

***Salmonella***  
**in Egg Production in Finland**  
**– a Quantitative Risk Assessment**



**Shell egg *Salmonella* Risk Assessment Team**

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## Kuvailulehti

<b>Julkaisija:</b>	<b>Eläinlääkintä- ja elintarvike tutkimuslaitos EELA</b>
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<b>Julkaisun nimi:</b>	<b>Salmonella suomalaisessa kananmunatuotannossa – kvantitatiivinen riskinarviointi</b>
<b>Tiivistelmä:</b>	<p>Suomessa on vuodesta 1995 alkaen valvottu kansallisen valvontaohjelman avulla kananmunatuotannon salmonellatartuntoja. Nyt valmistuneen riskinarvioinnin tavoitteina on kuvata kananmunien aiheuttamaa salmonellatartuntariskiä kuluttajille ja arvioida kansalliseen salmonellavalvontaohjelmaan liittyvien toimenpiteiden vaikutusta tähän riskiin. Arviointi kattaa ammattimaisen kananmunien tuotantoketjun alkutuotannosta kulutukseen asti ja koskee munia, joissa salmonellatartunta on munan sisällä. Tarkastelukohteeksi valittiin vuosi 2001, joka arviointityön alkaessa oli viimeisin vuosi, jolta tietoja oli kattavasti saatavilla. Arvio ihmisten tartuntatapaus-ten lukumäärästä perustuu vuoden 1999 tietoihin, koska kyseisenä vuotena salmonellaa todettiin tuotantoparvissa eniten sitten salmonellavalvontaohjelman käynnistämisen jälkeen ja se edustaa siten nk. ”worst case” –tilannetta. Arviointi tehtiin valvontaohjelman tietojen, kuluttajille ja ammattikeittiöille suunnattujen kyselytutkimusten tulosten sekä muun käytettävissä olevan aineiston perusteella.</p> <p>Tämän arvion mukaan keskimäärin 0,3 %:ssa munantuotantoparvista esiintyisi salmonellaa vuoden 2001 mukaisessa perustilanteessa, vaikka valvontaohjelmassa ei todettu yhtään positiivista tuotantoparvea. Arvio todellisesta esiintyvyydestä on korkeampi kuin todettu esiintyvyys, koska mallin avulla arvioidaan myös toteamatta jääneiden tartuntojen määrää. Mallin mukaan salmonellatartunnan saaneet tuotantoparvet olisivat tuottaneet 0–7400 salmonellan saastuttamaa kananmunaa vuonna 2001 (95 % vaihteluväli), keskiarvon ollessa 1800 kappaletta. Samana vuonna kananmunien kaupallinen vuosituotanto Suomessa oli noin 54,5 miljoonaa kiloa eli noin 850 miljoonaa kappaletta.</p> <p>Mallin perusteella voidaan arvioida, että raportoiduista ihmisten salmonellatapauksista hyvin pieni osa eli 0–50 kpl (95 % vaihteluväli, keskiarvo 10 kpl) olisi ollut kananmunien aiheuttamia. Jos salmonellapositiivisiksi todettuja parvia ei poistettaisi tuotannosta, todellinen salmonellaesiintyvyys tuotantoparvissa nousisi mallin mukaan keskimäärin yhteen prosenttiin ja ihmisillä raportoitaisiin kananmunien välittämiä salmonellatartuntoja 0–140 kpl vuodessa (95 % vaihteluväli, keskiarvo 40 kpl). Positiiviseksi todetun parven poistaminen tuotannosta osoittautui siten tehokkaak-</p>

si riskinhallintakeinoksi, joka vähentää ihmisten salmonellatartuntojen lukumäärää merkittävästi myös silloin, kun salmonellan esiintyminen parvissa on harvinaista (kuten Suomessa).

Mikäli salmonellavalvontaohjelman näytteenottoa lisättäisiin EY:n uuden zoonosiasetuksen ((EC) No 2160/2003) mukaisesti ja positiivisen näytetuloksen aiheuttamat toimenpiteet pysyisivät ennallaan, esiintyisi ihmisillä raportoituja kananmunien välittämiä salmonellatartuntoja mallin mukaan keskimäärin 10 kpl vuodessa (95% vaihteluväli 0–40 kpl) verrattuna nykyisen järjestelmän mukaisessa tilanteessa keskimäärin todettuun 10 tapaukseen. Siten salmonellanäytteenottomäärän lisääminen yhdellä näytteenotokerralla munintakanojen seurannassa uuden zoonosiasetuksen vaatimusten mukaiseksi vähentäisi kuluttajan riskiä vain erittäin vähän tai ei lainkaan nykytilanteeseen verrattuna.

Mallin avulla simuloitiin myös tilannetta, jossa 20 % vanhempaispolven parvista saisi tartunnan munintakauden alussa. Silloin ennuste tuotantarvien todelliselle keskimääräiselle salmonellaesiintyvyydelle olisi mallin mukaan 0,6 % ja ihmisillä raportoituja kananmunien välittämiä salmonellatartuntoja olisi 0–80 kpl vuodessa, keskiarvon ollessa 30 kpl. Jos salmonellapositiivisiksi todettuja parvia ei poistettaisi tässä tilanteessa tuotannosta, tuotantarvien keskimääräinen salmonellaesiintyvyys tässä skenaariossa olisi 4,2 % ja ihmisillä raportoituja kananmunien välittämiä salmonellatartuntoja olisi 10–520 kpl vuodessa (95 % vaihteluväli, keskiarvo 170). Salmonellaesiintyvyyden noustessa positiivisten parvien poistamisen kuluttajaa suojaava merkitys korostui, sillä ihmisillä raportoitujen tartuntojen määrä kasvaisi kuusinkertaiseksi, mikäli todettuja positiivisia parvia ei siinä tilanteessa poistettaisi tuotannosta.

Suomelle on myönnetty kansallisen salmonellavalvontaohjelman vuoksi oikeus nk. erityistakuisiin eli samaa turvallisuustasoa voidaan vaatia sekä koti- että tuontikanamunilta. Nykyinen tilanne on johtanut siihen, että Suomessa tuotetuissa ja kulutetuissa kananmunissa esiintyy erittäin vähän salmonellaa (mallin mukaan keskimäärin 0,0002 %). Mikäli 30 % kananmunien kokonaiskulutuksesta korvautuisi munilla, joiden salmonellaesiintyvyys olisi samalla tasolla kuin monissa Euroopan yhteisön jäsenmaissa on raportoitu (0,06 %, 0,5 % tai jopa 1 %), ihmisillä raportoituja kananmunien välittämiä salmonellatartuntoja olisi mallin mukaan vuodessa 90–1730 kpl (munista 0,06 % saastuneita) tai jopa 1430–28 550 kpl (munista 1 % saastuneita) (95 % vaihteluväli). Arvio ihmisten tartuntatapauksista olisi siten 70–1000-kertainen vuoden 2001 mukaiseen perustilanteeseen verrattuna. On kuitenkin

kin huomattava, että nämä skenaarioiden tulokset ovat herkkiä arviolle kananmunan-annoksen salmonellasolujen lukumäärästä syöntihetkellä, vaikka perustilanteen ennusteeseen sillä ei ole suurta vaikutusta. Tuloksen mukaan kansallisen salmonellavalvontaohjelman perusteella saaduilla erityistakuilla on tuontikananmunien osalta selvä kuluttajan terveyttä suojaava vaikutus, mutta vaikutuksen suuruutta on ongelmallista arvioida.

**Malliin sisältyy olettamuksia, epävarmuuksia ja rajoituksia, kuten laskennan rajoittuminen kananmuniin, joiden sisällä on salmonellaa ja joiden esiintyvyyden laskenta nojaa S. Enteritidis-serotyypistä tunnettuun esiintyvyysetietoon, sekä epävarmuus parven testaamisen kokonaisherkkyydestä. Nämä on esitelty raportissa tarkemmin. Suora vertailu muualla raportoituihin tuloksiin saattaa olla vaikeaa vertailtavien tietojen puutteellisuudesta tai yhteismitattomuudesta johtuen. Raportin avulla voidaan kuitenkin vetää seuraavia johtopäätöksiä:**

1. Riskinarviointimallin perusteella keskimäärin 0,3 %:lla kananmunatuotantoparvista esiintyy salmonellaa ja noin 0,0002 % tuotetuista kotimaisista kananmunista sisältää salmonellaa. Tämä on kansainvälisesti erittäin matala taso ja alittaa selvästi kansalliselle valvontaohjelmalle asetetun 1 %:n tavoitetaso.
2. Kansallisen valvontaohjelman mukainen salmonellaposiitiviseksi todetun parven pakollinen poisto tuotannosta osoittautui arvioinnin tulosten perusteella tehokkaaksi riskinhallintakeinoksi, joka suojaa kuluttajaa merkittävästi myös silloin, kun salmonellan esiintyminen munantuotantoketjussa on harvinaista. Mikäli nykyisessä tilanteessa ei positiiviseksi todettuja parvia poistettaisi tuotannosta, ihmisten salmonellatapausten lukumäärä kasvaisi todennäköisesti nelinkertaiseksi. Torjuntatoinen suojaava vaikutus korostuu salmonellaesiintyvyyden kasvaessa.
3. Tuotantopolven salmonellanäytteenottotiheyden lisääminen vastaamaan EY:n zoonoosiasetuksen ((EC) No 2160/2003) vaatimuksia vähentäisi nykyisessä matalan esiintyvyyden tilanteessa kuluttajan salmonellariskiä erittäin vähän tai ei lainkaan verrattuna nykyisen valvontaohjelman mukaiseen näytteenottoon.
4. Mikäli 30 % kananmunien kulutuksesta korvautuisi kananmunilla, joissa salmonellaa esiintyy saman verran kuin monissa Euroopan yhteisön jäsenmaissa on raportoitu, (0,06%, 0,5% tai 1%), kuluttajien riski saada salmonellatartunta kananmunien välityksellä 70–1000-kertaistuisi.

5. Mallin rakentamista varten tehtyjen kyselytutkimusten perusteella raakaa tai löysää kananmunaa sisältävien ruokalajien käyttö suomalaisissa kotitalouksissa ja ammattikeittiöissä oli alle 20 %:a kananmunien kokonaiskäytöstä. Tulos ei poikennut muiden maiden saatavilla olevista tutkimustuloksista. Siten kananmunien välittämien salmonellatartuntojen tai ruokamyrkytysten vähäinen määrä ei johdu suomalaisten kuluttajien erityisen turvallisesta kananmunien käytöstä vaan kananmunien todellisesta matalasta salmonellaesiintyvyydestä.

**Avainsanat:** Salmonella, kananmuna, valvonta, Kansallinen salmonellavalvontaohjelma

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## Presentationsblad

<b>Utgivare:</b>	<b>Forskningsanstalten för veterinärmedicin och livsmedel, EELA</b>
<b>Författare:</b>	<b>Satu Lievonen, Jukka Ranta och Riitta Majjala</b>
<b>Titel:</b>	<b>Salmonella i finländsk äggproduktion – en kvantitativ riskvärdering</b>
<b>Referat:</b>	<p>I Finland har man sedan år 1995 övervakat salmonellasmittor inom äggproduktionen inom ramen för ett nationellt övervakningsprogram. Syftet med denna riskvärdering är att beskriva risken för att konsumenterna skall smittas med salmonella via ägg samt att utvärdera hur de åtgärder som anknyter till det nationella programmet för övervakning av salmonella påverkar denna risk. Värderingen omfattar den yrkesmässiga produktionskedjan för hönsägg från primärproduktion till konsumtion och gäller ägg där salmonellasmittan finns inne i ägget. För granskningen valdes år 2001. Då värderingen inleddes var detta det senaste året för vilket heltäckande uppgifter fanns att tillgå. Det uppskattade antalet smittofall hos människor bygger på uppgifterna från år 1999 eftersom man under detta år konstaterade de flesta fallen av salmonella i produktionsflockar sedan programmet för övervakning av salmonella startade. Året i fråga representerar därmed ett s.k. "worst case"-scenario. Värderingen utfördes på basis av uppgifterna från övervakningsprogrammet, enkäter till konsumenter och storkök samt annat tillgängligt material.</p> <p>Enligt denna bedömning skulle salmonellasmitta förekomma i medeltal hos 0.3% av de äggproducerande flockarna i en liknande situation som år 2001, även om man inte konstaterade en enda positiv produktionsflock inom ramen för övervakningsprogrammet. Den uppskattade faktiska förekomsten är större än den konstaterade förekomsten, eftersom man med modellens hjälp även gör en uppskattning av antalet icke konstaterade smittofall. Enligt modellen skulle de salmonellasmittade produktionsflockarna år 2001 ha producerat 0–7400 ägg med salmonellasmitta (95% Bayes konfidens intervall) med ett medelvärde på 1800 stycken. Under samma år uppgick den kommersiella äggproduktionen i Finland till cirka 54.5 miljoner kilogram, dvs. cirka 850 miljoner stycken ägg per år.</p> <p>På basis av modellen kan man approximera att en mycket liten del av de rapporterade salmonellafallen hos människor, dvs. 0–50 stycken (95% Bayes konfidens intervall, medelvärde 10 st.) är orsakade av hönsägg. Om flockar som konstaterats vara salmonellapositiva inte tas ur produktion skulle den faktiska salmonellaförekomsten i produktionsflockarna enligt modellen öka till i genomsnitt en procent och hos människorna rapporteras 0–140 äggburna salmonellasmittor per år (95%</p>



Bayes konfidens intervall, medelvärde 40 st.). Att ta en konstaterat salmonella positiv flock ur produktion visade sig därmed vara en effektiv riskhanteringsmetod som avsevärt minskar antalet salmonellasmittor hos människor, också då salmonella smitta i flockarna, liksom i Finland förekommer på en låg nivå.

Om provtagningen inom programmet för övervakning av salmonella utökas i överensstämmelse med EG:s nya zoonosförordning ((EC) nr 2160/2003), och de åtgärder som orsakar ett positivt provresultat förblir oförändrade, skulle det i genomsnitt förekomma 10 stycken rapporterade äggburna salmonellasmittor hos människor per år (95% Bayes konfidens intervall, medelvärde 0–40 st.) jämfört med de 10 fall som i genomsnitt konstateras enligt det nuvarande systemet. Att vid uppföljningen av värphöns utöka antalet salmonellaprovtagningar med en, så som kraven i den nya zoonosförordningen anger, medför således att konsumentrisken jämfört med nuläget skulle reduceras endast i mycket liten utsträckning eller inte alls.

Med modellens hjälp simulerades också en situation där 20 % av föräldragenerations flockar får smittan i början av värpperioden. Prognosen för den faktiska genomsnittliga förekomsten av salmonella i produktionsflockarna är enligt modellen då 0.6 % och antalet rapporterade äggburna salmonellasmittor hos människor 0–80 stycken per år, med ett medelvärde på 30 stycken. I fall att de flockar som konstaterats vara salmonellapositiva inte tas ur produktion skulle den genomsnittliga salmonellaförekomsten hos produktionsflockarna i detta scenario vara 4,2 % och antalet rapporterade äggburna salmonellasmittor hos människor 10–520 stycken per år (95% Bayes konfidens intervall, medelvärde 170). Då salmonellaförekomsten ökar framhävs betydelsen av avlägsnande av positiva flockar för konsumentskyddet, eftersom antalet rapporterade smittor hos människor skulle ha ökat sexfaldigt om de konstaterat positiva flockarna inte hade tagits ur produktion.

Till följd av det nationella programmet för övervakning av salmonella har Finland beviljats rätt till s.k. särskilda garantier, vilket innebär att samma säkerhetsnivå kan krävas av såväl inhemska som importerade ägg. Salmonellaförekomsten i ägg som produceras och konsumeras i Finland (enligt modellen i medeltal 0.0002 %) är i nuläget ytters låg. Om 30 % av den sammanlagda äggkonsumtionen ersätts med ägg för vilka salmonellaförekomsten ligger på samma nivå som i många av Europeiska gemenskapens medlemsstater (0.06 %, 0.5 % eller rentav 1 %), skulle det enligt modellen årligen rapporteras 90–1730 stycken äggburna salmonellasmittor hos människor (0.06 % av äggen kontaminerade) eller rentav 1430–28 550 stycken (1 % av äggen kontaminerade) (95% Bayes konfidens intervall). Det uppskattade an-

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talet smittofall hos människor vore därmed 70–1000 gånger större jämfört med situationen år 2001. Observeras bör att resultaten i dessa scenarier är sensitivt för ändringar i det uppskattade antalet salmonellaceller i en portion ägg vid konsumtionen, även om detta inte har någon större effekt på prognosen i enlighet med grundsituationen. Resultatet anger att de särskilda garantier som bygger på det nationella programmet för övervakning av salmonella har en klart skyddande verkan för konsumenthälsan när det gäller importerade ägg, men det är problematiskt att bedöma hur omfattande denna verkan är.

**I modellen ingår antaganden, osäkerhetsfaktorer och gränsdragningar. Modellkalkylen begränsas bland annat till enbart ägg med salmonellasmitta inne i äggetoch vars estimerade salmonella förekomst bygger på publicerade uppgifter om förekomsten av serotypen S. Enteritidis. Vidare råder det osäkerhet kring den flockspecifika sensitiviteten för testning av flockar med avseende på salmonella. Dessa faktorer har beskrivits närmare i rapporten. Till följd av bristfälliga eller ojämförbara bakgrundsuppgifter kan det vara svårt att direkt jämföra resultaten i denna värdering med resultat som rapporterats på annat håll. Med rapportens hjälp kan dock följande slutsatser dras:**

1. På basis av riskvärderingsmodellen bär i snitt 0.3 % av de äggproducerande flockarna på salmonella medan cirka 0.0002 % av de inhemska äggen innehåller salmonella. Internationellt sett är nivån ytterst låg och den underskrider klart målnivån på 1 % som fastställts för det nationella övervakningsprogrammet.
2. Att som en obligatorisk åtgärd enligt det nationella övervakningsprogrammet ta en konstaterat salmonellapositiv flock ur produktion visade sig med stöd av värderingsresultaten vara en effektiv riskhanteringsmetod som avsevärt skyddar konsumenten också med en låg salmonellaförekomst i äggproduktionskedjan. Om man i nuläget inte tar konstaterat positiva flockar ur produktion leder detta sannolikt till att antalet salmonellafall bland människor fyrdubblas. Bekämpningsåtgärdernas skyddande effekt accentueras då förekomsten av salmonella ökar.
3. En ökad provtagningsfrekvens avseende salmonella hos produktionsflockar i överensstämmelse med kraven i EG:s zoonosförordning ((EC) nr 2160/2003) jämfört med det nuvarande salmonellaövervakningsprogrammet skulle under rådande omständigheter med låg förekomst reducera konsumentrisken endast i mycket liten utsträckning eller inte alls.

4. Om 30 % av äggkonsumtionen ersätts med ägg med en salmonellaförekomst på samma nivå som i många av Europeiska gemenskapens medlemsstater (0.06 %, 0.5 % eller 1 %), skulle risken för att konsumenterna smittas med salmonella via ägg 70–1000-faldigas.

5. På basis av de enkäter som utarbetades med tanke på konstruerandet av modellen utgör andelen maträtter innehållande råa eller löskokta ägg mindre än 20 % av den sammanlagda äggkonsumtionen i finländska privathushåll och storkök. Resultatet avvek inte från de forskningsresultat som finns att tillgå från andra länder. Det obetydliga antalet äggburna salmonellasmittor eller matförgiftningar beror därmed inte på att de finländska konsumenterna använder ägg på ett synnerligen säkert sätt utan på en låg salmonella förekomst i ägg.

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## Description

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<b>Title:</b>	<b><i>Salmonella</i> in Egg Production in Finland – a Quantitative Risk Assessment</b>
<b>Abstract:</b>	<p>Since 1995, the Finnish <i>Salmonella</i> Control Programme (FSCP) has been monitoring <i>Salmonella</i> infection in egg production. This risk assessment examines the risk to consumers of <i>Salmonella</i> infection from shell eggs in Finland, and evaluates the effects of the interventions mandated by the <i>Salmonella</i> Control Programme on this risk. This risk assessment covers the commercial egg production chain from primary production through consumption, and is limited to internally-contaminated eggs. This assessment focuses on 2001, the last year for which complete surveillance data was available when work was begun. The number of estimated human <i>Salmonella</i> cases is based on data from 1999, however, since this year had the highest rates of detected <i>Salmonella</i> in egg production flocks since the inception of the FSCP and thus represents a “worst case” scenario. This risk assessment is based on FSCP data, surveys of consumers and institutional kitchens, as well as on other available data.</p> <p>This assessment finds that <i>Salmonella</i> would be present in an average of 0.3% of egg production flocks in the default situation based on 2001 data, although no positive flocks were detected by the control programme. The estimate of true prevalence is thus higher than reported prevalence, since the model also estimates the number of undetected infections. According to the model, in 2001 <i>Salmonella</i>-infected flocks would have produced 0–7,400 infected eggs (95% credible interval), with a mean of 1,800 eggs. The same year, the annual commercial production of eggs was 54.5 million kilos, or about 850 million eggs.</p> <p>Based on the model, we can estimate that a very small percentage of human <i>Salmonella</i> infections, 0–50 cases (95% credible interval, with a mean of 10) were caused by shell eggs. If detected <i>Salmonella</i>-positive flocks were not removed from production, according to the model the true <i>Salmonella</i> prevalence in egg production flocks would go up an average of one percent, and the reported number of human cases caused by eggs would be 0–140 cases per year (95% credible interval, with a mean of 40 cases). The removal of infected flocks is thus an effective intervention, significantly reducing the number of human <i>Salmonella</i> cases even in a situation (like Finland) where the prevalence of <i>Salmonella</i> is very low.</p>

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If sampling frequency under the FSCP were increased in accordance with the EU's new zoonosis regulation ((EC) No 2160/2003) while the interventions mandated by positive test results stayed the same, the model predicts that the reported number of human *Salmonella* cases caused by shell eggs would average ten cases per year (95% credible interval, 0–40 cases), compared to the current 10 cases under the present system. Therefore, increasing the sampling frequency of production flocks in accordance with the new zoonosis regulation (i.e., adding one sample) would have little or no effect on consumer risk compared to the present situation.

The model was also used to simulate a situation where 20% of the parent flocks were infected at the beginning of the laying phase. In this scenario, the predicted true prevalence of *Salmonella* in production flocks would be 0.6%, and the reported human *Salmonella* cases caused by eggs would be 0–80 per year, with a mean of 30 cases. If *Salmonella*-positive flocks were not removed from production, the average *Salmonella* prevalence in production flocks would in this scenario be 4.2%, and the reported human infections caused by eggs would be 10–520 cases per year (95% credible interval, with a mean of 170). Moreover, as *Salmonella* prevalence rises, the significance to consumer safety of removing positive flocks increases even more, as in this scenario the reported number of human infections would increase sixfold if detected positive flocks were not removed from production.

Due to its national *Salmonella* Control Programme, Finland has been granted so-called special guarantees which require the same level of safety in both domestic and imported eggs. In the current situation, the *Salmonella* prevalence in eggs produced and consumed in Finland is extremely low (according to the model, an average of 0.0002%). If 30% of total egg consumption were replaced with eggs with *Salmonella* prevalence equivalent to what has been reported in many European Union member states (0.06%, 0.5% and even 1%), according to the model the number of reported human *Salmonella* cases caused by eggs would be 90–1,730 cases per year (if 0.06% of eggs are infected) or even up to 1,430–28,550 cases (if 1% of eggs are infected) (95% credible interval). The estimate of human infections would thus be 70–1000 times the default situation of 2001. It is important to note, however, that these results depend to a great extent on the estimate of the CFU/g per contaminated serving at the time of consumption, although in the default situation this figure does not have a great effect on the results. These results show that the special guarantees under the Finnish *Salmonella* Control Programme do have a positive effect on consumer safety, though it is problematic to estimate the size of this effect.

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**This model contains certain assumptions, uncertainties and limitations. For example, it is limited to internally-contaminated eggs, given that the only applicable prevalence data is on the *S. Enteritidis* serovar. In addition, there is uncertainty about the overall flock level sensitivity of the tests used. These limitations are detailed more fully in the report. Direct comparison with results published elsewhere may also be difficult due to incomplete or incommensurate data. Based on this report, however, we can draw the following conclusions:**

1. According to this risk assessment model, *Salmonella* is present in an average of 0.3% of egg production flocks, and approximately 0.0002% of domestic eggs contain *Salmonella*. Internationally, this is an extremely low level, clearly below the 1% target set by the Finnish *Salmonella* Control Programme.
2. According to the model, the removal of infected flocks, as mandated by the Finnish *Salmonella* Control Programme, is an effective intervention, significantly reducing the number of human *Salmonella* infections even in cases where the prevalence of *Salmonella* in egg production chain is very low. If, in the current situation, detected positive flocks were not removed from production, the number of human *Salmonella* cases would likely quadruple. Moreover, the safety effect of this intervention increases as the prevalence of *Salmonella* increases.
3. Increasing the sampling frequency of production flocks in accordance with the new EU zoonosis regulation ((EC) No 2160/2003) would, in the current situation of low *Salmonella* prevalence, have little or no effect on consumer safety compared to the present sampling frequency.
4. If 30% of shell egg consumption were replaced with eggs with a *Salmonella* prevalence equivalent to that reported in many EU member states (0.06%, 0.5%, or 1%), the risk of *Salmonella* infection to consumers would increase 70–000 times.
5. According to surveys completed for this risk assessment, the use of raw or undercooked eggs in Finnish households and institutional kitchens is under 20% of total shell egg consumption, which is in line with findings in other countries. Therefore, we can conclude that the low levels of *Salmonella* infection or food poisoning caused by shell eggs in Finland are not due to particularly safe egg consumption by Finns, but rather to the fact that the true *Salmonella* prevalence in shell eggs is low.

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<b>Key words:</b>	<i>Salmonella</i> , shell eggs, control, Finnish <i>Salmonella</i> Control Programme
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## 1. Some abbreviations, acronyms and definitions

### **Bayesian inference, probabilistic inference**

Method of inferring the probable values of unknown quantities by conditioning on observed data, i.e. updating prior distributions to posterior distributions.

### **Breeder flock**

A parent flock or a grandparent flock in the shell egg production chain.

### **Censored observation**

When the exact value of an observation is not known, but instead it is only known that the value lies above (or below) a known boundary, or within a known interval, it is said to be (statistically) censored.

### **CFU**

Colony Forming Units. CFU/g represents the amount of colony forming bacterial units per gram of sample.

### **CI**

Credible Interval. Bayesian “confidence interval” derived by taking e.g. the 2.5 and 97.5 percentage points of a distribution for a 95% CI. Thus the true value has a 95% probability of being within the 95% CI.

### **CIM**

Consumption Inference Model. The model is used for joint estimation of the average final CFU/g at the time of consumption per contaminated serving and the true number of human cases of illness, accounting for under-reporting. It uses Bayesian probabilistic inference (MCMC sampling, WinBUGS).

### **EDSM**

Egg Distribution Simulation Model. The model is used to estimate (1) the proportion of shell eggs consumed in private households and the catering industry, (2) the proportion of raw and undercooked egg dishes prepared in these kitchens and (3) the distribution of servings per eggs. It uses Monte Carlo simulations based on assigned distributions.

**ECFIM**

Egg Contamination Frequency Inference Model. The model is used to estimate the true frequency of contaminated shell eggs originating from an infected flock, based on data from literature. It uses Bayesian hierarchical modelling (WinBUGS).

**EELA**

National Veterinary and Food Research Institute

**ETT**

Association for the Prevention of Animal Diseases

**FSCP**

Finnish *Salmonella* Control Programme. The national *Salmonella* control programme, approved by Commission Decision 94/968/EC on December 1994 and started in 1995. It covers beef, pork and poultry production and is intended to keep the annual incidence of *Salmonella* below 1%.

**Internally-contaminated egg (sisäisesti kontaminoitunut muna)**

An egg whose internal liquid content has been infected by *Salmonella*, resulting from early infection during egg formation due to infection of the hen's reproductive tissues.

**KTL**

National Public Health Institute

**KTTK**

Plant Production Inspection Centre

**Marginal distribution (or density)**

Distribution of one or a few random variables derived from a joint distribution containing a larger number of random variables ( $f(x) = \int f(x,y)dy$ ). A distribution can be defined by a probability mass function for discrete points or by a continuous probability density for continuous values. A density may also assume a general form and hence include both discrete and continuous situations as special cases. A cumulative distribution function is the probability  $F(x) = P(X \leq x) = \int_{-\infty}^x f(x)dx$ .

**MC**

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

**MCMC**

Markov chain Monte Carlo sampling. Monte Carlo simulation based on Markov chain sampling techniques.

**MMM**

The Ministry of Agriculture and Forestry

**MMMTIKE**

The Information Center of the Ministry of Agriculture and Forestry

**Posterior distribution (or density)**

Conditional distribution describing the remaining uncertainty about an unknown quantity after observing data ( $f(x | data, prior)$ ). See also 'marginal distribution'.

**PPIM**

Primary Production Inference Model. The model is used for simulating *Salmonella* prevalence in the production chain from grandparent flocks to shell eggs at the retail level. It uses Bayesian probabilistic inference (MCMC sampling / WinBUGS and Matlab).

**Prior distribution (or density)**

Conditional distribution describing initial uncertainty about an unknown quantity before observing data ( $f(x | prior)$ ). See also 'marginal distribution'.

**QMRA**

Quantitative microbiological risk assessment

**Reported cases**

Number of reported cases is an estimated number of registered human infections due to the consumption of *Salmonella* contaminated eggs based on the serovars and phagetypes of isolated strains from humans, poultry and eggs.

**Special guarantees**

Finland is allowed to require the same level of safety from imported consignments as is provided by the National *Salmonella* Control Programme (FSCP).

**Underreporting (aliraportointi)**

A human with salmonellosis is registered as a human *Salmonella* case in Finland if s/he seeks a doctor, if a specimen is taken and submitted to a clinical laboratory, and if a laboratory identifies the causative organism, confirms the case and reports it to the National Infectious Disease Register. In this risk assessment, it has been estimated that 10 – 30% of all *Salmonella* cases actually occurring in Finland annually are diagnosed and, therefore, have been reported to the National Infectious Disease Register.

**WinBUGS**

Software with model specification language for computing posterior distributions using MCMC sampling methods.

## 2. Yhteenveto ja johtopäätökset

### 2.1 Johdanto

Suomella on ollut vuodesta 1995 alkaen EU:n hyväksymä kansallinen salmonellavalvontaohjelma. Valvontaohjelmassa tutkitaan säännöllisesti salmonellan esiintymistä tuotantotiloilla, hautomoissa, teurastamoissa ja lihanleikkaamoissa. Ohjelman tavoitteena on pitää salmonellan vuotuinen esiintyvyys tuotantoeläimissä ja niistä saatavissa lihassa ja munissa enintään 1 % tasolla. Tätä kautta pyritään varmistamaan ruoan turvallisuus kuluttajille.

Valvontaohjelmaan kattaa tärkeimmät kotimaiset tuotantoeläimet: naudat, siat ja siipikarjan sekä niistä saatavan lihan ja kananmunat. Kananmunatuotannon osalta kansallisen valvontaohjelman näytteenottoon kuuluvat isovanhempaisparvet, vanhempaisparvet, hautomot ja tuotantoparvet. Salmonellan löytyminen johtaa aina riskinhallintatoimiin, joiden tavoitteena on katkaista bakteerin leviäminen edelleen tuotantoketjussa. Valvontaohjelma antaa Suomelle myös mahdollisuuden vaatia salmonellatutkimuksia muista maista tuotavilta naudan-, sian- ja siipikarjanlihalla ja kananmunilla sekä elävältä siipikarjalta, ellei lähtömaassa ole EU:n vahvistamaa vastaavatasoista valvontaohjelmaa kuin Suomessa (nk. erityistakuut). Käytännössä ainoastaan Ruotsi ja Norja ovat tällaisia maita.

Kanojen salmonellavalvontaohjelmaa on nyt noudatettu kymmenen vuotta. Tällä riskinarvioinnilla haluttiin selvittää kananmunien aiheuttamaa salmonellariskiä kuluttajille ja salmonellavalvontaohjelmaan liittyvien riskinhallintatoimenpiteiden vaikutusta tähän riskiin. Lisäksi arvioitiin, miten riski muuttuisi, jos 20 % vanhempaispolven parvista saisi salmonellatartunnan tai jos Suomessa kananmunien kokonaiskulutuksesta 30 % korvautuisi munilla, joiden salmonellaesiintyvyys olisi nykyistä korkeampi. Arviointi tehtiin valvontaohjelman ja omien kyselytutkimusten tulosten sekä muun käytettävissä olevan aineiston perusteella. Työ on tehty maa- ja metsätalousministeriön pyynnöstä.

### 2.2 Riskinarviointimalli

Tämä riskinarviointimalli on yksinkertaistettu kuvaus siitä, miten salmonellatartunta voi kulkea kananmunien tuotantoketjussa ja päätyä kuluttajalle asti. Riskinarviointimallissa on hyödynnetty salmonellavalvontaohjelman tietoja erityisesti vuodelta 2001, joka arviointityön alkaessa oli viimeisin vuosi, jolta tietoja oli kattavasti saatavilla. Arvio ihmisten tartuntatapausten lukumäärästä perustuu vuoden 1999 tietoihin, koska kyseisenä vuotena salmonellaa todettiin tuotantoparvissa eniten sitten

ohjelman käynnistämisen jälkeen ja se edustaa siten pahinta mahdollista tilannetta (nk. worst case –skenaario). Valvontaohjelmasta saatuja tietoja on täydennetty kuluttajille ja ammattikeittöille suunnatuilla kyselyillä, kananmunatuotannon ja siipikarja-alan asiantuntijoiden arvioilla sekä kirjallisuudesta ja suomalaisista tilastoista ja rekistereistä kerätyillä tiedoilla. Mallissa ei ole tehty eroja eri salmonellaserotyypien välillä alkutuotannossa, sillä kansallinen salmonellavalvontaohjelmakin käsittelee niitä samalla tavalla.

