2.4. Model Validation and Sensitivity Analysis

To assess the part of the SPSM concerning slaughterhouses, the output of salmonella-positive broiler meat in the SPSM can be compared to information on the retail level obtained by a study done by municipal food control laboratories, EELA and the National Food Agency. In 1999, 147 Finnish and 11 foreign samples of retail poultry meat were studied; none were positive for salmonella (Hatakka et al. 2000). In 2000, 161 broiler samples from the retail market were studied; no positive samples were detected. Two of these were of foreign origin (Hatakka et al. 2001). The mean of the predictive distribution (Figure 21) of true salmonella prevalence in Finnish broiler meat (0.21%) is a little lower than the apparent prevalence reported in the FSCP in 1999 (0.61%). The latter prevalence is based on only 2 positive samples out of 329 samples studied in 1999 (Table 20). EELA and EVI have collected data from the official samples of various foodstuffs analysed in municipal food control

laboratories in the last few years (Hatakka & Maijala 2000). In 1999, none of 10 fresh poultry meat samples obtained from industry and 5 of 153 (3.3%) fresh poultry meat samples obtained from retail were positive for salmonella. In 2000, 2 of 34 fresh poultry meat samples (5.9%) obtained from industry and 5 of 178 (2.8%) samples obtained from retail were positive for salmonella. Unfortunately, these data do not differentiate the country of origin of the samples of broiler and turkey meat, and can also include several samples from the same source, e.g. in the case of a food-borne outbreak investigation.

In the simulation of secondary production we must move from describing flocks to actual numbers of birds. First, flock sizes need to be described. There were some data available about typical flock sizes, but the information was not accurate. However, the total amount (kg) of annual broiler meat produced is known. Ideally, the model should utilize this known data point for making inferences about the less accurately known flock sizes. Unfortunately, such probabilistic inference is not possible with @RISK simulations and is a difficult ill-conditioned inference problem in general. Therefore, the total amount of annual broiler meat is treated as random in the SPSM. In 1999, the total amount of broiler meat was 61 million kilograms. The flock sizes in the simulated predictive distribution were adjusted so that the resulting total amount has its expected value close to 61 million kg, and the variance was large enough to cover the values 61 ± 2 million kg (Figure 22).

Table 20.
Information on salmonella in poultry meat at cutting plants.

Domestic meat	Source of information	Year	% positive
Poultry meat (kg)	Own-cheks – inquiry	1999	0.03 %
Poultry meat (samples)	Own-cheks – inquiry	1999	0.25 %
Broiler meat (kg)	Own-cheks – inquiry	1999	0.03 %
Broiler meat (samples)	Own-cheks – inquiry	1999	0.32 %
Broiler and turkey meat	FSCP	1996	0.0 %
Broiler and turkey meat	FSCP	1997	3.1 %
Broiler meat	FSCP	1998	0.76 %
Broiler meat	FSCP	1999	0.61 %

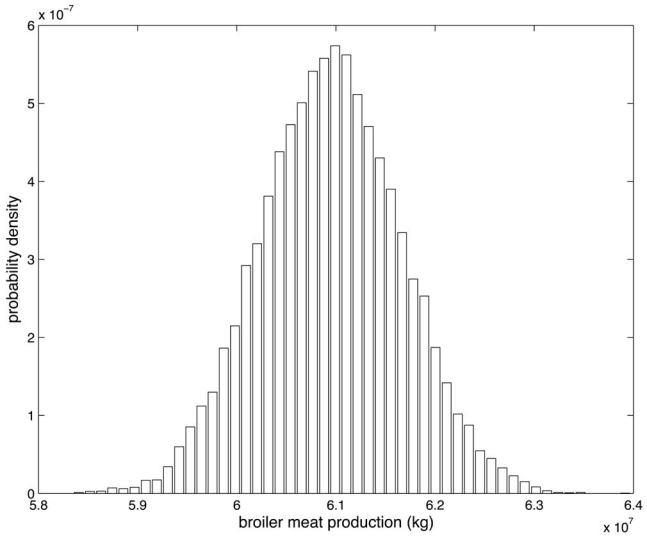


Figure 22.
Predictive distribution (from SPSM, @RISK) of the total annual amount of Finnish broiler meat (kg) produced, based on the simulated numbers of broiler flocks and data from 1999. Mean 61×10^6 kg, 95% probability interval $[59,62] \times 10^6$ kg. (20,000 Monte Carlo iterations).

Table 21.
The percentage of salmonella-positive samples in fresh broiler carcasses or parts of carcasses.

Year	No. Of samples	Salmonella positive (%)
1991*	25	4
1992*	95	10,5
1993*	100	4
1994*	109	9,2
1995*	101	1
1996*	100	3
1998*	114	0,9
1999**	147 (domestic)	0
1999**	11 (imported)	0
2000**	159 (domestic)	0
2000**	2 (imported)	0

* Data from National Veterinary and Food Research Institute
** Data from National Veterinary and Food Research Institute and National Food Authority

6.3.2.5. Limitations of the Secondary Production Simulation Model

In 1996-99, the size of broiler flocks sent to slaughter increased. However, no precise data were available, so we used information based on a 1999 slaughter house inquiry. In the model, we did not take into account the cross-contamination of salmonella from broiler meat to foodstuffs which are not heat-treated before consumption. Also, the effect of import depends a lot on the country of origin, but we did not consider different EU or third countries separately; rather, we quantified a total prevalence for broiler meat entering Finland.

The simulation model exploits the results of the inference model (PPIM). Ideally, the input distributions of the simulation model should equal the multidimensional joint posterior distribution obtained from the PPIM. However, @RISK software only allows us to specify input distributions one-by-one, i.e. as marginal distributions. It is possible to specify the correlation between different input variables but this only works well if there are linear dependencies between variables. It is also possible to import a set of simulated values (e.g. a MCMC sample from the PPIM) as a ”simulation table”, but this option is not very flexible with large simulations. Due to these software limitations, it is not very easy to construct a manageable large simulation model which can be based on multidimensional input distributions. Also, graphical visualization of results (multidimensional large samples) is limited in @RISK. Technical limitations become apparent when e.g. (posterior) probability distributions of some variables for a specific year are needed. Such probabilistic inference is not feasible with a Monte Carlo ”forward” simulation approach. Consequently, the simulation model cannot ”learn backwards” e.g. from the observed number of reported infections which, after all, is fairly well known compared to many other quantities, such as the CFU/g level per contaminated serving. Such, probabilistic learning was implemented in the CIM model, which takes the predicted number of servings from the SPSM as a prior distribution. The resulting prediction of the number of human infections is computed in the CIM, and not as a direct prediction from the SPSM. Even though the SPSM originally covered grandparent flocks down to human infections, for all these reasons it can only effectively simulate up to the amount of contaminated meat at retail.

6.3.2.6. Mathematics of the Secondary Production Simulation Model

Parameters p, η, θ, h and h_3 were given marginal probability distributions obtained from the corresponding marginal distributions of the joint posterior computed

in PPIM. The correct way to simulate the process onwards would be to utilize directly the multidimensional sample from the posterior. This can be done in e.g. Matlab (or WinBUGS) but is difficult or impossible to do with other software, such as @RISK. In our case, the joint posterior of these parameters was not extremely different from the independent samples of each marginal distribution. In general, it is important to consider the full joint distribution, and all simulations should respect the multidimensional probabilistic dependencies. However, @RISK software and Excel tools are not well-suited for such heavy numerical computation. Therefore, the @RISK implementation of the input distributions in the SPSM can be seen, at best, as an approximation of the actual multidimensional parameter distribution. Results concerning the PPIM and the CIM were obtained with WinBUGS and Matlab. The SPSM was effective only for Monte Carlo predictions of the processing steps and import. These simulations act as a link between the PPIM and the CIM, thus transforming the predictive distributions of the PPIM into priors for the CIM.

In general, a simulation model produces a conditional joint distribution $\pi(\bullet \mid \bullet)$ of all the variables, given some parameter values:

$$\pi(A,B,C,D \mid \text{parameters}).$$

Here, for the sake of simplicity, the variables are denoted arbitrarily by A,B,C and D, even though these letters do not correspond to the names of the actual variables in the SPSM. In practice this density is specified in a hierarchical form by defining further conditional densities which only depend on the "previous" variable(s):

$$\pi(A,B,C,D \mid \text{parameters}) = \pi(D \mid C, B, A, \text{parameters}) \times \pi(C \mid B, A, \text{parameters}) \times \pi(B \mid A, \text{parameters})\, \pi(A \mid \text{parameters})$$

In this way, each variable along the chain A,B,C,D depends on the values of the preceding variables and/or some parameters. The chain of variables eventually describes the assumed causal relationships in the production chain. However, the conditional probabilities do not themselves express causality as such, but rather the information content. In other words P(Y|X) can be interpreted as an uncertainty statement addressing the question: "what would be our uncertainty about the possible values of Y if we knew the value of X". In principle, a joint distribution can be defined in a number of different ways as a chain of conditional distributions. A complete list of conditional distributions in the SPSM is given in the table below. Only some of these are effectively used in the SPSM because the PPIM and the CIM already cover the inferential analysis.

The simulation model of the primary production chain is based on the conditional distributions introduced in the PPIM. The posterior distribution of model parameters from the PPIM were treated as input (prior) distributions for the SPSM. The number of grandparent and parent flock houses is known for each year, but the exact temporal flow of different flocks is not, and the corresponding flock lifetimes can fall partly within two consecutive years. Therefore, uncertainty about the temporal shifts of different flocks was modelled as a uniform discrete distribution over all possible shifts, as in the PPIM.

The total number of broiler flocks is n_3 , but n_3^{small} of them are simulated as "small" flocks with a given flock size distribution, while n_3^{large} of them are simulated as "large" flocks with a (possibly) different flock size distribution, specified by the user.

Table 22. The conditional distributions used in the SPSM. The parts covered by the PPIM or the CIM are shaded and do not reproduce the computation of these inference modules.

Quantity	Depends on	Conditional distribution or function
	Primary production	
p	Year 1999 Before 1999	Uniform{0.65,0.85} Uniform{0.3,0.5}
η	PPIM results	Beta{8.0514 , 1.0689}
θ	PPIM results	Beta{1.0564 , 127.8169}
h	PPIM results	Beta{2.1268 , 708.4709}
h_3	PPIM results, h	Beta{7.5423 , 320.2677} x (1-h)+h
I_{1j1}	h	Bernoulli{h}
I_{1jt}	$I_{1j,t-1}$ = 0, h $I_{1j,t-1}$ = 1, h, η	Bernoulli{h} Bernoulli{1-(1-h)(1-η)}
Q_1^{eff}	I_{1jt} 4< t<9	(Σ I_{1jt}) / (No. of grandparent flock tests during laying period)
v_2	θ, Q_1^{eff}	Q_1^{eff} + θ (1-Q_1^{eff})
I_{2j1}	v_2	Bernoulli{v_2}
I_{2jt}	$I_{2j,t-1}$ = 0, h $I_{2j,t-1}$ = 1, h, η	Bernoulli{h} Bernoulli{1-(1-h)(1-η)}
Q_2^{eff}	I_{2jt} 4< t<9	(Σ I_{2jt}) / (No. of parent flock tests during laying period)
v_3	θ, Q_2^{eff}	Q_2^{eff} + θ (1-Q_2^{eff})
x_3	v_3, h_3, n_3	Binomial{n_3,1-(v_3)(1-h_3)}, Alternatively a predictive distribution from a scenario computed in the PPIM.
Q_3^{eff}	x_3, n_3	x_3 / n_3
w_j	Prior of temporal shift of flock j.	Categorical{1/6,1/6,1/6,1/6,1/6,1/6}
	Secondary production	
f	Prior	0.825
n_3^{small}	f, n_3	Binomial(n_3,f)
n_3^{large}	n_3^{small}, n_3	n_3 - n_3^{small}
n_{inf}^{small}	x_3, n_3^{small} , n_3	Hyperg{x_3, n_3^{small} , n_3}
n_{inf}^{large}	x_3, n_{inf}^{small}	x_3 - n_{inf}^{small}
n_{clean}^{small}	n_3^{small} , n_{inf}^{small}	n_3^{small} - n_{inf}^{small}
n_{clean}^{large}	n_3^{large} , n_{in}^{flarge}	n_3^{large}- n_{inf}^{large}
d_3^{small}	p , n_{inf}^{small}	Binomial{n_{inf}^{small},p}
d_3^{large}	p , n_{inf}^{large}	Binomial{n_{inf}^{large},p}
d_3	d_3^{small}, d_3^{large}	d_3^{small} + d_3^{large}
B_{clean}^{small}	μ^{small} , σ^{small} , n_{clean}^{small}	Normal{ n_{clean}^{small} x μ_{small} , σ_{small} x n_{clean}^{small} }
B_{clean}^{large}	μ^{large} , σ^{large} , n_{clean}^{large}	Normal{ n_{clean}^{large} x μ_{large} , σ_{large} x n_{clean}^{large} }
B_{test-}^{small}	μ_{small} , σ_{small}, n_{inf}^{small} , d_3^{small}	Normal{(n_{inf}^{small} - d_3^{small}) x μ_{small} , σ_{small} x (n_{inf}^{small} - d_3^{small})}
B_{test-}^{large}	μ_{large} , σ_{large}, n_{inf}^{large} , d_3^{large}	Normal{(n_{inf}^{large} - d_3^{large}) x μ_{large} , σ_{large} x (n_{inf}^{large} - d_3^{large})}
B_{test+}^{small}	μ^{small} , σ^{small} , d_3^{small}	Normal{ d_3^{small} x μ_{small} , σ_{small} x d_3^{small} }
B_{test+}^{large}	μ_{large} , σ_{large}, d_3^{large}	Normal{d_3^{large}) x μ_{large} , σ_{large} x d_3^{large} }
I_{test+}^{large}	B_{test+}^{large} , P_{b2}	Binomial{B_{test+}^{large},P_{b2} }
I_{test+}^{small}	B_{test+}^{small} , P_{b2}	Binomial{B_{test+}^{small},P_{b2} }
I_{test-}^{large}	B_{test-}^{large} , P_{b1}	Binomial{B_{test-}^{large},P_{b1} }
I_{test-}^{small}	B_{test-}^{small}, P_{b1}	Binomial{B_{test-}^{small},P_{b1} }
B_{norm}	B_{clean}^{small}, B_{clean}^{large}, B_{test-}^{small} , B_{test-}^{large}	B_{clean}^{small} + B_{clean}^{large} + B_{test-}^{small} + B_{test-}^{large}
u	Prior	0.26
mkg	Prior	1.28 kg
Stdkg	Prior	0.122 kg
B'_{normkg}	B_{norm} , mkg, stdkg	Round{Normal{B_{norm} x mkg, stdkg x B_{norm}}}
B_{normkg}	B'_{normkg} , u	Round{B'_{normkg} x (1-u)}
I_{norm}	I_{test-}^{small} , I_{test-}^{large}	I_{test-}^{small} + I_{test-}^{large}
I_{normkg}	I_{norm} , mkg, stdkg	Round{Normal{I_{norm} x mkg, stdkg x I_{norm}}}
I_{norm2}	Cs, B_{norm} , I_{norm}	Binomial{Bnorm-Inorm,1-e $^{-Cs\ x\ (Inorm/Bnorm)/(1-Inorm/Bnorm)}$} + I_{norm}
$I'_{norm2kg}$	I_{norm2} , mkg , stdkg	Round{Normal{I_{norm2} x mkg, stdkg x I_{norm2}}}
$I_{norm2kg}$	$I'_{norm2kg}$	Round{$I'_{norm2kg}$ x (1-u)}
Prevalence2	I_{norm2} , B_{norm}	I_{norm2}/B_{norm}
B_{ht}	B_{test+}^{small} , B_{test+}^{large}	B_{test+}^{small} + B_{test+}^{large}
B_{htkg}	B_{ht}, B'_{normkg}, u, mkg, stdkg	Round{Normal{B_{ht} x mkg, stdkg x B_{ht}} + u x B'_{normkg} }
I_{ht}	I_{test+}^{small} , I_{test+}^{large}	I_{test+}^{small} + I_{test+}^{large}
I_{htkg}	I_{ht} , $I'_{norm2kg}$, u, mkg, stdkg	Round{Normal{I_{ht} x mkg, stdkg x I_{ht}} + u x $I'_{norm2kg}$ }
P_{ht}	Prior	0
I_{ht2kg}	P_{ht} , I_{htkg}	Binomial{I_{htkg},P_{ht}}
I_{ht3kg}	Cc, prevalence2, B_{htkg} , I_{ht2kg}	Binomial{B_{htkg} - I_{ht2kg} ,1-e $^{-Cc\ x\ (prevalence2)/(1-prevalence2)}$} + I_{ht2kg}
Prevalence3	I_{ht3kg} , $I_{norm2kg}$, B_{normkg} , B_{htkg}	(I_{ht3kg} + $I_{norm2kg}$)/(B_{normkg} +B_{htkg})
Minftotal	I_{ht3kg} , $I_{norm2kg}$	I_{ht3kg} + $I_{norm2kg}$
Mtotal	B_{normkg} , B_{htkg}	B_{normkg} + B_{htkg}
MPRFIN	Output variable	B_{htkg}
CMPRFIN	Output variable	I_{ht3kg}
MRFIN	Output variable	B_{normkg}
CMRFIN	Output variable	$I_{norm2kg}$
	Import	
P_{ir}	Prior	Uniform{0.05,0.3}
P_{ip}	Prior	Uniform{0,0.05}
P_I	Prior	Uniform{0.3,0.6}
MRimp	Prior	Uniform{340000,840000}
MPRimpFIN	Output variable	Round{MRimp x u}
CMPRimpFIN	MRimp, u, P_{ir} , P_I	Round{MRimp x u x P_{ir} x P_I }
CMPRimpFINht	$P_{ht,}$ CMPRimpFIN	Binomial{CMPRimpFIN, P_{ht} }
CMPRimpFIN2	Output variable	Binomial{MPRimpFIN-CMPRimpFINht, 1-e $^{-Cc\ x\ (CMRimp/\ MRimp')/(1-CMRimp/MRimp')}$} +CMPRimpFINht
MRimp'	Output variable	Round{MRimp x (1-u)}
CMRimp	Output variable	Round{MRimp x (1-u) x P_{ir} x P_I }
MPRimp	Output variable	Uniform{240000,850000}
CMPRimp	Output variable	Round{MPRimp x P_{ip} x P_I}
	Consumption	
nser	CMtotal , Ssize	(CMPRFIN+CMRFIN+CMPRimpFIN2+CMRimp+CMPRimp)/ssize
cfu	CIM result	In current situation: joint posterior distribution (CIM) with total number of servings nser. Other scenarios: marginal posterior distribution Beta{2.99,17185.4} (CIM).
ssize	Prior	Normal{126,20}
p	cfu, ssize, α , β	1-(1+cfu x ssize/α)$^{-\beta}$
α	Prior	21.159
β	Prior	0.2767
nc	p, nser	Binomial{nser,p}
psel	Prior	Beta(20,80)
ncobs	psel, nc	Binomial(nc, psel)

Furthermore, the number of ”small” flocks is random (uncertain) according to a defined probability, with an expected proportion of small flocks equal to f.

The total number of infected broiler flocks is x_3, which has a conditional binomial distribution. This variable can also be assigned a predictive distribution according to the scenarios implemented in the PPIM. Given the value of x_3, and the values of n_3^{small} and n_3 , the number of ”small” infected broiler flocks x_3^{small} is hypergeometrically distributed within these parameters. The number of ”large” infected broiler flocks is then simply x_3 - x_3^{small}. The numbers of detected ”small” and ”large” flocks are d_3^{small} and d_3^{large} which have conditional binomial distributions with a common probability parameter p (i.e. the sensitivity). The total number of detected broiler flocks d_3 is the sum of these two.

B_{clean}^{small} is the total number of birds from completely infection-free flocks with a ”small” flock size given by mean μ_{small} and standard deviation σ_{small} per flock. Likewise, B_{clean}^{large} is the total number of birds originating from completely infection free flocks with a ”large” flock size given by mean μ_{large}, and standard deviation σ_{large} per flock.

B_{test+}^{small} is the total number of birds in those flocks which were detected (i.e. test positive) and ”small”. This has a normal distribution arising from the sum of d_3^{small} approximately normally-distributed flock sizes. Likewise, B_{test+}^{large} is the total number of birds in those flocks which were detected and ”large”. B_{test-}^{small} is the total number of birds in flocks which were infected and ”small” and test negative. This has a conditional normal distribution arising from the sum of x_3^{small} - d_3^{small} normally-distributed flock sizes. B_{test-}^{large} has an analogous definition.

I_{test+}^{small} is the total number of infected birds in flocks which were detected and ”small”. It has a conditional binomial distribution with parameters P_{b2} and B_{test+}^{small} where P_{b2} represents the expected within flock prevalence in a flock which is known to be test positive. I_{test+}^{large} has the same interpretation with ”large flocks”.

I_{test-}^{small} is the total number of infected birds from all ”small” flocks which were truly infected but test negative. This has a conditional binomial distribution with the parameters P_{b1} and B_{test-}^{small}. Similarly, I_{test-}^{large} is defined for ”large” flocks. P_{b1} is the expected within-flock prevalence in a flock which is test negative, yet truly infected.