Mallin perusrakenteita ovat säädelleet käytettävissä olevan tiedon lisäksi myös ne riskinhallintatoimenpiteet ja tapahtumavaihtoehdot (skenaariot), joiden vaikutusta mallilla halutaan kuvata. Mallin tuloksia ovat arvio salmonellan todellisesta esiintyvyydestä tuotantoparvissa sekä arviot ammattimaisesti tuotetusta vuosittaisesta kananmunamäärästä, niiden kananmunien lukumäärästä, joissa salmonellatartunta on munan sisällä, ja ihmisten tartuntatapausten lukumäärästä seuraavissa tilanteissa: a) nykyisessä tuotantotilanteessa (vuoden 2001 tietojen mukainen perustila), b) jos 30% kananmunien kokonaiskulutuksesta korvautuisi munilla joiden salmonellaesiintyvyys on nykyistä korkeampi tai c) jos 20 % vanhempaispolven emoparvista saisi salmonellatartunnan esimerkiksi rehujen välityksellä. Lisäksi on tutkittu, miten muutokset kahdessa valvontaohjelmaan kuuluvassa toimenpiteessä vaikuttaisivat tuloksiin: a) positiivisten tuotanto- ja emoparviin poistaminen tuotannosta nykyisen valvontaohjelman mukaisesti ja b) salmonellanäytteenottoitiheyden lisääminen vastaamaan EY:n zoonoosiasetusta ((EC) No 2160/2003).

Riskinarviointi on tehty Codex alimentariuksen periaatteiden mukaisesti (Codex Alimentarius Commission 1999) ja se jakautuu neljään eri riskinarvioinnin osaan: vaaran tunnistaminen, vaaran kuvaaminen, altistuksen arviointi ja riskin kuvaaminen.

### 2.2.1 Vaaran tunnistaminen

Salmonelloosi on *Salmonella enterica* –bakteerin aiheuttama tauti. *S. enterica* –serotyyppejä tunnetaan yli 2500. Kaikki serotyypit voivat aiheuttaa tautia ihmiselle, joskin taudinaiheutuskyvyssä on eroja eri serotyyppien välillä. Salmonella lisääntyy elintarvikkeissa, jos säilytys- ja kuljetuslämpötilat ovat sille otolliset. Salmonella tuhoutuu yleensä prosesseissa, joissa lämpötila ylittää 70 °C, joten salmonella voi säilyä elossa matalassa lämpötilassa käsitellyissä elintarvikkeissa. Kuumennuksen teho on riippuvainen tuotteen kosteudesta. Joissakin tapauksissa salmonellan tuhoamiseen tarvitaan jopa 130 °C.

Vuosina 1995–2001 Suomessa raportoitiin ihmisillä vuosittain noin kolme tuhatta salmonellatapausta (54–67 tapausta / 100 000 asukasta / vuosi). Vuosina 2002–2004 ilmoitettiin keskimäärin 2300 salmonellatapausta vuodessa (43–45 tapausta / 100 000 asukasta / vuosi) (KTL 2005). Salmonellatartuntoja aiheuttaa Suomessa vuosittain noin 100 serotyyppiä. Yli puolet tartunnoista on *Salmonella* Enteritidis ja *Salmonella* Typhimurium –serotyyppien aiheuttamia. *Salmonella* Enteritidis –tartunnoista suurin osa (90–96 % vuosina 1997–2003) oli peräisin ulkomailta, kun taas *Salmonella* Typhimurium –tartunnoista suurin osa (38–78 % vuosina 1997–2003) oli kotimaisia tartuntoja. Vuosina 1997–2003 oli ulkomaista alkuperää olevien raportoitujen salmonellatapausten osuus 63–81 % kaikista tapauksista (KTL 2004).

Yhdessäkään munantuotannon emokasvattamossa tai emokanalassa ei Suomessa vuosina 1995–2003 todettu salmonellaa. Tuotantopolven kasvattamoissa ja kanaloissa salmonellaa on todettu 0–4 tilalla vuodessa. Siten salmonellavalvontaohjelman tavoite pitää salmonellan vuotuinen esiintyvyys munintakanoissa ja niistä saatavissa kananmunissa enintään 1 % tasolla on toteutunut erittäin hyvin (EELA

1997; EVI-EELA-MMM 2003; MMM 2000; Seuna 1998, 1999, 2000). Salmonellan aiheuttamia ruokamyrkytys-epidemiaa raportoitiin vuosina 1998–2003 vuosittain yhdestä yhdeksään (Hatakka & Wihlman 1999; Hatakka & Halonen 2000; Hatakka et al. 2001, 2002, 2003, 2004). Kanamunien aiheuttama salmonellaruokamyrkytys-epidemia raportoitiin viimeksi vuonna 1995, kun *Salmonella* Enteritidis todettiin yhdeltä munantuotantotilalta ja tilalla tuotettujen kananmunien selvitetiin aiheuttaneen kaksi ruokamyrkytys-epidemiaa (MMM 2000).

### 2.2.2 Vaaran kuvaaminen

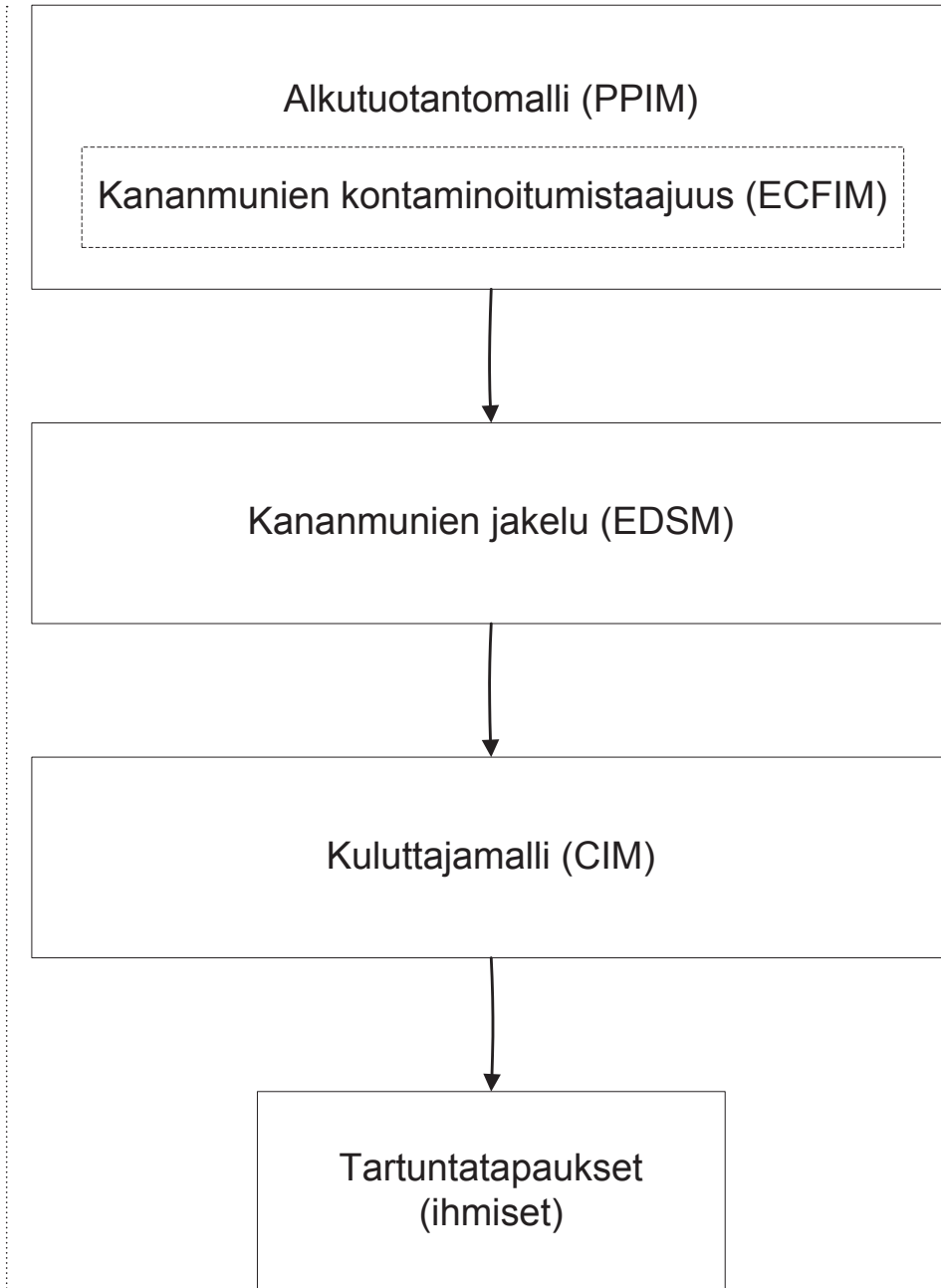
Salmonellabakteeri voi kasvaa 5–46 °C:ssa, mutta sen optimikasvulämpötila on 35–37 °C. Kasvun minimi vesiaktiivisuustaso on 0,95, mutta solut voivat säilyä kuivassa materiaalissa hengissä pitkään. Yhdeksän prosentin suolapitoisuus ja pH alle 4,0 tai yli 9,5 estävät salmonellan kasvun (Jay 2000; Ray 2001).

Salmonellainfektio aiheuttaa harvoin kanoilla oireita. Myös ihmisten salmonellatartunta saattaa 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 osa potilaista saa jälkioireita kuten nivel- ja silmätulehduksia. Reaktiivista nivel-tulehduksista todetaan 1–15 %:lla akuutin salmonelloosin sairastaneista henkilöistä. Niveloireet alkavat yleensä 7–15 päivän kuluttua ruuansulatuskanavan oireiden alkamisesta. Useimmat potilaat paranevat 3–5 kuukaudessa. 16 %:lla näistä tapauksista oireet muuttuvat kuitenkin kroonisiksi (Leirisalo-Repo et al. 1997; Ekman 2000). Salmonellainfektioon on myös liitetty lisääntynyt pitkäaikaisuus (Helms et al. 2003).

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 käyttää normaaliväestön, puhumattakaan riskiryhmien annos-vasteiden arvioimiseen. Yleisesti oletetaan, että vasta annokset  $10^7$ – $10^9$  salmonellasolua aiheuttavat sairastumisen. Eräissä ruokamyrkytyksissä on kuitenkin raportoitu sairastumisia jopa alle  $10^3$  solun annoksella. Tässä riskinarviointimallissa on käytetty normaaliväestölle sovitettua ns. beta-Poisson annos-vastemallia (WHO/FAO 2002).

### 2.2.3 Altistuksen arviointi

Altistuksen arvioinnissa salmonellan tartuntareittiä on mallinnettu alkutuotannosta kuluttajalle tarjottaviin annoksiin asti. Altistuksen mallinnus sisältää kaksi osamallia (Kuva 1, s. 26), joiden tulos ilmaistaan todennäköisyysjakaumina. Altistuksen arvioinnista saatu tieto yhdistetään lopulta riskin kuvaamisessa annos-vaste yms. tietojen kanssa tartunnan saaneiden ihmisten lukumäärän arvioimiseksi.



**Kuva 1.** Kananmunista kuluttajalle aiheutuvan salmonellariskin arviointimalli osamalleineen.

Mallinnus alkaa **Alkutuotantomallilla** (Primary Production Inference Model, PPIM), jonka avulla arvioidaan salmonellan esiintymisen todennäköisyyttä alkaen maahan tuotavista isovanhempaispolven untuvikoista ja päätyn myytävänä oleviin kananmuniin saakka. Alkutuotantomalli jakautuu rakenteeltaan kahteen osaan: Arvioitaessa tartunnan esiintymistodennäköisyyttä isovanhempais- ja vanhempaisparvissa hyödynnettiin broilerisalmoneellariskinarviointia varten tehtyä matemaattista mallia (Ranta & Majala 2002; Majala & Ranta 2003). Tartunnan todennäköisyyttä tuotantoparvissa mallinnettiin tasapainojakaumalla, joka kuvaa yleisellä tasolla parven elinkaaren aikaisten tilojen (esim. infektiot, ei infektiota, parven ikä) tapahtumistodennäköisyyksiä valvontaohjelmaan kuuluvilla kanaloilla joissa kullakin aikajaksolla voi olla tietyn ikäinen infektoitunut tai infektoitumaton parvi tasapainojakauman to-



dennäköisyyksien mukaan. Mallinnuksen perusaineiston muodostivat salmonella-valvontaohjelman tiedot vuonna 2001 otettujen valvontanäytteiden lukumääristä kananmunatuotantoketjun eri tasoilla (isovanhempais- ja vanhempaisparvet sekä tuotantoparvet) sekä todettujen positiivisten näytteiden lukumäärästä. Kanaparvet voivat saada salmonellatartunnan joko vanhempaisparvista muninnan tai haudonnan kautta (nk. vertikaalinen tartuntareitti) tai tuotantotilalla esimerkiksi rehun, ihmisten tai haittaeläinten välityksellä (nk. horisontaalinen tartuntareitti). Rehuperäinen altistus sisältyy horisontaalisen tartunnan yleiseen malliparametriin, sillä tietoja rehujen aiheuttamista salmonellaepidemioista kananmunatuotannossa ei ollut käytettävissä. Lisäksi käytettiin hyväksi osittain elinkeinolta ja osittain tilastoista ja asiantuntija-arvioina saatuja tietoja parvien lukumäärästä ja kokojakaumasta. Mallissa otettiin huomioon myös se, että kasvattamoissa ja kanaloissa voi vuoden aikana olla useampikin parvi peräkkäin. Edelleen oletettiin, että parvien välillä pidetään tuotantokatko. Arvioinnissa käytettiin samoja asiantuntija-arvioihin perustuvia priorijakaumia salmonellan viljelymenetelmän herkkyydestä, parven horisontaalitartunnan todennäköisyydestä sekä infektion säilymistodennäköisyydestä, joita on käytetty myös aiemmin valmistuneessa broilersalmonellan riskinarviointityössä (Ranta & Maijala 2002; Maijala & Ranta 2003).

Alkutuotantomallissa tarvittava arvio siitä, miten usein salmonellatartunnan saaneen parven kanat munivat kananmunia, joissa salmonella on munan sisällä, tuotettiin erillisellä, rakenteellisesti Alkutuotantomallin sisään sijoittuvalla, **Kananmunien kontaminoitumistaajuus** -osamallilla (Egg Contamination Frequency Inference Model, ECFIM). Se perustuu julkaistuun tietoon infektoituneiden yhdysvaltalaisen munantuotantoparvien havaitusta salmonellaa sisältävien kananmunien munimistaajuudesta (Henzler et al. 1998). Mallissa tietoa havaitusta munimistaajuudesta täydennettiin arviolla julkaisussa käytetyn määrittämenetelmän herkkyydestä.

**Kananmunien jakelu** -osamalli (Egg Distribution Simulation Model, EDSM) kuvaa kananmunien ja erityisesti salmonellalla saastuneiden kananmunien jakautumista kotitalouksien, ammattikeittiöiden ja elintarviketeollisuuden käyttöön ja sitä todennäköisyyttä, jolla kontaminoituneesta kananmunasta valmistetaan raakaa tai löysää kananmunaa sisältävä ruokalaji kotitaloudessa tai ammattikeittiössä. Arviot kananmunien käytön jakautumisesta kotitalouksien, ammattikeittiöiden ja elintarviketeollisuuden kesken perustuvat markkinatutkimuslaitosten kulutustutkimustietoon ja asiantuntija-arvioihin. Sitä, miten suuri osa kananmunista käytetään raakaa tai löysää kananmunaa sisältäviin ruokalajeihin selvitettiin kuluttajille ja ammattikeittiöille suunnatuilla kyselytutkimuksilla (Lievonon et al. 2004; Lievonon & Maijala 2005). Kyselyvastausten perusteella ja keittokirjojen reseptejä apuna käyttäen tuotettiin todennäköisyysjakaumat yhdestä kananmunasta valmistettavien raakaa tai löysää kananmunaa sisältävien annosten lukumäärälle kotitalouksissa ja ammattikeittiöissä.

#### 2.2.4 Riskin kuvaaminen

Se, miten monta salmonellasolua ruokailija saa kontaminoitunutta kananmunaa sisältävän ruokalajin syöntihetkellä, riippuu salmonellan esiintymistiheydestä, salmonellasolujen määrästä kananmunassa, annoksen koosta, ruoan kypsennysasteesta sekä keittiössä tapahtuvasta ristikontaminaatiosta. Määrän arvioiminen on siten hyvin vaikeaa. Kolmannessa riskinarviointimallin osassa, **Kuluttajamallissa** (Consumption Inference Model, CIM), hyödynnettiin siksi ns. Bayes-inferenssimallia, joka perustuu arvioituun kananmunasta peräisin olevaan tartuntatapausten lukumäärään vuoden 1999 tilastoitujen tartuntatapausten perusteella (KTL 2002; Maijala et al. 2005). Vuosi 1999 valittiin tarkasteluvuodeksi, koska kyseisenä vuonna salmo-

nellan esiintyvyyden munintakanojen tuotantoparvissa oli valvontaohjelman käynnistämisen jälkeisistä vuosista korkein (nk. worst case -skenaario). Tartuntatapausten maksimimääräksi valittiin niiden kotimaista alkuperää olevien salmonelloosien lukumäärä, joita vastaavat serotyypit oli eristetty joistakin munintakanojen valvontaohjelman mukaisista näytteistä (MMM 2000). Näin kananmunien välittämien raportoitujen tartuntatapausten määrän arvioksi saatiin 0–44 tartuntatapausta vuonna 1999. Mallissa huomioitiin myös tapausten aliraportointi, jotta todellista tartuntatapausten määrää voitiin kuvata valitulla annosvastemallilla.

Käyttämällä näin tietoa tartuntatapausten lukumäärästä, annosvastemallista ja Kananmunien jakelu-osamallilla simuloitusta annosten määrästä, saatiin ennusteet kalibroitua havaintovuoden (1999) tietojen mukaan. Mallissa annoskohtainen sairastumistodennäköisyys jäi kuitenkin riippumaan hyvin paljon siitä mikä salmonellasolujen määrän oletetaan olevan syöntihetkellä. Tällä seikalla on merkitystä skenaarioiden ennusteiden laskennassa, joissa annosmäärä vaihtuu skenaarion mukaan toiseksi, muiden parametrien arvojen säilyessä muuttumattomina. Skenaarioiden tulokset ovat siis herkkiä arviolle syöntihetken salmonellasolujen lukumäärästä, mutta perustilanteen ennusteeseen sillä ei ole suurta vaikutusta. Tämä johtuu siitä, että perustilanteen arviointi perustuu kaikkien parametrien yhteisjakaumaan, joka kokonaisuutena kalibroituu annettuun nykytilanteen tapausmäärään.

### 2.3 Riskinhallintatoimien vaikutus

Riskinhallintatoimi, jonka vaikutusta kananmunien aiheuttamaan tartuntariskiä arvioitiin, oli positiiviseksi todetun emo-/tuotantoparven poistaminen tuotannosta. Positiivisten parvien poistamisen vaikutusta arvioitiin sekä vuoden 2001 mukaisessa perustilanteessa että simuloitaessa salmonellanäytteenottotaajuuden muuttumista ja tartunnan leviämistä 20 prosenttiin vanhempaispolven parvista (kts. luku 2.4).

Vuoden 2001 mukaisessa perustilanteessa munantuotantoparvien todellisen salmonellaesiintyvyyden arvioitu 95 %:n vaihteluväli oli 0,1–0,6 % ja arvioitu todellinen keskimääräinen esiintyvyys oli 0,3 %. Ilman salmonellaposiitiviksi todettujen parvien poistoa todellinen salmonellaesiintyvyys munantuotantoparvissa olisi mallin mukaan ollut 1,0 % eli noin kolminkertainen (95 % vaihteluväli [0,3;3,3]). Munantuotantoparvien todettu salmonellaesiintyvyys oli 0 % vuonna 2001, sillä kyseisenä vuonna ei salmonellavalvontaohjelmassa todettu yhtään positiivista tuotantoparvea. Mallin mukainen odotusarvo todettujen positiivisten määrälle on noin 0,3 % × mikrobiologisen viljelymenetelmän sensitiivisyys (0,75) eli noin 2 todettua positiivista jokaista 1000 testausta kohti, olettaen että infektoituneen parven sisäinen prevalenssi on ainakin 5%, jolloin parvikohtaisen osanäytteistä poolatun testin sensitiivisyys olisi likimain sama kuin mikrobiologinen sensitiivisyys. Perustilanteessa ihmisten raportoitujen salmonellatartuntojen määrän arvioitu 95 % vaihteluväli oli 0–50, keskiarvon ollessa 10 tartuntatapausta vuodessa. Todellisten salmonellatartuntojen 95 % vaihteluväli oli 0–250 ja keskiarvo 60 tartuntatapausta vuodessa. Jos positiiviksi todettuja parvia ei poistettaisi, ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 0–140 ja keskiarvo 40 tartuntatapausta vuodessa. Vastaavasti todellisten salmonellatartuntojen 95 % vaihteluväli olisi 0–740 ja keskiarvo 190 tartuntatapausta vuodessa.

**Skenaariot:****1) Munintakanojen salmonellanäytteenottomäärää lisätään zoonosiasetuksen ((EC) No 2160/2003) mukaiseksi**

Tässä skenaariossa arvioitiin seuraavien muutosten vaikutusta: tuotantopolven kasvatusparvet testataan päivän ikäisinä untuvikkoina (nykyisen valvontaohjelman mukaan untuvikkoja ei testata) ja tuotantarvet testataan munituskaudella joka 15. viikko eli noin 35, 50 ja 65 viikon ikäiset munivat kanat testataan (nykyisen valvontaohjelman mukaan munivat kanat testataan 20–25, 55–60 ja 70–74 viikon ikäisinä). Mikäli salmonellanäytteenotto muutettaisiin zoonosiasetuksen mukaiseksi, munantuotantarvien todellisen salmonellaesiintyvyyden 95 %:n vaihteluväli olisi mallin mukaan 0,1–0,5 % ja arvioitu todellinen keskimääräinen esiintyvyys olisi 0,3 %. Ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 0–40, keskiarvon ollessa 10 tartuntatapausta vuodessa ja todellisten salmonellatartuntojen 95 % vaihteluväli olisi 0–220, keskiarvon ollessa 50 tartuntatapausta vuodessa. Ilman positiivisten parvien poistoa munantuotantarvien todellisen salmonellaesiintyvyyden 95 %:n vaihteluväli olisi tässä skenaariossa 0,3–3,2 % ja arvioitu todellinen keskimääräinen esiintyvyys olisi 1,0 %. Vastaava ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 0–140, keskiarvon ollessa 40 tartuntatapausta vuodessa ja todellisten salmonellatartuntojen 95 % vaihteluväli olisi 0–730, keskiarvon ollessa 190 tartuntatapausta vuodessa. Riskinarviointimallin mukaan munivien kanojen tuotantopolven salmonellanäytteenoton lisääminen zoonosiasetuksen mukaiseksi ei siten nykytilanteessa oleellisesti vaikuttaisi salmonellan esiintyvyyteen tuotantarvissa tai kananmunien välittämiin salmonellatartuntoihin ihmisissä.

**2) Vanhempaispolven parvista 20 % saa tartunnan munintakauden alussa**

Tässä skenaariossa tutkittiin tilannetta, jossa 20 % eli yhteensä 6 parvea kaikkiaan 26 vanhempaisparvesta todetaan salmonellapositiivisiksi munintakauden alussa. Lisäksi oletettiin, että isovanhempaispolven siitosparvet eivät ole infektoituneita, ts. vanhempaispolven parvet ovat saaneet tartunnan horisontaalisen tartuntareitin kautta. Tällainen tilanne voisi olla esimerkiksi salmonellaa sisältävien rehujen välityksellä leviävä epidemia. Mikäli todetut positiiviset parvet poistettaisiin, munantuotantarvien todellisen salmonellaesiintyvyyden 95 %:n vaihteluväli olisi mallin mukaan 0,3–1,1 % ja arvioitu todellinen keskimääräinen esiintyvyys olisi 0,6 %. Ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 0–80, keskiarvon ollessa 30 tartuntatapausta vuodessa ja todellisten salmonellatartuntojen 95 % vaihteluväli olisi 10–420, keskiarvon ollessa 130 tartuntatapausta vuodessa. Ilman positiivisten parvien poistoa munantuotantarvien todellisen salmonellaesiintyvyyden 95 %:n vaihteluväli olisi tässä skenaariossa 0,9–11,6 % ja arvioitu todellinen keskimääräinen esiintyvyys olisi 4,2 %. Vastaava ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 10–520, keskiarvon ollessa 170 tartuntatapausta vuodessa ja todellisten salmonellatartuntojen 95 % vaihteluväli olisi 40–2620, keskiarvon ollessa 850 tartuntatapausta vuodessa. Ilman positiivisten parvien poistoa ihmisillä todettujen sairastapausten määrä kasvaisi noin kuusinkertaiseksi.

**3) 30 % kulutuksesta korvautuu kananmunilla joissa on nykyistä korkeampi salmonellaesiintyvyys**

Tässä skenaariossa tutkittiin tilannetta, jossa 30 % kulutetuista kananmunista korvautuisi kananmunilla, joissa salmonellaa esiintyy saman verran kuin monissa Euroopan unionin jäsenmaissa käytetyissä kananmunissa on raportoitu esiintyvän. Valittu osuus (30%) vastaa tuontimunien osuutta Tanskassa vuonna 2001 (FAOSTAT 2005). Kananmunien kulutuksen oletettiin pysyvän nykytasolla, jolloin skenaario kuvaa joko tuonin osuuden kasvamista 30 %:iin tai salmonellaesiintyvyyden kasva-

mista 30 %:ssa kotimaisista kananmunista esimerkiksi rehuepidemian seurauksena. Skenaariossa korkeamman salmonellaesiintyvyyden oletettiin olevan 0,06 %, 0,5 % tai 1 %. Alin taso, 0,06 %, vastaa Kananmunien kontaminoitumistaajuus -osamallissa kirjallisuuden perusteella arvioitua keskimääräistä kananmunien munansiäistä salmonellaesiintyvyyttä infektoituneissa parvissa. Tasot 0,5 % ja 1 % vastaavat tyypillisiä EU:n zoonoosiraporteissa ilmoitettuja kananmunien salmonellaesiintyvyyksiä (European Commission 2001, 2003a, 2004). Esimerkiksi vuonna 2001 seitsemän jäsenmaan ilmoitusten mukaan salmonellaa esiintyi 0–10,4 %:ssa tutkituista kananmunista, tyypillisen esiintyvyyden ollessa 0,6–1,5 %. Tuloksia ilmoitettaessa ei kuitenkaan ole kerrottu, olivatko kyseessä markkinoilla olevat vai infektoituneiden parvien tuottamat kananmunat eikä sitä, oliko salmonellaa tutkittu kananmunien pinnalta vai sisältä tai minkälaisella otannalla näytteet oli kerätty, joten tulosten täsmällisempi tulkinta on ongelmallista. Skenaarion mukaisessa 0,06 %:n tilanteessa ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväli olisi 90–1730, keskiarvon ollessa 860. Todellisten salmonellatartuntojen 95 % vaihteluväli olisi 450–7780 ja keskiarvo 4350. Jos taas skenaariossa oletetaan 1 %:n prevalenssi 30 %:ssa kulutetuista kananmunista, saadaan ihmisten raportoitujen salmonellatartuntojen 95 % vaihteluväliksi 1430–28 550, keskiarvon ollessa 14 260 tartuntatapausta vuodessa. Todellisten salmonellatartuntojen 95 % vaihteluväli olisi 7440–128 440, keskiarvon ollessa 71 920 tartuntatapausta vuodessa. Skenaarioiden tuloksiin vaikuttaa suuresti epävarmuus salmonellapitoisuudesta syöntihetkellä. Tästä johtuen annoskohtainen sairastumistodennäköisyys voitiin arvioida heikosti, ollen noin 0–50 %. Kaikki skenaariot perustuvat tähän sairastumistodennäköisyyteen, sillä skenaarioissa muuttuu vain annosmäärä muiden parametrien säilyessä perustilanteen mukaisina estimaatteina.

## 2.4 Johtopäätökset

Kansallisen salmonellavalvontaohjelman testaustulosten perusteella on jo pitkään tiedetty, että suomalaisessa kananmunantuotannossa todetaan vain vähän salmonellaa. Sen sijaan salmonellaesiintyvyyden todellista tasoa munintaparvissa, tuetuissa kananmunissa tai salmonellaa sisältävien kananmunien välittämien salmonellatartuntojen lukumäärää ihmisissä ei ole koskaan tieteellisesti arvioitu. Nyt raportoitavaan kvantitatiiviseen riskinarviointiin sisältyvän matemaattisen riskinarviointimallin avulla voitiin arvioida sekä kananmunatuotantoketjun todellista salmonellaesiintyvyyttä että tuotettujen salmonellaposiitivisten kananmunien lukumäärää. Riskinarvioinnin aikana selvitettiin, miten salmonellaposiitiviset kananmunat jakautuvat jakeluketjun mukana tuotantotiloilta kulutukseen ja tutkittiin kotitalouksien ja ammattikeittiöiden kananmunankäyttöä. Mm. näiden tietojen avulla voitiin laskea arvio ihmisten raportoitujen ja todellisten kananmunavälitteisten salmonellatartuntojen vuosittaisesta lukumäärästä.

Matemaattinen malli mahdollisti nykyiseen valvontaohjelmaan kuuluvien riskinhalintatoimenpiteiden (positiivisen parven poisto ja erityistakeet) kansanterveydellisten vaikutusten arvioimisen. Samoin mallin avulla voitiin arvioida, miten valvontaohjelman kuluttajaa suojaava vaikutus muuttuisi, jos nykyisen salmonellavalvontaohjelman mukaista munintaparvien näytteenottotaajuutta lisättäisiin vastaamaan EY:n zoonoosiasetuksen esittämää näytteenottotaajuutta.

Matemaattisen riskinarviointimallin avulla laskettu arvio salmonellan todellisesta esiintyvyydestä tuotantoparvissa mallin perusvuonna 2001 oli 0,3 %. Vuosina 1996–2000 kansallisessa valvontaohjelmassa todettiin vuosittain 0,02–0,2 % valvontanäytteistä olevan positiivisia. Vuosina 2001–2003 munintakanojen kansalli-

sessä valvontaohjelmassa ei ole todettu yhtään positiivista näytettä eikä munantuotantoparvea, mutta vuonna 2004 todettiin sekä yksi positiivinen emo- että tuotantoparvi. Mallin herkkyyksianalyysissä haluttiin tarkistaa, miten ns. normaalitilanne eli muutaman positiivisen tuotantoparven toteaminen vuosittain vaikuttaisi mallin antamaan arvioon tuotantoparvien todellisesta salmonellaesiintyvyydestä. Tästä syystä laskettiin todellinen esiintyvyys vuoden 2001 kaltaiselle vuodelle olettaen että nollan sijaan olisi todettu kaksi positiivista tuotantoparvea. Tällöin mallin arvio salmonellan todellisesta esiintyvyydestä tuotantoparvissa oli edelleen 0,3 %.

Mallin mukaan vuonna 2001 Suomessa tuotettiin keskimäärin 1800 kananmunaa, joiden sisällä oli salmonellaa (95% vaihteluväli [0;7400]). Samana vuonna kananmunien kaupallinen vuosituotanto oli noin 54,5 miljoonaa kiloa eli noin 850 miljoonaa kappaletta. Karkeasti arvioiden salmonellan esiintyvyys kananmunissa oli siten noin yksi sisäisesti kontaminoitunut kananmuna 500 000 tuotettua kananmunaa kohti (0,0002 %). Riskinarviointimallin tulosten perusteella sekä suomalaisten munantuotantoparvien että kananmunien todellinen salmonellaesiintyvyys on kansainvälisesti erittäin matala ja alittaa selvästi kansalliselle valvontaohjelmalle asetetun 1 %:n tavoitetason.

Kansalliseen munintakanojen salmonellavalvontaohjelmaan sisältyvistä riskinhallintatoimenpiteistä tässä riskinarvioinnissa simuloitiin todetun positiivisen parven poistamisen vaikutusta salmonellan esiintyvyyteen tuotantoparvissa, kananmunissa ja ihmisissä. Positiivisten parvien poistaminen osoittautui tehokkaaksi riskinhallintakeinoksi, jota ilman todettujen ihmisten salmonellatapausten lukumäärä kasvaisi todennäköisesti nelinkertaiseksi, jos salmonellan esiintyminen munintakanoissa pysyy nykyisellä erittäin matalalla tasolla. Simuloitaessa tilannetta, jossa salmonellan esiintyvyys munantuotantoketjussa äkillisesti kasvoi, positiivisen parven poistamisen merkitys korostui. Tilanteessa, jossa 20 % vanhempaispolven parvista sai salmonellatartunnan munintakauden alussa esimerkiksi saastuneen rehun välityksellä, todettujen ihmisten salmonellatapausten lukumäärä kasvoi kuusinkertaiseksi, mikäli todettuja positiivisia parvia ei poistettu tuotannosta. Toisaalta tällöin valvontaohjelman kustannukset olisivat myös korkeammat ja vaikutus kananmunien tuotantotilanteeseen voimakkaampi.

Valvontanäytteenottomäärän lisääminen tuotantopolven kasvatusvaiheeseen ja tuotantovaiheen näytteenottoajankohdtien muuttaminen joka 15. viikko tapahtuvaksi ei nykyisellä erittäin matalan salmonellaesiintyvyyden tasolla vaikuttanut oleellisesti arvioon salmonellan esiintyvyydestä tuotantoparvissa tai ihmisten salmonellatapausten lukumäärään.

Kun simuloitiin tilannetta, jossa 30 % kulutuksesta korvautui kananmunilla, joissa salmonellaa esiintyy saman verran kuin esim. monissa Euroopan yhteisön jäsenmaissa on raportoitu esiintyvän, kuluttajien mahdollisuus saada salmonellatartunta 70–1000-kertaistui. Tällainen tilanne voisi olla esimerkiksi kananmunien tuonti Suomeen tai kotimaisessa kananmunien tuotantopolvessa leviävä salmonellaepidemia. Vertailua tehtäessä on huomioitava kuitenkin vertailtavien tietojen puutteellisuus ja/tai yhteensopimattomuus. EU:n zoonoosiraporteissa on puutteellisesti tulkittavissa otannan tilastotieteelliset ominaisuudet, eivätkä tiedot ole suoraan vertailtavissa tässä laskettuun esiintyvyyteen kananmunille, joiden sisällä on salmonellaa.

Riskinarviointimallin rakentamista varten tehdyn kyselytutkimuksen perusteella suomalaisten kuluttajien kuorimunien kulutuksesta 4 % selittyi raakaa kananmunaa sisältävien ruokalajien ja 12 % löysää kananmunaa sisältävien ruokalajien käytöllä.