All test negative flocks undergo normal treatment. Therefore, the total number of such birds is the sum of all birds in all truly clean flocks and all test negative (but truly infected) flocks. The total is $B_{norm} = B_{clean}^{small} + B_{clean}^{large} + B_{test-}^{small} + B_{test-}^{large}$. The number of infected birds among them is $I_{norm} = I_{test-}^{small} + I_{test-}^{large}$. The ratio of these gives the initial infection prevalence in the normal treatment.

All test positive flocks are assumed to undergo heat treatment. The number of heat-treated birds is $B_{ht} = B_{test+}^{small} + B_{test+}^{large}$ and the number of infected birds among them is equal to $I_{test+}^{small} + I_{test+}^{large}$. The ratio of these gives the initial infection prevalence before heat treatment.

It is assumed that due to heat treatment the infection prevalence drops to zero for those birds undergoing heat treatment. However, in normal treatment it is possible that infection spreads due to secondary infections between birds and due to the slaughter process. The resulting infection prevalence depends on the initial prevalence and the assumed increment model describing the increase of prevalence, expressed in total annual numbers. The following binomial distribution was adopted to describe the total number of such secondary infections:

$$Binomial(B_{norm} - I_{norm}, probability)$$

where B_{norm} is the total number of birds undergoing normal treatment and I_{norm} is the number of initially infected birds among them. The probability parameter of the

binomial distribution is a function of the initial prevalence I_{norm}/B_{norm}:

$$probability = 1 - e^{\left(\frac{-Cs \times I_{norm}}{B_{norm}}\right) \Big/ \left(1 - \frac{I_{norm}}{B_{norm}}\right)}$$

where Cs is a parameter defining the shape of the function. A value of Cs=10 was chosen to obtain a curve in agreement with expert opinion. The final annual number of infected birds is computed by adding the number of annual secondary infections to the annual initial number of infected birds in normal treatment. The number of birds is then converted to kilograms. The weight of each broiler is assumed to follow a normal distribution with a mean mkg=1.28 kg and standard deviation stdkg=0.122 kg. Solving the distribution of the sum of independent and identically-distributed normal random numbers gives the total amounts of both infected and clean broiler meat annually after slaughtering and possible heat treatment. Some of the raw meat is used for producing processed food products, and these also undergo heat treatment. The proportion of such raw meat is u and this is accounted for when computing the kilograms that end up either as sold raw or sold processed meat.

Some heat-treated birds can get contaminated afterwards by cross-contamination. This increment of prevalence is modelled in a similar fashion to secondary infections above. The number of heat-treated meat kilograms B_{htkg} (all clean after treatment) that were afterwards cross-contaminated is modelled by a binomial distribution

$$Binomial(B_{htkg}, probability)$$

where the probability parameter is defined as a function of the salmonella prevalence (prevalence2, after accounting for the secondary infections above) among the birds which were not heat-treated:

$$probability = 1 - e^{\frac{-Ccxprevalence2}{(1-prevalence2)}}$$

and where parameter Cc defines the shape of the function. A value of Cc=0.05 was chosen to obtain a curve in agreement with expert opinion. Consequently, the expected prevalence due to cross-contamination among heat-treated meat is low, but an increasing function of the prevalence among birds in normal treatment. The resulting total prevalence (prevalence3) describes the total proportion of salmonella-contaminated broiler meat in Finnish production, after slaughterhouse and processing.

Meat entering Finland is divided into two groups: raw meat (MRimp) and processed meat (MPRimp). Uncertainty about the quantities of each is described by a uniform distribution whose range is defined by the minimum and maximum value over the years 1996-1999. Likewise, uncertainty about the salmonella prevalence in each group is described by a uniform distribution in agreement with expert opinion. Uniform distributions were derived both for the proportion of contaminated lots (P_{ir} and P_{ip}) and for the within-prevalence (P_I) of a lot. The overall prevalence of infected meat entering Finland (raw and processed) is then the product of these two, (P_{ir} x P_I and P_{ip} x P_I), assuming the lots are of equal size. The amount of contaminated meat entering Finland (raw and processed) is obtained as the product of the amount and the corresponding prevalence.

Finally, consumed meat is divided into five groups: (A) domestic processed meat made from domestic broilers, (B) domestic processed meat from broiler meat entering

Finland, (C) processed meat entering Finland, (D) domestic raw meat and (E) raw meat entering Finland. The amount of meat in groups (A,B) is obtained as proportion, u, of the total amount of raw (domestic and non-domestic) meat. Likewise, the amount of meat in groups (D,E) is obtained as proportion, 1-u, of the corresponding total amount. The amount of meat sold in group (A) is denoted as MPRFIN in the above table. The amount of meat sold in group (B) is MPRimpFIN. The amounts of meat sold in groups (C-E) are MPRimp, MRFIN and MRimp. The amount of contaminated meat in each group is denoted by a similar notation. Raw meat entering Finland used for producing processed meat is heat-treated, so the salmonella contamination is assumed to be zero. However, there may be cross-contamination after heat treatment. This is modelled to depend on the initial prevalence in raw meat entering Finland. The mathematical form is the same as above with other cross contaminations. The model does not consider further food preparation or processing by consumers. The amount of contaminated meat represents a computational estimate of the total amount of broiler meat that has a nonzero level of contamination before final storage and preparation in homes, restaurants, retail etc.

6.4. Risk characterization

The ultimate goal of this risk assessment was to estimate the risk of human cases of illness caused by salmonella in broilers. This depends on the estimated number of contaminated servings (computed from the SPSM, following the PPIM results), but also on the assumed dose-response model and its parameters, including the unknown level of contamination at the time of consumption. Furthermore, only some of the true cases of illness end up as reported cases. We chose a beta-Poisson model with fixed parameters as the dose-response model. This model was calibrated to the current situation (1999) by estimating the CFU-parameter using data on the reported cases and knowledge about under-reporting (CIM). The predictive distribution of the number of reported human cases caused by salmonella in broilers is shown in Figure 31. This is based on the current situation (1999), so we assume that detected positive breeder flocks are eliminated and that meat originating from broiler flocks detected positive for salmonella are heat treated.

6.4.1. Consumption Inference Model (CIM)

6.4.1.1. Summary of the Consumption Inference Model (CIM)

The dose-response model specifies the probability distribution for the number of human cases of illness for each specified set of values for (1) the parameters in the model, (2) the number of contaminated servings, (3) the average size of the servings, (4) and the average CFU/g levels in such servings. The number of contaminated servings was described by a probability distribution resulting from the secondary production simulation model (SPSM). This represents the number of servings that would be contaminated at least before final preparation and storage.

We took the parameters for the dose-response model from the literature. The size of servings was quantified as a distribution deduced from the consumption data. CFU/g levels at the time of actual consumption are highly uncertain, as there are no reliable data sources available and experts are consequently also unsure of these figures. If a probability distribution for CFU/g were specified so that it would represent this uncertainty, it would need to support a wide range of values, in fact so wide that the resulting predictive distribution of human cases would be unrealistic. However,

for the observed years, e.g. 1999, the total number of reported human cases of salmonella is known. From this figure we can estimate the likely number of cases due to broiler meat, for example on the basis of the serotypes and phagetypes detected in broilers, broiler food, and the types detected from the human cases. This estimate may contain less uncertainty than direct opinions of the CFU/g in the total population of contaminated servings – at the actual time of consumption. Therefore, we can treat the estimate of human cases of illness due to broiler meat as an ”observed” data value, or expert opinion, and compute a posterior distribution for average CFU/g, given this estimate and the prior densities for the number of servings and the average size of the servings. Furthermore, we can simultaneously take into account the under-reporting of human cases within the same inference model. This approach accounts for many of the uncertainties while, at the same time, utilizing the only truly observed consumption-related data: reported human infections. The inputs and sources of information are listed in Table 23.

Based on data from 1999, if detected positive breeder flocks were not removed this could result in 1.6-fold more human cases of illness compared to the situation under the FSCP. If heat treatment were not used, this could result in 4.1-fold more human cases of illness compared to the situation under the FSCP. If neither of these were in use, this could result in 5.6-fold more human cases of illness.

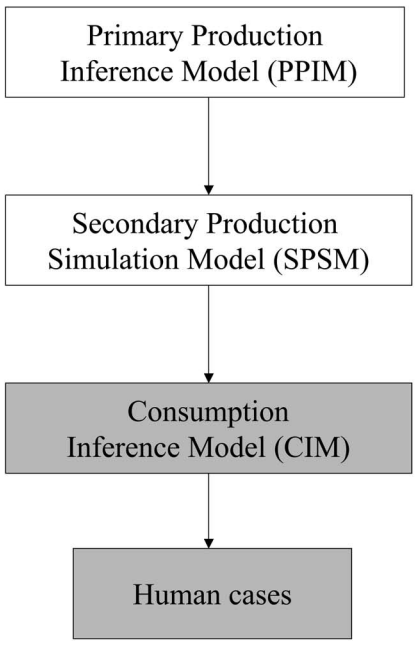


Figure 23.
The Consumption Inference Model (CIM) in the whole risk assessment model.

6.4.1.2. Inputs and parameters of the Consumption Inference Model

Data variables

Share of broiler-borne cases of human cases of illness (ncobs)

An estimate of the human cases caused by salmonella from broiler meat is not directly available in Finland. Therefore, we compared the serotypes isolated from broilers or broiler meat with the reported human cases in order to estimate the proportion of broiler-caused cases among all reported cases. For this calculation, we used data from 1999. All the common serotypes were included, taking into account the proportion of domestic cases out of all reported human cases caused by these serotypes. This resulted in total of 423 domestic cases with common serotypes, including 386 cases of *S.* Typhimurium.

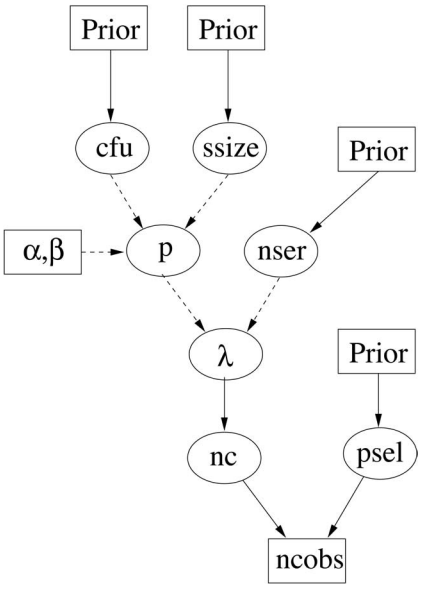


Figure 24.
Graph of the conditional distributions in the CIM. Rectangular nodes denote observed or given data values. See also Table 26.

Table 23.
Input variables and parameters used in the CIM.