Vastaavasti ammattikeittiöiden kananmunankulutuksesta enintään 15 % oli raakaa tai löysää kananmunaa sisältävien ruokalajien käyttöä. Tulos ei poikennut muiden maiden saatavilla olevista tutkimustuloksista. Siten kananmunien välittämien salmonellatartuntojen ja epidemioiden vähäinen määrä ei johdu suomalaisten kuluttajien erityisen turvallisesta kananmunien käytöstä vaan kananmunien todellisesta matalasta salmonellaesiintyvyydestä.

**Malliin sisältyy olettamuksia, epävarmuuksia ja rajouksia, kuten laskennan rajoittuminen kananmuniin, joiden sisällä on salmonellaa ja joiden esiintyvyyden laskenta nojaa S. Enteritidis-serotyypistä julkaistuun esiintyvyystietoon, sekä epävarmuus parven testaamisen kokonaisherkkyydestä. Nämä on esitelty raportissa tarkemmin. Suora vertailu muualla raportoituihin tuloksiin saattaa olla vaikeaa vertailtavien tietojen puutteellisuudesta tai yhteismitattomuudesta johtuen. Raportin avulla voidaan kuitenkin vetää seuraavia johtopäätöksiä:**

1. Riskinarviointimallin perusteella keskimäärin 0,3 %:lla kananmunatuotantoparvista esiintyy salmonellaa ja noin 0,0002 % tuotetuista kotimaisista kananmunista sisältää salmonellaa. Tämä on kansainvälisesti erittäin matala taso ja alittaa selvästi kansalliselle valvontaohjelmalle asetetun 1 %:n tavoitetasoa.
2. Kansallisen valvontaohjelman mukainen salmonellaposiitiviseksi todetun parven pakollinen poisto tuotannosta osoittautui arvioinnin tulosten perusteella tehokkaaksi riskinhallintakeinoksi, joka suojaa kuluttajaa merkittävästi myös silloin, kun salmonellan esiintyminen munantuotantoketjussa on harvinaista. Mikäli nykyisessä tilanteessa ei positiiviseksi todettuja parvia poistettaisi tuotannosta, ihmisten salmonellatapausten lukumäärä kasvaisi todennäköisesti nelinkertaiseksi. Torjuntatoimenpiteen suojaava vaikutus korostuu salmonellaesiintyvyyden kasvaessa.
3. Tuotantopolven salmonellanäytteenottotiheyden lisääminen vastaamaan EY:n zoonoosiasetuksen ((EC) No 2160/2003) vaatimuksia vähentäisi nykyisessä matalan esiintyvyyden tilanteessa kuluttajan salmonellariskiä erittäin vähän tai ei lainkaan verrattuna nykyisen valvontaohjelman mukaiseen näytteenottoon.
4. Mikäli 30 % kananmunien kulutuksesta korvautuisi kananmunilla, joissa salmonellaa esiintyy saman verran kuin monissa Euroopan yhteisön jäsenmaissa on raportoitu, (0,06%, 0,5% tai 1%), kuluttajien riski saada salmonellatartunta kananmunien välityksellä 70–1000-kertaistuisi.
5. Mallin rakentamista varten tehtyjen kyselytutkimusten perusteella raakaa tai löysää kananmunaa sisältävien ruokalajien käyttö suomalaisissa kotitalouksissa ja ammattikeittiöissä oli alle 20 %:a kananmunien kokonaiskäytöstä. Tulos ei poikennut muiden maiden saatavilla olevista tutkimustuloksista. Siten kananmunien välittämien salmonellatartuntojen tai ruokamyrkytysten vähäinen määrä ei johdu suomalaisten kuluttajien erityisen turvallisesta kananmunien käytöstä vaan kananmunien todellisesta matalasta salmonellaesiintyvyydestä.

## 3. Summary and conclusions

### 3.1 Introduction

Since 1995, Finland has had an EU-approved national *Salmonella* Control Programme. The Finnish *Salmonella* Control Programme (FSCP) regularly collects samples for *Salmonella* control from farms, hatcheries, slaughterhouses and cutting plants. 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%. The purpose of this surveillance is to ensure the safety of food for consumers.

The programme covers the most important domestic production animals: cattle, pigs and poultry, as well as their meat and eggs. In terms of egg production, the FSCP collects samples from grandparent flocks, parent flocks, hatcheries, and production flocks. Detection of *Salmonella* always leads to risk control measures, whose aim is to prevent the spread of bacteria in the food production chain. The control program allows Finland to demand that a portion of imported beef, pork and poultry meat, eggs and live poultry are examined for *Salmonella* in the country of origin if that country does not have an EU-approved *Salmonella* control program comparable to Finland's (so-called special guarantees). In practice, only Sweden and Norway have such programs.

The Finnish *Salmonella* Control Programme for laying hens has now been in effect for ten years. This risk assessment analyses the risk of infection to consumers of shell eggs produced in Finland, as well as the effects the risk management measures included under the programme have on this risk. In addition, we analyzed how these risks would change if 20% of grandparent flocks were infected or if 30% of the total shell egg consumption were replaced by eggs with a higher *Salmonella* prevalence. This risk assessment has been based on data gathered for the control program, on data received from postal surveys conducted during the risk assessment project, as well as on other available data. This work has been done at the request of the Ministry of Agriculture and Forestry.

### 3.2 The Risk Assessment Model

This risk assessment model is a simplified picture of how a *Salmonella* infection might be transmitted through the egg production chain and end up in consumption. This risk assessment especially makes use of FSCP data from 2001, the latest year with complete surveillance data available at the beginning of this risk assessment work. The estimated number of human *Salmonella* infections is based on data from

1999, however, because 1999 had the highest rates of detected *Salmonella* in egg production flocks since the inception of the FSCP and thus represents a “worst case” scenario. The FSCP data have been supplemented with surveys of private households and institutional kitchens, expert opinions from the egg production sector and information obtained from scientific literature as well as statistics and registers collected in Finland. The model does not differentiate between different *Salmonella* serovars in primary production, as the FSCP treats all of them in the same way.

The model’s basic structure has been determined not only by the availability of information, but also by the interventions and scenarios whose effects the model seeks to simulate. The model estimates the total amount of eggs produced by commercial egg producers, the amount of *Salmonella* contaminated eggs (internally-contaminated eggs) and the number of human *Salmonella* infections in the following cases: a) in the current production conditions (the default situation based on data from 2001), b) if the sampling frequency of *Salmonella* control samples is increased to be equivalent to the zoonosis regulation (Regulation (EC) No 2160/2003), c) if 20% of parent flocks are infected at the beginning of the laying phase, or d) if 30% of total shell egg consumption is replaced by eggs with higher *Salmonella* prevalence. The effects of removing positive flocks, the main risk management measure according to the FSCP for laying hens, is also studied.

This risk assessment is based on the principles of the Codex Alimentarius Commission (Codex Alimentarius Commission 1999) and is divided into four parts: hazard identification, hazard characterization, exposure assessment and risk characterization.

### 3.2.1 Hazard identification

Salmonellosis is caused by the *Salmonella enterica* bacteria. Over 2500 serovars of *S. enterica* are known. All serovars can cause infection in humans, although there are differences between different serovars in how easily they can cause infections. *Salmonella* bacteria can multiply in food products if the temperature during storage and transportation allows. *Salmonella* is usually destroyed in processes where the temperature exceeds 70 °C, so it may persist in products processed at lower temperatures. In addition, the effectiveness of heat treatment depends on the humidity of the product: in some cases, temperatures as high as 130 °C are needed to destroy *Salmonella*.

In 1995–2001, the number of human *Salmonella* infections in Finland was about 3,000 cases per year (54–67 / 100,000 inhabitants / year). In 2002–2004, an average of 2,300 cases per year was reported (43–45 cases / 100,000 inhabitants / year) (KTL 2005). About 100 *Salmonella* serovars are responsible for *Salmonella* infections each year. Over half of all infections were caused by the serovars *Salmonella* Enteritidis and *Salmonella* Typhimurium. The vast majority of the *Salmonella* Enteritidis infections (90–96% in 1997–2003) came from abroad, while the majority of *Salmonella* Typhimurium infections (38–78% in 1997–2003) were of domestic origin. In 1997–2003, 63–81% of all salmonellosis infections came from abroad (KTL 2004).

In 1995–2003, no *Salmonella* was detected in any of the breeding units of egg production in Finland. In rearing and production units of laying hens, *Salmonella* has been detected on 0–4 farms per year. Thus, the FSCP has well met its goal of keeping the prevalence of *Salmonella* in hens and in eggs under 1% (EELA 1997; EVELA-MMM 2003; MMM 2000; Seuna 1998, 1999, 2000). In 1998–2003, from 1 to 9 human *Salmonella* outbreaks were reported annually (Hatakka & Wihlman 1999;



Hatakka & Halonen 2000; Hatakka et al. 2001, 2002, 2003, 2004). The last human *Salmonella* outbreak caused by eggs was reported in 1995, when *S. Enteritidis* was detected at one egg production farm and two *Salmonella* outbreaks caused by the eggs produced on that particular farm were traced back (MMM 2000).

### 3.2.2 Hazard characterization

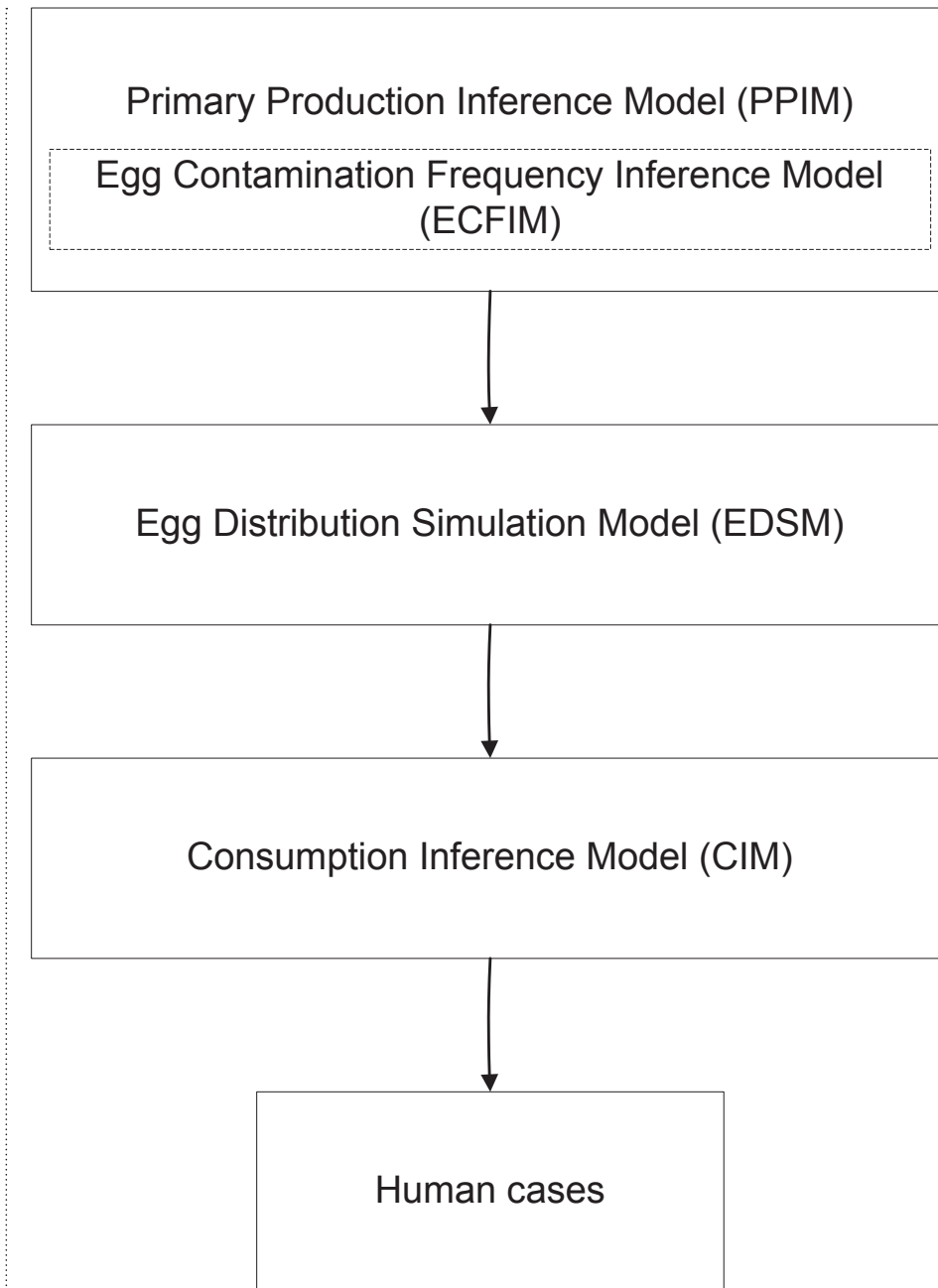
*Salmonella* bacteria can grow in temperatures of 5–46°C, although the optimal temperature is 35–37°C. The minimum water activity is 0.95, but cells can survive long periods in dry material. Nine percent NaCl prohibits the growth of *Salmonella*, as well as a pH outside the range 4.0–9.5 (Jay 2000; Ray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

A *Salmonella* infection rarely causes symptoms in hens. 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, some patients suffer sequelae such as arthritis and ophthalmia. Reactive arthritis is observed in 1–15% of patients with acute salmonellosis. Onset typically occurs from 7 to 15 days after the beginning of gastrointestinal symptoms and most patients recover within the first 3 to 5 months. However, in 16% of patients the symptoms become chronic (Leirisalo-Repo et al. 1997; Ekman 2000). Furthermore, there is new evidence for increased relative mortality within one year after *Salmonella* infection (Helms et al. 2003).

One of the problem areas in assessing microbiological risks is estimating the dose-response, and this is true for *Salmonella* as well. Most dose-response tests have been conducted either with animals or with healthy, young adults; thus, the results cannot be directly applied to the assessment of dose-responses for the normal population, let alone for specific risk groups. It is generally assumed that it takes a dose of at least  $10^7$ – $10^9$  cells/g to cause salmonellosis. However, data from outbreaks of salmonellosis have indicated that sometimes doses even below  $10^3$  cells/g are able to cause gastroenteritis. In this risk assessment model, we used a Beta-Poisson dose-response model adapted for the normal population (WHO/FAO 2002).

### 3.2.3 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. The entire exposure assessment modelling consists of two separate submodels (Figure 1), whose results are presented as probability distributions. 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.



**Figure 1.** The risk assessment model with its submodels for assessing the risks to consumers of *Salmonella* in shell eggs.

In the first part of the model, the **Primary Production Inference Model (PPIM)**, the probability of *Salmonella* prevalence and transmission along the production chain from the flocks of imported grandparent chicks up to shell eggs at the retail level are modelled. The PPIM is divided into two parts. First, a previous mathematical model for the *Salmonella* prevalence in broiler flocks (Ranta & Majjala 2002; Majjala & Ranta 2003) was utilized to assess the probability of *Salmonella* infection in breeder flocks. Then, a generic stationary distribution was constructed to assess the prevalence of *Salmonella* in production flocks. The distribution produces general probabilities of different states of a production flock (e.g. infected, not-infected) at a number of age periods during its life cycle. These age periods then correspond to possible testing times. The whole PPIM is based on the FSCP statistics in 2001,

which gives the number of control samples taken and the number of positive isolations at each level of the egg production chain (rearing and production flocks of breeders and laying hens). Layer 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 transmission, since reports of *Salmonella* epidemics in egg production traced to contaminated feed were not available. In addition, we used information provided by the industry and expert opinions to evaluate the number of breeder and production flocks. The data for a size distribution of the production flocks was obtained from the Information Centre of the Ministry of Agriculture and Forestry. In the model, we also took into account the fact that in a given calendar year, breeding and production farms might have several different flocks in succession, rather than just one flock for the whole year. A quantitative risk assessment on *Salmonella* in broiler production in Finland provided prior distributions, based on expert opinions, for the sensitivity of the *Salmonella* testing method, the chance of horizontal infection and the chance of vertical infection, as well as the likelihood that an ongoing infection would persist (Ranta & Majjala 2002; Majjala & Ranta 2003).

As input for the Primary Production Inference Model, it was necessary to estimate how frequently hens in *Salmonella* infected flocks laid *Salmonella*-contaminated eggs. This estimate was modelled by a submodel called the **Egg Contamination Frequency Inference Model (ECFIM)**, which is a submodel of the PPIM and was based on published information on the apparent prevalence of contaminated eggs laid by infected egg production flocks in the US (Henzler et al. 1998). In the model, sensitivity of the *Salmonella* testing method used in the US study was assessed using scientific literature. The result of the ECFIM is a posterior distribution which provides an input for the PPIM.

The second part of the model, the **Egg Distribution Simulation Model (EDSM)**, describes how shell eggs and especially contaminated shell eggs flow downwards along the distribution chain and how they become divided between households, institutional kitchens and the food industry. The probability of a contaminated egg ending up in a raw or undercooked egg dish is also described, and servings per egg are modelled. Proportions of egg consumption in households and in institutional kitchens were based on information obtained from market research companies and expert opinions. We studied the proportion of raw and undercooked egg dishes prepared in private households and institutional kitchens using postal surveys, which, along with recipes from cookery books, also provided data for estimating the probability distribution for servings per egg (Lievonon et al. 2004; Lievonon & Majjala 2005).

### 3.2.4 Risk characterization

Estimating the number of *Salmonella* cells consumed is difficult, since it depends on the frequency of *Salmonella* contamination, the number of *Salmonella* cells in eggs, the serving size, 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 utilized a so-called Bayesian inference model which estimates the number of human cases of illness caused by *Salmonella* from eggs based on records of reported domestic human cases of illness in 1999. In 1999, the prevalence of *Salmonella* in flocks of laying hens was the highest it had been since the control program was initiated (a so-called "worst case scenario"). To estimate the realized maximum number based on these

records, we first chose the salmonellosis cases of domestic origin which had a corresponding serovar isolated from a FSCP specimen. Then, the relative shares of beef, pork and poultry as a cause for human salmonellosis cases was estimated by dividing the number of human cases in proportion to the serovar isolates made from different domestic and animal species and food products. Thus we arrived at an estimate of 0–44 reported human cases of illness caused by eggs in 1999.

Using the estimate of the reported number of egg-borne human cases of illness and the number of contaminated servings calculated from the Egg Distribution Simulation Model, we applied a specific dose-response model (WHO/FAO 2002) to estimate the chance of illness per contaminated serving. This was done with the Consumption Inference Model, which also accounts for underreporting. The chance of illness was analysed in two ways: firstly, by directly assigning it a uniform prior, and secondly, by assigning different informative priors on the average CFU/g per serving, in the specified dose response model. The resulting joint posterior density of the unknown parameters and variables was used to compute causal predictive distributions under different scenarios and interventions with differing numbers of contaminated servings.

### 3.3 Effects of interventions

The model was also used to assess the effects of one intervention: the removal of the parent and production flocks which tested *Salmonella* positive. These effects were studied in a situation like 2001 (the default year) and in two scenarios: a) increasing the sampling frequency of *Salmonella* control samples to be equivalent to the zoonosis regulation ((EC) No 2160/2003) and b) if 20% of the parent flocks were infected at the beginning of the laying phase (see chapter 3.4).

The estimated 95% credible interval of true *Salmonella* prevalence in production flocks was 0.1–0.6% and the estimated mean was 0.3% in a default situation based on figures from 2001. Without removal of the positive flocks, the true *Salmonella* prevalence in production flocks would have been threefold (1.0%) (95% credible interval [0.3;3.3]) according to the model. The apparent *Salmonella* prevalence in egg production flocks was 0% in 2001, because the FSCP did not detect a single positive flock that year. According to the model, the expected value for the number of detected positive flocks is about 0.3% x the sensitivity of the microbiological culture method (0.75), which means about 2 detected positive flocks per 1,000 tests, assuming that within-flock prevalence in an infected flock is at least 5%. With this assumption, the sensitivity of a pooled sample would be nearly the test sensitivity of a culture method. In the default situation, the estimate for the number of reported human *Salmonella* cases ranged from 0–50 (95% credible interval), with a mean of 10 human cases per year. The 95% credible interval of the true human *Salmonella* cases was 0–250 with a mean of 60 human cases per year. Without removal of the positive flocks, the 95% credible interval of the reported human *Salmonella* cases would be 0–140 with a mean of 40 human cases per year. The 95% credible interval of the true human *Salmonella* cases would be 0–740 with a mean of 190 human cases per year, respectively.

## Scenarios

### 1) Increasing the sampling frequency of *Salmonella* control samples to be equivalent to the zoonosis regulation ((EC) No 2160/2003).

The effects of the following changes were assessed in this scenario: 1) Rearing flocks of laying hens are tested as day-old chicks (day-old chicks are not tested in the present FSCP) and 2) production flocks are tested every 15<sup>th</sup> weeks during the laying phase, which means that laying hens are tested at the age of around 35, 50 and 65 weeks (currently they are tested at the age of 20–25, 55–60 and 70–74 weeks). If the *Salmonella* sampling was changed according to the zoonosis regulation, the 95% credible interval of true *Salmonella* prevalence in production flocks would be 0.1–0.5% and the estimated mean would be 0.3%, according to the model. The 95% credible interval of the reported human *Salmonella* cases would be 0–40 with a mean of 10 human cases per year. The 95% credible interval of the true human *Salmonella* cases would be 0–220 with a mean of 50 human cases per year. Without the removal of positive flocks, the 95% credible interval of true *Salmonella* prevalence in production flocks would be 0.3–3.2% and the estimated mean would be 1.0%, according to the model in this scenario. The respective 95% credible interval of the reported human *Salmonella* cases would be 0–140 with a mean of 40 human cases per year. The 95% credible interval of the true human *Salmonella* cases would be 0–730 with a mean of 190 human cases per year. According to the risk assessment model, therefore, increasing the sampling frequency of *Salmonella* control samples to be equivalent to the zoonosis regulation ((EC) No 2160/2003) would not substantially affect *Salmonella* prevalence in production flocks or the number of human *Salmonella* cases transmitted by shell eggs in the current situation.

### 2) 20% of the parent flocks were infected at the beginning of the laying phase.

This scenario simulates a situation where 20% of all parent flocks (6 flocks out of 26) are detected to be *Salmonella* positive at the beginning of the laying phase. It was also assumed that the grandparent flocks are not infected, so the parent flocks have been infected via horizontal transmission. Such a situation could be caused, for instance, by the spread of a *Salmonella* epidemic via contaminated feeding stuffs. If the *Salmonella* positive flocks were removed, the 95% credible interval of true *Salmonella* prevalence in production flocks would be 0.3–1.1% and the estimated mean would be 0.6%, according to the model. The 95% credible interval of the reported human *Salmonella* cases would be 0–80 with a mean of 30 human cases per year, while the 95% credible interval of the true human *Salmonella* cases would be 10–420 with a mean of 130 human cases per year. Without removal of the *Salmonella* positive flocks, the 95% credible interval of true *Salmonella* prevalence in production flocks would be 0.9–11.6% and the estimated mean would be 4.2% in this scenario. The respective 95% credible interval of the reported human *Salmonella* cases would be 10–520 with a mean of 170 human cases per year, while the 95% credible interval of the true human *Salmonella* cases would be 40–2,620 with a mean of 850 human cases per year. Therefore, without removal of the *Salmonella* positive flocks, the number of reported human *Salmonella* cases would increase about sixfold.

### 30% of the total shell egg consumption is replaced by eggs with a higher *Salmonella* prevalence

This scenario simulates a situation where 30% of total shell egg consumption is replaced by eggs with the *Salmonella* prevalence reported to exist in shell eggs used by several EU member states. In order to create a realistic scenario, we chose this 30% proportion of shell eggs with a higher *Salmonella* prevalence, as this figure cor-

responds to the amount of shell eggs Denmark imported in 2001 (FAOSTAT 2005). The consumption of shell eggs was assumed to remain at the current level, so this scenario could happen if Finland imported eggs from countries with a high *Salmonella* prevalence in shell eggs or if there was an increase of *Salmonella* prevalence in domestic shell eggs, for instance, as a result of infections transmitted by contaminated feeding stuffs. The higher *Salmonella* prevalence was assumed to be 0.06, 0.5 or 1.0% in this scenario. The lowest percentage, 0.06%, corresponds to the mean result of the ECFIM, which, based on literature, estimates the *Salmonella* prevalence of internally-contaminated shell eggs laid by hens of infected flocks. The other percentages, 0.5 and 1.0% are equivalent to the typical *Salmonella* prevalences in shell eggs reported in annual zoonosis reports of the EU (European Commission 2001, 2003a, 2004). For instance, in 2001 *Salmonella* was detected in 0% to 10.4% of tested shell eggs according to seven member states. The typical *Salmonella* prevalence reported was 0.6–1.5%. It was not reported, however, if the eggs tested originated from retail sale or from infected flocks and whether the content, the shell or both were analyzed. Also, the sampling remained unclear. Therefore, it is problematic to interpret these results. When a prevalence of 0.06% in 30% of consumed shell eggs was simulated, the 95% credible interval of the reported human *Salmonella* cases would be 90–1,730 with a mean of 860 human cases per year, while the 95% credible interval of the true human *Salmonella* cases would be 450–7,780 with a mean of 4,350 human cases per year. When a prevalence of 1.0% in 30% of consumed shell eggs was simulated, the 95% credible interval of the reported human *Salmonella* cases would be 1,430–28,550 with a mean of 14,260 human cases per year, while the 95% credible interval of the true human *Salmonella* cases would be 7,440–128,440 with a mean of 71,920 human cases per year. Uncertainty about the number of *Salmonella* cells at the time of consumption had a significant effect on the results of these scenarios, however. Therefore, the probability of becoming ill from a single serving could only be vaguely estimated, the result being from 0 to 50%. All scenarios are based on this probability of illness, because the only changing parameter is the number of servings while all other parameters remain as they are in the default situation.

### 3.4 Conclusions

As a result of the Finnish *Salmonella* Control Programme, it has long been known that *Salmonella* is rarely detected in egg production. On the other hand, the true prevalence of *Salmonella* in laying flocks, in eggs produced, as well as the number of human infections caused by shell eggs, has never been scientifically studied. Using the mathematical risk assessment model developed for this quantitative risk assessment, we can estimate the true *Salmonella* prevalence in the egg production chain as well as the number of *Salmonella*-positive eggs. In addition, this risk assessment examines the distribution of *Salmonella*-positive eggs along the distribution chain, and studies the ways shell eggs are used in private households and institutional kitchens. Based on this information, it is possible to estimate the reported and true numbers of human *Salmonella* cases caused by shell eggs.

The mathematical model also makes it possible to assess the effects on public health of the current interventions (removal of detected positive flocks and the special guarantees provided under the FSCP). Similarly, we can also use the model to assess changes in consumer safety if the current sampling frequency mandated by the FSCP were changed in accordance with the new EU zoonosis regulation.

According to the mathematical risk assessment model, the true prevalence of *Salmonella* in production flocks in the default year 2001 was 0.3%. From 1996–2000, 0.02–0.2% of samples tested by the FSCP were positive. From 2001–2003 there were no positive samples detected by the control programme, but in 2004 one positive parent and one positive production flock were detected. Given the very low numbers of positive test samples, we thought it important to test the model's estimate of true *Salmonella* prevalence in a so-called normal situation, where a few infected production flocks are detected per year. For this sensitivity analysis, the calculations were repeated using surveillance data from 2001, but with two detected positive production flocks. Even using these figures, the model still estimated that the true prevalence of *Salmonella* in production flocks was 0.3%.

According to the model, in 2001 an average of 1,800 eggs were internally-contaminated with *Salmonella* (95% credible interval [0;7,400]). In the same year, a total of 54.5 million kilos, or about 850 million eggs, were produced in commercial facilities. We can thus roughly estimate that one in 500,000 egg was internally-infected with *Salmonella* (0.0002%). Based on this risk assessment model, we can conclude that the true *Salmonella* prevalence in production flocks and in shell eggs is exceptionally low in Finland by international standards, and is well under the target of 1% set by the FSCP.

In this risk assessment, we also simulated the effects of the interventions mandated by the FSCP (removal of detected positive flocks) on the prevalence of *Salmonella* in production flocks, shell eggs and in humans. Removing positive flocks is an effective risk management measure, as the number of confirmed human cases would likely quadruple if the prevalence of *Salmonella* in laying hens remained at the current low levels, and positive flocks were not removed. In a simulated situation where the prevalence of *Salmonella* in the egg production chain suddenly rises, the significance of removing infected flocks increases still further. For example, if 20% of grandparent flocks were infected with *Salmonella* at the beginning of the laying phase, for example through consuming infected feed, the number of confirmed human cases would increase sixfold if the infected positive flocks were not removed from production. In this case, the costs of the control programme would also increase, and its effect on egg production would be greater.

Increasing the number of samples taken during the rearing of production flocks and changing the frequency of sampling to every 15<sup>th</sup> week during the laying phase of production flocks would not in the present situation of very low *Salmonella* prevalence have a significant effect on the estimate of *Salmonella* prevalence in production flocks or in the number of human cases.

When simulating a situation where 30% of eggs consumed were replaced with eggs with a *Salmonella* prevalence equivalent to what has been reported in many European Union member states, the consumer's risk of being infected with *Salmonella* increases 70–1000 times. Such a situation could be caused by the import of eggs to Finland or by a *Salmonella* epidemic in domestic egg production flocks. When making such comparisons, however, it is important to recognize the lack and/or incomensurability of data. For example, the EU zoonosis reports are difficult to interpret due to deficient background information about the statistical features of the reported results, and therefore, these data are not directly comparable to the estimated prevalence of internally-contaminated eggs in Finland.

Surveys conducted in conjunction with this risk assessment reveal that 4% of shell eggs are consumed in dishes containing raw eggs, while a further 12% are consumed in undercooked dishes. In institutional kitchens not more than 15% of total shell egg consumption was in the form of dishes containing raw or undercooked eggs, a figure in line with findings in other countries. The low levels of *Salmonella* infection or epidemics caused by shell eggs in Finland are thus not due to particularly safe egg consumption by Finns, but rather to the fact that the true prevalence of *Salmonella* in eggs is low.

**This model contains certain assumptions, uncertainties and limitations. For example, it is limited to internally-contaminated eggs, given that the only applicable prevalence data is on the *S. Enteritidis* serovar. In addition, there is uncertainty about the overall flock level sensitivity of the tests used. These limitations are detailed more fully in the report. Direct comparison with results published elsewhere may also be difficult due to incomplete or incommensurate data. Based on this report, however, we can draw the following conclusions:**

1. According to this risk assessment model, *Salmonella* is present in an average of 0.3% of egg production flocks, and approximately 0.0002% of domestic eggs contain *Salmonella*. Internationally, this is an extremely low level, clearly below the 1% target set by the Finnish *Salmonella* Control Programme.
2. According to the model, the removal of infected flocks, as mandated by the Finnish *Salmonella* Control Programme, is an effective intervention, significantly reducing the number of human *Salmonella* infections even in cases where the prevalence of *Salmonella* in egg production chain is very low. If, in the current situation, detected positive flocks were not removed from production, the number of human *Salmonella* cases would likely quadruple. Moreover, the safety effect of this intervention increases as the prevalence of *Salmonella* increases.
3. Increasing the sampling frequency of production flocks in accordance with the new EU zoonosis regulation ((EC) No 2160/2003) would, in the current situation of low *Salmonella* prevalence, have little or no effect on consumer safety compared to the present sampling frequency.
4. If 30% of shell egg consumption were replaced with eggs with a *Salmonella* prevalence equivalent to that reported in many EU member states (0.06%, 0.5%, or 1%), the risk of *Salmonella* infection to consumers would increase 70–1000 times.
5. According to surveys completed for this risk assessment, the use of raw or undercooked eggs in Finnish households and institutional kitchens is under 20% of total shell egg consumption, which is in line with findings in other countries. Therefore, we can conclude that the low levels of *Salmonella* infection or food poisoning caused by shell eggs in Finland are not due to particularly safe egg consumption by Finns, but rather to the fact that the true *Salmonella* prevalence in shell eggs is low.



## 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 diarrhoea. The excretion of *Salmonella* in faeces usually ceases in about a month, but a small number of infected persons may become chronic asymptomatic *Salmonella* carriers. Therefore, occasionally people who come in contact with an infected person can acquire the disease. Only very few *Salmonella* serovars can cause severe disease in animals, including *Salmonella* Gallinarum/Pullorum in poultry or *Salmonella* Dublin in cattle.

When Finland joined the European Union in 1995, its extraordinary good *Salmonella* situation in animal production was acknowledged and it was granted special permission to run its own procedures for controlling *Salmonella* infection in meat and egg production. This EU-approved programme is called the Finnish *Salmonella* Control Programme (FSCP) (MMMEEO 1994). The aims of the programme are to keep the occurrence of *Salmonella* low both in domestic animals and food of animal origin, and thus to ensure the safety of food for consumers with respect to *Salmonella*. 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, the Feedingstuff Act has been applied in Finland to detect *Salmonella* in feeds for over 40 years. Because of this tight domestic production control and negligible imports, the *Salmonella* situation was good when Finland joined the EU. And, as a result of the serious commitment of farms and production plants, the *Salmonella* situation in Finland has remained good after joining the EU. The good *Salmonella* situation in broiler and pork production was recently verified (Maijala & Ranta 2003; Ranta et al. 2004). However, the *Salmonella* risk to consumers caused by shell eggs has never been assessed scientifically 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. 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; a quantitative risk assessment report was published in 2003. Also, quantitative risk assessments for *Salmonella* in Finnish pork and beef production were launched in 2001; the pork risk assessment was published in 2004. The present quantitative risk assessment for *Salmonella* in egg production in Finland was started in early 2003. This report uses the principles of the Codex Alimentarius Commission on microbiological risk assessment (Codex Alimentarius Commission 1999).

## 4.2 Objectives

The objectives of this risk assessment on *Salmonella* in egg production were:

1. To create a model of *Salmonella* transmission from layer grandparents to consumers in Finland.
2. To assess the effect of the FSCP on the *Salmonella* risk caused by shell eggs to Finnish consumers based on the situation in 2001.
3. To assess the effect of the removal of infected flocks on consumer risk.
4. To study the effects of changes in sampling frequency (Regulation (EC) No 2160/2003) and two other scenarios on consumer risk.