Code	Data variable	Source of information
nser	Number of contaminated servings	Output from SPSM
ncobs	Estimated number of registered human infections due to salmonella from broiler meat	Zoonoses in Finland 1995-1999. Ministry of agriculture and Forestry
ssize	Size of one serving (g)	The 1997 dietary survey of Finnish adults, National Public Health Institute
cfu	Average colony forming units / gram at the time of consumption.	No prior information required. (Uninformative prior distribution chosen).
Code	Model parameter	Source of information
α	Dose-response model parameter (Beta-Poisson)	WHO/FAO, p 40 (2002)
β	Dose-response model parameter (Beta-Poisson)	WHO/FAO, p 40 (2002)
psel	Probability that a human disease case becomes reported (under reporting)	Elintarvike-eritystilanne –työryhmän muistio 1997, UK tutkimus

S. Typhimurium is one of the main domestic serotypes in humans in Finland. Based on phagetyping in 1999, two isolates from broiler flocks were of the same phagetype with humans, namely FT 1 (248 human cases, 1% of foreign origin). However, in 1995-98, FT1 was not detected in broilers or broiler meat at all, but it is the typical phagetype of cattle and pig production. Therefore, an estimate of 246 human reported cases was still felt to be an overestimate of the number of cases due to broilers. As a crude estimate, the percentage of two broiler isolates out of all isolates of *S.* Typhimurium FT1 from animals and food (25) was used as the upper level (8%), resulting in 20 human cases of illness in 1999. Even this might still be an overestimate, since in other years no FT1 isolations were detected in broilers. Therefore, we estimated that a total of 58 cases (Typhimurium + others) were caused by broilers in 1999. Although this estimate was derived manually, it would be possible to develop a formal model for this estimate, based on the total number of reported cases, phagetype information, and consumption data, but this remains a topic for further research. The graph of the CIM is shown in Figure 24.

This estimate can be compared to Danish data, where 10-14% of human salmonellosis cases (276 infections in 2000) were estimated to have been caused by imported poultry and 2-4% by broilers (71 infections in 2000) (Ministry of Food, Agriculture and Fisheries 2001).

Average level of contamination (cfu)

The level of contamination at the time of consumption is an important factor in the risk to consumers. This level depends, for example, on the characteristics of the strain, the microbiological ecology of the food, the initial contamination of raw material including consideration of regional differences and seasonality of production, the level of sanitation and process controls, the methods of processing, packaging, distibution and storage of the foods as well as any preparation steps such as cooking and holding (Codex Alimentarius Commission 2000). One approach would have been to ask experts about all these issues and build a model for all these steps. The experts could have been asked to estimate the level of contamination at the time of consumption (including storage, preparation, cross-contamination, etc.) bearing in mind the information presented in Table 24 and Figure 25.

In the Netherlands, most fresh (89%) and frozen chicken (68%) samples taken from local stores (n = 89) contained less than 10 salmonella cells per carcass (Dufrenne et al. 2001).

The processing of broiler meat in the consumer's kitchen involves two types of risks: inefficient cooking and cross-contamination. For example, humidity levels during processing significantly affected the survival of salmonella in a study where 107 CFU/g were inoculated into chicken breast patties and processed in an air convection oven at 177°C (Murphy et al. 2001). With low humidity, salmonella cells survived such heat treatment.

The heat treatment of broiler meat in an oven has recently been modelled by Hartnett et al. (2001), who formulated a theoretical model for heat treatment as $T(t)=50.789\ln(t)-106.12$. Based on a Finnish study (25 families), this model could also be applied relatively well to the Finnish situation (Virtanen S-M 2001), although it was not included in this model.

Table 24.
The level of salmonella contamination in fresh broiler carcasses at retail shops in Finland (National Veterinary Institute – personal communication Tuula Johansson).

Year	No. Samples	% positive	CFU /g
1991	25	4.0	9
1991	9	78,0	7-116**
1992	95	10.5	4-33*

* one sample > 387
**based on one positive lot

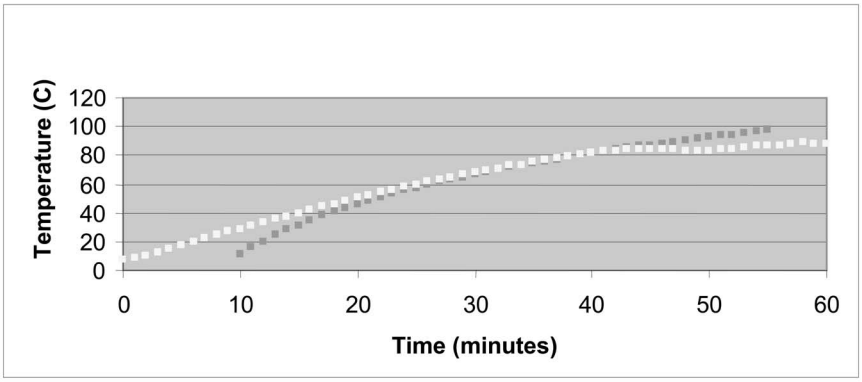


Figure 25.
The average temperature of chicken processed in Finnish consumers' ovens compared to the theoretical model (Virtanen S-M 2001).

Unfortunately, very little data existed in Finland concerning the various steps of food preparation and storage, so it was not possible to quantify the actual CFU/g level (at the time of consumption), even as an expert opinion. Therefore, Bayesian inference was used in the CIM for computing the likely average contamination level based on the available information on the true number of reported human cases, the chosen dose-response model, the serving size and the number of contaminated servings. The latter is obtained from the SPSM as a probability distribution. Hence, it is possible to start with an uninformative prior distribution for the average CFU/g, e.g. a uniform distribution over a suitably wide range to cover all the plausible values (Figure 26). As a result, a posterior distribution of CFU/g is obtained, representing the plausible average values according to information on these other quantities.

Number of contaminated servings (nser)

The number of contaminated servings is calculated simply by dividing the total amount of contaminated meat by the average serving size. The total amount (kg) of contaminated meat is given by the SPSM as a probability distribution (Figure 27). Different interventions and scenarios considered in this assessment have an effect on this total amount only, and hence on nser. The probability distributions are then taken as prior distributions in the CIM.

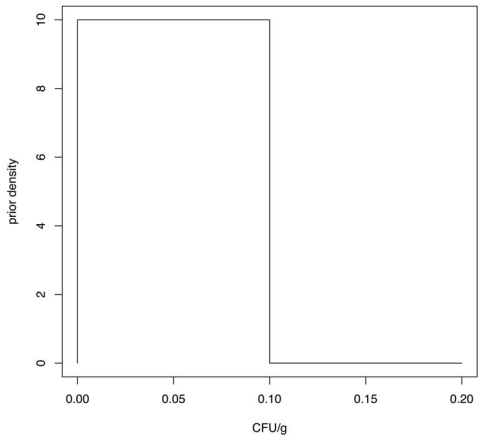


Figure 26.
Prior density of final average CFU/g in a originally contaminated serving.

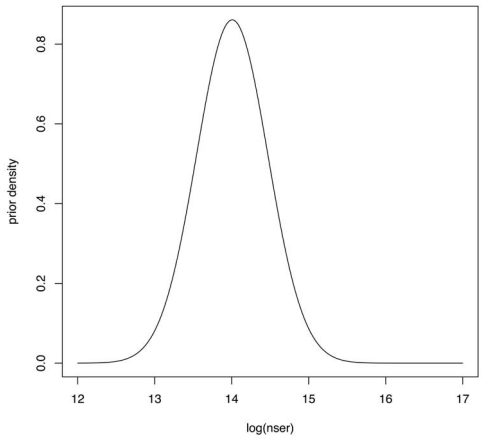


Figure 27.
Prior density of the logarithm of the number of contaminated servings (ln(nser)).

Serving size of broiler meat (ssize)

Consumption of broiler meat has been steadily increasing in Finland for many years. In 1996-1999, annual consumption increased from 8.6 kg to 11.2 kg per person, i.e. 29% (Table 13). In the model, it was assumed that this increased consumption is not due to an increase in portion size but to an increased frequency of eating broiler meat in its various forms.

The consumption of poultry meat in the National FINN DIET 1997 survey probably also includes some turkey meat (National Public Health Institute 1998). Therefore, the average consumption of females (126 g/day) was used in the model (Figure 28). The average consumption of males was 170 g/day. 11% of female respondents (1,501) had consumed poultry meat the previous day compared to 9% of male respondents (1,361). This database does not cover children nor people over 65. In the model, it

was assumed that this amount is eaten only once a day and could therefore be used as a portion size. Furthermore, it was assumed that the propotion of boneless meat was not important since most pieces of poultry include some bones.

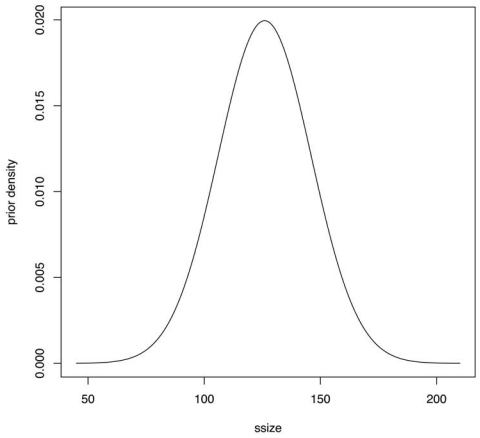


Figure 28.
Prior density of the size (in grams) of one serving (ssize)

Model parameters

Dose-response model (α,β)

A Beta-Poisson dose-response model was chosen with parameters (α,β) for a normal population taken from the WHO/FAO report (WHO/FAO 2002).

Expected reporting of infections in humans (psel)

In Finland, physicians have to notify clinical cases caused by *S.* Typhi and *S.* Paratyphi B to the Contagious Disease Register in the National Public Health Institute. Laboratories have to notify all confirmed salmonella cases, usually based on bacteriological culturing. Samples are taken from persons suffering from diarrhea, people in close contact with them, and from asymptomatic persons working in risk professions. Salmonella species identification is done with biochemical methods and by the agglutination of cultures by salmonella antisera. Phagetyping is done for *S.* Paratyphi, *S.* Typhimurium, and *S.* Enteritidis.

Wheeler et al. (1999) conducted a study on the reporting rate of some foodborne diseases. According to them, 72.7% of salmonella cases visited a physician, 36.5% were positive for salmonella in laboratory analysis and 31.8% were reported to the national register. In Finland, it has been estimated that approximately 10% of all salmonella cases are reported to the national registers (Ruutu 2001). Since this information is relatively weak, we used a range of 10-30% for reporting activity

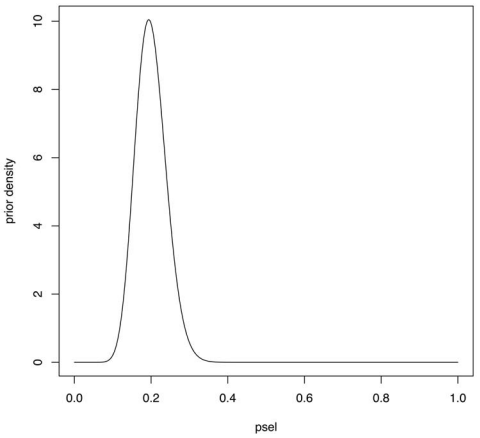


Figure 29.
Prior density of the chance (psel) that an individual (salmonella) case of illness is reported as a case of salmonella.