## 5. Background information

### 5.1 Egg production in Finland

Egg production in Finland is mainly concentrated in the southwestern part of the country. The total number of laying hens was estimated to be 4.2 million in 1995 and 3.2 million in 2002 (MMMTIKE 2003a). In 1995, when Finland joined the European Community, more than 7,000 farms carried on egg production (MMMTIKE 1996). Most of them (58%) were family farms with fewer than 100 egg layers. In the nine years from 1995 to 2003, the number of egg production farms decreased significantly, to only 1,815 in 2003 (Figure 2). In particular, the number of small farms decreased, while the number of large farms, those containing over 5000 egg layers, increased from 88 in 1995 to 165 in 2003 (MMMTIKE 2004). Because of this transition towards more professional egg production in larger units, the number of hens did not change as significantly as the number of farms (Figure 3). As a result, the average number of hens per farm increased. When taking into account farms with at least 100 hens, the average-sized farm had 2,412 hens in 1998 (MMMTIKE 2000). By 2003, the corresponding average was 3,535 (MMMTIKE 2004). Egg production and self-sufficiency in eggs decreased during the late 1990's, but overproduction has remained a problem. Self-sufficiency in eggs was 116% in 2003 (Figure 4) (MMMTIKE 2004). As a result, Finland exports shell eggs mainly to Sweden, Denmark, and Germany. Because of national overproduction, low prices and the special guarantees provided by the Finnish *Salmonella* Control Programme, Finland has not imported shell eggs for human consumption. Import of egg products, however, has increased rapidly in the few last years, though it was still only 1.6% of total egg consumption in 2002 (Table 1) (MMMTIKE 2003a).

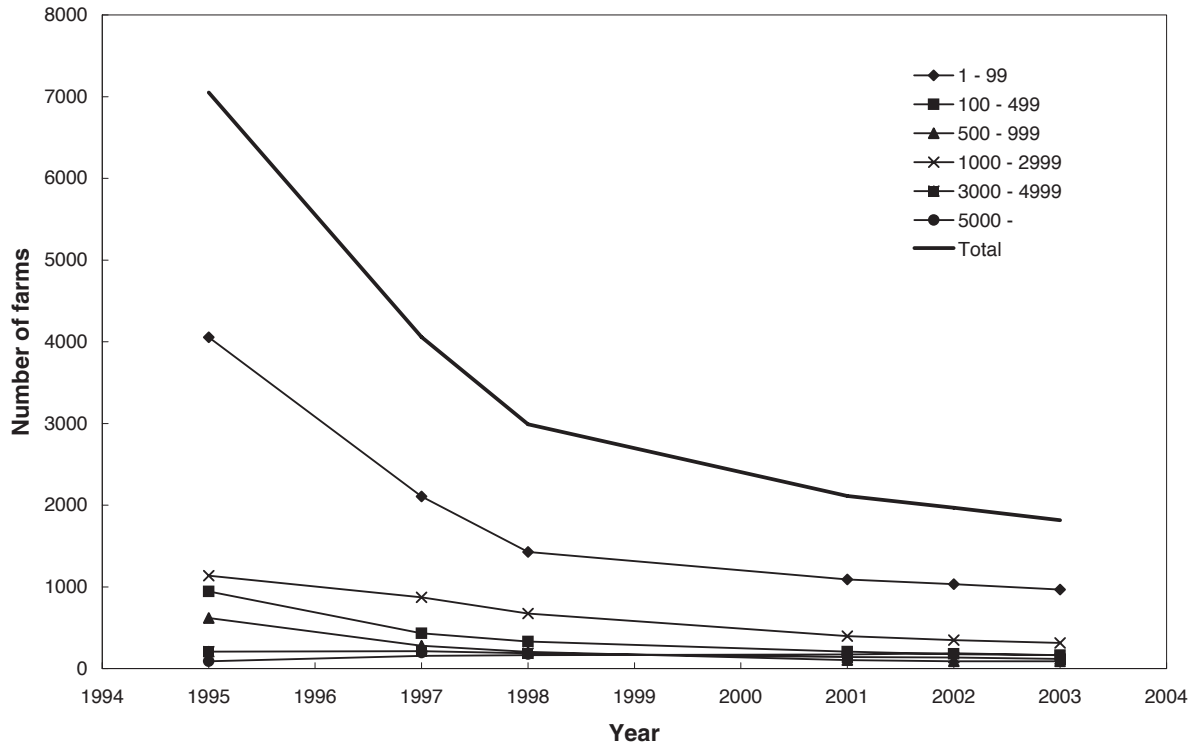


Figure 2. Number of egg production farms by size of flock in 1995–2003 (MMMTIKE 1996, 1999, 2000, 2002, 2003a, 2004).

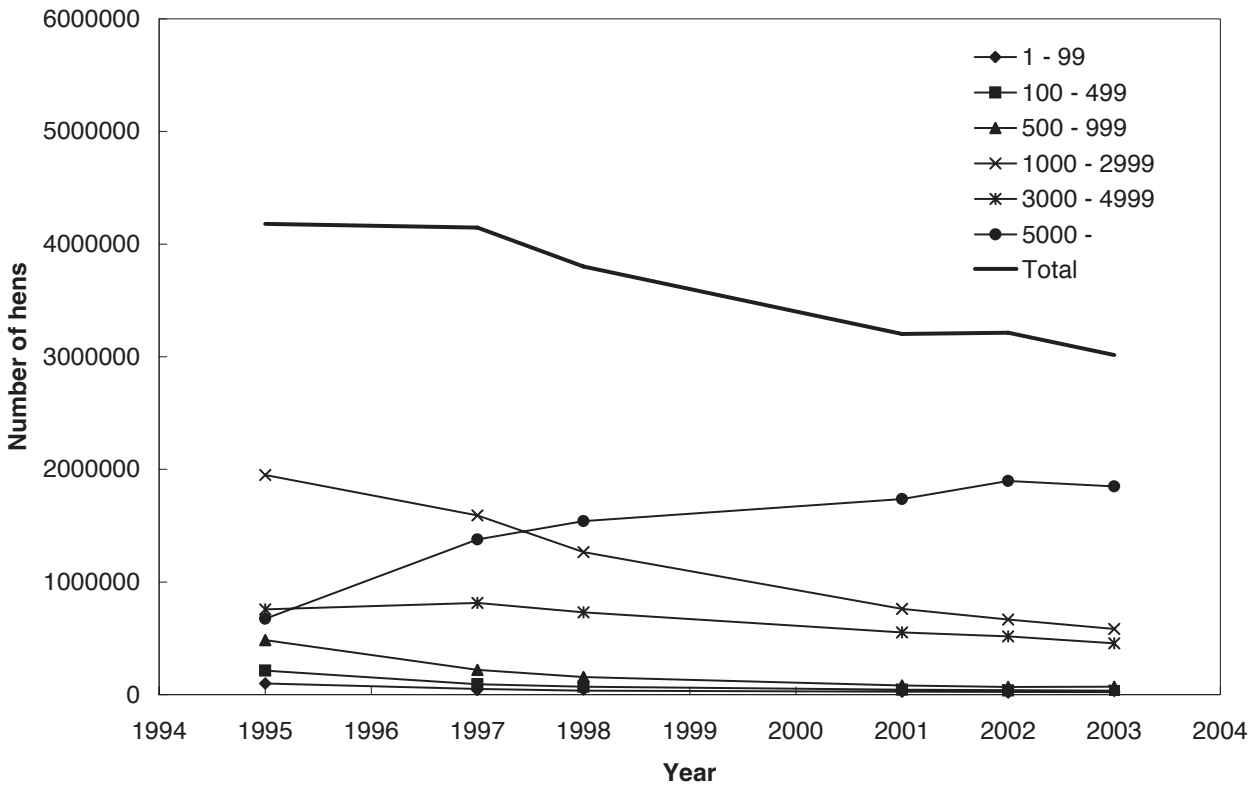
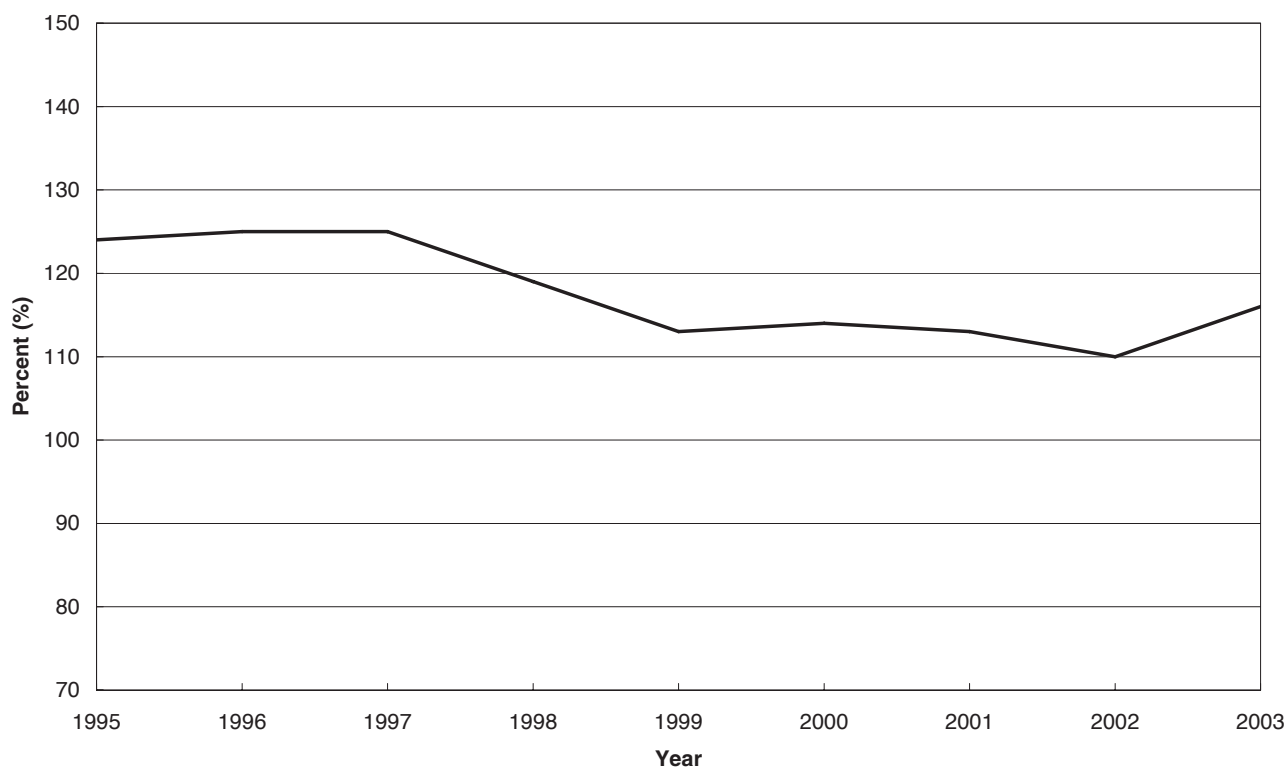


Figure 3. Number of hens by size of flock and the total number of hens in 1995–2003 (MMMTIKE 1996, 1999, 2000, 2002, 2003a, 2004).



**Figure 4.** Self-sufficiency in shell egg production 1995–2003 (MMMTIKE 2004).

**Table 1.** The Finnish production, consumption, and export of eggs and import of egg products in 1995–2003 (MMMTIKE 2002, 2003a, 2004).

Year	Total egg production (Million kg)	Consumption (Million kg)	Export (Million kg)	Import (egg products) (Million kg)
1995	74.7	59.9	13.7	0.049
1996	70.8	56.0	13.8	0.104
1997	66.7	52.6	12.8	0.083
1998	63.9	52.9	10.6	0.100
1999	58.9	51.4	6.9	0.132
2000	59.0	51.4	6.4	0.184
2001	56.5*	52.0	7.1	0.184
2002	54.7	51.7	4.7	0.820
2003	56.2	50.7	8.9	0.825

### 5.1.1 Structure of egg production in Finland

There is no domestic grandparent production in Finland: grandparents and parents of egg layers are transferred from Canada, France, Germany and the United States to two rearing holdings by two importers (Table 2). In 2002, the imported hybrids were HY-line, Lohmann and Shaver. Isabrown was a popular hybrid as well during the 1990s, but its import ceased in 2001. In Finland, there are two holdings for grandparent rearing flocks and 12 holdings for parent rearing flocks. Adult parent breeding flocks are farmed in 13 holdings. Rearing flocks of laying hens are farmed

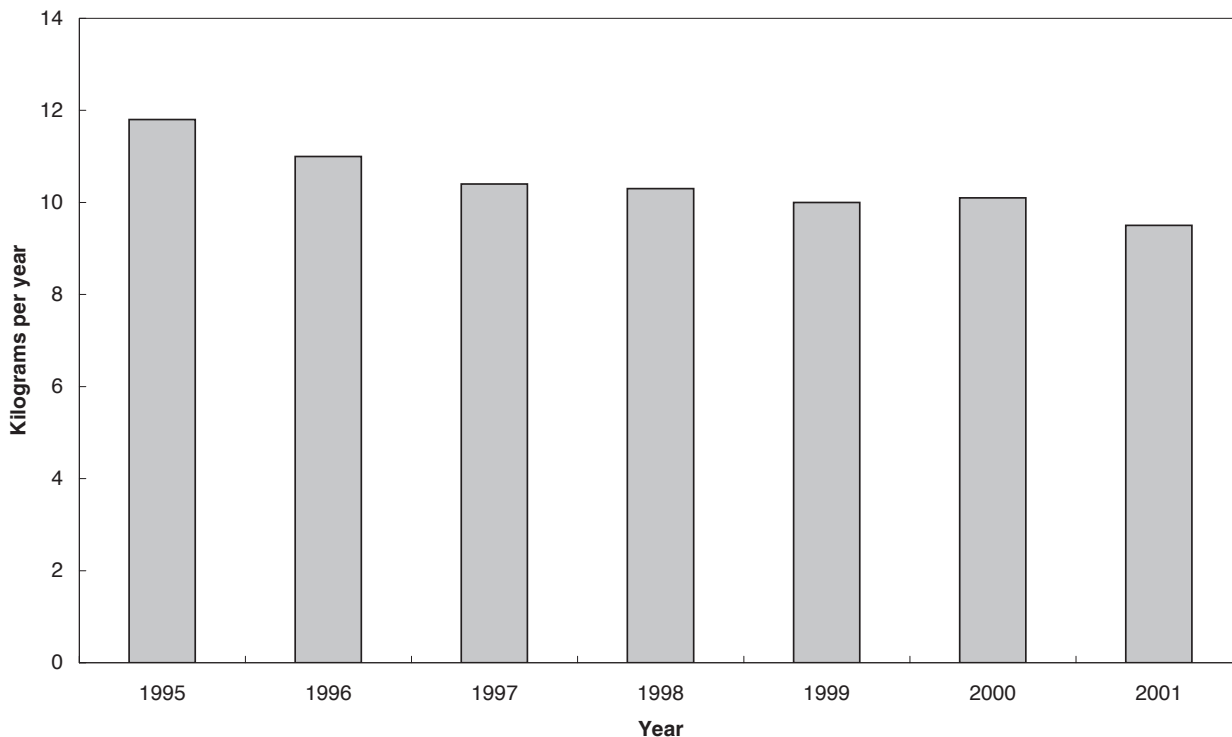
in approximately 50 commercial holdings. In addition, there are many producers who breed laying hens for their own production. In 2003, there were 847 egg producers with more than 100 layers (MMMTIKE 2004).

**Table 2.** Import of grandparent and parent chicks in 1995–2003 (ETT 2003).

Hybrid	Number of imported grandparent chicks								
	1995	1996	1997	1998	1999	2000	2001	2002	2003
Isabrown	1,000	900		900	990		1,000		
Shaver	1,000	995		995	995		1,000	1,000	
Lohmann White		1,560	1,311	1,311	1,311	1,440	1,440	1,440	1,440
HY-Line Brown								1,350	
Hybrid	Number of imported parent chicks								
	1995	1996	1997	1998	1999	2000	2001	2002	2003
Lohmann Brown			4,480	4,480	2,240	4,800	2,500	2,400	2,200
Lohmann Tradition									2,240
HY-Line Brown								19,250	
HY-Line W-36/C-20								6,435	11,600

## 5.2 Egg consumption in Finland

According to food balance sheets, Finnish people consume an average of 10 kilograms of eggs per person per year. Consumption increased in 1995 when Finland joined the EU, but then quickly levelled off and has now slowly decreased for several years (Figure 5). Egg consumption per capita in Finland is lower than in most EU countries or in the USA (Table 3).



**Figure 5.** Egg consumption per capita in Finland in 1995–2001 (MMMTIKE 2002).

**Table 3.** Egg consumption in the Nordic countries, in some EU countries and in the USA in 2002 (MMMTIKE 2003a, 2004; FAOSTAT 2005).

Country	Consumption per capita (kg/year)
Iceland	9.2
Norway	10.1
Sweden	11.9
Finland	9.8
Denmark	15.4
United Kingdom	13.0
France	15.0
Germany	14.0
Italy	13.0
USA	14.6

The official food balance sheets calculate national egg consumption using the equation

$$\text{Consumption} = \text{Production} + \text{Import} - \text{Export} - \text{Hatching} - \text{Feed use.}$$

The result is an internationally comparable statistical value, but it provides no information on different egg consumption patterns in the Finnish population.

In addition to official statistics, information on shell egg consumption is collected by commercial market research companies and the National Public Health Institute (KTL). According to recent national dietary surveys, the average egg consumption of Finnish men was 8 kg/year in 1997 and 7.7 kg/year in 2002. The corresponding numbers for women were 5.8 kg/year in 1997 and 5.5 kg/year in 2002 (National Public Health Institute 1998; Männistö et al. 2003). These results differ from the amounts reported in the food balance sheets. The dietary survey method used was a 24-hour recall in 1997 and a 48-hour recall in 2002. It should be noted, therefore, that these dietary surveys were designed to assess the average diet and nutrient intake of Finnish adults (25–64 years old), not to estimate the total annual consumption of different food items. Estimating the total annual consumption of food items consumed infrequently, such as shell eggs, is especially difficult on the basis of information obtained for one or two days. Because of different starting points of each individual register and study, the estimated consumptions of shell eggs from different data sources differ from each other and are not directly comparable.

In addition to specialized dietary surveys, KTL regularly monitors the shell egg consumption of the adult and elderly population as part of two large health behaviour studies called Health Behaviour and Health among the Finnish Adult Population (Helakorpi et al. 2003) and Health Behaviour and Health among Finnish Elderly (Sulander et al. 2004). The former is carried out annually and the latter every second year. According to Health Behaviour and Health among the Finnish Adult Population research series, the shell egg consumption of adult people has been stable in recent years (Table 4). When elderly persons and persons of working age are compared, the elderly tend to eat more eggs. A smaller percentage of the elderly reports no use of eggs at all (20.3–28% of the elderly vs. 37.6 % of the working population) and more of them reported using eggs several times a week (Helakorpi et al. 2003; Sulander et al. 2004).

**Table 4.** Eggs eaten by the 15-64-year-old population during the previous week in 1999–2003 (Helakorpi et al. 1999, 2000, 2001, 2002, 2003).

How many days did you consume eggs last week?	Year				
	1999	2000	2001	2002	2003
	Proportion of the respondents (%)				
Not at all	35.4	35.3	34.1	35.8	37.6
On 1-2 days	52.9	54.2	56.0	53.6	52.1
On 3-5 days	10.3	9.2	8.8	9.8	9.1
On 6-7 days	1.4	1.3	1.2	0.8	1.2

### 5.3 Egg market legislation

The European Union has at least the following directly applicable regulations which control marketing and welfare standards for hen eggs:

- Council Regulation (EEC) No 1907/90 on certain marketing standards for eggs as last amended by Council Regulation (EC) No 1039/2005.
- Commission Regulation (EC) No 2295/2003 introducing detailed rules for implementing Council Regulation (EEC) No 1907/90 on certain marketing standards for eggs as last amended by Commission Regulation (EC) 1515/2004.
- Council Directive 1999/74/EC laying down minimum standards for the protection of laying hens.
- Commission Directive 2002/4/EC on the registration of establishment keeping laying hens, covered by Council Directive 1999/74/EC.

The regulations lay down uniform rules throughout the European Community for the quality and weight grading, labelling, packaging, storage, transport and retailing of hen eggs. The aim of the regulations is to lay down the minimum standards for the welfare of laying hens and to ensure that the quality of eggs is maintained.

These regulations apply to all hen eggs marketed within the European Community, with certain exceptions. These regulations do not apply to eggs sold directly by producers to consumers at the farm or through door-to-door selling. Such eggs must be the producer's own and cannot be quality or weight graded. A producer may also sell ungraded eggs at a local public market, but since 1 July 2005 these eggs must carry the code of the producer's distinguishing number (Council Regulation (EC) No 1039/2005). In addition to the general exceptions throughout the Community, Finnish egg producers have the right to sell ungraded eggs directly to local retailers in certain sparsely inhabited areas of northern and eastern Finland (the provinces of Lappi and Oulu, the municipalities formerly belonging to the provinces of Pohjois-Karjala and Kuopio and the islands of Åland). Despite these exceptions, all Finnish producers delivering shell eggs to packing stations must be part of the Finnish *Salmonella* Control Programme. According to the National Food Agency Finland, there were 1,000 producers who delivered shell eggs to packing stations in 2001. Furthermore, institutional kitchens and bakeries are allowed to use only class A graded shell eggs from packing stations.

Since June 2003, every egg production site must be registered and issued a distinguishing number. This obligation covers egg production establishments of all sizes, including the above-mentioned areas of northern and eastern Finland. Registration is not mandatory, however, for producers practising direct sale at their own farm or



through door-to-door selling. This registration of establishments, and the assigning of distinguishing numbers, is a condition for tracing eggs placed on the market for human consumption. Since January 2004, each shell egg must be marked with the distinguishing number of the production site. The obligatory marking covers grade A shell eggs which are graded at the packaging stations, but not shell eggs for direct sale from producers to consumers. This labelling guarantees the traceability of eggs and ensures that their origin and production method can be verified.

## 5.4 The Finnish *Salmonella* control programme (FSCP)

In community legislation, minimum measures for monitoring and controlling *Salmonella* in fowl flocks have been laid down in the zoonosis directive 2003/99/EC and the zoonosis regulation (EC) No 2160/2003 which repealed the previous zoonosis directive 92/177/EEC in April 2004. This legislation prescribes measures for both breeding flocks and egg production flocks of poultry and covers all *Salmonella* serovars with public health significance. The more specific target for breeder flocks has been laid down in Commission regulation (EC) No 1003/2005, according to which preventive measures for breeding flocks of *Gallus gallus* cover *Salmonella* Enteritidis, *Salmonella* Hadar, *Salmonella* Infantis, *Salmonella* Typhimurium and *Salmonella* Virchow. During the transitional period measures for laying hens cover *Salmonella* Typhimurium and *Salmonella* Enteritidis. Thereafter, Community targets for the reduction of the prevalence of zoonosis will specify the *Salmonella* serovars covered.

Because of the favourable *Salmonella* situation in Finland, the EU Commission granted Finland the so-called Finnish *Salmonella* Control Programme (FSCP) (Commission Decision 94/968/EC). An objective of the programme is to keep the prevalence of *Salmonella* in production animals, meat and eggs less than 1% at a national level (MMMEEO 1994). The Finnish *Salmonella* Control Programme (FSCP) started in May 1995.

### 5.4.1 The Finnish *Salmonella* control programme for egg laying hens

The Finnish *Salmonella* control programme for live poultry covers laying hens, broilers and turkeys (MMMEEO 1994). All serovars of *Salmonella* are covered. The *Salmonella* control programme for egg production was originally started in 1995, and was amended in 2001 (MMM 24/EEO/2001). The programme for layers covers breeding flocks as well as commercial egg production flocks. The structure of the FSCP for egg production is shown in Figure 6.

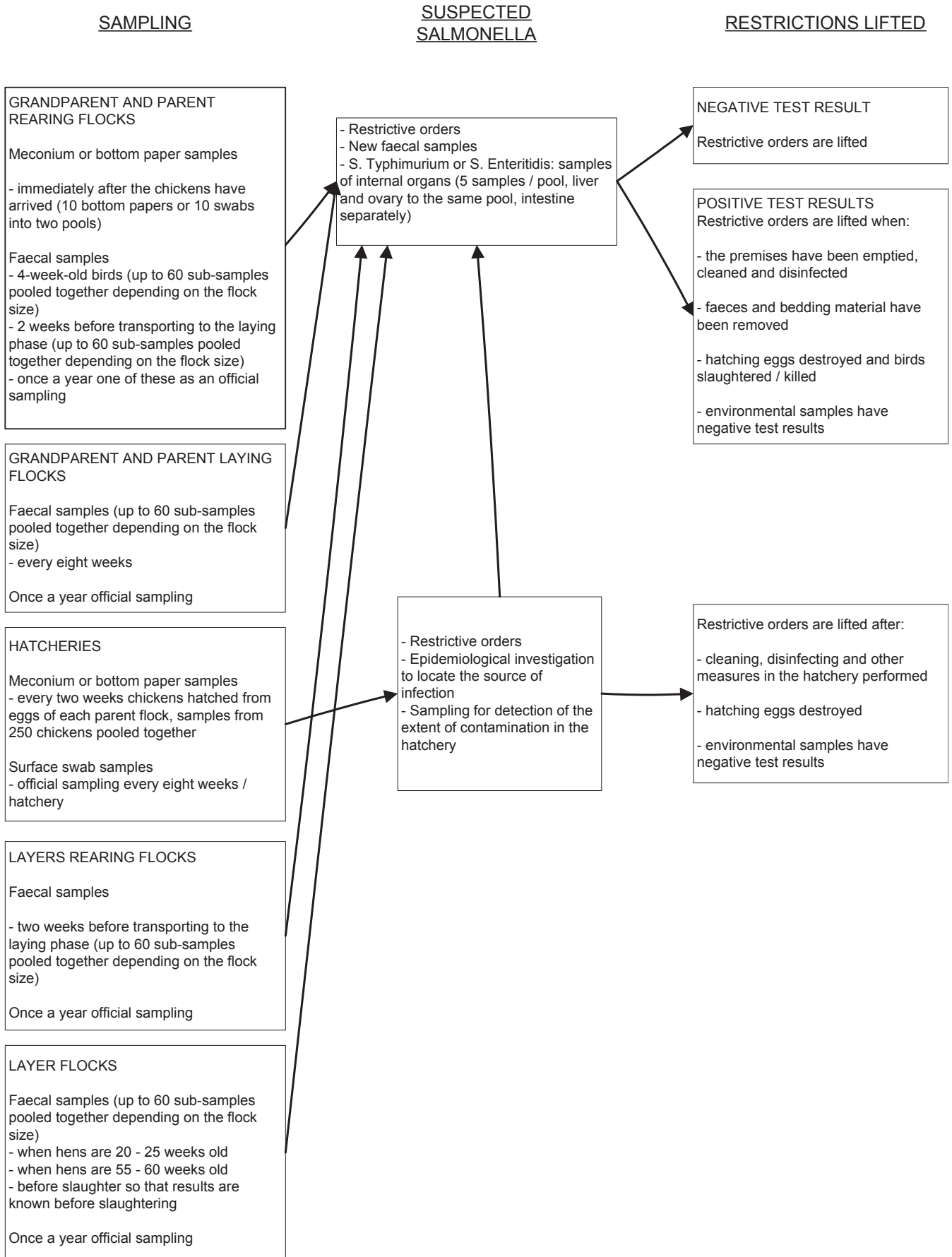


Figure 6. Structure of the FSCP for egg production (MMM 24/EEO/2001).

The control of *Salmonella* in shell eggs by FSCP is based on the controlling of flocks on farms, since bacteriological testing of eggs for *Salmonella* is not cost-effective in a country with low *Salmonella* prevalence. Sampling of breeding flocks of egg layers is identical to sampling of breeding flocks of broilers (MMM 23/EEO/2001). According to the *Salmonella* control programme for laying hens (MMM 24/EEO/2001), breeding flocks (grandparent and parent flocks) are examined by bottom paper or meconium sampling when the birds are one day old, and by faecal sampling twice prior to entering the laying phase. In the laying period, breeding flocks are examined by faecal sampling every eight weeks. At hatchery, chicks hatched from eggs supplied by each breeding flock are examined by bottom paper or meconium sampling every two weeks. Egg production flocks are sampled by faecal samples once during the rearing period. Negative test results for rearing flocks must be received before breeders or layers can be transported to the production unit. During the laying period, faecal samples of egg laying flocks are examined three times. The poultry meat inspection veterinarian must be notified of the result of the last examination before sending the flock to the slaughterhouse. Official sampling taken in the presence of an official veterinarian has to be conducted once a year at each level of the shell egg production chain. Exceptions are hatcheries where official samples are taken every eight weeks.

If *Salmonella* is detected at any level of the shell egg production chain, the positive flock is put under official restrictions, including prohibition of transportation of animals and eggs. A positive result is confirmed by official faecal sampling, or if infection by *Salmonella* Typhimurium or *Salmonella* Enteritidis is suspected, samples of liver, ovary and intestine must be examined. If *Salmonella* infection is confirmed, all hens, chickens and eggs must be destroyed. Shell eggs laid by infected hens can either be heat-treated or destroyed. In practice, any shell eggs laid by infected hens are destroyed. Furthermore, an epidemiological investigation must be done to identify the source and possible spread of infection. Restrictions on flocks are lifted after the premises have been emptied, cleaned and disinfected, and surface swabs taken thereafter have given negative results (MMM 24/EEO/2001).

Based on this intensified surveillance in domestic shell egg production, the European Community authorized Finland to require special guarantees regarding *Salmonella* on consignments of day-old chicks, breeders, laying hens and shell eggs imported to Finland (Commission Decision 2003/644/EC; Commission Decision 2004/235/EC; Commission Regulation (EC) No 1688/2005). These decisions require that consignments must be accompanied by a certificate of negative test results asserting that a flock of origin is free either for all *Salmonella* serovars (consignments of day-old chicks and breeding poultry) or for the following invasive *Salmonella* serovars: *Salmonella* Gallinarum, *Salmonella* Pullorum, *Salmonella* Enteritidis, *Salmonella* Berta, *Salmonella* Typhimurium, *Salmonella* Thompson and *Salmonella* Infantis (consignments of laying hens) (Commission Decision 2003/644/EC; Commission Decision 2004/235/EC). For shell eggs imported or dispatched to retail, negative test results for all *Salmonella* serovars are required (Commission Regulation (EC) No 1688/2005). These special guarantees do not apply, however, to egg products, eggs intended for the manufacture of processed products by a process that guarantees the elimination of salmonella or eggs produced under a corresponding *Salmonella* control programme as in Finland (Regulation (EC) No 853/2004; Commission Regulation (EC) No 1688/2005).

## 5.5 *Salmonella* control of feeds

In the European Union, control of feeds is based on Regulation (EC) No 882/2004 of the European Parliament and of the Council on official controls performed to ensure the verification of compliance with feed and food law, animal health and animal welfare rules. Regulation (EC) No 178/2002 of the European Parliament and of the Council lays down the general principles governing food and feed safety at the Community and national level. Production, processing, use, storage and transport of raw materials of animal origin for feeds are regulated by Regulation (EC) No 1774/2002 laying down health rules concerning animal by-products not intended for human consumption. Regulation (EC) No 1831/2003 of the European Parliament and of the Council describes general rules on feed hygiene, conditions and arrangements ensuring the traceability of feed and conditions and arrangements for registration and approval of establishments.

In Finland, the Feedingstuff Act (MMM 396/1998) regulates manufacture, transport, circulation, use, trade, storage and import and export of feeds. Control of production, processing, use, storage and transport of animal by-products intended for animal feed is described in the Decree of the Ministry of Agriculture and Forestry (MMM 850/2005). The Act on Veterinary Border Inspection (MMM 1192/1996) applies to the import of feed material of animal origin.

The Decision of the Ministry of Agriculture and Forestry on undesirable substances, products and organisms in animal feed (MMM 163/1998) includes requirements for hygienic quality of feedingstuffs. According to this decision, feeds in Finland must not be contaminated with *Salmonella*. According to the Feedingstuff Act, responsibility for feeds being *Salmonella*-free is on the feed operator, and they are liable to pay compensation for damages caused by *Salmonella*-contaminated feeds.

The supreme authority for control of feedingstuffs in Finland is the Department of Food and Health of the Ministry of Agriculture and Forestry, which is responsible for legislation, for general guidance about control measures, and for controlling import of feedingstuffs of animal origin from third countries (border inspection veterinarians).

The Plan Production Inspection Centre (KTTK) carries out inspections of feedingstuffs concerning manufacturing, marketing and import from Member States and from third countries, as well as inspections of the quality control systems of feed operators. The control of imports is focused on feedingstuffs of plant origin. All lots of feed material of plant origin are analysed for *Salmonella* either by KTTK or by the operator. KTTK is responsible for issuing prohibitions and approvals of imported lots.

When *Salmonella* is found in domestic production, in a marketing sample or in imported feedingstuff, a prohibition concerning the whole lot is immediately issued. If *Salmonella* is found in domestic feed production, the production line or the entire plant is halted until the source of the contamination is identified and the contamination is eliminated. Efforts are made to ensure that *Salmonella* does not spread any further, to other feed plants or to farms.

KTTK may upon request grant permission to decontaminate the lot, and this decontamination must be carried out in accordance with instructions provided by the KTTK. After decontamination, KTTK resamples the lot. If the lot is verified to be free of *Salmonella*, KTTK may give permission for the lot to be used. In marketing con-

trol, the shop where the *Salmonella* was found is contacted. The importer or the representative is also immediately informed, and the shop and the importer or representative are responsible for withdrawing the product from the market in accordance with instructions provided by the KTTK. The operator must inform KTTK when *Salmonella* is found in products, raw materials or manufacturing processes. If *Salmonella*-positive raw materials are detected, they must be decontaminated before they can be cleared for use.

## 5.6 Other measures to combat *Salmonella*

### 5.6.1 Finnish food legislation

In Finland the control and handling of foodstuffs was mainly based on three acts: the Act on the Hygiene of Foodstuff of Animal origin (Hygiene Act, 1196/1996); the Food Act (361/1995); and the Health Protection Act (763/1994). These Acts, as well as the Decrees based on them, also dealt with zoonotic agents in foodstuffs. The Hygiene Act regulated the handling of foodstuff 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 the requirements involved were laid down in the Decisions and Decrees of the Ministry of Agriculture and Forestry, issued on the basis of the Hygiene Act. In March 2006, these three acts were superseded by a new Food Act (The Finnish Government 2005). Now a single act regulates requirements for food hygiene and zoonotic agents.

### 5.6.2 Voluntary activities of the egg production branch

In addition to official control measures, voluntary *Salmonella* control is practiced in animal import, feed production and egg production. The Association for Animal Disease Prevention was founded in 1994 with most Finnish abattoirs, dairies and egg packing companies as members. The association provides instructions on risk management to farmers and importers and controls the import of production animals, semen, embryos and animal feed. The association keeps an open register of feed importers, manufacturers and mixers whose standards are higher than the official standards for *Salmonella*-free feeds, e.g. who test every batch of imported feeding-stuff for *Salmonella*.

In 2002, the biggest Finnish egg packing centre launched a new control-based production system which allows the egg packer to control egg production in accordance with the market situation. As part of the system, producers agree to comply with good agricultural practices, i.e. they obey legislation, buy feed materials and compound feeds from sellers approved by the Association for Animal Disease Prevention, buy chicks from farmers who have been approved by the authorities and by the egg packer, and take control samples for analysis according to the Finnish *Salmonella* Control programme. In 2003, about 400 egg producers took part in the control-based egg production system, producing about 66% of the shell eggs sold in the grocery trade to consumers (Munakunta 2003).

## 5.7 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 sourc-

es 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 Matlab 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 egg production

This risk assessment on *Salmonella* in egg production has been done following the principles of the Codex Alimentarius Commission (1999). Therefore, this risk assessment process has been divided into four parts:

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

The modelling is focused on production of domestic shell eggs which are sold in Finland. At the beginning of the project, no distinction between different serovars was made. In practice, however, the *Salmonella* prevalence in shell eggs was estimated based on data of *S. Enteritidis* and on internal contamination only. Shell eggs produced by commercial farms delivering shell eggs to egg packing centres and complying with the legislation of the Finnish *Salmonella* Control Programme were taken into account. These shell eggs accounted for 96.5% of the total egg production in 2001, which is the default year of the model (MMMTIKE 2003b). This assessment excludes shell eggs produced for a farmer's own consumption or distributed via direct sale. Furthermore, ungraded shell eggs provided directly to a local grocery in certain sparsely inhabited areas of northern and eastern Finland are excluded.

### 6.1 Hazard identification

#### 6.1.1 *Salmonella* and salmonellosis

Salmonellosis is most often caused by the ingestion of foods containing *Salmonella enterica* bacteria and is one of the major zoonoses in many countries worldwide. In 2001, salmonellosis was the most frequently reported zoonosis in Europe, with approximately 160,000 cases reported (European Commission 2003a). *Salmonellae* are gram-negative, facultatively anaerobic, rod-shaped bacteria that belong to the genus *Enterobacteriaceae*. They are widely distributed in nature, with humans and animals being their primary reservoirs. At least 2,422 different serovars of *Salmonella* are known; these have been divided into two species, *S. enterica* and *S. bongori* (Jay 2000; Popoff et al. 1996). *S. enterica* is divided into six subspecies: *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae* and *indica* (Popoff & Le Minor 1992). Serotyping of *Salmonellae* is done by identifying the O- and H- antigens (phase 1 and 2) in order to name the serovar. Names for *Salmonella* serovars were 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. For epidemiological purposes, Jay (2000) divided the *Salmonellae* into three groups: (1) Serovars *S. Typhi*, *S. Paratyphi A* and *S. Paratyphi C* that infect humans only and cause typhoid and paratyphoid fevers. (2) The host-adapted serovars like *S. Gallinarum* / *Pullorum* (poultry), *S. Abortus equi* (horses), *S. Abortus ovis* (sheep), *S. Choleraesuis* (swine). Some of these serovars are also human pathogens and may be contracted from foods. (3) Unadapted serovars with no host preference. These serovars are pathogenic for humans and animals, and they include most food borne serovars. In this risk assessment, only the *Salmonella* serovars belonging to group 3 are discussed.

All mammals, birds and reptiles may act as carriers of *Salmonella* without symptoms. An infected animal sheds *Salmonella* in the faeces, thus enabling the bacteria to spread in the environment. Wild animals, such as birds, mice and rats, may spread the infection to feed and production animals unless proper pest control is employed on the farm. 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 serovars, 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).

### 6.1.2 *Salmonella* in Finland

Finland, Sweden and Norway have traditionally fought against *Salmonella* with strict measures, resulting in a good situation compared to that in many other European countries. In Finland, *Salmonella* surveillance in egg production is implemented according to the FSCP of laying hens, and *Salmonella* samples are taken regularly on different levels of the egg production chain. In 1995–2000 *Salmonella* was not detected in any of the breeding units of egg production in Finland. The number of *Salmonella* isolations in egg production farms varied annually between 1 and 4, which corresponds to a *Salmonella* crude prevalence of 0.02 to 0.1%. In addition, in 1997 *S. Typhimurium* was isolated on one farm rearing pullets (EELA 1997; EVI-EELA-MMM 2003; MMM 2000; Seuna 1998, 1999, 2000). In 2001–2003, positive *Salmonella* samples were not detected in the egg production chain (EVI-EELA-MMM 2003). One positive breeder flock as well as one positive production flock was detected in 2004 (EFSA 2006). According to a baseline study on the prevalence of *Salmonella* in *Gallus gallus* laying flocks in the EU, one holding out of the 268 sampled was positive for *Salmonella* (MMM 2005).

In 1995–2001, the number of human *Salmonella* cases reported annually was on average 3,000 in Finland. In the last two years, the number of reported cases has clearly decreased, to only 2,279 in 2003 (National Public Health Institute 2004). Since 1995, the annual incidence of human salmonellosis has varied between 44 and 65 registered cases / 100,000 inhabitants. Due to the good domestic *Salmonella* situation, the majority of human infections are contracted abroad. Of these annually-reported cases, 12–35% were of domestic origin in 1995–2003 (National Public Health Institute 2000, 2004). Each year infections are caused by more than 100 different *Salmonella* serovars. From year to year, the most common serovars of both domestic and foreign origin have been *S. Typhimurium* and *S. Enteritidis* (National Public Health Institute 2004). In 1997–2003, *S. Enteritidis* caused 10–20% of human *Salmonella* cases of domestic origin and 44–52% of human *Salmonella* cases of foreign origin annually (National Public Health Institute 2004).

In Finland, occupational *Salmonella* control for food industry and hospital workers includes over 50,000 samples annually. 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, an average of 0.11% (range 0.06–0.20%) have been infected with *Salmonella*. New workers had about the same infection rate, 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 2000, personal communication). It has been estimated that about 10% of all human *Salmonella* infections are diagnosed and reported in Finland (Ruutu 2001).

### 6.1.3 *Salmonella* in other countries

Norway and Sweden also have a very favourable *Salmonella* situation. In Norway no *Salmonella* has been detected in poultry breeders for egg production or in laying hens since the Norwegian *Salmonella* Control Programme was initiated in 1995, though the incidence rate of human salmonellosis increased from 32 / 100,000 to 42 / 100,000 in 1999–2001. Most cases (80–90%) were of foreign origin. The most common serovars have been *S. Enteritidis*, *S. Typhimurium*, *S. Hadar* and *S. Virchow* (The Norwegian Zoonosis Centre 2000, 2001, 2002). In Sweden, an average of six positive egg production farms have been identified annually since 1995. The dominating serovar has been *S. Livingstone* which accounted for about 67% of cases in the 1990s (SVA 2001). No cases have been reported in breeders. Between 1992 and 2002 the annual incidence of notified domestic *Salmonella* cases in humans varied between 5 to 10 / 100,000. Domestic cases account for around 15% of all *Salmonella* cases in Sweden (SVA 2003).

In the annual zoonoses report of the European Commission (European Commission 2004), member countries used to be divided into those running an approved *Salmonella* control programme and those applying a monitoring scheme based on the sampling under the old Zoonoses Directive (Council Directive 92/117/EEC). Between 1999–2001, however, the number of countries running an approved control programme increased from four to seven. Denmark, Ireland, Finland and Sweden have been running control programmes for several years. In addition, beginning in 1999 or thereafter, Austria, France and the Netherlands have started approved control programmes covering rearing flocks of hens and the production period of layers. Other countries monitored *Salmonella* according to the old Zoonoses Directive (European Commission 2004). With the exception of Finland, Sweden and Norway, *Salmonella* has regularly been found both in breeders and in laying hens. The general trend seems to be that the reported prevalence of *Salmonella* in layer breeder flocks is lower than in production flocks. In 2001, the prevalence of *Salmonella* in breeder flocks varied from 0% in Finland, Norway and Northern Ireland to 6.8% in Italy and 14.7% in Greece. In 2001, the *Salmonella* prevalence in production flocks varied from 0% in Finland and Norway, to 14.3% in The Netherlands, and to 37% in Spain (European Commission 2003a). In 2002, the prevalences were lower in many countries (Table 5).

**Table 5.** Apparent *Salmonella* prevalence (%) in flocks of laying hens in some European countries in 2001 and 2002 (European Commission 2003a, 2004).

Country	2001	2002
	Prevalence of <i>Salmonella</i> in laying flocks (%)	
Denmark <sup>1</sup>	4.1	2.6
Finland <sup>1,2,3</sup>	0	0
Ireland	0.7	1.2
Sweden <sup>1</sup>	0.45	0.3
Norway <sup>1,2</sup>	0	0
Austria	n.a.	n.a.
France <sup>4</sup>	2.8	1.8
Germany <sup>5</sup>	2.3	1.5
Spain	37	9.6
United Kingdom	n.a.	n.a.
Italy	10.1	5.2
Belgium	n.a.	n.a.
Netherlands <sup>6</sup>	9.3	5.3
Greece	16.7	5.7
Portugal	0.6	n.a.

<sup>1</sup> Rearing and production flocks

<sup>2</sup> Includes granparent flocks

<sup>3</sup> Numbers include several tests per flock

<sup>4</sup> Number includes *S. Enteritidis* and *S. Typhimurium* only

<sup>5</sup> Only production period

<sup>6</sup> Plan of Approach

n.a. Data not available

#### 6.1.4 Food as a source of *Salmonella*

As they are intestinal bacteria, *Salmonellae* naturally inhabit the gastro-intestinal tract of different animals. Therefore animal-derived foods such as meat, meat products, poultry and eggs are the most common vehicles of salmonellosis to humans (Jay 2000). In addition, *Salmonella* have been found in various foods, including dry food products, fats, chocolate, spices, herbs, fresh fruits and vegetables, sprouts, fish and shellfish (Cox 2000; D'Aoust 2001). According to the World Health Organisation (2001), the most important food vehicles of *Salmonellae* which caused outbreaks in Europe between 1993 and 1998 were:

Egg and egg products: 35%

Cakes and ice cream: 28%

Meat and meat products: 8%

Poultry and poultry products: 4%

Salads, dressings and mayonnaise: 4%

From the mid-1980s to the mid-1990s, there was a dramatic increase in reported *Salmonella* infections caused by *S. Enteritidis* both in the USA and in Europe (Humphrey 2000). The number of reported *S. Enteritidis* isolates peaked in 1995 in the United States and has steadily decreased thereafter (Centers for Disease Control and Prevention 2003; Patrick et al. 2004). In Europe, the trend has not been equally well-defined. The proportion of *Salmonella* infections caused by *S. Enteritidis* has

decreased in some countries, e.g., England (Cogan & Humphrey 2003), while the total share of all reported *Salmonella* Enteritidis isolations in Europe increased from 73.8% in 1993 to 83.6% in 1998 (WHO 2001). According to the European Union, *S. Enteritidis* accounted for 71.0% and 67.1% of reported human salmonellosis in 2001 and 2002, respectively (European Commission 2003a, 2004). The major food sources for the human *Salmonella* cases caused by *S. Enteritidis* have been shell eggs and different egg-containing food products. Consumption of raw eggs and dishes containing raw or only lightly prepared eggs are considered especially unsafe (European Commission 2003b). More than 75% of the 1,117 reported European *S. Enteritidis* outbreaks investigated between 1993 and 1998 were related to the consumption of undercooked eggs, egg products or foods containing raw eggs such as ice creams or cream pastry fillings (WHO 2001). Furthermore, eggnog, mayonnaise, milk shakes, ice cream, mousse, custard and hollandaise sauce are mentioned as sources of food poisoning (Poppe 1999). Among single foods implicated in egg-associated outbreaks in the United States between 1985 and 1999, 28% were foods that contained raw eggs (e.g., homemade ice cream, Caesar salad dressing, tiramisu, eggnog). Traditional egg dishes such as omelettes, French toast, pancakes, and foods that use egg batter accounted for 27% of the egg-associated outbreaks. Twenty-six per cent of outbreaks were attributed to well-cooked dishes known to contain eggs, such as lasagne, and 15% of outbreaks to egg dishes that were lightly cooked (e.g., hollandaise source, meringue, cream pies) (Patrick et al. 2004).

In Europe, *Salmonella* spp. was responsible for 77.1% of the food borne outbreaks reported in 1993–1998. The most common serovar was *S. Enteritidis* which caused 34.7% of the confirmed cases. Among the 22,386 outbreaks where a food vehicle was identified, eggs, egg products, egg-containing dishes and mayonnaise were involved in 36.5% of outbreaks (WHO 2001).

During the period 1993–1998, the Danish Veterinary and Food Administration reported 324 food borne outbreaks of which 82 were identified to be caused by *S. Enteritidis*, while 8 were caused by *S. Typhimurium*. The source of infection was typically desserts with raw eggs and other non-heat-treated foods with raw eggs (WHO 2001). Denmark reported 30 and 27 outbreaks of zoonotic gastrointestinal infections registered by the Regional Veterinary and Food Authorities in 2002 and 2003, respectively (the Danish Zoonosis Centre 2003; 2004). Of these, one outbreak was identified to be caused by *S. Enteritidis* in 2002 and four outbreaks in 2003. The outbreak in 2002 was caused by a Japanese omelette and one outbreak in 2003 was caused by sandwiches with salad, eggs, shrimps and dressing (the Danish Zoonosis Centre 2003, 2004).

There were 526 reported food borne or waterborne outbreaks in Sweden in 1993–1998. One outbreak in 1993 was identified to be caused by eggs (WHO 2001). In 1999 and 2000, 121 and 75 food borne or waterborne outbreaks were investigated. The causative agent was identified in 26% and 53% of the outbreaks investigated in 1999 and 2000, respectively. None of them was caused by eggs (WHO 2003).

In Norway, 134 confirmed food-borne outbreaks were reported from 1993 to 1998. Eggs were identified as a source of one outbreak in 1998 (WHO 2001). In 1999 and 2000, the incriminated food was identified in all food borne outbreaks studied (20 in 1999 and 22 in 2000). Eggs and egg products caused one outbreak in 2000 (WHO 2003).

In Finland, 1–9 *Salmonella* outbreaks per year have been reported during the period 1998–2003. The most common food vehicles were unpasteurized milk products, meat and sprouts (Hatakka & Wihlman 1999; Hatakka & Halonen 2000; Hatakka et al. 2001, 2002, 2003, 2004). Shell eggs caused two outbreaks in 1995, when *Salmonella* Enteritidis was found on one egg production farm (MMM 2000). Since then, there have not been any reported *Salmonella* outbreaks caused by shell eggs in Finland.

## 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 when the temperature exceeds 70°C. However, the matrix, especially humidity, affects this, and sometimes even temperatures over 100°C are needed to destroy *Salmonella* in dry feedstuffs. There are variations in the ability of different strains and serovars to survive in the environment, e.g. in dry heat and pH resistance (Jay 2000).

The virulence mechanisms of *Salmonella* continue to be unravelled. 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-phagocytic cells by attaching to the intestinal mucosa.

### 6.2.2 Poultry host

*Salmonella* infections in poultry are usually divided into infections caused by the two host-adapted serovars, *S. Pullorum* and *S. Gallinarum*, and by unadapted serovars with no host preference (Wray & Davies 2001). The host-adapted serovars typically produce severe systemic disease and are rarely involved in human infections. *Salmonella* Pullorum causes Pullorum disease, which was last recorded in 1961 in Finland (MMMELO 2004a). *Salmonella* Gallinarum infection, fowl typhoid, has never been reported in Finland.

Poultry can also be infected with unadapted *Salmonella* serovars, but the unadapted serovars produce severe systemic disease in birds only in special circumstances (Barrow 1999). The occurrence of salmonellosis in poultry is influenced by factors including the age of the bird, the infectious dose, the route of infection, the invasiveness of the *Salmonella* strain or serovar and the breed of chicken. Infection is usually confined to the gastrointestinal tract without any symptoms (Poppe 2000). The disease with clinical symptoms is uncommon and is mostly seen in young chicks. Morbidity and mortality varies considerably, though usually less than 20% of the affected animals die. Clinical signs, such as depression and diarrhoea, are not specific and are similar whichever serovar of *Salmonella* is involved (Wray & Davies 2001). Infected birds often excrete *Salmonella* in their faeces. Most infected birds free themselves of infection, but some of them remain symptomless carriers which excrete *Salmonella* continuously or intermittently for long periods (Poppe 2000). Some serovars, such as *S. Typhimurium* and *S. Enteritidis*, are capable of becoming localized in the ovary or oviduct, resulting in contamination of egg contents, or contaminating the egg surface as it passes through the cloaca. Thus, the contents of eggs can become contaminated via vertical transmission, resulting in the hatching of infected progeny (Barrow 1999).

### 6.2.3 *Salmonella* in eggs

Shell eggs mainly become contaminated with *Salmonellae* as a result of infection of the oviduct, as a result of a persistent intestinal infection or as a result of faecal contamination. The prevalence of egg shell contamination usually exceeds that of egg contents (Humphrey 1994). With *S. Enteritidis* strains, infection of the reproductive organs of laying hens is often the main factor affecting the production of contaminated eggs. With other *Salmonella* serovars, horizontal transmission via faeces is more important (Humphrey 1994; De Buck et al. 2004).

In shell eggs, *S. Enteritidis* is the predominant serovar isolated from egg contents. Other *Salmonella* serovars, for instance *S. Typhimurium* and *S. Heidelberg*, have also been isolated from the ovaries of laying hens but they have only sporadically been isolated from eggs (International Commission on Microbiological Specifications for Food 1998; De Buck et al. 2004). The site of infection in the reproductive tract affects the site of contamination in eggs. If the ovaries are infected, the yolk may be contaminated, while infection of the oviduct leads to contamination in albumen. Egg content can also be contaminated due to penetration of *Salmonellae* through the shell or because *Salmonellae* on the shell contaminate egg contents during breaking (Humphrey 1999). Penetration through the shell is facilitated by cracks and dirt in the shell, humidity and a fall in temperature (International Commission on Microbiological Specifications for Food 1998). In addition to horizontal faecal contamination, surface contamination may result from infection in the lower reproductive tract or it may happen during passage through the cloaca (De Buck et al. 2004).

The number of infected eggs produced by an infected flock depends on how many hens in a flock are infected (within-flock prevalence), how many of them actually lay contaminated eggs and how frequently contaminated eggs are laid. In the risk assessment of *Salmonella* in eggs and broiler chickens, WHO/FAO (2002) concluded that although the reported within-flock prevalence varied considerably, from 0.33% to 16.4% (Hogue et al. 1997; Poppe et al. 1992), low within-flock prevalence was more frequent than high within-flock prevalence. Infected hens are known to lay contaminated eggs in a clustered and intermittent way (Humphrey 1994). Variable prevalences of *Salmonella* positive eggs have been observed in scientific surveys (Table 6) and also reported by several EU countries (Table 7).

**Table 6.** Observed prevalence of *Salmonella* bacteria in shell eggs.

Population	Country	Type of sample	Serovar	Prevalence in eggs (%)	Reference
Naturally infected layer flocks	USA	Egg pools	<i>S. Enteritidis</i> PT8	0.03 - 0.90	Henzler et al. 1994
A naturally infected layer flock	Finland	Egg pools	<i>S. Enteritidis</i> PT1	0.8 - 8	Johansson et al. 1996
Naturally infected layer flocks (cage birds)	USA	Egg pools	<i>S. Enteritidis</i> PT4	0.015 - 0.0419	Kinde et al. 1996
Naturally infected layer flocks (free range birds)	USA	Egg pools	<i>S. Enteritidis</i> PT4	0.15 - 0.19	Kinde et al. 1996
Naturally infected layer flocks	USA	Egg pools	<i>S. Enteritidis</i>	0.026 (overall prevalence)	Henzler et al. 1998
Naturally infected layer flocks	USA	Egg pools	<i>S. Enteritidis</i>	0 - 0.625 (flock-specific prevalence)	Henzler et al. 1998
Domestic shell eggs on retail sale in Denmark	Denmark	Egg pools	All <i>Salmonella</i>	0.06 on shell; 0.02 in contents	The Danish Zoonosis Centre 2003
Domestic shell eggs on retail sale in the United Kingdom	UK	Egg pools	<i>S. Enteritidis</i> , <i>S. Infantis</i> , <i>S. Livingstone</i>	0.06	Food Standards Agency 2004

**Table 7.** Reported prevalence of *Salmonella* bacteria in shell eggs in some EU countries in 1999–2003 (European Commission 2003a, 2005).

Country	1999	2000	2001	2002	2003
	Prevalence of <i>Salmonella</i> spp in eggs (%)				
Austria	n.a.	0.2	1.4	1.1	0.5
Germany	0.4	0.5	0.6	0.6	0.6
Ireland	n.a.	0.0	0.0	0.0	0.1
Italy	0.9	0.1	0.7	3.1	0.7
Spain	0.7	3.9	4.9	8.1	1.9
Netherlands	n.a.	0.0	0.0	0.0	n.a.

n.a. Value is not available.

### 6.2.4 Human host

Infections in humans with the non-human adapted *Salmonella* sp. are characterised 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 resulting from gastrointestinal symptoms, patients can have a variety of extraintestinal symptoms. 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 within the first 3 to 5 months. Nevertheless, many patients continue to have mild joint symptoms after the acute phase of ReA and in 16% of patients the disease even remains chronic, mainly in patients who are HLA-B27-positive (Leirisalo-Repo et al. 1997; Ekman 2000; Hannu et al. 2002). Furthermore, there are results suggesting increased mortality within one year after contracting salmonellosis (Helms et al. 2003).

#### 6.2.4.1 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 2000). 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. 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 has 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 is important to remember, however, that the severity of illness may be higher in susceptible individuals, thereby increasing the risk (since risk is a combination of probability and severity). In addition, it has been suggested that excess mortality is 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 (even fewer than 10 organisms) (Fontaine et al. 1980; Blaser & Newman 1982; Kapperud et al. 1990).

Unfortunately, for ethical and practical reasons, data on dose-response in humans is difficult to obtain. Therefore, it is not surprising that 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 maxi-



mum 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 WHO microbiological risk assessment on food, five dose-response models were studied in detail. They concluded that at present, any single model presentation for the relationship between dose and response is not vastly superior to any other model (WHO/FAO 2002).

## 6.3 Exposure assessment

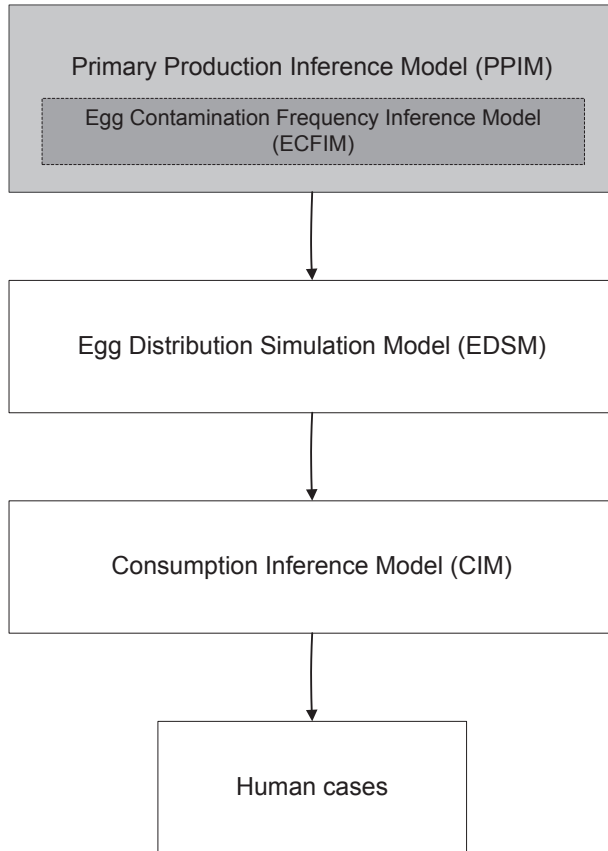
The occurrence of contamination at the time of consumption depends on the previous steps of the production chain. Therefore, the whole production chain from the grandparent chickens up to consumers was modelled. The exposure model was divided into two parts: the Primary Production Inference Model (PPIM) and the Egg Distribution Simulation Model (EDSM). Chapter 6.3 provides a general overview of the model's structure. It also reports the results and discusses the sensitivity and limitations of each part of the model. More detailed information about the mathematics of the model is provided in Appendix A.

### 6.3.1 Primary Production Inference Model (PPIM)

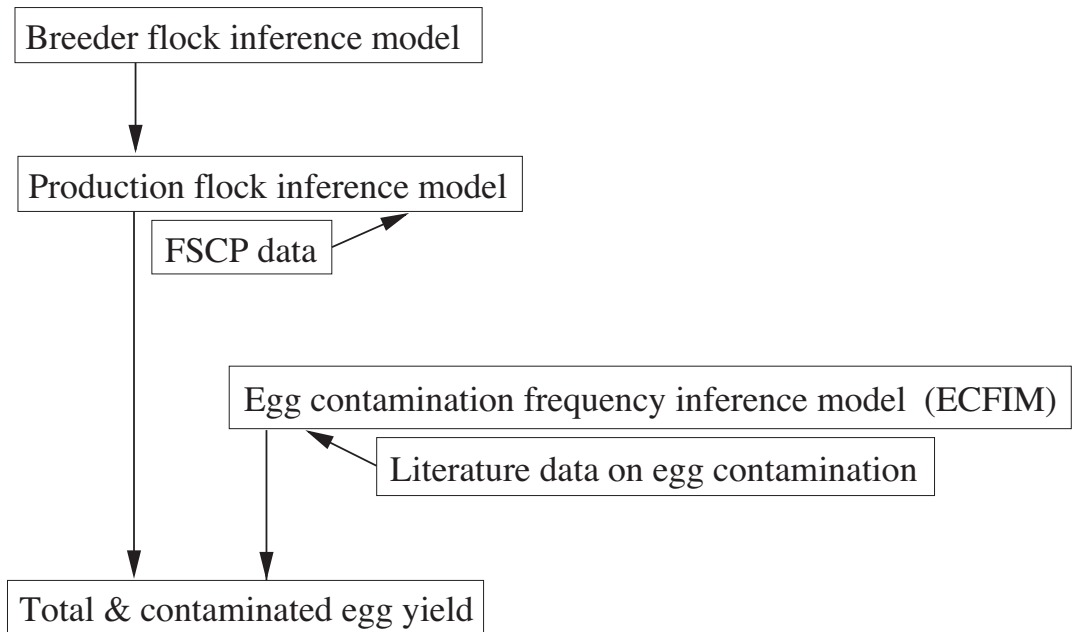
#### 6.3.1.1 Summary of the PPIM

The Primary Production Inference Model (PPIM) estimates total commercial shell egg production and the true production of contaminated shell eggs, based on data reported in 2001 (Figure 7). The model utilizes Bayesian inference with data concerning primary production (breeder and production flocks). The first part of the model (breeder flocks) is a modification of the previously published model on broiler production (Maijala & Ranta 2003; Ranta & Maijala 2002). Based on the testing results of breeder flocks, an estimate of true flock prevalence was obtained as well as a posterior distribution of model parameters. This was further used as a prior distribution for the second part of the PPIM concerning production flocks. Infection prevalence in production flocks was modelled as a generic stationary, i.e. as a long run distribution for a large population of production flocks. Using the result of Bayesian inference concerning breeder flocks and the production flock data (testing results), a final posterior density of model parameters and production flock prevalence was obtained. Together with flock size distribution and estimated egg contamination frequency, the stationary infection probabilities were used to calculate the total annual production of contaminated eggs. Primary production was modelled as two separate production pyramids, since in practice there are two unconnected production chains of shell eggs in Finland. Total egg production was the sum of these two production pyramids. The basic structure of the PPIM is shown in Figure 8.

To estimate the true annual production of contaminated shell eggs, the frequency with which infected flocks produce contaminated eggs must first be evaluated. In this risk assessment, the true egg contamination frequency was estimated using a separate model called the Egg Contamination Frequency Inference Model (ECFIM) (Figure 7, page 68). The model summarizes information on egg contamination frequency in an infected flock, using data from literature on apparent egg contamination in 60 infected flocks (Henzler et al. 1998). True *Salmonella* prevalence in eggs is estimated based on these data, also accounting for the sensitivity of the laboratory culture technique. The result of the ECFIM is a posterior distribution which provides an input for the PPIM.



**Figure 7.** The Primary Production Inference Model (PPIM) and the Egg Contamination Frequency Inference Model (ECFIM) in the whole risk assessment model.



**Figure 8.** The basic structure of the Primary Production Inference Model (PPIM).

According to the PPIM, in 2001 the mean true *Salmonella* prevalence in egg laying flocks was 0.3%, with the 95% credible interval [0.1;0.6]. The estimated mean of total commercial egg production was 821,000,000 eggs (53 million kg). The 95% credible intervals were [755 million eggs;889 million eggs] and [48 million kg;57 million kg], respectively. The estimated mean number of contaminated eggs was 1,800 [0;7,400].

### 6.3.1.2 The Egg Contamination Frequency Inference Model (ECFIM)

In a country with low *Salmonella* prevalence such as Finland, sampling of eggs is not a cost-effective surveillance method (WHO/FAO 2002). Therefore, control of *Salmonella* in egg production is based on controlling flocks, and thus there is no domestic surveillance data on the prevalence of *Salmonella* in shell eggs. In an article describing the first *Salmonella* Enteritidis PT1 infection reported in a commercial production flock in Finland, Johansson et al. (1996) estimated that the egg contamination level was within a range of 0.8–8%. Due to the lack of original Finnish surveillance data, we estimated the egg contamination frequency of Finnish shell eggs based on an American article, Henzler et al. (1998). This particular article was chosen because it reports results from several unconnected egg production farms which belonged to a voluntary surveillance program. These farms were detected positive during normal surveillance, not during a *Salmonella* outbreak. Thus the starting point of the study was considered to be similar to the present situation in Finland, where all egg production flocks are under regular *Salmonella* testing.

#### 6.3.1.2.1 Inputs of the ECFIM

All the inputs to the ECFIM are presented in Table 12 in Appendix B.

##### Number of infected flocks studied

Sixty flocks voluntarily enrolled in a *Salmonella* Enteritidis prevention project for which at least one environmental sample (manure or egg-handling equipment) was positive for *S. Enteritidis* (Henzler et al. 1998).

##### Number of eggs tested in each infected flock ( $n_i$ )

When *S. Enteritidis* was isolated from environmental samples, 1,000 eggs were collected from the house every 2 weeks for 8 weeks (Henzler et al. 1998). Thus the number of eggs tested in the flock ( $i=1, \dots, 60$ ) was 4,000.

##### Number of apparent positive eggs (apparent <sub>$i$</sub> )

This input parameter describes number of apparent positive eggs among the  $n_i$  tested eggs (assuming that in each test-positive pool there is only one positive egg in a pool of 10–20 eggs). The egg shells were disinfected before the eggs were broken and pooled, and therefore only eggs with contaminated contents were taken into account. In summary, the apparent positive eggs per 4,000 tested eggs were 0 for 42 flocks, 1 for 8 flocks, 2 for 2 flocks, 3 for 2 flocks, 4 for 3 flocks and 6, 8 and 25 for 1 flock each (Henzler et al. 1998). However, we also did the analysis by assuming there could be any number of positive eggs (not zero) in a positive pool of 10 eggs (10\*400 eggs in total per flock).

##### Sensitivity of the laboratory culture technique ( $ps$ )

In our opinion, the laboratory culture techniques used by Henzler et al. (1998) to detect *Salmonella*-positive pools were unsensitive, due to a relatively short incubation period of egg pools (first 48 h, later 72–96 h) and the lack of a pre-enrichment period before inoculation onto agar plates. Both steps are considered necessary, especially when low counts of *Salmonella* cell are studied (Gast 1993a, 1993b). Accord-

ing to the literature, most contaminated shell eggs contain only a few *Salmonella* cells (Humphrey et al. 1991; Gast and Beard 1992). Therefore we thought it was important to take the possibility of false negative test results into account, and so produced a probability distribution of test sensitivity. The techniques used by Henzler et al. (1998) were considered to be at least as sensitive as a comparable culture method used by Gast (1993b), which detected 21 out of 66 positive egg pools (sensitivity 32%). For the maximum value of sensitivity, we referred to Valentín-Bon et al. (2003), who reported a sensitivity of 71% using a 4-day incubation of egg pools and a pre-enrichment step in trypticase soy broth supplemented with ferrous sulfate. The most probable sensitivity value for such culture methods as used by Henzler et al. (1998) was assessed to be 50%, according to USDA-FSIS (2004).

In the model, therefore, for the prior distribution of the sensitivity of the laboratory culture technique to detect *Salmonella* from shell eggs, we chose Beta(12,12) density which has a mean of 0.5 and std of 0.1.

#### Hyper parameters of the model ( $\alpha$ , $\beta$ )

Hyper parameters defined the prior density (Beta( $\alpha$ ,  $\beta$ )) of true contamination frequency. Prior density exp(0.001) was chosen for both  $\alpha$  and  $\beta$ , leading to a non-informative uniform U(0,1) predictive prior for the true prevalence. The exponential prior density was also chosen to be fairly non-informative over the realistic range of values for the hyper parameters so that these would be estimated from the data.