(Figure 29). This may still be an overestimate since the origin (domestic/foreign) of many of the reported cases cannot be identified. In the CIM, the variable ncobs describes the number of cases which are reported and identified as of domestic origin, and attributable to broiler salmonella.

Table 25.
The prior distributions used in the CIM, based on expert opinions and their basic assumptions.

Code	Parameter	Value / distribution used	Basic assumptions
α	Dose-response model parameter (Beta-Poisson)	21.159	The model used can be fitted also for Finnish population
β	Dose-response model parameter (Beta-Poisson)	0.2767	The model used can be fitted also for Finnish population
ncobs	Estimated number of registered human infections due to salmonella from broiler meat	58	The comparision with sero- and phagetypes was used
psel	Chance that an infected human case becomes reported as a disease case (under reporting)	Beta(20,80)	Value should be in the range 0.1-0.3
cfu	Final contamination (cfu/g) at the time of consumption	Uniform(0,0.1)	Uninformative prior density over a wide range of values expressing vague prior knowledge.
ssize	Size of one serving (g)	Normal(126,20)	The data of this one survey can be used for this model
ln(nser)	Logarithm of the number of contaminated servings.	Normal(14.286,0.4659)	Fitted distribution from the output of the simulation model (SPSM)

6.4.1.3. Outputs of the Consumption Inference Model

The marginal posterior distribution of mean CFU/g and the number of contaminated servings, based on the estimated number of human cases of illness (ncobs = 58), is shown below. As a result, the most probable values appear along the ”boomerang” shaped distribution (Figure 30). Large values of CFU/g together with a small number of contaminated servings is just as probable as small values of CFU/g together with a large number of contaminated servings. This is the summary information we get from the CIM as an output. When simulating predictions under the same assumptions and background scenario (such as conditions in 1999), the number of human infections are simulated with parameters taken from this joint distribution (Figure 31).

The resulting number of human cases depends on the total number of consumed contaminated meals and the dose-response model. The former quantity is provided by the previous steps of the simulation model (SPSM), and the latter can be chosen among several equally plausible models.

We have chosen a Beta-Poisson dose-response model whose parameters were taken from Fazil et. al (2000). The distributions of numbers of infections have

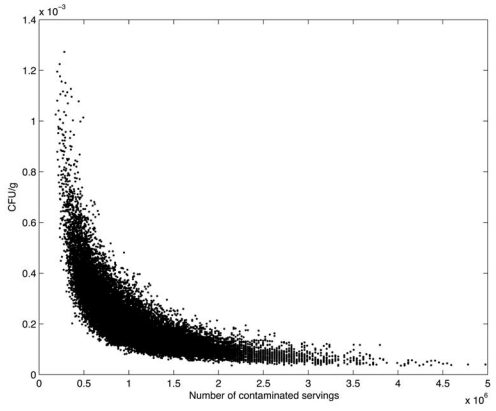


Figure 30.
MCMC sample from the marginal joint posterior distribution (CIM) of the mean number of colony forming units at the time of consumption (CFU/g) and the number of initially contaminated servings (nser) (100,000 MCMC iterations). The marginal mean of CFU is 0.0002, Std 0.0001.

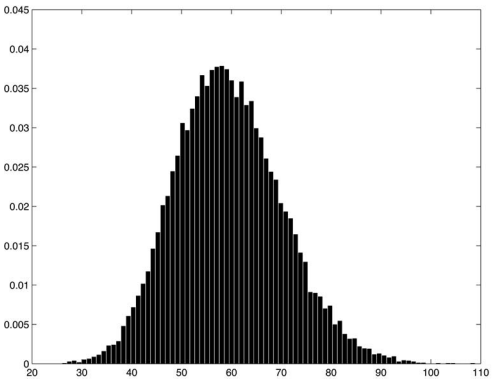


Figure 31.
Predictive distribution of the number of annually reported salmonella cases in humans. Mean 59, mode 58. Result based on data from 1999, 100,000 MCMCiterations. 95% probability interval [39-82].

extremely long tails which means that there is a small probability of a very large outbreak. Different dose-response models can yield different predictions.

The Beta-Poisson model we chose was presented by the USDA/FDA in the *Salmonella* Enteritidis Risk assessment, and is based on human feeding trial data for *Shigella dysenteriae*. Fazil et al. (2000) compared it to outbreak data and, on a purely empirical basis, concluded that this curve does tend to capture the upper range of these data.

6.4.1.4. Model Validation and sensitivity analysis

The effect of different estimates of the number of reported human cases due to broiler salmonella was studied by allowing ± 20% deviation from the estimate. This corresponds to 46 or 70 reported infections instead of 58. The resulting marginal posterior means and standard deviations of mean CFU/g were then (1.349E-4, 7.703E-5) and (2.04E-4, 1.198E-4), respectively. Since the default estimate, 58, produced a result of (1.741E-4, 1.007E-4), the difference was not significant. If needed, larger uncertainty could be included in the inference model, which would then account for it. Indeed, this approach is being developed further in ongoing risk assessments on salmonella. The inference model was also expanded by describing our estimate, 58, to follow a conditional Poisson distribution with a mean equal to the unknown true number of reported human infections due to broiler salmonella. This resulted in a posterior distribution of the latter quantity to be in the range of 40-80. The marginal mean and standard deviation of mean CFU/g were then (1.735E-4, 1.033E-4), respectively. Validation and comparison against an observed value of CFU/g is not currently possible, because there are no data about levels of CFU/g at the actual time of consumption. However, by definition, a contaminated serving must have at least one colony-forming unit of salmonella bacteria. If the average serving

size is 126g, the average level of contamination should be at least 1/126=0.008 CFU/g for such servings. The posterior mean was 0.0002 CFU/g. This is because the SPSM estimates the amount of contaminated meat as a total that would be contaminated before the final storage and preparation, but these steps were not included in the model. If the food is prepared properly, the actual contamination level at the time of consumption can be smaller than 0.008, because many initially contaminated servings will then have 0 CFU/g, as indicated by the low posterior mean.

We were able to compare these predictions of reported human cases with the actual records for years closely resembling 1999. These numbers were in reasonable agreement, although it would be better to account for the differences in total production before making such comparisons, i.e. by computing a scenario prediction with a different production volume.

6.4.1.5. Limitations of the Consumption Inference Model

The model can only describe the average levels of CFU/g in the total population of contaminated servings at the time of consumption. It would be interesting to describe the levels separately in different groups of broiler meat products because there may be important differences between them. However, this would ideally require an estimate of the reported number of human cases of illness resulting from each group of products, which is difficult to make. The same problem concerns e.g. different types of restaurants and different habits of preparing food. Alternatively, a direct survey of contamination at the time of consumption would be needed, but this would be expensive because large samples would be needed due to the current low prevalence of salmonella contamination. However, the interventions that are assessed here only affect the numbers of resulting contaminated servings and not the final levels of CFU/g. Hence, it can be sufficient for our present purposes to quantify average levels of CFU/g for the total population.

Another limitation of the model is that, although it is straightforward to compute (using WinBUGS) the posterior distribution of model parameters, especially CFU and nser, and to generate posterior predictive distributions from these, it is more difficult to generate predictions using different scenarios concerning the number of contaminated servings. A new scenario is fictitious, so we do not have a realized data value for the number of reported human cases (ncobs) for that scenario. We do still have the marginal posterior density of cfu obtained from the CIM, but the joint posterior of cfu and nser no longer exists. Instead, we use a new marginal prior density, $nser^{scen}$. Sampling independently of these two marginal densities (cfu and $nser^{scen}$) would yield an unrealistically large variance for the prediction. Another approach is to use pointwise stochastic coupling between the two marginal densities, the marginal posterior of nser obtained from the CIM, and the marginal prior of $nser^{scen}$ according to the new scenario. This coupling mechanism was applied when computing predictions under different (counterfactual) scenarios. In some simulation literature stochastic coupling is also known as syncronization of simulations.

6.4.1.6. Mathematics of the Consumption Inference Model

The final dose (CFU/g) at the time of consumption is uncertain, as is described by the posterior distribution obtained from the CIM. The prior distribution was chosen to be uniform over a range of plausible values. The size of each serving is also uncertain; this is described by a normal prior distribution based on data about consumption. The number of consumed contaminated servings is obtained by dividing the amount of contaminated meat by the serving size. The conditional probability of illness is obtained using a beta-poisson model with the parameters given in Fazil et. al. (2000).

In the beta-Poisson model, the probability of illness was calculated as

$$p = 1-(1+dose/21.159)^{(-0.2767)}.$$

Using these probabilities, the final number of human cases of illness (nc) is derived from a binomial distribution with the corresponding number of consumed servings. Finally, the number of reported cases (ncobs) depends on the chance of becoming a reported case (psel) and the total number of all cases of illness. The result is given by the conditional binomial distribution Bin(psel, nc).

The following joint posterior distribution was computed using WinBUGS software:

$$\pi(cfu, nc, nser, psel, ssize \mid ncobs, \alpha, \beta) \propto$$
$$\pi(ncobs \mid psel, nc)\, \pi(nc \mid nser, cfu, ssize, \alpha, \beta)\, \pi(psel)\, \pi(ssize)\, \pi(nser)$$

where (α,β) are the parameters of the dose-response model chosen, nc is the true number of cases of illness due to broiler, nser is the true number of contaminated servings due to broiler, ssize is the serving size, and psel is the selection probability that a human case of illness is reported. ncobs is the estimated number of reported human cases due to broiler. The marginal posterior density of CFU/g was used with various scenarios affecting the amount of contaminated servings, but not the level of CFU/g per serving.

Table 26.
A short summary of the conditional distributions used in the CIM.

Quantity	Depends on	Conditional distribution, or function
ssize	Prior	Normal{126,20}
ln(nser)	Prior, SPSM results	Normal{14.29,0.466}
$\ln(nser^{scen})$	Prior, SPSM results	Pointwise stochastic coupling with nser.
cfu	Prior	Uniform{0,0.1}
psel	Prior	Beta{20,80}
p	cfu,ssize,α, β	$1-(1+cfu \times ssize/\alpha)^{-\beta}$
λ	p,nser	p x nser
nc	λ	Poisson{λ}
ncobs	nc,psel	Binomial{nc,psel}

7. The effects of interventions

Four scenarios were studied using the model: A, describing the current situation estimated on the basis of year 1999; B, the situation where one grandparent flock is infected; C, the situation where five parent flocks are infected; and D, the situation where half of the domestic retail broiler meat would be replaced by 20-40% contaminated meat.