#### **6.3.1.2.2 Output of the ECFIM**

The egg contamination frequency was taken as a probability distribution, modelled using the data reported by Henzler et al. (1998). They studied 60 naturally infected flocks (a total of 238,900 eggs or 18,740 egg pools of 10–20 eggs were analyzed), and found that flock-specific prevalence ranged from 0 to 62.5/10,000 eggs. Even within contaminated flocks, production of *Salmonella* Enteritidis contaminated eggs was rare, and only a few flocks produce contaminated eggs with high frequency. The true egg contamination frequency (in a contaminated flock) was estimated using Bayesian hierarchical modelling (ECFIM, Egg Contamination Frequency Inference Model) accounting for test sensitivity and the apparent results of these 60 naturally infected flocks. The posterior predictive distribution for egg contamination frequency was approximately Beta(0.16, 257.82) with mean 0.06%, median 0.003% and std 0.15%. The 95% credible interval was [0%;0.52%]. The distribution produced had a long tail, but the most probable egg contamination frequency was zero. In other words, the ECFIM estimates that the majority of infected laying flocks won't produce many contaminated eggs, while a few will produce contaminated eggs with high frequency. On average, 0.06% of the eggs produced by an infected flock would be contaminated. In comparison, the average estimate (apparent frequency) given by Henzler et al. (1998) was 0.026%.

#### **6.3.1.2.3 Sensitivity and limitations of the ECFIM**

The aim of this project was to quantify all serovars of *Salmonella*. During the project, however, it became obvious that quantitative *Salmonella* prevalence data of shell eggs were available only for shell eggs internally-contaminated by *S. Enteritidis*. Therefore, in the ECFIM, all positive flocks generated by the model were treated as if they were infected by *S. Enteritidis*, which is able, unlike most other serovars, to contaminate not only egg shells but also vertically to contaminate egg contents. Thus, these estimates, interpreted as overall prevalence in eggs, are likely to overestimate the significance of internally contaminated eggs in Finnish egg production. In practice, egg shell contamination is more common than egg content contamina-

tion and many different serovars have been isolated from egg shells (Humphrey 1999; Advisory Committee on the Microbiological Safety of Food 2001). Higher *Salmonella* prevalences (0.6%-8%) in eggs have for instance been reported in the annual zoonoses report of European Union (European Commission 2004). It is not clear, however, whether these results reflect true differences in the prevalence rates or different sampling schemes. Another question is whether the data, which originated in the United States in the early 1990s, represent the current situation in Finland. The estimates of true prevalence also depend on test sensitivity, which could not be quantified in a more detailed fashion.

### 6.3.1.2 Inputs of the PPIM

All the inputs to the PPIM are presented in Table 13 in Appendix B.

#### Number of imported grandparent chicks and flocks

We obtained the number of imported grandparent and parent chicks from the statistics of the Association for Animal Disease Prevention in Finland. In 2001, three batches of grandparent chicks were imported. These three batches included one batch of 1,440 Lohmann chicks, one batch of 1,000 Shaver chicks and one batch of 1,000 Isabrown chicks. Each batch was assumed to form one single flock and thus the total number of three grandparent flocks was used in the Primary Production Inference Model.

#### Number of imported parent chicks

According to the statistics of the Association for Animal Disease Prevention in Finland, one batch of 2,500 Lohmann brown parent chicks was imported in 2001.

#### Number of parent flocks

Data on the number of parent flocks were collected from the two importer companies and their contracting parties. Both the importer of Lohmann LSL and LB hybrids and the importer of Shaver and Isabrown hybrids reported that the number of parent flocks of their hybrids was 13. Thus, the total number of parent flocks was 26 in the PPIM.

#### Length of rearing and production period of grandparent and parent flocks

We used an expert opinion for information about the general length of rearing and the production period of grandparent and parent flocks. The case-specific length of these periods depends, for instance, on the hybrid in question, on the production method (cage or floor), and on the current market situation. According to this expert opinion (a poultry counsellor), the average rearing period was 16–18 weeks for both grandparent and parent pullets. The length of the production period was assumed to be 38–43 weeks for grandparent flocks. For parent flocks, the production period was estimated to be slightly longer, lasting from 45 to 50 weeks.

#### Number of production flocks

In 2001, there were 2,111 egg-producing farms in Finland (MMMTIKE 2002). Over half of them (1,091 or 52%) were small family farms having fewer than 100 layers. These farms accounted for approximately 0.8% of the annual shell egg production, mainly producing eggs for consumption on the farms or for direct sale. In this risk assessment, only commercial farms delivering shell eggs to egg packing centres and complying with the regulations of the FSCP were taken into account.

According to information obtained from the National Food Agency Finland, there were 1,000 registered egg producers delivering shell eggs to packing centres in

2001. Unfortunately, no data on the numbers of laying flocks in each farm was available. Traditionally, the average number of laying hens in a single farm has been small. In 2001, in farms with at least 100 hens, the average number of hens was only 3,114 (MMMTIKE 2002). In addition, the number of small farms was larger than the number of big farms. According to MMMTIKE (2002), 92% of Finnish egg producers had less than 5000 laying hens in 2001. Therefore, it seems probable that the majority of farms had only one flock. Because there was no exact data on the total number of laying flocks for these 1,000 registered egg producers, each farm was thought to represent one flock of laying hens, and thus the total number of production flocks of laying hens in the PPIM was modelled as 1,000.

#### Number of production flocks of different hybrids amongst the 1,000 production flocks

We estimated the number of Lohmann Classic (LSL) and Lohmann Brown (LB) production flocks, as well as the number of Isabrown and Shaver production flocks, based on information from a newspaper article about the market shares of different hybrids (Joensuu 2002) and on a record of accepted pullet suppliers maintained by Finland's Poultry Association and published in every issue of their magazine. Based on these sources, the market share of Lohmann hybrids was assumed to be 70% and the market share of Isabrown and Shaver hybrids was assumed to be 30%. Furthermore, the number of production flocks of Lohmann hybrids was assumed to be 700 and the total number of Isabrown and Shaver hybrids was assumed to be 300, respectively. These constitute two independent production pyramids for which the PPIM was applied separately, after which the values were added together.

#### Length of rearing and production period of egg production flocks

According to an expert opinion (a poultry counsellor), the average rearing period was 14–18 weeks for layer pullets. The length of the production period was assumed to be 50–54 weeks for production flocks.

#### Number of samples taken and positive samples

Data on the number of samples taken for *Salmonella* control and on the number of positive samples detected in different stages of egg production were taken from the annual statistics of the FSCP (Table 8) (EELA 2000, EVI-EELA-MMM 2003, MMME-LO 2004b). In 1999–2003, the apparent *Salmonella* prevalence in shell egg production was well below the 1% objective level.

**Table 8.** Number of control samples and positive isolates in breeder flocks and commercial egg layer flocks according to the FSCP in 1999–2004 (EELA 2000; EVI-EELA-MMM 2003; MMELO 2004b; EFSA 2006).

Poultry production unit	Year	Sampling	Number of positives
<b>Egg layer breeders</b>			
Rearing	1999	227	0
	2000	83	0
	2001	290	0
	2002	221	0
	2003	184	0
	2004	44	0
Production	1999	36	0
	2000	145	0
	2001	144	0
	2002	262	0
	2003	112	0
	2004	33	1
<b>Egg production</b>			
Rearing	1999	113	0
	2000	104	0
	2001	77	0
	2002	281	0
	2003	175	1
	2004	167	0
Commercial egg layers	1999	2,443	6
	2000	2,118	1
	2001	1,728	0
	2002	1,883	0
	2003	1,974	0
	2004	1,944	1

Number of production flocks from which three *Salmonella* control samples are taken during the production period

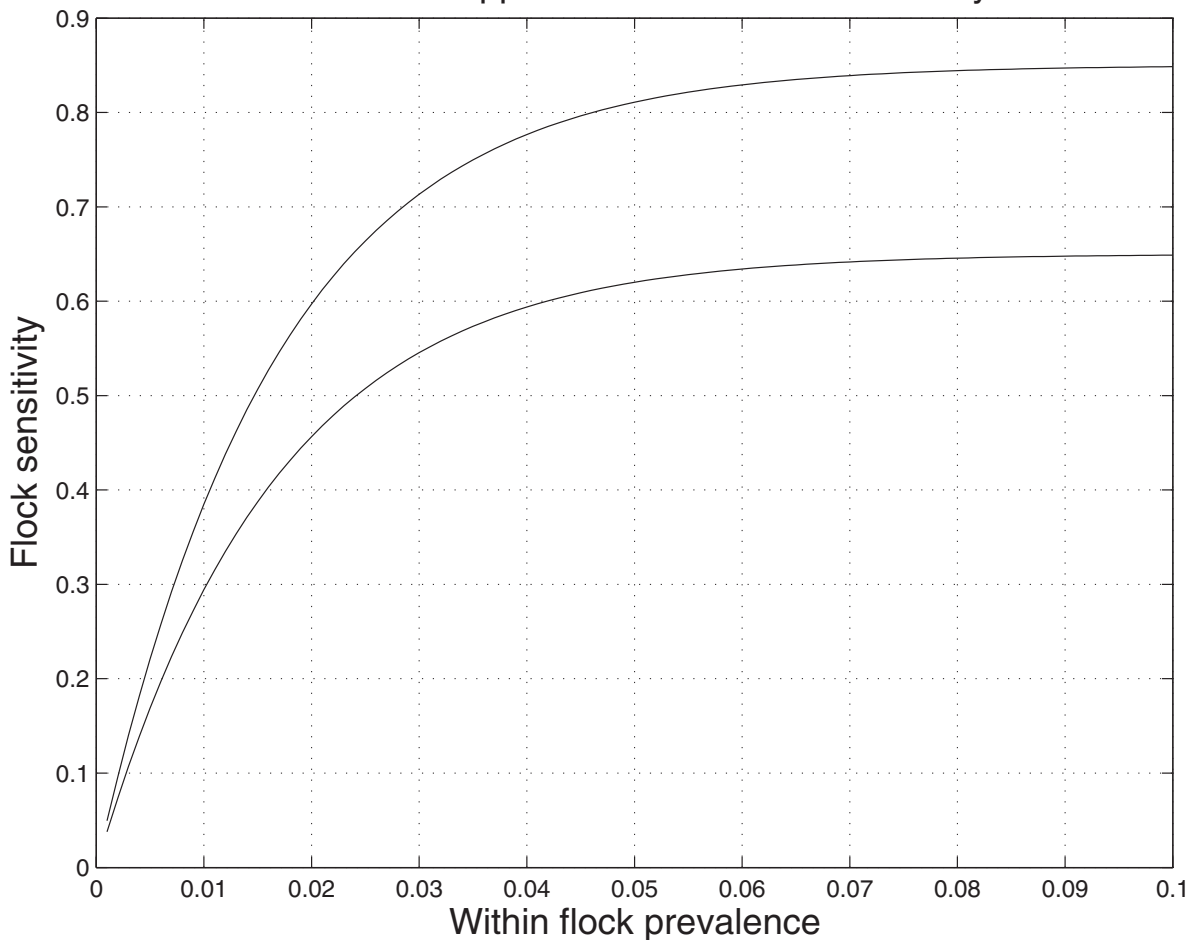
To calculate the share of egg producers who had taken three *Salmonella* control samples during the production period, we estimated the time between two production flocks assuming that producers followed the all-in all-out principle. According to the expert (a poultry counsellor), pullets are usually transferred to a production unit at the age of 16 weeks, and start laying eggs at the age of 20 weeks. The laying period lasts a maximum of 54 weeks. After one production flock, the producers have a production break of 9 weeks (Uusitalo 2003). With this calculation, the time between two consecutive production flocks is 67 weeks. If all 1,000 registered egg producers included in our model had taken 3 *Salmonella* samples during the production period, the annual number of *Salmonella* samples should have been 2,328. According to the annual statistics of the FSCP, in 2001 the number of *Salmonella* control samples taken during egg production period was 1,728 (Table 8). Theoretically, this value can be interpreted to mean that all producers took two *Salmonella* control samples during the production period and 176 out of 1,000 took three samples. The number of *Salmonella* samples taken amongst different hybrids was divided in the proportion of 70% for Lohmann hybrids to 30% for Isabrown and Shaver hybrids.

### Flock sensitivity

The flock sensitivity should describe overall flock level sensitivity, accounting not only for the sensitivity of the laboratory method (test sensitivity) but also other factors such as the within-flock prevalence, the sampling method and sampling practices as well as the effects of pooling. Unfortunately, applicable data both on *Salmonella* spp. prevalence within naturally infected flocks of laying hens as well as on the effects of pooling are practically non-existent. For instance, three large quantitative risk assessments estimated the within-flock percentage of infected hens based on the same data from the early 1990s (USDA-FSIS 1998, USDA-FSIS 2004, WHO/FAO 2002).

Generally, if the within-flock prevalence is  $p_w$ , the size of a pool is  $k$  (subsamples in a pool), and test sensitivity  $s$ , the flock level sensitivity can be calculated as  $(1-(1-p_w)^k)s$ , assuming  $s$  is not affected by pool size (dilution). Assuming a large pool of  $k=60$  and within-flock prevalence of  $p_w=5\%$ , this gives  $0.954 \times s$ , i.e. almost equal to the test sensitivity. For prevalence values below 5%, the sensitivity becomes significantly worse as shown in Figure 9. We thus assumed that the within-flock prevalence is above 5% in all infected flocks in this model. If this were not the case, the model's predictions of true prevalence should be adjusted accordingly higher. On the other hand, if the within-flock prevalence decreased, the number of infected hens laying contaminated eggs would be smaller and the number of contaminated eggs would also decrease.

Lower and upper estimate of flock sensitivity



**Figure 9.** Sensitivity of the pooled test as a function of within-flock prevalence. The upper curve assumes laboratory sensitivity 0.85, lower curve 0.65.



The exact effect of dilution due to pooling is difficult to estimate because there is little published information on the effects of pooling on the sensitivity of faecal culture methods (Kivelä et al. 1999; Arnold et al. 2005). For theoretical calculations, the number of *Salmonella* cells in faeces should be known but this information is unfortunately not available. While pooling has a dilution effect, there is on the other hand an increased probability of capturing positive faeces in the pool as the number of individual subsamples is increased. Arnold et al. (2005) studied the sensitivity of pooled faecal samples for isolation of *Salmonella* in pigs, finding that dilution of positive samples with negative samples may actually increase the possibility of isolating *Salmonella* due to dilution of *Salmonella*-inhibiting factors excreted by infected animals. In this risk assessment, we assumed that the test sensitivity for a pooled sample was not significantly affected by the dilution effects of pooling due to the enrichment methods used. For *Salmonella* detection, the FSCP only allows the use of ISO 6579:2002 or NMKL 71:1999 methods (ISO 2002; NMKL 1999). Since 1999, a culture method including a pre-enrichment step and a sample size of 1 g has been used. Siiskonen (2000) showed that without pre-enrichment, test sensitivity was 23%, but with pre-enrichment it was 92%. 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; Majjala et al. 1992). In a 1996 collaborative study organized by the community reference laboratory for *Salmonella* (CRLS), the overall sensitivity of 17 laboratories to detect 120 CFU/g *Salmonella* Typhimurium from a 1 g sample with pre-enrichment was 85% (215/255) (Voogt et al. 1997). Furthermore, in a 2003 validation study organized by CRLS, the overall sensitivity to detect *S. Enteritidis* was 73–83% and to detect *S. Typhimurium* was 62–70%, using Rappaport-Vassiliadis medium with soya (Mooijman 2005).

Because of the lack of applicable data, the flock test sensitivity in this risk assessment was assumed to be the same as in the previous risk assessment on *Salmonella* in broiler production (Ranta & Majjala 2002; Majjala & Ranta 2003). In the model, the prior distribution for flock test sensitivity of the isolation methods was chosen as a Beta-distribution with a mean of 0.75 and standard deviation of 0.05. For comparison, the calculations in the default situation (data from 2001) were repeated with a lower flock test sensitivity ( $0.5 \pm 0.3$ ). The results of the comparison are shown in Tables 9, 10 and 11. Since all suspected strains are verified by serotyping in the reference laboratory, the specificity was estimated to be virtually 100%.

#### Chance of vertical infection of grandparent flocks ( $v_1$ )

There is no domestic grandparent production in Finland, but day-old grandparent chicks are imported from Canada, France, Germany and the United States (ETT 2005). In the international breeding units, parent birds are maintained at high health status. Before import to Finland, a negative *Salmonella* test result of a parent flock is required. In Finland, importers voluntarily put the imported grandparent chicks in quarantine to make sure that the flocks are free of disease. All these precautions provide great certainty that *Salmonella* bacteria are not present in the imported flocks. Therefore, the chance of vertical infection of grandparent flocks was taken as zero.

#### 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

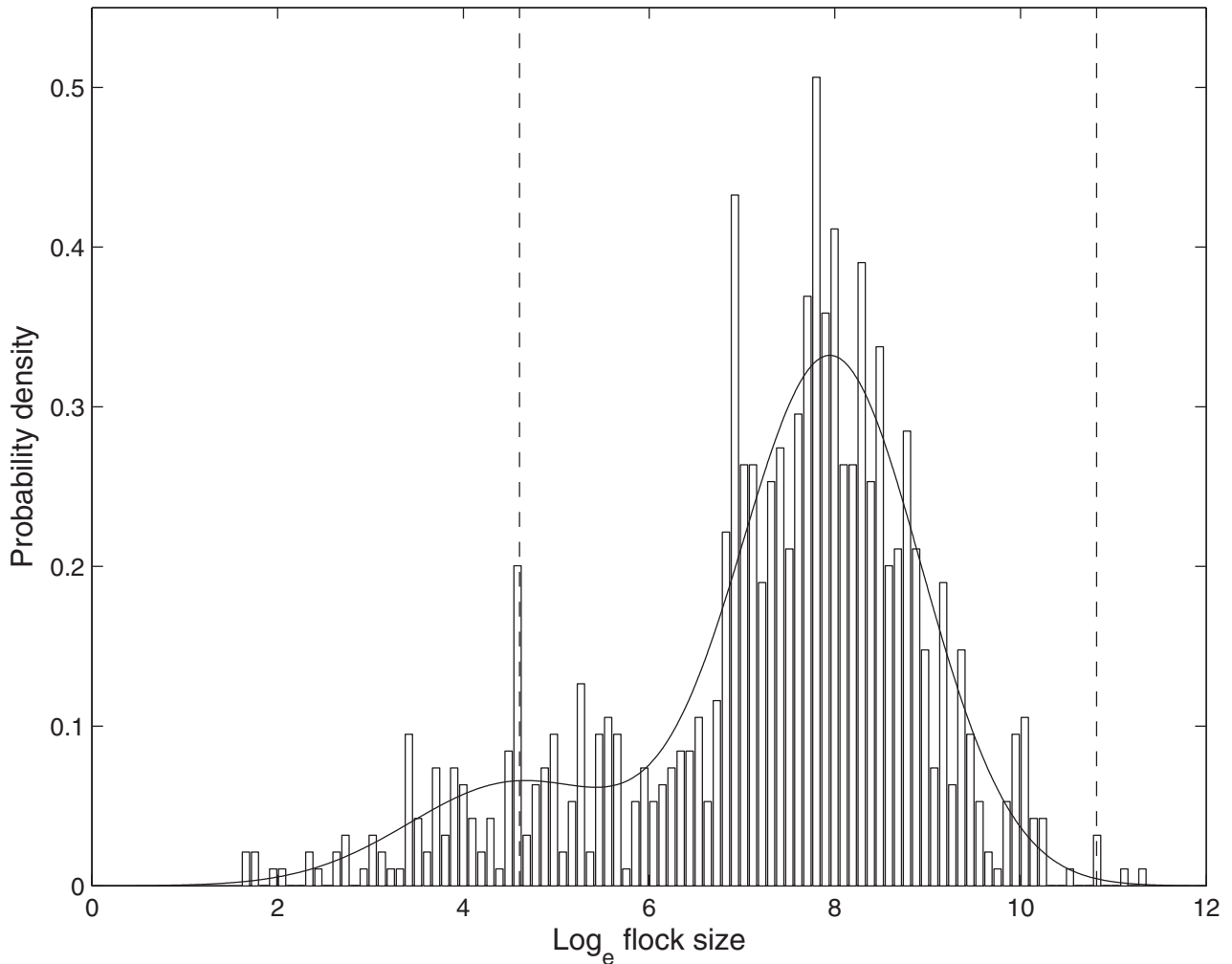
transmission of *Salmonella* could be modelled if the effect of these various routes were known. Unfortunately, no such official data exist in Finland. In this risk assessment, the prior distributions of  $h$  and  $h_3$  were taken from the previous risk assessment of *Salmonella* in the broiler production chain (Maijala & Ranta 2003; Ranta & Maijala 2002). The distributions were based on information obtained from experts, namely, that the chance of horizontal infection during an 8-week time step in production flocks ( $h_3$ ) is the same or higher compared to that of breeder flocks ( $h$ ). The prior distribution of  $h_3$  was thus 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  $[0, 1]$ , accepting only values for which  $h_3 > h$ .

#### Chance of ongoing infection to persist between two consecutive visits ( $\eta$ )

Once a flock is infected, the infection is likely to persist if no intervention is taken. Parameter  $\eta$  accounts for the natural duration of *Salmonella* in such a situation. Since the model was defined stepwise according to the possible testing scheme (i.e. regular 8-week periods), this parameter represents the conditional probability that a *Salmonella* infection would last at least over one time step, given that the flock was infected at the time of the previous time step. According to expert knowledge, this probability is high if interventions are not taken. Hence, Beta (9,1) prior density with mean 0.9, sd 0.091 was chosen.

#### Distribution of sizes of egg laying flocks

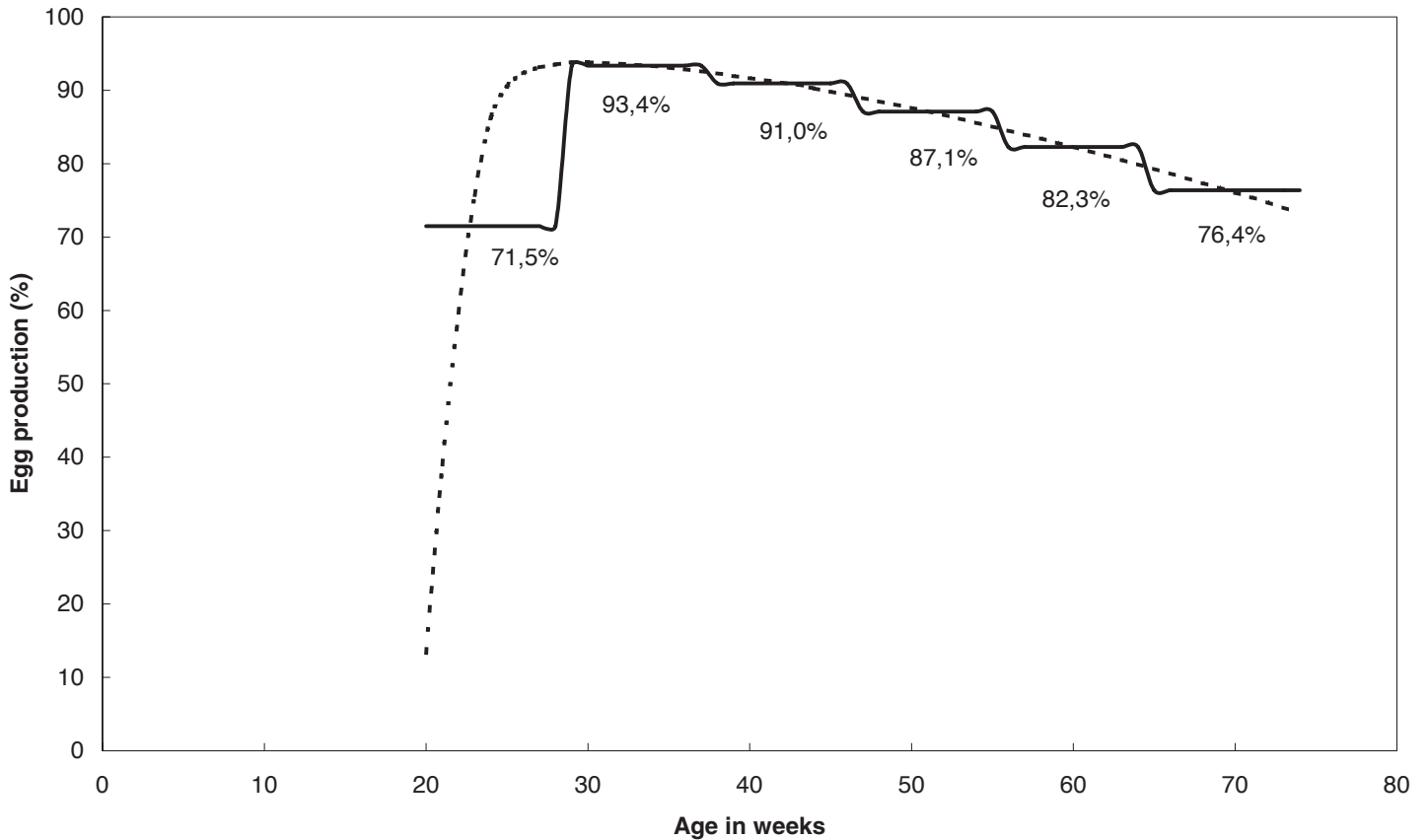
Primary data about the sizes of egg producing flocks were from an annual sampling survey called the Farm Survey, which is carried out by the Information Centre of the Ministry of Agriculture and Forestry (MMM-TIKE). This survey collects data on the disposal calculation for the most important cereals and potatoes, the number of livestock, the yields of livestock and their use. The annual sample covers about 10,000 farms picked from the population of the Statistical Farm Register (MMM-TIKE 2003a). At our request, TIKE reported the exact flock size of all farms surveyed which had either chickens or hens for egg production in 2001. The report included data on 797 flocks of laying hens. The minimum flock size was zero, which was interpreted to mean a production break between two consecutive flocks, and the maximum flock size was 48,400. We estimated the flock size distribution using these data after removing all flocks of zero size (Figure 10). The fitted  $\log_e$ -transformed distribution was a mixture density  $0.81 * N(7.95, 0.98^2) + 0.19 * N(4.59, 1.17^2)$ . These parameter estimates were obtained as maximum likelihood estimates. In simulations, this mixture density was truncated at 100 and 50,000 to ensure flock sizes are between these realistic bounds describing production flocks under the FSCP.



**Figure 10.** Estimated distribution of flock sizes of laying hens based on data from the Information Centre of the Ministry of Agriculture and Forestry. The dashed lines show the truncation points at  $\log(100)$  and  $\log(50,000)$ .

#### Ideal egg production per hen per day

We obtained information on egg production per hen per day from management guides for the different hybrids. For Lohmann hybrids, we found management guides on the web ([www.ltz.de](http://www.ltz.de)), and for Shaver and Isabrown hybrids we received information from the importer (Haaviston Siitoskanala). We thus obtained egg production information for three hybrids (Lohmann White, Lohmann Brown and Shaver 2000). Since the egg production curves of the different hybrids closely resemble each other, we felt that the average curve provided an adequate illustration for modelling. In keeping with the structure of the PPIM, this average egg production curve was further divided into six gradual, equally long production periods resulting in egg production rates of 0.715, 0.934, 0.91, 0.871, 0.823 and 0.764 (Figure 11, page 78).



**Figure 11.** The average egg production curve as such, and divided into the six periods used in the model.

#### Egg production per hen in Finland in 2001

The ideal egg production rate per hen per day obtained from the management guides was corrected with the average egg production per hen, which was 17.2 kg in 2001 (MMMTIKE 2002). The corrected egg production rates for six 8-week periods were then 0.6839, 0.8934, 0.8705, 0.8332, 0.7873 and 0.7308.

#### Production break

According to a postal survey of egg producers done by Uusitalo (2003), in 2001 the average production break between flocks was 9 weeks.

#### Death rate of laying hens

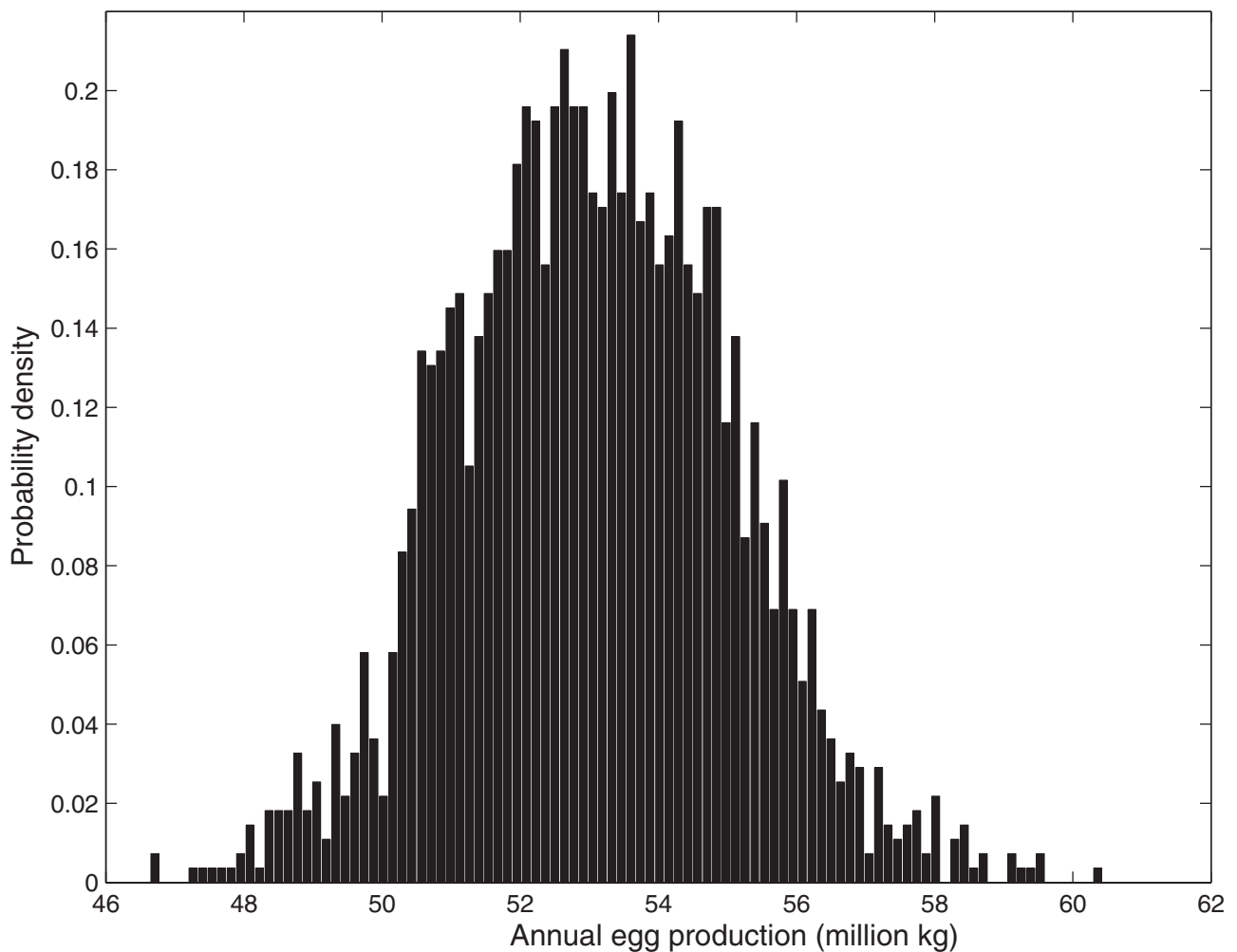
According to an expert opinion (a poultry veterinarian), the average death rate amongst flocks of laying hens in Finland varies between 4 and 6% during the production period. Therefore, during each stepwise part of the production period, a death rate of 1% was taken into account. After the whole production period,  $0.99^6 = 94.15\%$  of the original number of the hens was thought to exist.

#### Weight distribution of shell eggs

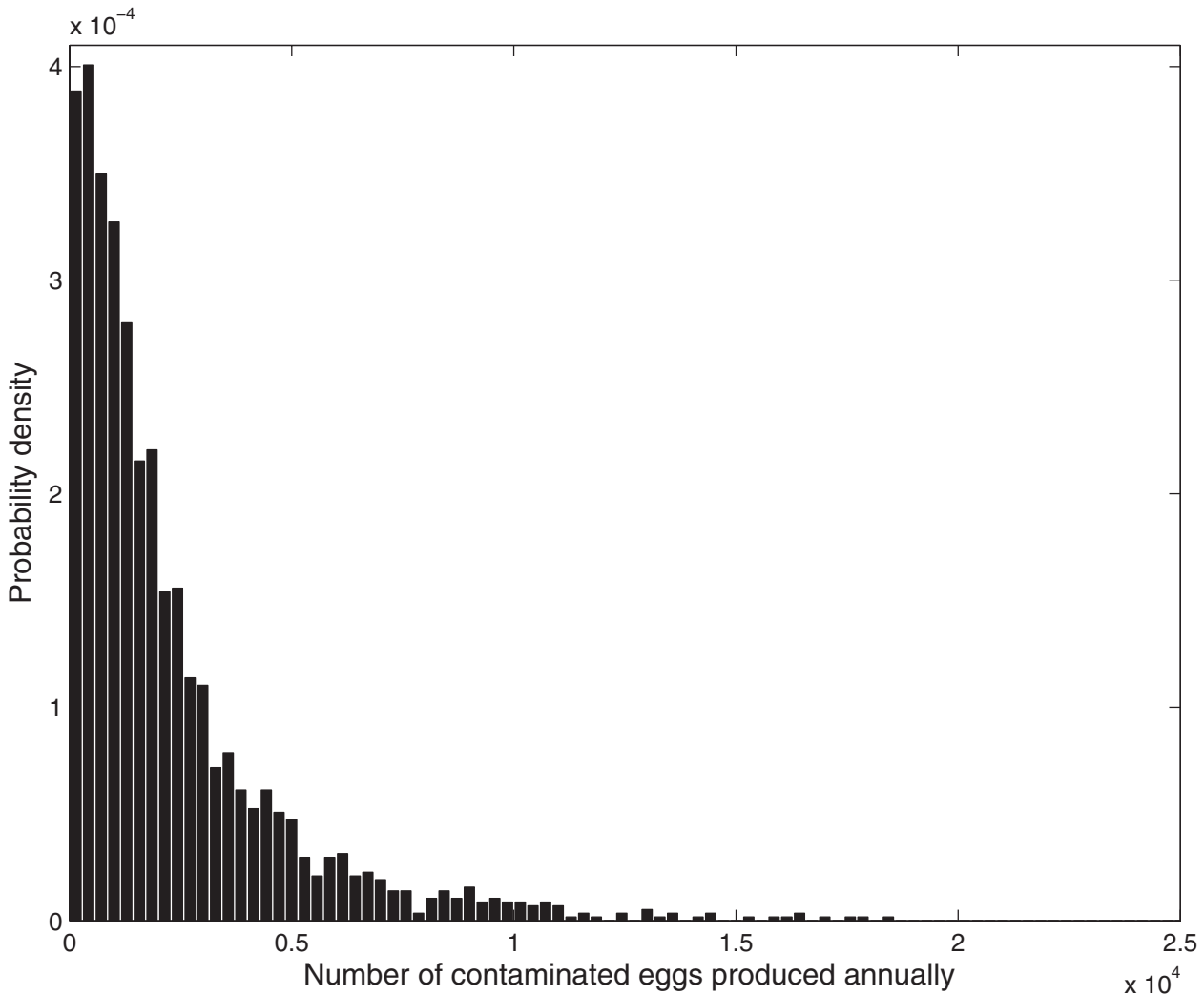
The estimated number of shell eggs produced in 2001 was converted into the amount produced (kilograms) using data on shell egg weights received from the National Food Agency Finland. Based on these data, estimates of parameters of weight distribution of shell eggs was obtained as  $N(0.064 \text{ (kg)}, 0.006^2)$ . This estimate is explained in appendix A.

### 6.3.1.3 Output of the PPIM

The amount of eggs produced annually and the amount of contaminated eggs were obtained as posterior predictive distributions based on the primary production data in 2001. The mean of the total egg distribution was 821,000,000 eggs (53 million kg) and the mean number of contaminated eggs was 1,800. The 95% credible intervals were [755,000,000; 889,000,000], [48 mill.kg; 57 mill.kg], and [0; 7,400], respectively. The probability that there is a truly infected laying flock at a randomly chosen flock house was 0.3%, which can also be interpreted as the expected laying flock prevalence. In terms of flock prevalence, the 95% CI, summed pointwise over all flock ages was [0.14%;0.58%]. The posterior predictive distributions are shown in Figures 12 and 13, respectively.



**Figure 12.** Predictive distribution of the total amount of commercially produced shell eggs in Finland in 2001.



**Figure 13.** Predictive distribution of the total number of contaminated eggs commercially produced in Finland in 2001.

According to the Information Centre of the Ministry of Agriculture and Forestry, egg producers delivered 54.6 million kg of shell eggs to packing plants in 2001 (MMM-TIKE 2003b). Therefore, the estimated mean of 53 million kg produced by the present model was taken as a satisfactory prediction of the real life situation in 2001.

The estimated annual mean of contaminated eggs in this model was 1,800, which corresponds to a *Salmonella* prevalence of  $1.8 \times 10^{-6}$  in eggs.

#### 6.3.1.4 Sensitivity and limitations of the PPIM

Technically, the PPIM was divided into two submodels: for breeder flocks and for production flocks. This creates computational limitations. While the breeder flocks could be modelled using a modified version of our previous model on broilers (WinBUGS), the stationary distribution for the production flock process could not be implemented within the same model in WinBUGS. On the other hand, expanding the breeder flock model to embrace individual flock life histories for a thousand production flocks by repeating the same model structure in WinBUGS would jam the MCMC computation. Therefore, an approach based on stationary distribution for production flocks was preferred, and implemented in Matlab. For Bayesian estimation, the prior density was obtained from the result of the breeder flock model in Win-

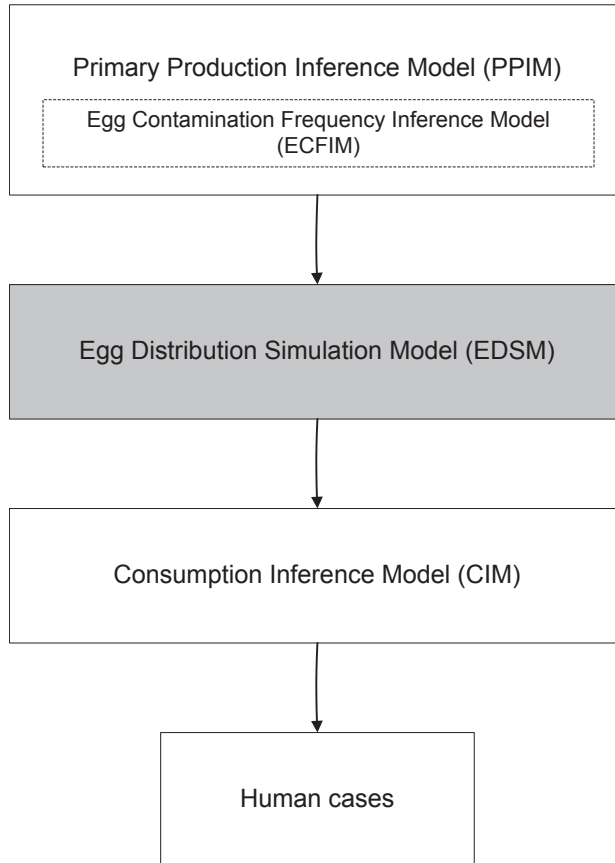
BUGS. This still utilizes the information gained from breeder flocks when estimating the parameters and prevalence in production flocks, but is inconvenient in practice. Ideally, the whole model should be computed within a single MCMC simulation using a single software program. The sensitivity and limitations of the breeder flock model have been discussed in the broiler *Salmonella* risk assessment (Majala & Ranta 2003).

A limitation of the stationary probability model is that stationary probabilities are not defined for periodic Markov chains. With badly chosen parameters, a transition probability matrix may lead to such a situation. Such periodicity was avoided by inserting a low nominal probability for some transition probability. Since the default data included no detected positive flocks, the model was also computed assuming two positive test results from production flocks, one from each production pyramid, which is not an unusual annual result. The parameter estimates and the estimated flock prevalence were nearly identical to the default results, indicating that the number of detected positive flocks must be clearly higher than just a few flocks in order to draw the conclusion that there is enough evidence about increased flock prevalence. Finally, the within-flock prevalence in infected flocks determines the overall flock sensitivity of the pooled testing method. No reliable Finnish data were available to estimate within flock-prevalence, and it was assumed to be at least 5% in each infected flock. If it were lower, the overall flock sensitivity and the resulting estimates of true flock prevalence should be revised accordingly.

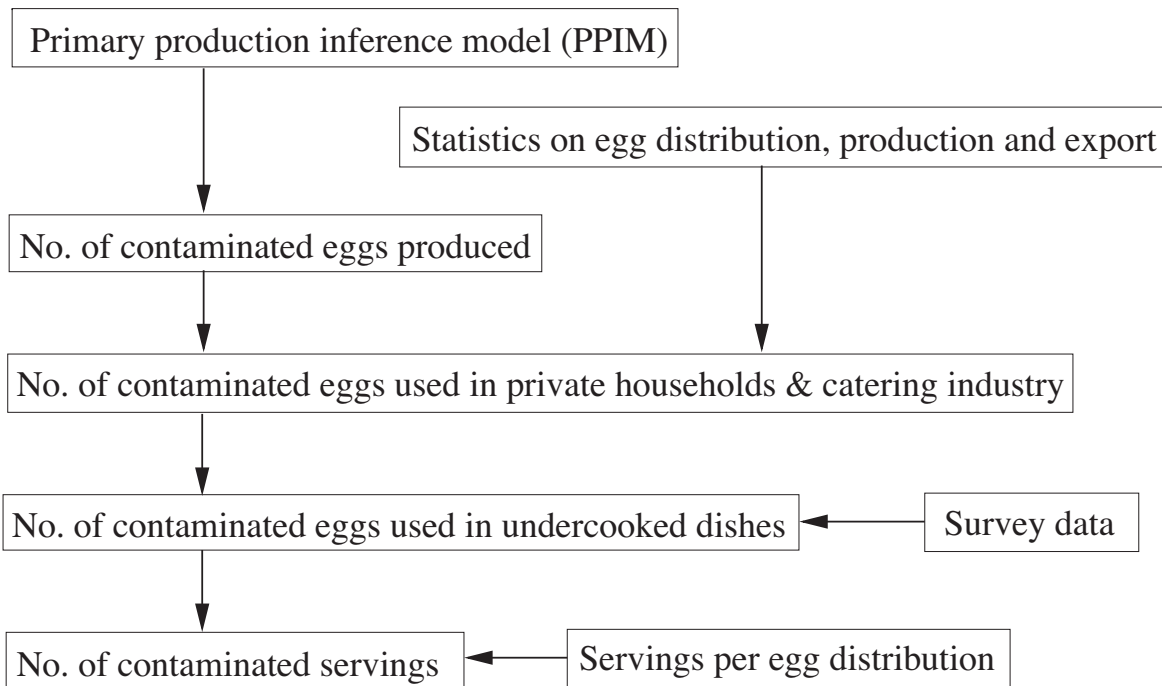
### 6.3.2 The Egg Distribution Simulation Model (EDSM)

#### 6.3.2.1 Summary of the EDSM

In this risk assessment, shell eggs were assumed to be consumed in three categories: 1) in private households, 2) in the catering sector and 3) in the food industry. The Egg Distribution Simulation Model describes the probability and number of contaminated eggs in each consumption category based on the total annual number of contaminated eggs and the proportion of each consumption category in the whole (Figure 14). The total annual number of contaminated eggs is predicted by the PPIM as a probability distribution. The output of the EDSM is the distribution of contaminated eggs in each category which is finally converted into the number of undercooked servings potentially contaminated at the time of consumption. The basic structure of the EDSM is shown in Figure 15.



**Figure 14.** The Egg Distribution Simulation Model (EDSM) in the whole risk assessment model.



**Figure 15.** The basic structure of the Egg Distribution Simulation Model.



According to the EDSM, the conditional predictive means of the number of contaminated eggs used in each consumption category were the following: 1,134 in private households, 187 in the catering sector and 47 in the food industry. The predictive 95% credible intervals were [22;4,650], [3;767] and [0;192], respectively. The shell eggs ending up in the food industry were assumed to be consumed only in well-cooked egg dishes and were therefore excluded from further analysis. For undercooked egg dishes, private households and the catering sector used 188 contaminated eggs in total with a 95% credible interval of [3;772]. The predictive mean of the total number of servings of undercooked egg dishes annually eaten in private households and the catering sector was 266 with a 95% credible interval of [4;1,101].

### 6.3.2.2 Inputs of the EDSM

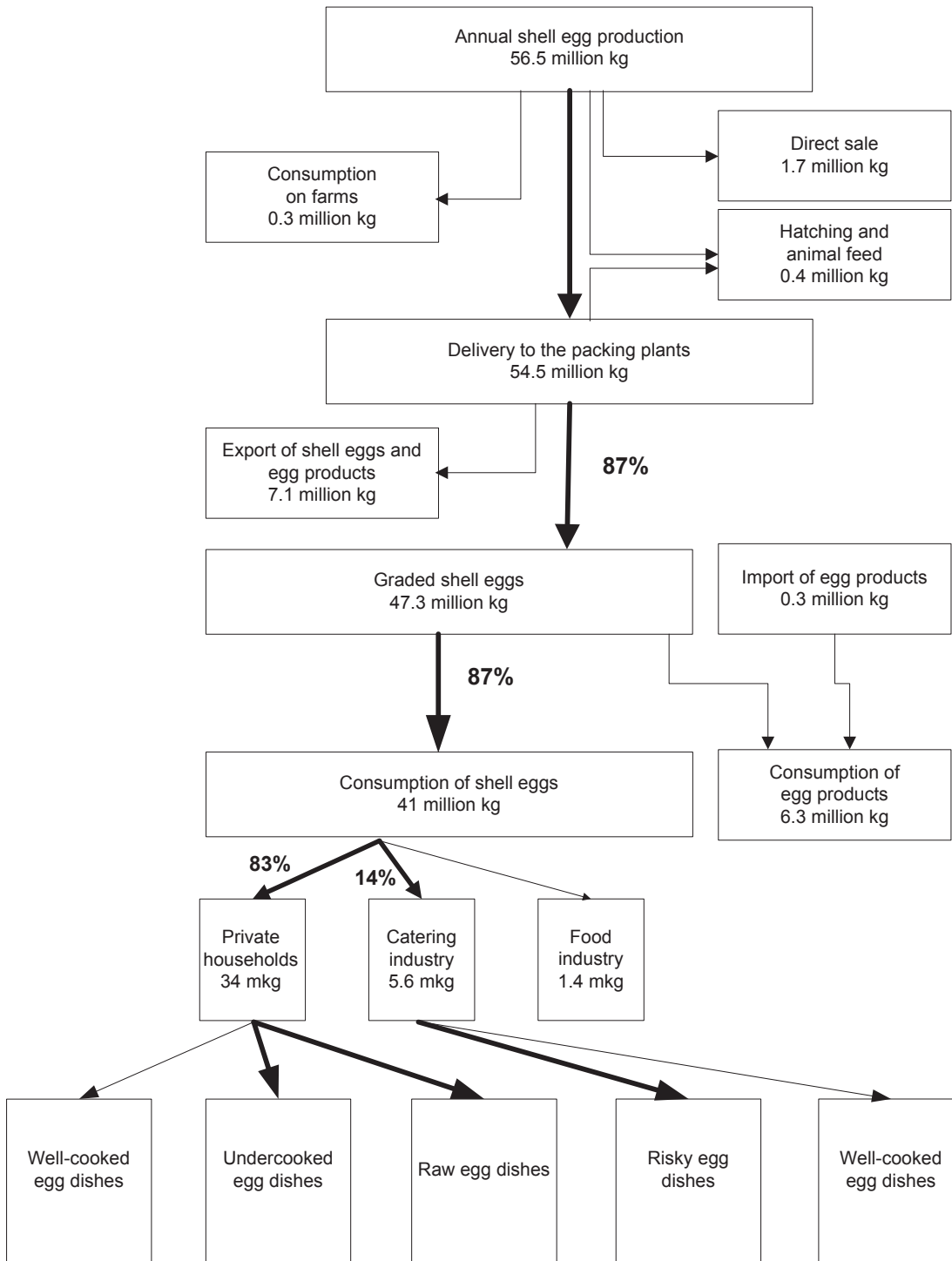
All the inputs of the EDSM are presented in Table 14 in Appendix B.

#### Number of contaminated eggs

The estimated number of contaminated eggs (per year) was received as an output from the PPIM.

#### Proportion of shell eggs used in private households and in the catering industry

To assess the risk of *Salmonella* to Finnish consumers caused by eggs, we had to estimate the proportion of shell eggs used in private households and in the catering sector as well as in the food industry. Figure 16 shows a flow chart of the distribution of shell eggs in Finland in 2001. The data used for constructing this flow chart were collected from various sources. Estimates of annual shell egg production, the amount delivered to the packing centres, consumption for producers' own food management and direct sale on farms as well as the amount of eggs used for hatching or animal feed were taken from the statistics of the Information Centre of the Ministry of Agriculture and Forestry (MMMTIKE 2002). Data concerning the import and export of shell eggs and egg products were gathered from the trade statistics of the National Board of Customs. On the consumption of egg products, we used data from Suomen Gallup Elintarviketieto Oy (Food and Farm Facts, Ltd) (Gallup Elintarviketieto 2002).



**Figure 16.** The estimated distribution of Finnish shell eggs from production to consumption in 2001. Sources of data MMTIKE 2002; the trade statistics of the National Board of Customs; Food and Farm Facts, Ltd.

In 2001, the consumption of shell eggs in private households, the catering sector and the food industry was estimated to be approximately 41 million kg in total. According to an expert opinion, based on industry information and results of commercial follow-up surveys of the Finnish retail market, private households used 34 million kg shell eggs in 2001. The proportion of shell eggs consumed by the catering industry was estimated using data from two commercial surveys. The amount of money spent by the catering sector (institutional kitchens, restaurants, bars, cafeterias, etc.) on purchasing shell eggs was obtained from a 1999 AC Nielsen survey of catering purchases; this survey gathered information on where the catering branch bought foodstuffs and how much money they spent on purchasing, and reported a sample size of around 1,000 kitchens. According to this survey, the Finnish catering sector spent 8.2 million euros on buying eggs in 1999. Institutional kitchens usually buy foodstuffs at wholesale. To convert the known sum of money into kilograms consumed, information about the average price of shell eggs at the wholesale level was obtained from the Finnish Hotel and Restaurant Association, which commissions Statistics Finland to gather information about wholesale prices twice a year. According to this data, the wholesale price of shell eggs was 1.26 € / kg in February 1999 and 1.68 € / kg in September 1999. In our calculation, we therefore used an average, 1.47 € / kg. This information was from 1999, not 2001, the year we were modelling, but at the time of calculation was the only information available. We assumed that changes in consumption patterns of shell eggs in the catering industry between 1999 and 2001 were relatively insignificant, and thus the estimates obtained in 1999 were considered to be adequate for 2001. Using these figures, we thus estimated that the catering industry consumed 5.6 million kg of shell eggs in 2001. Finally, we calculated the amount of shell eggs used in the food industry (1.4 million kg) by simply subtracting the amounts used in private households (34 million kg) and the catering industry (5.6 million kg) from the total amount of 41 million kg. In this risk assessment, the shell eggs ending up in the food industry were assumed to be consumed only in well-cooked egg dishes and were therefore excluded from further analysis.

To summarize, the proportions of shell eggs used in private households, in the catering sector, in the food industry and in the remaining category "other" were assessed to be 62.39%, 10.28%, 2.57% and 24.76%, respectively, out of the delivery of 54.5 million kgs of shell eggs to the packing plants.

#### Fraction of undercooked egg dishes in private households

The cooking method with which an egg dish is prepared affects the possibility that the dish could cause a *Salmonella* infection. Well-cooked egg dishes are generally considered safe. Because consumption of raw eggs and dishes containing raw or only lightly prepared eggs are considered the main source of egg-borne *Salmonella* infections, we needed to estimate their proportion out of the total shell egg consumption in Finnish households. Using a postal survey, we determined that consumption of undercooked eggs accounted for 12% and consumption of raw eggs accounted for 4% of the total shell egg consumption in Finnish private households (Lievonen et al. 2004). To account for the uncertainty of a combined proportion, the exact percentages of undercooked and raw egg dishes were treated as two normally distributed variables and summed up (Appendix A).

#### Fraction of undercooked egg dishes in the catering industry

To calculate the proportion of undercooked egg dishes prepared in the catering industry, a survey was made of 141 catering establishments which used shell eggs (Lievonen & Majjala 2005). In the survey, respondents were divided into three cate-

gories according to the size of the establishment: small (serving less than 200 portions a day), medium-sized (serving 200–1999 portions a day) and large (serving at least 2000 portions a day). Within the catering industry, the amounts of eggs used in these three types of establishments were distributed as 44.65%, 49.59% and 5.76%, respectively. In addition, for each category we estimated the proportion of undercooked egg servings from the total number of all servings of egg dishes in a year. In each of the categories, a considerable proportion (28/54, 28/59 and 21/28) of the respondents did not prepare raw or undercooked eggs at all. Hence, the fraction of undercooked servings in each category was modelled as a mixture density with a probability  $p_0$  of zero and probability  $1 - p_0$  of nonzero values. The posterior predictive distribution of proportions of undercooked egg dishes in each category was computed with WinBUGS. The model is explained in Appendix A.

#### Servings per egg

Eggs are served in various types of dishes. Therefore, a single egg may be consumed by a single person, but it may feed many people as well. In this report, the number of servings per egg was produced as a probability distribution based on egg consumption data gathered from private households and catering establishments.

To model a probability distribution for the number of servings per egg in private households, egg dishes consumed by only one person were first assessed. Soft-boiled eggs, eggs fried sunny side up, poached eggs and raw eggs as such were considered to be eaten by one person. Half of the servings of runny omelettes and runny scrambled eggs were assumed to be consumed by one person in accordance with USDA-FSIS (2004). In addition, the size of a single portion of whipped egg white was taken as one albumen. According to the survey of Lievonen et al. (2004), consumption of these egg dishes accounted for 87.9% of the total amount of soft-boiled and raw egg dishes consumed. The average servings per egg of other soft-boiled and raw egg dishes were estimated using recipes obtained from cookery books (Heikkilä & Lampi 1998; Lehto & Patala 1996) and from the electronic nutrition database of Palmia, the service centre of the city of Helsinki. The share of consumption for each individual dish was taken from the survey of Lievonen et al. (2004).

To estimate the servings per egg in the catering establishments, a corresponding probability distribution was constructed using data gathered by the postal survey sent to the catering establishments. For calculation, soft-boiled eggs and eggs fried sunny side up, poached eggs, raw eggs as such, cold drinks and whipped egg white as well as half of the servings of runny omelettes and runny scrambled eggs were assumed to be consumed by one person. According to the survey, egg dishes eaten by a single person accounted for 56.4% of the total amount of portions of soft-boiled and raw egg dishes in the catering establishments. In the same way as with private households, the average servings per egg of other soft-boiled and raw egg dishes were evaluated using recipes obtained from cookery books (Heikkilä & Lampi 1998; Lehto & Patala 1996) and from the electronic nutrition database of Palmia, the service centre of the city of Helsinki. The share of consumption for each individual dish was taken from the catering survey.

While modelling the probability distributions, the maximum and minimum amounts of servings per egg were specified, because extremely high and low values were considered unrealistic. A single egg divided into 58 portions of 1 gram was taken as a minimum portion size and five eggs consumed by one person were taken as a maximum portion. All reasonable values should fall between these boundaries. Next, the probability of a single egg being consumed by one person was assessed

separately for private households and for small, medium and large catering establishments. The majority of eggs fell into this category, even though the probability was higher in private households than in catering establishments. Then, for eggs not consumed exactly as one egg per portion, separate probability distributions for the number of servings per egg in private households and in catering establishments were constructed.

Paired estimates of servings per egg and the percentage of consumption were derived over the range of all meal types. These discrete estimates resulting from a discrete number of meal types were transformed into a continuous distribution. However, each percentage point could be interpreted either as the upper or lower percentage point in a continuous distribution, leading to two different continuous distributions. The final probability distribution for servings per egg was taken as an average of these two, i.e. as a mixture distribution with equal weight. Such a mixture distribution was estimated separately for both private households and the catering industry. Thus, for each egg the resulting number of servings could be generated from a distribution. However, due to the large number of eggs, the total number of servings was generated from the normal distribution based on the law of large numbers.

### 6.3.2.3 Output of the EDSM

#### Fraction of undercooked egg dishes in the catering industry

Fifty-two percent [95% credible interval 38–65%] of small catering establishments, 48% [95% credible interval 35–60%] of medium-sized and 73% [95% credible interval 56–87%] of large catering establishments did not prepare risky egg dishes at all. Given that they are prepared, the conditional predictive means of consumption of undercooked egg dishes in small, medium-sized and large catering establishments were 22, 28 and 28% with respective 95% credible intervals of [0.00;0.87], [0.00;0.93] and [0.00;1.00]. Accounting for both those who do and do not prepare risky dishes at all, and the proportion of consumption if prepared, the unconditional predictive total values were 11%, [0;76%] 15%, [0;87%], and 7% [0;96%], respectively. The results show, on average, a fairly low total fraction (7–15%) of undercooked dishes in all three groups of establishments although uncertainty is large. Especially if the fraction is not exactly zero, there is large uncertainty about its value due to the heterogeneity of the responses in the survey, ranging from nearly zero values to high proportions.

#### Number of contaminated eggs used for preparing egg dishes

In the model, shell eggs were assumed to be consumed in private households, in the catering sector and in the food industry. The predictive means of the number of contaminated eggs used in each category were 1, 130, 190 and 50, respectively. The predictive 95% credible intervals were [20;4,650], [3;770] and [0;190]. In total, the predictive mean was 1,370 and the corresponding 95% credible interval [30;5,600]. The shell eggs ending up in the food industry were assumed to be consumed only in well-cooked egg dishes and therefore were excluded from further analysis.

#### Number of contaminated eggs used for undercooked egg dishes

The predictive means of the number of contaminated eggs used for undercooked egg dishes was 180 in private households and 10 in the catering sector with 95% credible intervals of [0;730] and [0;50], respectively. The total amount of contaminated eggs used for undercooked egg dishes was 190 with a 95% credible interval of [0;770]. In Table 10, the respective rounded values are 200 with a 95% credible interval of [0;800].

#### Number of undercooked servings

The predictive mean of the total number of contaminated risky servings of undercooked egg dishes was 300 with a 95% credible interval of [0;1,100].

#### Average serving size

The average serving size (in grams) was computed as  $0.9 \times 64 \times (\text{number of eggs used for undercooked servings}) / (\text{number of undercooked servings})$ . The mean value and standard deviation were 42.9 and 8.9.

#### **6.3.2.4 Sensitivity and limitations of the EDSM**

The model assumes complete mixing of eggs after they have been produced so that each egg has an equal multinomial probability of ending up in the different consumption categories. Hence, the distribution of eggs is assumed to follow a conditional multinomial distribution, given the total number of such eggs and the fixed probabilities for consumption groups. The model does not account for any clustering effects. The estimated number of servings resulting from a certain number of eggs depends on assumptions concerning meal types and their consumption, for which we made a gross estimation based on typical recipes and limited survey data.

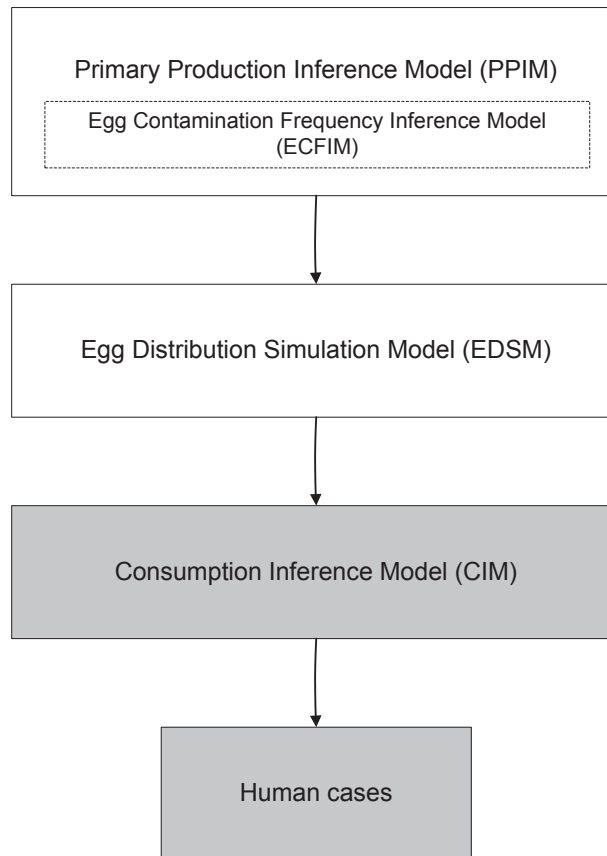
### **6.4 Risk characterization**

The goal of this risk assessment was to quantify the risk of human infections caused by shell eggs. This depends on the estimated number of contaminated servings, but also on the level of contamination per such serving. The estimate of the number of contaminated servings depends on the results of the previous inference models (PPIM, ECFIM) and the simulation model (EDSM). The estimated levels of contamination (hence, probability of illness) at the time of consumption depends on the results of the Consumption Inference Model (CIM) which includes an assumed dose-response model and its parameters. The CIM also uses data on the reported number of human cases and underreporting. The model thus was calibrated to the current situation (based on 2001) by using these data and the results of the previous modules.

#### **6.4.1 Consumption Inference Model (CIM)**

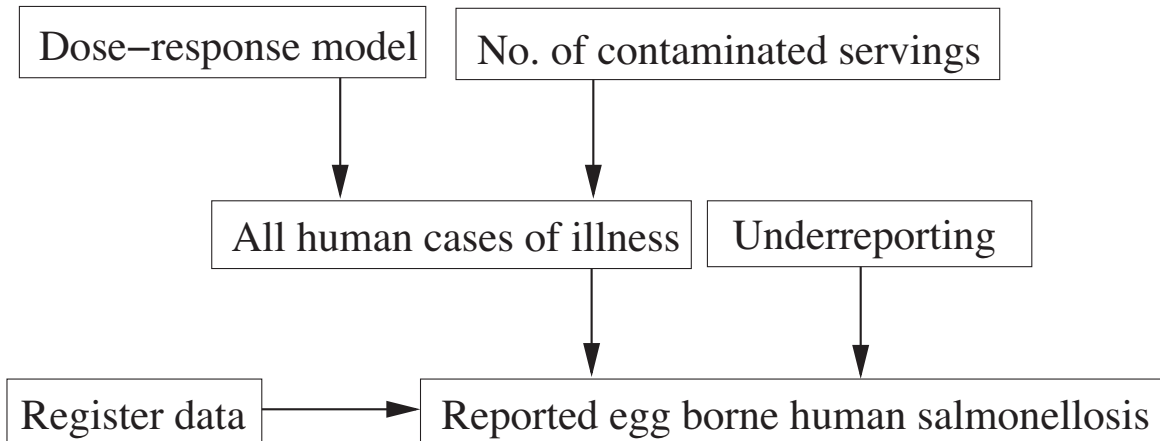
##### **6.4.1.1 Summary of the CIM**

The number of human cases of illness due to *Salmonella* from eggs was assessed by a hierarchical Bayesian model, based on the records of the reported number of domestic human cases of illness and phagetype information (Figure 18). The meta-level model utilizes a given dose-response model that is assumed to be fixed. The CIM combines information from two directions: the observed records of human cases of illness and the predicted number of contaminated servings resulting from the Egg Distribution Simulation Model. As a result, the model aims to estimate the average CFU/g level per contaminated serving jointly with other uncertain quantities. The resulting information can be further used when predicting the number of human cases under different scenarios (Figure 17).



**Figure 17.** The Consumption Inference Model (CIM) in the whole risk assessment model.

The dose-response model specifies a 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 size of servings; and (4) the average CFU/g levels in such servings. Uncertainty about the number of contaminated servings was described by a probability distribution resulting from the Egg Distribution Simulation Model (EDSM), representing the number of “risky” servings (raw and undercooked) egg dishes that could be contaminated. The parameters of the dose-response model were taken from the literature and treated as fixed constants. The serving size was quantified as a distribution deduced from the consumption data in the EDSM. The CFU/g levels at the time of actual consumption are highly uncertain, as there are no reliable data sources available and also expert opinions present large uncertainties. Therefore, this most uncertain quantity was described by a prior distribution that was designed to be uninformative. This was done using a normal distribution centred at zero and then restricted to the positive axis. By choosing the prior median, the width of this half-normal density was controlled. As a default value we used a median of 1 CFU/g on the basis of information from previous risk assessments (USDA-FSIS 1998; USDA-FSIS 2004), but for the sensitivity analysis 10 and 10,000 CFU/g were also used as a median. The CIM was also computed without any specific dose-response model by simply using one parameter to describe the probability of illness, which was assigned a uniform prior. The basic structure of the CIM is shown in Figure 18.

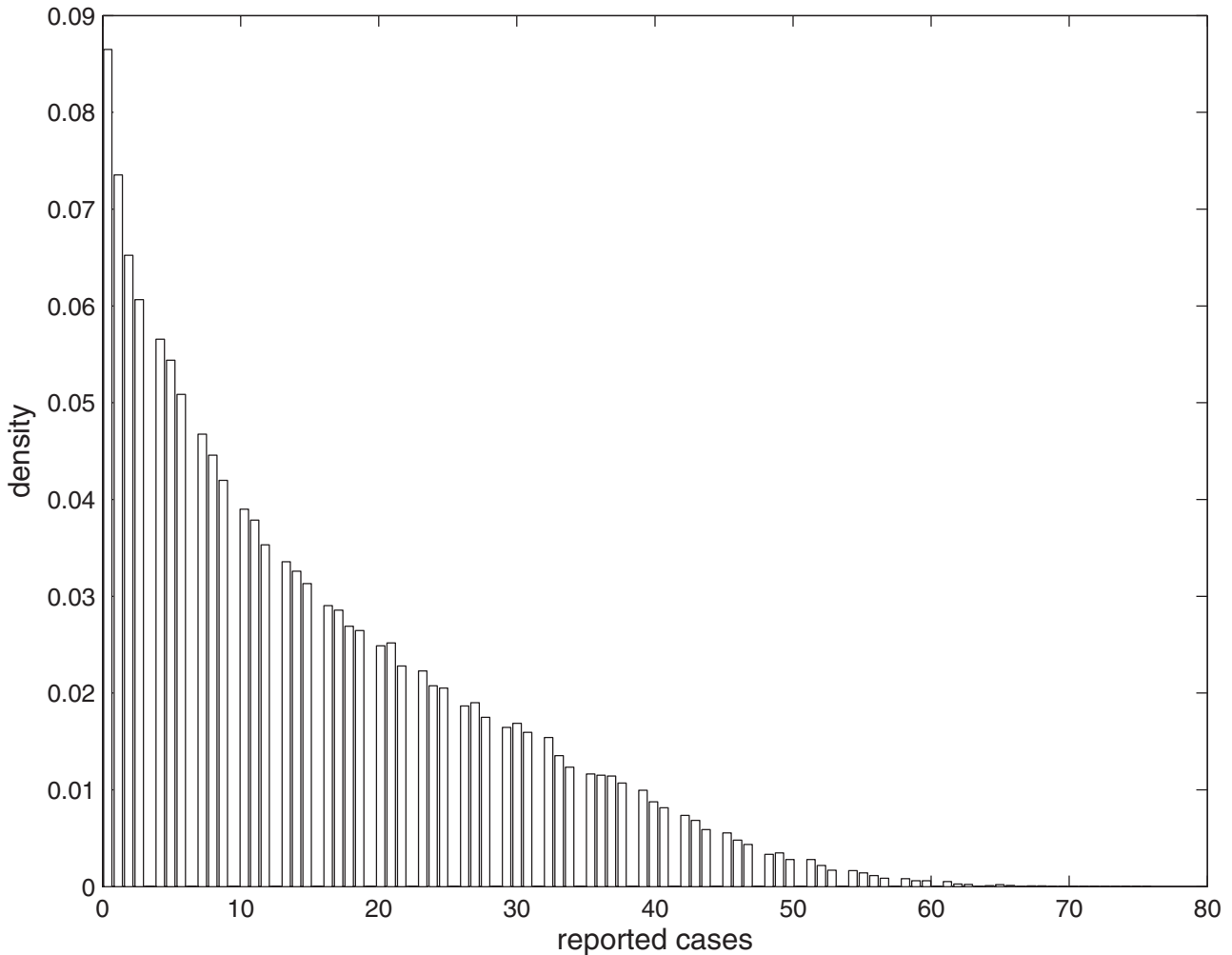


**Figure 18.** The basic structure of the Consumption Inference Model.

The annual number of reported human infections of *Salmonella* is known. From the 1999 data (the year with the highest annual number of positive testing results in the Finnish *Salmonella* Control Programme for laying hens since 1995), we can deduce an estimate (minimum, maximum) for the number of infections due to eggs. This was done on the basis of the serovars and phagetypes detected in breeders and layers in the egg production chain, and the human infections. Therefore, we can treat the estimate of human infections due to eggs as a censored data value and compute a posterior distribution for the unknown parameters and variables, given the prior densities of model quantities. Also, the underreporting of human infections was accounted for simultaneously 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: the reported human infections.