Two interventions were studied in each scenario: the removal of detected positive breeder flocks, and the heat treatment of meat originating from detected positive broiler flocks. All intervention combinations were studied: without both interventions, with both interventions, and with only one of the two interventions.

In terms of broiler production, the FSCP contains several interventions to prevent the spread of salmonella. These include:

1) Giving restrictive orders for breeder flocks detected positive for salmonella. This results in slaughtering of the birds.
2) Cleaning and disinfecting the infected poultry farm and negative sampling results after cleaning and before new birds are taken in.
3) Epidemiological investigations in order to identify the source of infection.
4) Slaughtering salmonella-positive flocks at the end of the day.
5) Heat treatment of meat originating from broiler flocks detected as positive for salmonella.
6) Demanding salmonella certifications for poultry meat entering Finland.

In this model, only the effect of slaughtering breeder flocks and the heat treatment of salmonella-positive meat were taken into account as possible interventions, as the effects of the other interventions were difficult to quantify.

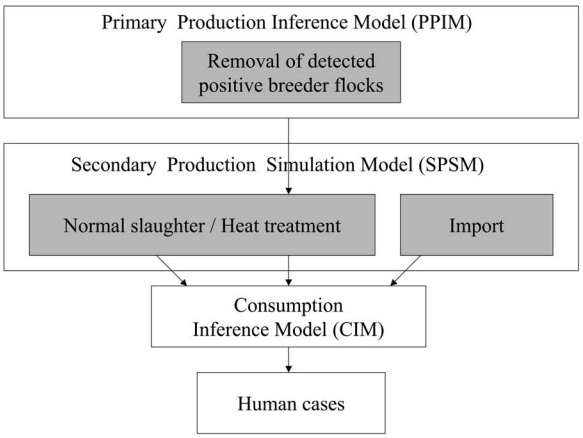


Figure 32.
Schematic picture of the modelled interventions.

The PPIM provides a probability distribution of the number of truly infected broiler flocks for any given year for which we have data. Similarly, with a given dose-response model, the CIM yields a probability distribution of the average level of contamination per serving (CFU/g) for a specified year for which we have observations on the reported number of cases. To assess interventions predictively, simulations provide the computation of predictive probability distributions for ”another year of the same kind”. This means that the posterior distribution of the controlling parameters is first computed describing the parametric uncertainty, and then events in the production process are random according to the parameter values drawn from this posterior distribution. Additionally, some parameters may still need to be given solely by expert opinion as point values or as (prior) probability distributions. The posterior distribution of the parameters is based on available data concerning some previous year(s) and is a probabilistic summary of what can be inferred, or learned, from such observations. This task calls for an inferential approach which can be implemented by WinBUGS, for example.

7.1. The effect on the number of infected broiler flocks

In scenario A, the current situation was modelled. First, the effect of removing salmonella positive breeder flocks was studied. In predictive simulations, it is possible to experiment with two alternative control strategies. In the first, no intervention is taken. In the second, a flock in the grandparent and parent populations is removed whenever a positive test result is made, thus reducing the number of infective laying periods and the chance of vertical transmission. Consequently, this affects the number of truly infected broiler flocks. These predictive distributions can be drawn from the PPIM alone and can be further used as input distributions for the simulation model describing the production process at the slaughterhouse stage and onwards.

Based on 1999 data, the predicted mean number of truly infected broiler flocks was 145 out of 2,939 (SD 119) if the salmonella positive breeder flocks would not have been removed, with a 95% probability interval [1.3%, 17.4%]. With removal of positive breeder flocks, it was 91 (SD 34), with a 95% probability interval [0.9%,5.8%] (Figure 33) (Ranta & Maijala 2002).

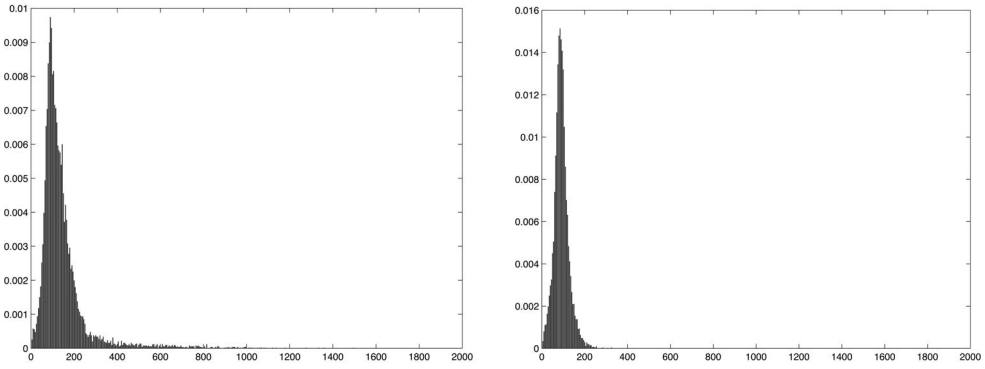


Figure 33.
Posterior predictive distribution (based on observed data in 1999) of the number of infected broiler flocks, with no intervention (left), and with intervention (right). The total number of flocks is 2,939. Reproduced from Ranta & Maijala (2002).

In scenario B, where one grandparent flock is infected at the beginning of the laying period, the effect of removal becomes more dramatic. The predicted mean number of infected flocks under no intervention was 575 out of 2,939 (SD 364), with a 95% probability interval [2.8%,45.1%]. With removal of positive flocks, the probability interval for salmonella in broiler flocks sent to slaughter would not differ much from the current situation resulting in 95 flocks (SD 36), with a 95% probability interval [1.0%-5.9%] (Figure 34) (Ranta & Maijala 2002).

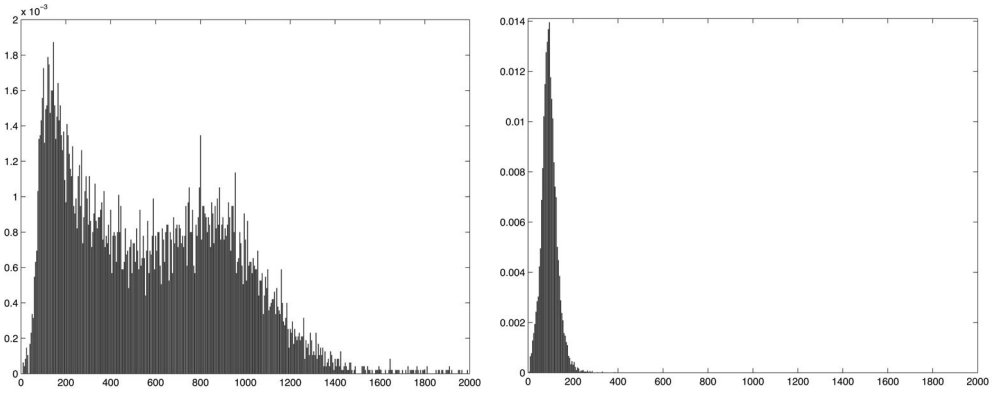


Figure 34.
Posterior predictive distribution (based on observed data in 1999) of the number of infected broiler flocks with no intervention, given that one of the grandparent flocks is truly infected at visit 4 but not detected at visits 1,2,3 (left). Similarly, the predictive distribution with intervention (right). The total number of flocks is 2,939. Reproduced from Ranta & Maijala (2002).

7.1.1. Computation of interventions for broiler flocks

For computing the predictive distribution for a scenario, we first used WinBUGS software. Data from 1999 was used as in the default setting. In addition, replicate variables were defined for a replicate process describing the scenario. For example, in the first scenario, one of the replicate grandparent flocks is said to be infected at the 4th visit. This information is included as data about this replicate process. Therefore, the model also makes inferences about the infection status of this flock at the first 3 visits. The full joint posterior distribution consists of the variables and parameters concerning the study year, 1999, for which there were data, and the replicate process up to the last data point of the scenario. Predictions for the next steps in the replicate process can then be sampled from this joint posterior density by using standard forward direction Monte Carlo, e.g. with Matlab.

7.2. The effect on the number of human cases

The risk of human cases of illness caused by salmonella in broiler meat was quantified using three modules, the PPIM, the SPSM, and the CIM. Even if they provide only a rough estimate of this risk, we can compare the relative effectiveness of the different interventions in the FSCP. For this purpose, all modules up to the predicted numbers of reported human cases were used in four different scenarios A-D.

In scenario A, the current situation was modelled (A-0). Due to the lack of detailed information on the effects of e.g. cleaning and sanitary slaughter, only two of domestic interventions and combinations thereof were chosen for modelling (A 1-3).

The following combinations of interventions were used:
(1) heat treatment of meat, but no elimination of the positive breeder flocks,
(2) no heat treatment of meat, but elimination of the detected positive breeder flocks, and
(3) neither heat treatment nor elimination of positive breeder flocks.

In scenario B, one grandparent flock was modelled to be infected at the beginning of the laying phase (B-0) and the three combinations of domestic interventions were computed (B 1-3). In scenario C, five parent flocks (but no grandparent flocks) were modelled to be infected at the beginning of the laying phase due, for example, to an infection from contaminated feed (C-0), and the three combinations of domestic interventions were computed (C 1-3).

In the basic model, the distribution of salmonella-positive lots in raw meat entering Finland and meat products currently included in the FSCP was, using some available statistics and expert opinions, modelled as Uniform (0.05,0.3) and Uniform (0,0.05), respectively. Within a positive lot, only a proportion of the meat was expected to be contaminated by salmonella (Uniform (0.3,0.6)). In order to study the effect of FSCP control measures on meat entering Finland, scenario D, where half the retail broiler meat is replaced by more contaminated meat, was simulated. This could happen as a result of increased imports from countries with a higher salmonella prevalence in raw broiler meat or due to a very large domestic outbreak with poor management. The distribution Uniform (0.2, 0.4) for a contamination level of 50% of the total production was based on information from various countries (European Commission 2001; Domínguez et al. 2002; Ghafir et al. 2002; KvW & RIVM 2002).

When comparing the prediction under no removal of the detected positive breeder flocks to the default prediction, the increase in prediction mean was 1.6-fold. If no heat treatment of the detected broiler flocks is assumed, the increase in prediction mean was 4.1-fold compared to the default. Finally, if no heat treatment is assumed and the detected positive breeder flocks are not removed, the increse in prediction mean was 5.6-fold. The distributions of the numbers of resulting human cases display large uncertainty. The comparison can be based on the relative differences, e.g. by comparing the relative change in predictive means (Table 27).

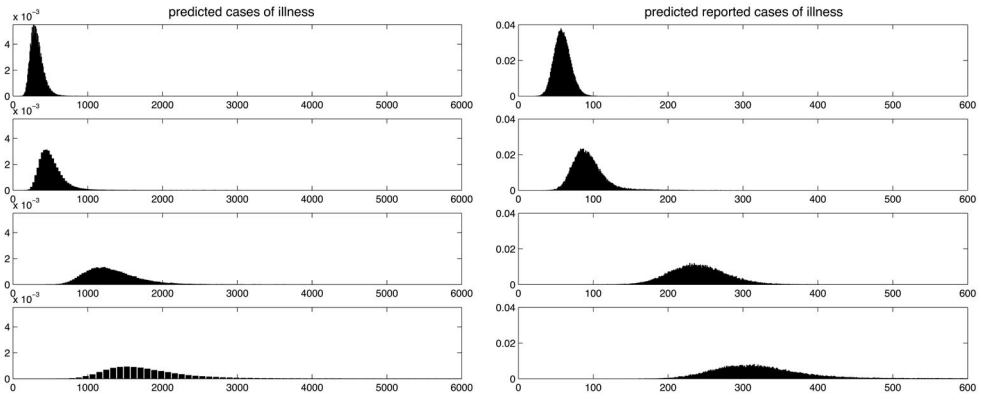


Figure 35.
Comparison of the predictive distributions for the number of all cases of illness (left) and reported cases (right). From top down: (0) In current situation (based on 1999), (1) Only heat treatment applied, (2) Only detected positive breeder flocks removed, (3) Heat treatment not applied and detected positive breeder flocks not removed.

If FSCP were not applied and one grandparent flock were infected at the beginning of the laying period, the predictive mean of human cases of illness would increase 17.8-fold compared to the situation with FSCP in this scenario. With heat treatment only, the increase would be 4.7-fold, and with removal of detected positive flocks only, it would be 3.4-fold. In this scenario, the removal of salmonella-positive breeder flocks was more effective compared to the heat treatment of meat. Removals of positive flocks are applied on two levels of production, namely grandparent and parent flocks. This is an advantage when the infection occurs in grandparent flocks.

If the FSCP were not applied and five parent flocks were infected at the beginning of the laying phase, the predictive mean of human cases of illness would increase 7.7-fold compared to the situation with the FSCP in this scenario. With heat treatment only, the increase would be 2.0-fold, and with removal of detected positive flocks

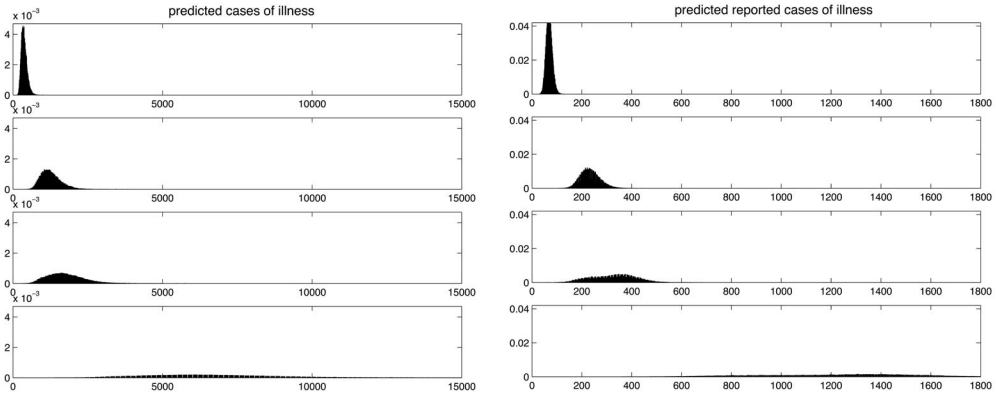


Figure 36.
Comparison of predictive distributions for the number of all cases of illness (left) and reported cases (right). In this scenario, one grandparent flock is infected at the 4th visit. From top down: (0) Both interventions applied, (1) Only detected positive breeder flocks removed, (2) Only heat treatment applied, (3) Heat treatment not applied and detected positive breeder flocks not removed.

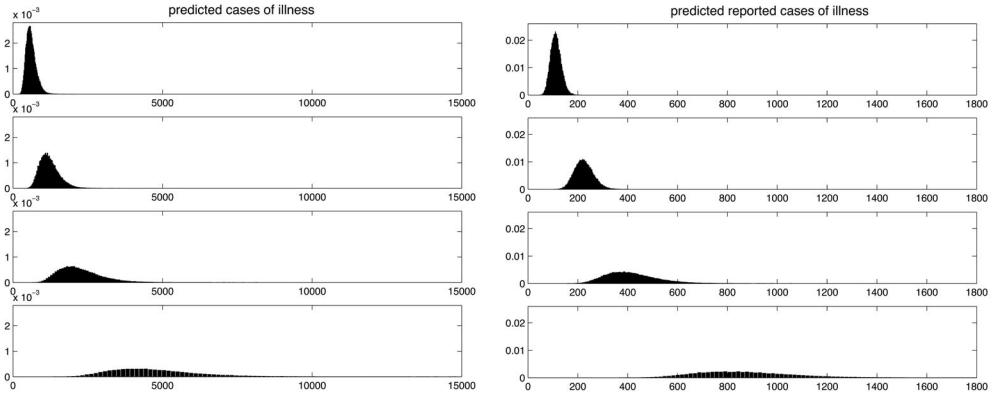


Figure 37.
Comparison of predictive distributions for the number of all cases of illness (left) and reported cases (right). In this scenario, 5 parent flocks are infected at the 4th visit but no grandparent flocks are infected. From top down: (0) Both interventions applied, (1) Only heat treatment applied, (2) Only detected positive breeder flocks removed, (3) Heat treatment not applied and detected positive breeder flocks not removed.

only, it would be 3.7-fold. In contrast to the first scenario, heat treatment alone would have a greater effect on public health than the removal of positive breeder flocks alone in this scenario.

Among scenario analyses A-D, the highest difference was seen in scenario D where the current situation with the FSCP was compared to a situation where half the retail broiler meat would be replaced by raw meat with a 20-40% contamination level (Figure 38). The increase of expected reported human infections would be 58-fold, resulting in a mean of 3,417 reported human infections.

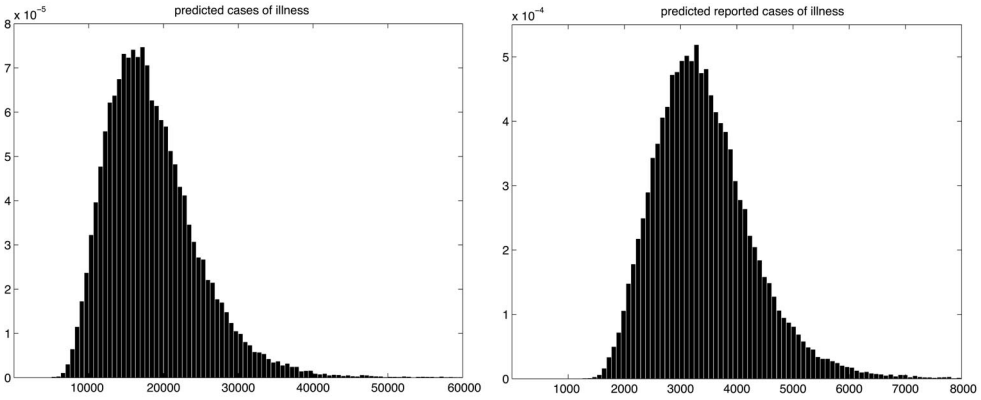


Figure 38
Predictive distributions for all cases of illness (left) and the number of reported cases (right), in a scenario where 50% of domestic production is replaced by broiler (raw) meat with 20-40% salmonella contamination. Processed meat entering Finland is simulated as default.

Table 27.
Summary of the predicted effects of two domestic interventions as currently performed and three different scenarios (positive grandparent flock, five positive parent flocks and 50% of retail broiler meat replaced by more contaminated meat) on numbers of human cases of illness.

	True number of cases of illness		Reported cases of illness	
	Scenario A			
	Mean	Std	Mean	Std
Both interventions are applied	319	82	59	11
Only heat treatment of pos. broiler flocks	509	169	94	24
Only removal of pos. breeder flocks	1308	335	241	37
Neither of the interventions are applied	1783	594	329	79
	Scenario B			
	Mean	Std	Mean	Std
Both interventions are applied	373	97	69	12
Only heat treatment of pos. broiler flocks	1760	615	325	87
Only removal of pos. breeder flocks	1264	336	233	39
Neither of the interventions are applied	6636	2240	1224	309
	Scenario C			
	Mean	Std	Mean	Std
Both interventions are applied	606	166	112	21
Only heat treatment of pos. broiler flocks	1214	322	224	38
Only removal of pos. breeder flocks	2238	723	413	102
Neither of the interventions are applied	4694	1435	867	192
	Scenario D			
	Mean	Std	Mean	Std
Both interventions are applied (domestic)	18489	6153	3417	872

7.2.1. Computation of interventions for public health

The CIM can be used to predict both the number of all human cases of illness and the reported number of cases. This posterior predictive distribution is straightforward to compute in WinBUGS, under the current default situation. The number of cases

of illness has a conditional binomial distribution (Bin(nser,p)) where the probability parameter p is given by the dose-response model, and the nser -parameter represents the number of contaminated servings per year. These parameters can be described by a joint posterior distribution, given current (or past) data about reported human cases. The posterior distribution of these parameters was the output of the CIM. The CIM then also produces a predictive distribution of cases by sampling the replicate number of cases from the binomial distribution, given the sampled parameters (p and nser) from their posterior distribution. The reported number of cases is predicted by further binomial sampling using the under-reporting parameter (psel), i.e. the selection probability of becoming a reported case.

However, when other (counterfactual) scenarios concerning the number of contaminated servings are simulated, this joint distribution no longer exists and we must simulate starting from other assumptions and hypotheses about this new scenario. If the CFU/g level and the number of contaminated servings are then considered independently, we can use the marginal distribution of CFU/g obtained from the CIM as our best prior predictive density, if no better information is available. The number of servings would be simulated separately from its marginal prior distribution according to the given scenario given by the SPSM. This approach will lead to unrealistically large prediction variance simply because any combinations of CFU/g and number of contaminated servings are then possible parameters. Information gained about the joint density as a result of the CIM would be lost.

Another approach is to use pointwise stochastic coupling between the number of contaminated servings in the posterior density and the number of contaminated servings in the prior density of the (counterfactual) scenario (Figure 39). Thus, pointwise stochastic coupling between nser and $nser^{scen}$ was applied as a solution combining information contained in the (old) posterior and the (new) prior of $nser^{scen}$ describing the scenario for a possible number of contaminated servings.

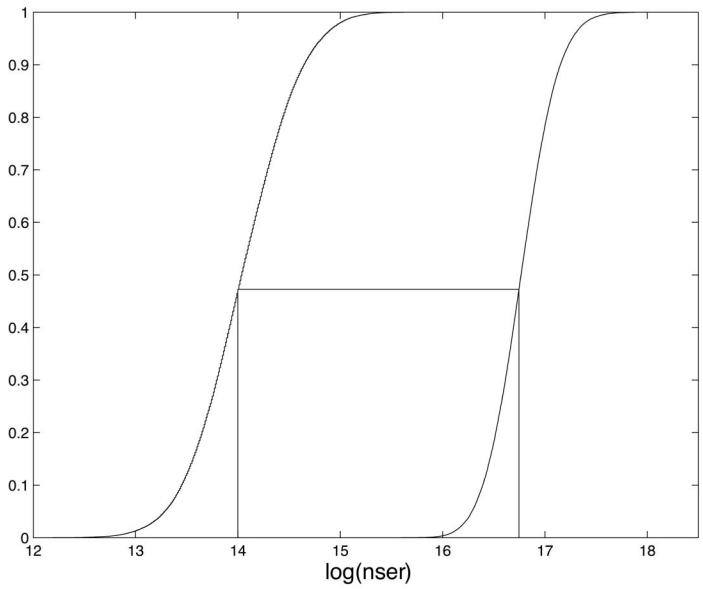


Figure 39.
Stochastic pointwise coupling of two random variables. Left curve: cumulative distribution of ln(nser) in the default situation with both domestic interventions. Right curve: cumulative distribution of ln(nser) under scenario 2 with no domestic interventions. Whenever the simulated value from the left distribution is 14, the coupled value from the right distribution would be 16.7.

8. Discussion

This risk assessment model provides a view of the effect of the Finnish Salmonella Control Program both on broilers and on humans. The strongest part of the model is on primary production, where the main interventions are also applied. The closer to the consumer, the more we have needed to include expert opinions in the model. The use of mathematical models in microbial risk assessments is a challenge for assessors as well as for risk managers. However, without these kinds of models it would be difficult to estimate the effectiveness of the work done by industry and government officials to combat salmonella. The results of this model have already been used to evaluate the economics of the FSCP (Kangas et al. 2003).

In general, removal of an infected breeder flock clearly reduces the risk of human infection, which is more evident in the scenarios with infected breeder flocks. This points out the effectiveness of salmonella control in the early steps of the production chain. Similarly, heat treatment of detected positive broiler flocks has a clear effect in those scenarios. Both of these interventions appeared to have effects when the true input prevalence is low, but their significance becomes more pronounced the higher the input prevalence.

It is questionable how realistic the model is in describing extreme situations, such as scenarios B and D (chapter 7). It is likely that other prevention mechanisms not included in the current model would come into effect, so the total number of human infections would be smaller. The current model computes the conditional expected number of human infections as a linear function of the number of contaminated servings. Therefore, multiplying the number of contaminated servings results in a multiplication of the conditional expected human infections by the same factor.

In scenario D, the amount of contaminated meat, and hence the amount of contaminated servings, is the largest among all the scenarios, resulting in 58 times more human cases. This figure can also be compared to the WHO/FAO (2002) report where it was estimated that with a 20% prevalence of contaminated broiler carcasses, the rate of illness per 100,000 people would be 29.38, and due to cross-contamination 68 illnesses per 100,000 (WHO/FAO 2002). This would imply that approximately 5,000 cases would occur due to broiler meat if the prevalence in carcassess were 20%. Although we cannot directly compare this risk assessment and the WHO/FAO study, both estimates are of the same magnitude. This also shows that salmonella control, both in domestic production and in the production of lots entering Finland, is very important in order to protect public health.

In terms of the whole assessment, we can make the following remarks. Firstly, a descriptive analysis and prediction of the concrete number of reported human infections could be done in a relatively straightforward manner if the annual records of reported infections from previous years are available. At minimum, this requires specifying a statistical model of the reported infections and data about these

reported numbers from past years. The statistical predictions could then be based on time series over several years. However, linking these reported human infections to specific sources of illness is more difficult, even though information about serotypes and phagetypes can be used. Quantification of the effects of various counterfactual scenarios is even more difficult, since in reality these could have an unexpected effect on other parameters and structural assumptions which are considered fixed, or "stable" in the model based analysis. Hence, it would be oversimplifying the situation to consider only the correlations between different inputs and outputs in a single model, since we also need to consider the uncertainty which is part of the model's whole structure and parameterization. We did this, for example, by considering different models for the probability of vertical transmission in the PPIM's sensitivity analysis. We also experimented with alternative prior distributions in some model parameters to see how this affects the results. These, as well as other uncertainties within the model, are discussed in the respective sections.

Our aim with this probability model of salmonella infections in the broiler production chain was to describe the dynamic course of the production process. A fairly detailed sequence of events was attempted to be modelled while at the same time maintaining the model's computability and estimation. In the case of primary production, the level of description was limited to the flock level. For such modelling, flock-specific surveillance data are needed. However, although data are originally gathered from specific flocks, they are generally not available in a flock-specific format; instead, data are available as annual total sums concerning the findings for different types of flocks. Therefore, important information about flock-specific lifetime histories is lost. It would be valuable to retain this information in order to model flock-specific events in different situations. If this dynamic information is lost, it is almost impossible to model and estimate dynamic properties of the more detailed production process, or to quantify how the process would change if specific changes concerning flocks and their treatment are made along their life span. Another difficulty related to analyzing infection dynamics is that there were no data about how long a salmonella infection persists in a flock under a natural course of infection, i.e. without intervention. In general more useful data could be gathered by organizing targeted experiments in addition to the annual records of the Salmonella Control Program. Also current data from the control program could be exploited more fully if temporal information about flock-specific events in calendar time were preserved. In addition, more data would be needed about secondary infections and cross-contamination effects at slaughterhouses and during processing. However, these are difficult or impossible to obtain because, ideally, a prospective observation of the course of an "undetected" salmonella contamination would be needed.

During this risk assessment process, we identified many gaps in data. In particular, data on the sensitivity of the testing method, differences in contamination levels during slaughter, cutting and retail as well as on the practices of quantitative analyses would have been beneficial. If they had been available, more detailed modelling would have been possible. However, these kinds of data are expensive due to the large number of samples needed to obtain nonzero results when there is a low prevalence of salmonella.

In order to fully exploit the results of a scientific inference based on both data and expert opinions about several quantities in the model, it is necessary to consider the multidimensional joint distribution representing the result of that inference. Spreadsheet modelling tools do not easily allow the computing of such multidimensional numerical integrations, which are nevertheless part of the task. A more flexible computing environment, however, is provided by professional software designed for

algorithmic programming often used in statistics and applied mathematics. For probabilistic inference models, one often needs tailored algorithms and/or special software.

The resulting number of human infections depends on the total number of consumed contaminated meals and the dose-response model chosen. The former quantity is provided by the previous steps of the simulation model (SPSM), while the latter can be chosen among several equally plausible models. These models require the quantification of the level of contamination (CFU/g) at the time of consumption. Due to the lack of such data, only expert opinions could be used, but these are very uncertain as well. An inference model was applied which utilized the comparatively more reliable information on reported human infections, with the associated sero- and phagetype information available. In this way, plausible average levels of CFU/g are estimated and the model is calibrated to the known records of human infections. However, knowledge about different sources of reported human salmonella infections can still be biased, due to sampling schemes which mainly focus on food of animal origin. The remaining parameters of the dose response model were taken from the FAO/WHO report (2002).

Due to uncertainties along the production and processing chain and consumption, the predictions cover a wide range of possible values for the resulting human infections, from almost zero to several thousand and are therefore not very accurate. Perhaps the only way to make them more accurate is to collect more data about consumers and the final doses of salmonella in broiler meat at the actual time of consumption.

Finally, the predictions made under different counterfactual scenarios cannot be fully validated until that scenario actually takes place. Pointwise stochastic coupling was used in order to take advantage of the posterior distribution (based on current or past data) and the marginal predictive distribution under a new scenario. This reduced the unrealistically large prediction variance that would result from treating the hyperprior densities in predictions as independent. However, instead of comparing predictions of the actual numbers of infections one should compare the relative differences under alternative scenarios. These relative effects may be more robust predictors than the plain numbers of infections.

9. References

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10. Appendix 1: Communication during the process

During this process, the principles and results of this assessment have been discussed in meetings with the co-operation group of salmonella risk assessment. The co-operation group consisted of experts on salmonella, broiler production, human medicine as well as representatives from authorities and industry. In addition, our work has been presented at the following occasions:

Maijala, R. & Nuotio, L. 2000. Risk of human salmonellosis posed by poultry in Finland. 9th International Symposium on Veterinary Epidemiology and Economics, August 2000, 1390. Colorado, USA. Poster.
Ranta, J. Detecting and preventing salmonella infections in primary production chain of broilers. A Bayesian approach to risk analysis. Seminar of the department of bio- and environmental sciences, University of Jyväskylä. 13.2.2001. Presentation.
Ranta, J. Estimating salmonella infections in the primary production chain of broilers. Statistics seminar at National Public Health Institute (KTL). 2.3.2001. Presentation.
Ranta, J. & Maijala, R. Predicting salmonella infections in the primary production chain of broilers. International Biometric Society Nordic Region Conference. June 7-9, 2001, Savonlinna, Finland. Presentation
Ranta J. Predicting salmonella infections in the primary production chain of broilers. Seminar of the department of statistics, Ludwig-Maximilians University, Muenchen. 3.7. 2001. Presentation.
Maijala, R. & Ranta, J. 2001. Risk assessment on salmonella transmission in the primary broiler production chain in Finland. International Congress on Food Safety and Toxiclogy, August 24-25th, 2001. Kuopio, Finland. Presentation.
Maijala, R. & Ranta, J. 2001. Broilertuotannon salmonellariskin tieteellinen arviointi. Eläinlääkäripäivät 2001, 28-30.11. Helsinki, Finland. Esitelmä.
Ranta J. Infektiotautien mallinnusta Bayes-menetelmillä (Modelling infectious diseases using Bayesian methods). Matematiikan päivät 9.1.2002, Joensuu. Esitelmä. (Mathematics symposium of Finnish Mathematical Society 9.1.2002. Presentation).
Maijala, R. & Ranta, J. 2002. Effect of the Finnish Salmonella Control Programme on Risk Caused by Salmonella in Broilers. International Symposium Salmonella & Salmonellosis (I3S). 29-31 May 2002. St.Brieuc, France, pages 561-564. Oral presentation.
Maijala, R. & Ranta, J. 2003. The use of predictive models to manage risks caused by Salmonella in broilers.The SAFE consortium, Fosare seminar series 1, Newly emerging pathogens, including risk assessment and risk management, 24-25 April 2003, Brussels. Oral presentation.

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Väitöskirja

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Riskinarviointi Echinococcus granulosus -loisesta Suomessa
Riskinarviointiraportti

05/2002: Meri Kokkonen
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Pro Gradu -tutkielma

06/2002
Klassisen sikaruton maahantulo ja leviäminen Suomessa
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07/2002
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