The predictive distribution of the number of reported human cases of illness, under conditions similar to 2001, was 10 (mean), with a 95% credible interval of [0;50] according to the CIM and the default priors. For the predictive distribution of the number of all human salmonellosis due to eggs, the CIM gave 60 (mean), with a 95% credible interval of [0;250]. The predictive distribution of the number of reported





**Figure 19.** The predictive distribution of the annual number of reported cases caused by *Salmonella* in shell eggs.

human cases of illness caused by *Salmonella* in shell eggs is shown in Figure 19.

#### 6.4.1.2 Inputs and parameters of the CIM

All the inputs to the CIM are presented in Table 15 in Appendix B.

##### Number of contaminated servings ( $n_{ser}$ )

This was taken as a prior distribution within the CIM. The distribution was derived from the output of EDSM as a fitted Gamma(0.8953,0.0034)-distribution.

##### Number of egg-borne reported cases of human infections ( $n_0$ )

Estimated numbers of human infections caused by *Salmonella* from shell eggs are not directly available in Finland. Therefore, comparison of serovars isolated from laying hens with the reported human infections was used to estimate the proportion of egg-caused infections. For this calculation, we used data from 1999, only taking into account the human cases of domestic origin. In 1999, 526 human cases of domestic origin, including 132 cases of *S. Enteritidis*, 386 cases of *S. Typhimurium* and 10 cases of *S. Infantis*, were caused by the same serovars as identified from laying hens.

In Finland, *S. Typhimurium* is one of the main serovars in humans. Based on page

typing in 1999, two isolates from flocks of laying hens were of the same phage type (PT1) as human isolates (248 human cases, where 1% were of foreign origin, thus 246 counted as domestic). However, PT1 is a typical finding in cattle and pig production, and is regarded as an endemic type of *Salmonella* in Finland. Therefore, this estimate of 246 reported human cases was regarded as an overestimate of the number of cases due to laying hens, because there are also other potential sources of such infections. As a crude estimate, the percentage of two laying hen isolates out of all isolates of *S. Typhimurium* PT1 from animals and food (25) was used as the upper level (8%), resulting in 20 human infections in 1999. The human cases caused by *Salmonella* Enteritidis PT4 and *Salmonella* Infantis from laying hens were estimated to be 24 and 0, respectively, with the same kind of calculation. In total, a maximum of 44 human infections were estimated to derive from laying hens in 1999. We used 1999 as a worst case scenario because there were exceptionally many *Salmonella* isolates from laying hens that year. The minimum was set at zero. Thus, we assumed that in 1999 the number of reported cases of human salmonellosis due to the shell eggs of laying hens was not larger than 44, and that this could be taken as a maximum for 2001 as well.

#### Serving size of egg (size)

The average serving size was estimated in the EDSM by dividing the number of resulting servings (EDSM output) by the corresponding number of eggs (PPIM output). This was calculated at each iteration during the simulation, resulting in a Monte Carlo sample. The resulting fitted prior distribution used in the CIM was  $N(42.9, 8.9^2)$ .

#### Level of contamination (cfu)

The level of contamination at the time of consumption is an important factor in consumer risk. It depends, for example, on the characteristics of the strain, the microbiological ecology of the food, the initial contamination of the raw material, taking into consideration regional differences and the seasonality of production, the level of sanitation and process controls, the methods of processing, packaging, distribution and storage of foods as well as any preparation steps such as cooking and holding. One approach would have been either to ask experts about all these issues and build a model for all these steps or to ask experts to estimate the level of contamination at the time of consumption (including storage, preparation, cross-contamination etc.).

Unfortunately, very little such data exist in Finland concerning these various steps in food preparation and storage and 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 available information on the number of reported human cases of illness, the selected dose-response model, the probability distribution of serving sizes of eggs and the number of contaminated servings. Hence, the approach was to start with a fairly uninformative prior distribution for the average CFU/g, e.g. a uniform distribution over a suitably wide range to cover all the plausible values. As a result, a posterior distribution of CFU/g is obtained as an output, representing the plausible average values according to information on the aforementioned quantities. However, it turned out that with these data, the resulting posterior density heavily depends on the chosen prior.

#### Dose-response model & parameters ( $\alpha, \beta$ )

A Beta-Poisson dose-response model was chosen with parameters ( $\alpha, \beta$ ) for a normal population taken from the WHO/FAO report (WHO/FAO 2002). Alternatively, the CIM was computed without any specific dose-response model by a simple one parameter model for the probability of illness, with a uniform prior.

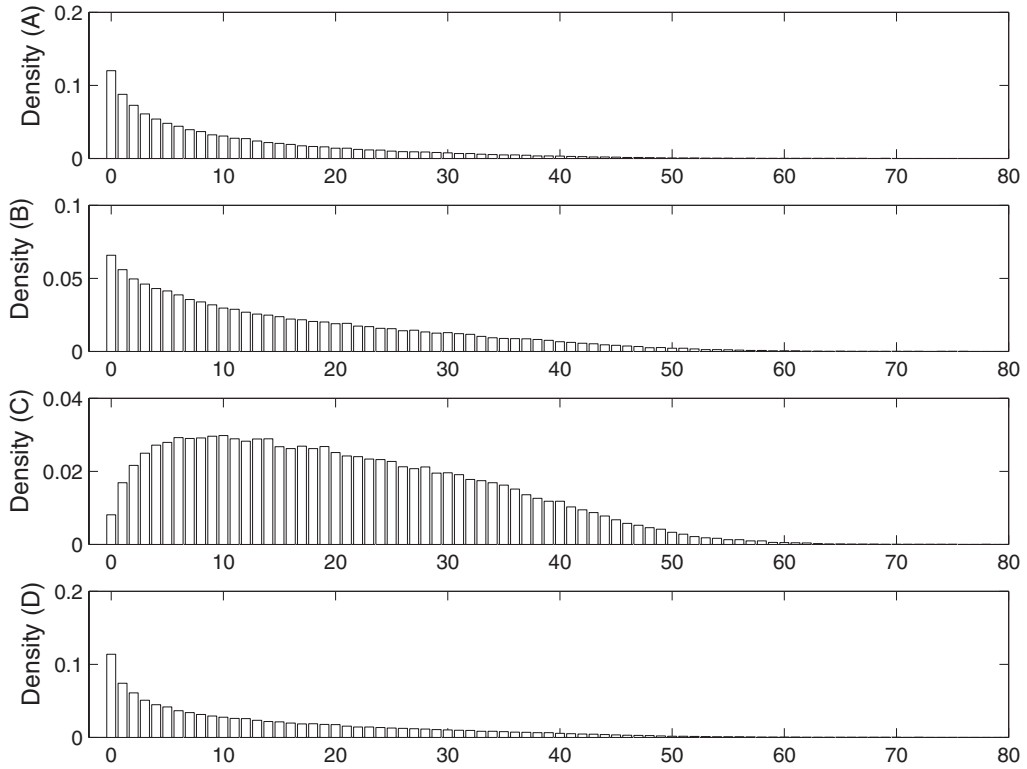
#### Expected reporting of human cases ( $p_{sel}$ )

In Finland, laboratories have to notify all confirmed *Salmonella* cases of any serovars, always based on bacteriological culturing. Samples are taken from persons suffering from diarrhoea, including their close contacts, and from asymptomatic persons working in risk professions. *Salmonella* species identification is done by biochemical methods and by agglutination of cultures of *Salmonella* antisera. Phage-typing is done for *S. Paratyphi*, *S. Typhimurium* and *S. Enteritidis*.

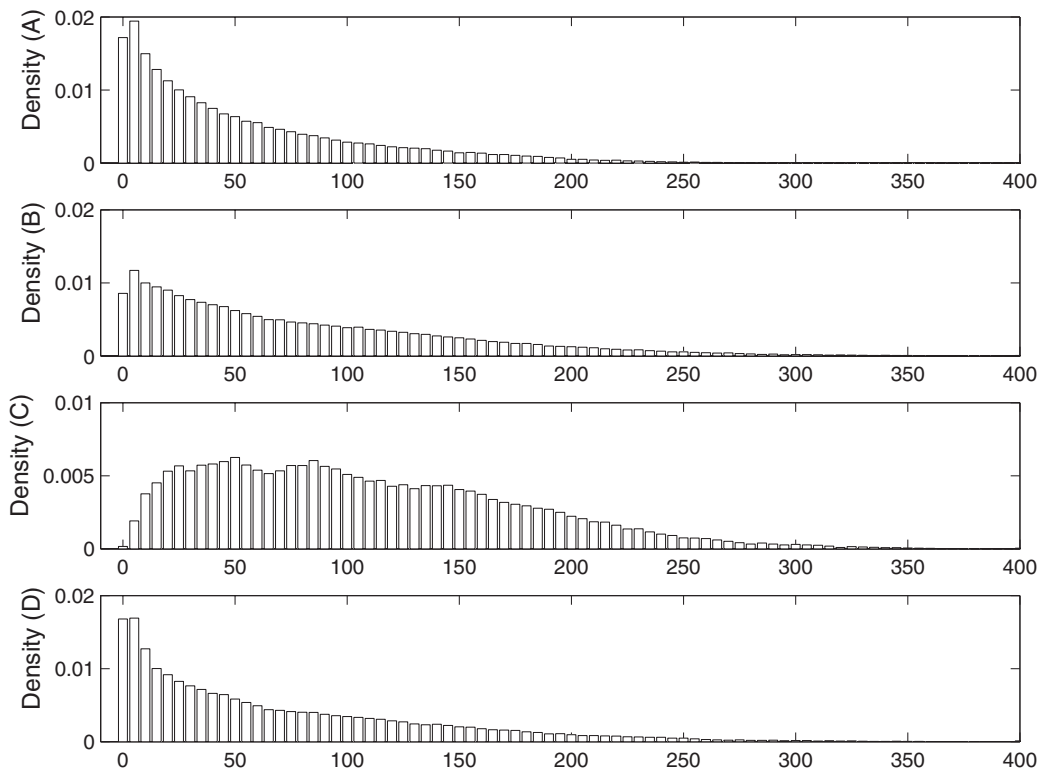
Wheeler et al. (1999) conducted a study on the reporting rate of some foodborne diseases. According to them, 72.7% of *Salmonella* cases visited a physician, 36.5% were positive for *Salmonella* in laboratory analysis and 31.8% were reported in the national register. It has been estimated that approximately 10% of all *Salmonella* cases actually occurring annually in Finland are diagnosed and, therefore, have been reported to the National Infectious Disease Register (NIDR). Since this information about underreporting is relatively weak, a Beta(20,80)-distribution for reporting activity in the range of 10–30% was used, but allowing lower and higher values as well (expected value 20%). This may still be an overestimate since the origin (domestic/foreign) of many of the reported infections cannot be identified.

#### **6.4.1.3 Outputs of the CIM**

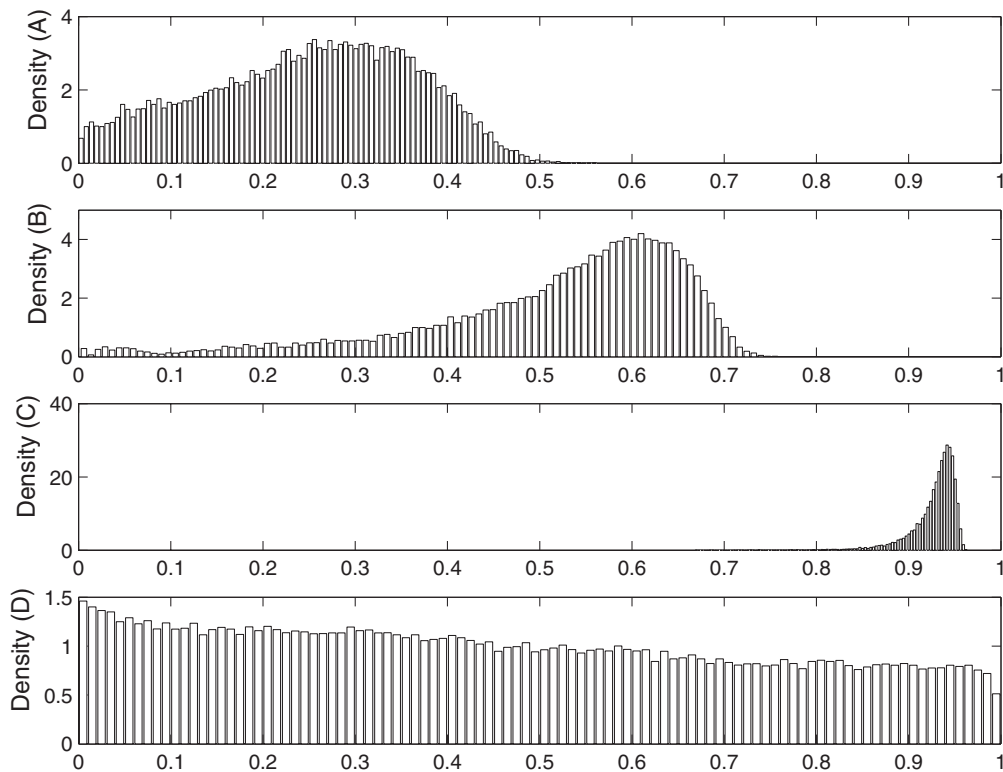
The predictive distribution of the number of reported human cases of illness, under conditions similar to 2001, was 10 (mean), with a 95% credible interval of [0;50] according to the CIM and the default priors, using 1 as the prior median of the CFU/g. For the predictive distribution of the number of all human cases due to egg consumption, the CIM gave 60 (mean), with a 95% credible interval of [0;250]. The respective predictive distributions are shown in Figures 20 and 21. The predictive distributions of frequencies of becoming a case resulting from a single serving are shown in Figure 22.



**Figure 20.** Posterior predictive distributions of the annual number of reported cases, assuming the prior median of CFU/g at the time of consumption as A) 1, B) 10, C) 10,000 or D) assuming a noninformative uniform prior directly on the chance of illness. The X-axis shows the number of reported cases.



**Figure 21.** Posterior predictive distributions of the annual number of all cases, assuming the prior median of CFU/g at the time of consumption as A) 1, B) 10, C) 10,000 or D) assuming a noninformative uniform prior directly on the chance of illness. The X-axis shows the number of all cases.



**Figure 22.** Posterior distributions of the chance of illness when eating a contaminated serving, assuming the prior median of CFU/g at the time of consumption as A) 1, B) 100, C) 10,000 or D) assuming a noninformative uniform prior directly on the chance of illness. The X-axis shows the chance of illness (i.e. a large population proportion of illness among those who had a single contaminated serving).

#### 6.4.1.4 Sensitivity and limitations of the CIM

While carrying out the computations for the CIM, we noted that in contrast to the broiler and pork *Salmonella* risk assessments (Majjala & Ranta 2003; Ranta et al. 2004) the estimates of probability of illness in this model depended heavily on the chosen prior assumption. Therefore, we tested different prior median CFU/g values. If the prior median CFU/g was chosen as 10,000, the results were: 20, [2;48] and 108, [12;260], respectively. If the dose-response model was replaced simply by a uniform prior for probability of illness, the results were: 13, [0;44] and 67, [0;236], respectively. These results were fairly similar, but the resulting estimate for the chance of illness (dose-response) changes with the prior. Therefore, the predictions under alternative scenarios concerning the number of servings are consequently influenced by the choice of priors affecting the chance of illness. The default prior distributions with prior median of CFU/g as 1 were chosen, based on information from the previous risk assessments. In 1998, USDA-FSIS concluded that the number of *Salmonella* Enteritidis per contaminated egg at the time of preparation and consumption ranged from 1 to 400 bacteria, with most eggs containing less than 40 bacteria (USDA-FSIS 1998). After more thorough modelling in 2004, it was suggested that the median number of *Salmonella* Enteritidis bacteria in contaminated eggs at the end of home storage was 10, while the 5<sup>th</sup> percentile was about 1 and the 95<sup>th</sup> percentile was  $10^6$  (USDA-FSIS 2004). The chosen median CFU/g value of 1 gave a median value of about 60 *Salmonella* bacteria per egg.

Although it is fairly straightforward to compute posterior predictive distributions for the number of cases (based on the estimated observed minimum and maximum cases, and the priors of model parameters), it is less so with hypothetical scenarios with increased or decreased numbers of servings. If, for example, we have a scenario where “the number of contaminated servings is doubled”, we can easily compute the result using the original MCMC sample from the posterior density by multiplying the *nser*-parameter by 2, while keeping the other sampled parameters as they were. The prediction can then be computed based on this transformed MCMC sample.

However, if the scenario concerns a different number of servings described by a new marginal density, it is not immediately clear how this density is combined with the original posterior density. Our approach was to use stochastic pointwise coupling applied to the original MCMC sample of *nser* and the MCMC sample under the scenario. Hence, each original point in the multidimensional posterior sample is shifted along the coordinate corresponding to *nser*, by the amount specified by the coupled marginal distributions. This requires some extra computation within Matlab.

The CIM draws information from the observed apparent number of human cases of *Salmonella* but this makes the model dependent on the validity and accuracy of such information. The number of observed apparent human cases is obtained from the National Infectious Disease Register run by KTL, an extensive but not faultless data collection system. Therefore, the total number of domestic human *Salmonella* cases used as the basis of calculations may not be absolutely correct. Some cases may be registered as origin unknown or acquired from abroad even though they truly are from domestic origin. In addition, the number of registered cases depends on how many persons seek a doctor and how many of them are diagnosed. In the CIM, the human cases are classified according to serovars but it is not clear which estimate would be best to use. Therefore, instead of choosing an exact number as a best guess, we specified a minimum and maximum so that there is reasonable confidence among experts that the true number is between those bounds. Only this (statistically) censored information was used, hence accounting for the inherent uncertainty.

The CIM also assumes that the specified dose-response model adequately describes the dose-response pattern of the Finnish population. When the number of contaminated servings is assumed to be low (by the prior derived from the EDSM), while the number of reported cases and underreporting cannot be assumed to be very low, the average cfu-level may not be identifiable from the joint posterior density. There may be many plausible combinations of the cfu-parameter and the number of servings, all explaining equally well the (statistically) censored number of human cases. The predictive distributions for the cases under the default situation may be fairly insensitive to the choice of dose-response model and the prior, but the cfu-parameter and the chance of illness are not.

## 7. Interventions and scenarios

In addition to modelling the default situation based on surveillance data from 2001, we simulated the effects of the Finnish *Salmonella* Control Programme on the annual estimates of reported and all cases of human salmonellosis caused by shell eggs in the following scenarios:

- 1) Increasing the sampling frequency of *Salmonella* control samples equivalent to the zoonosis regulation ((EC) No 2160/2003)
- 2) 20% of the parent flocks were infected at the beginning of the laying phase
- 3) 30% of the total shell egg consumption is replaced by eggs with higher *Salmonella* prevalence (0.06%, 0.5% or 1%).

We also studied the effects of the main intervention of the *Salmonella* Control Programme for laying hens (removal of the parent and production flocks tested to be *Salmonella* positive) on the consumer risk for obtaining salmonellosis via shell eggs.

Tables 9, 10 and 11 show the estimated true *Salmonella* prevalence in production flocks, the annual number of contaminated eggs, the contaminated eggs ending up in undercooked servings, the number of undercooked servings as well as annual estimates of reported and all human *Salmonella* cases caused by shell eggs in the default situation and under different scenarios and interventions. With the default situation we mean a simulation based on surveillance data from 2001. In that year, the *Salmonella* situation in shell egg production was excellent, as there were no positive *Salmonella* test results. We wanted to make sure that these excellent *Salmonella* test results had no effect on our estimation of *Salmonella* prevalence in production flocks, however, so we also simulated the effect of a “normal year” with a couple of positive test results on the estimated true *Salmonella* prevalence in production flocks. In Table 10, this simulation is called the default situation with 2 positive test results. In addition, alternative results of the default situation, based on a lower flock test sensitivity estimate, are also shown in Tables 9, 10 and 11. These results show that if the flock test sensitivity is expected to be only 50%, with large uncertainty about its true value, the predicted total amounts are correspondingly higher. Therefore, instead of using each absolute value of the predictions for comparisons, one could use the relative difference.

**Table 9.** Expected *Salmonella* prevalence (q) in production flocks with 95% credible interval (CI) in the default situation and under different interventions and scenarios.

	q <sup>a</sup>	95% point-wise summed CI <sup>b</sup> for flock prevalence	Relative change (within scenario) in expected flock prevalence
Default situation, positive flocks are removed	0.3%	0.14%-0.58%	
Default situation, no removal of positive flocks	1.0%	0.28%-3.26%	3.3
Default situation, positive flocks are removed, flock test sensitivity 0.5 ± 0.3	1.3%	0.32%-3.46%	4.3
Increased testing frequency, positive flocks are removed	0.3%	0.11%-0.47%	
Increased testing frequency, no removal of positive flocks	1.0%	0.28%-3.15%	3.3
20% of parent flocks infected, positive flocks are removed	0.6%	0.33%-1.12%	
20% of parent flocks infected, no removal of positive flocks	4.2%	0.93%-11.55%	7.0

<sup>a</sup> Note: this is the stationary probability that there exists a truly infected flock at the flock house, under the given scenario. For the probability of its being detected IF it were tested, multiply this with the test sensitivity.

<sup>b</sup> Note: pointwise summed CI is calculated by summing the point-wise CI of each infectious status prevalence over all ages.



**Table 10.** Annual number of contaminated eggs, contaminated eggs ending up in undercooked servings and number of undercooked servings with their 95% credible intervals in the default situation and under different interventions and scenarios.

	No of contaminated eggs	95%CI	No of contaminated eggs to risky servings	95%CI	No of contaminated risky servings	95%CI
Default situation, positive flocks removed	1,800	0-7,400	200	0-800	300	0-1,100
Default situation, without removal	5,700	300-22,100	600	0-2,300	800	0-3,300
Default situation, positive flocks removed, flock test sensitivity $0.5 \pm 0.3$	7,300	500-24,000	800	100-2,500	1,100	100-3,300
Increased sampling frequency, positive flocks removed	1,500	0-6,500	200	0-700	200	0-1,000
Increased sampling frequency, without removal	5,600	300-21,900	600	0-2,300	800	0-3,200
20% of parent flocks infected, positive flocks removed	3,700	400-11,900	400	0-1,200	500	100-1,800
20% of parent flocks infected, without removal	24,200	3,300-71,300	2500	300-7,400	3,600	500-10,500
Default situation with 2 positive test results, positive flocks removed	2,000	100-7,900	200	0-800	300	0-1,200
30% of eggs with 0.06% prevalence	149,000	136,900-162,000	15,400	13,100-17,700	17,600	15,200-20,200
30% of eggs with 0.5% prevalence	1,232,200	1,133,900-1,335,600	127,100	108,900-146,400	145,600	126,300-166,000
30% of eggs with 1% prevalence	2,463,100	2,266,900-2,669,700	254,100	217,600-292,700	291,000	252,400-331,800

**Table 11.** Annual estimates (with 95% credible intervals) of reported and all cases of human salmonellosis caused by shell eggs in the default situation and under different interventions and scenarios (Means & 95% CIs from predictive distributions).

	Reported cases	95%CI	All cases	95%CI	Relative change (within scenario) in expected reported cases
Default situation, positive flocks removed	10	0-50	60	0-250	4
Default situation, without removal	40	0-140	190	0-740	4
Default situation, without removal, flock test sensitivity $0.5 \pm 0.3$	50	0-170	250	10-830	5
Increased sampling frequency, positive flocks removed	10	0-40	50	0-220	4
Increased sampling frequency, without removal	40	0-140	190	0-730	4
20% of parent flocks infected, positive flocks removed	30	0-80	130	10-420	6
20% of parent flocks infected, without removal	170	10-520	850	40-2,620	6
30% of eggs with 0.06% prevalence	860	90-1,730	4,350	450-7,780	
30% of eggs with 0.5% prevalence	7,130	710-14,300	35,980	3,710-64,280	
30% of eggs with 1% prevalence	14,260	1,430-28,550	71,920	7,440-128,440	

The removal of detected positive flocks was quantified in the default situation, in the alternative testing frequency, and under the scenario of 20% infected parent flocks at the beginning of the laying period (and no infected grandparent flocks). When the parent flocks are infected, the estimate of horizontal infection naturally increases, since the vertical transmission probability was assumed to be zero. Because the horizontal infection parameter is common for all flocks, this also implies a higher infection probability for the remaining flocks whose infection status is not specified (not a fixed value) under the scenario.

If the *Salmonella* positive flocks were not removed, the estimated true *Salmonella* prevalence of production flocks and the estimated number of reported human cases would increase fourfold in the default situation and in the alternative testing frequency (Table 9 and 11). Thus the removal of detected positive flocks proved to protect public health even in the current situation, where the *Salmonella* prevalence in egg production is very low.

Under the current low prevalence, increased testing frequency does not have any special effect on the human risk of acquiring *Salmonella* from shell eggs. The expected burden of the reported and all human cases is of the same magnitude both with the current testing frequency and when testing according to the new zoonosis regulation ((EC) No 2160/2003) (Table 11). For this risk assessment we did not compare other testing frequency / *Salmonella* prevalence combinations. However, it would be interesting to determine the *Salmonella* prevalence at which increased testing frequency would have a cost-effective *Salmonella* risk-mitigating effect.

In the second scenario (a sudden increase of *Salmonella* prevalence in the production pyramid as 20% of the parent flocks infected), the effect of removing positive flocks was emphasized. If the *Salmonella* positive flocks were not removed when 20% of the parent flocks were infected, the estimated true *Salmonella* prevalence of production flocks and the estimated number of reported human cases would have been sixfold (Table 9 and 11).

The third scenario was that a proportion,  $f=30\%$ , of total consumption would be replaced by eggs with a higher *Salmonella* prevalence, 0.06%, 0.5% or 1%. The *Salmonella* prevalence in the remaining 70% of eggs was assumed to be similar to the default situation in this scenario ( $1.8 \times 10^{-6}$ ). The total number of infected eggs was calculated as  $N_{\text{inf\_eggs}} \times (1-f) + \text{prevalence} \times N_{\text{eggs}} \times f$ , where  $N_{\text{inf\_eggs}}$  and  $N_{\text{eggs}}$  denote the domestic number of infected eggs and the domestic total egg production in the default situation, respectively. The calculated value can be interpreted as a conditional expected value, given  $N_{\text{inf\_eggs}}$ ,  $N_{\text{eggs}}$ , share of a proportion  $f$ , and prevalence of 0.06%, 0.5% or 1%.

The number of contaminated eggs increases vastly in this scenario (Table 10), due to the estimated very low prevalence in domestic production. In short, the probability of a positive egg is the product of (1) the probability of an infected laying flock and (2) the probability of producing a contaminated egg among the eggs from an infected flock. Calculating with the estimated values for domestic production gives roughly  $0.3\% \times 0.06\% = 1.8$  per million eggs. However, these figures represent merely internally-contaminated eggs, excluding surface contamination, based on *S. Enteritidis* literature. The results of this scenario show that if the *Salmonella* prevalence in shell eggs consumed in Finland suddenly increased, for instance because of import from a country with different *Salmonella* status or because of a large epidemic in domestic production flocks, it would have an immediate and significant effect

on public health. According to surveys of private households and the catering sector, egg consumption patterns in Finland do not differ from those in countries where human *Salmonella* cases and outbreaks caused by eggs are more common (Lievonen et al. 2004; Lievonen & Majjala 2005). Therefore, the current low level of human *Salmonella* cases caused by eggs in Finland is not a consequence of particularly safe egg consumption but rather of the low true *Salmonella* prevalence in production flocks.

## 8. Discussion

The objectives of this risk assessment were to quantitatively estimate the true *Salmonella* prevalence in egg production in Finland and to study the effect of the Finnish *Salmonella* control programme on the prevalence of salmonellosis in Finnish consumers in the default situation and under different scenarios. According to the mathematical risk assessment model, the annual average true *Salmonella* prevalence in production flocks of laying hens in Finland was 0.3% (95% credible interval [0.1;0.6]). This result agrees with the result of the baseline study on the prevalence of *Salmonella* in laying flocks of *Gallus gallus* in the EU, according to which one holding out of 268 sampled was positive for *Salmonella* (MMM 2005). While the estimated *Salmonella* prevalences are at the same level as reported in Norway and Sweden, they are much lower than in many European countries or in the United States (European Commission 2001, 2003a, 2004, 2005; Ebel & Schlosser 2000). For instance, the USDA-FSIS *Salmonella* Enteritidis risk assessment (USDA-FSIS 1998) estimated a *Salmonella* Enteritidis prevalence of 0.5% on average in eggs annually produced in the United States. However, the average flock prevalence was 35% in their model, while the estimated true flock prevalence is 0.3% in Finland. According to WHO/FAO (2002), the risk of illness from *Salmonella* Enteritidis in eggs is proportional to flock prevalence. Therefore it seems reasonable to conclude even based on the estimates of true flock prevalence that consumer risk in Finland is much lower than it was in the United States in 1998.

According to this risk assessment, the annual average *Salmonella* prevalence in Finnish shell eggs was  $1.8 \times 10^{-6}$  (1,800 contaminated eggs / year, 95% credible interval [0;7,400]). This study aims to assess the risk caused by *Salmonella* spp. on consumers. Estimates for *Salmonella* prevalence in production flocks were based on surveillance data covering all *Salmonella* serovars. However, because of the lack of original experimental data, the submodel for estimating the proportion of contaminated eggs was based on literature. The applicable quantitative data available was unfortunately on *Salmonella* Enteritidis and internally-contaminated eggs only. Due to the data available, by a 'contaminated egg' we only meant eggs with *Salmonella* inside the egg, excluding contamination on the egg shell. Therefore, this value may underestimate the true number of eggs annually contaminated by any *Salmonella* serovars. On the other hand, the given value may also overemphasize the severity of *Salmonella* contamination of a single egg by presupposing that all contaminated eggs have *Salmonella* in the contents. In practice, the prevalence of shell contamination usually exceeds the contamination of egg contents (Humphrey 1994). While *Salmonella* outbreaks caused by eggs have been connected to eggs internally-contaminated by *S. Enteritidis* (Advisory Committee on the Microbiological Safety of

Food 2001), *Salmonella* on egg shells are likely to die rapidly in a dry environment (Humphrey 1994), although they may also be a source of cross-contamination during food preparation. By comparison, the recently published Belgian risk assessment on *Salmonella* Enteritidis in shell eggs used 25% prevalence as an input for infected laying flocks, and their estimate for the annual number of positive eggs varied from 29 up to 12.48 million with a mean of 70,990 contaminated eggs per year (prevalence from  $9.9 \times 10^{-9}$  to  $4.2 \times 10^{-3}$ ) (Grijnspeerdt et al. 2005). The large output range included in that study reflects the wide uncertainty associated with the model inputs, a common situation in many quantitative microbiological risk assessments.

According to this risk assessment, in 2001 the annual true number of human cases caused by eggs was 60 (95% credible interval [0;250] and the corresponding incidence 1.2 cases / 100,000 inhabitants) in Finland. In Denmark, in 1999 the annual number of sporadic human *Salmonella* cases caused by eggs was estimated to be 1,156 (95% credible interval [1,062;1,246] and the corresponding incidence 21.6 cases / 100,000 inhabitants), making up 47% of all human *Salmonella* cases (Hald et al. 2004). In that year the apparent *Salmonella* prevalence in Danish egg production flocks was 5.1% (The Danish Veterinary and Food Administration 2004); i.e. 17 times higher than the estimated true *Salmonella* prevalence in production flocks in Finland in 2001 (0.3%).

Since 1998, several quantitative microbiological risk assessments (QMRA) on *Salmonella* and in particular on *S. Enteritidis* in eggs have been published (USDA-FSIS 1998, 2004; Advisory Committee on the Microbiological Safety of Food 2001; WHO/FAO 2002; Grijnspeerdt et al. 2005). A common feature of these risk assessments is that they have been done as a response to an increasing number of human *Salmonella* cases associated with the consumption of shell eggs in different countries. This risk assessment differs from these assessments in two ways: it is being conducted in a country with an excellent *Salmonella* situation, and it has concentrated on mitigations in primary production instead of focusing on mitigation strategies in processing and consumption steps. That is, the main intervention studied is the removal of detected positive parent and production flocks, with a second focus on the effects of increased frequency of *Salmonella* sampling. By contrast, in this risk assessment we ignored the interventions usually studied in other QMRAs with high *Salmonella* prevalence in primary production, such as changing storage times and temperature during the distribution chain or pasteurization of shell eggs, since there was very little data to model these parts of the production chain in detail and since the authorities were mainly interested in the effect of the FSCP on human risk in Finland.

Based on this QMRA, the removal of positive flocks proved to be an effective intervention, with a clear effect both on *Salmonella* prevalence in the egg production chain and in humans. While the depopulation of an infected flock is admittedly a powerful risk management option (WHO/FAO 2002), its implementation may be impossible in practice if flock prevalence is high. For instance, the National *Salmonella* Control Programme of shell egg flocks established in Denmark in late 1996 was based on the elimination of all shell egg and pullet rearing flocks if *S. Enteritidis* or *S. Typhimurium* were detected. The extent of *Salmonella* infection, however, was greater than was anticipated at the outset. The programme turned out to be financially unsound and was suspended in 1997 (The Danish Veterinary and Food Administration 2004).

Another intervention, the frequency of *Salmonella* sampling of production flocks, was also modelled in this QMRA. Our results showed that increasing the current

sampling frequency in production flocks from three to four times did not have any significant effect on the true *Salmonella* prevalence in egg production or on the number of human cases in Finland. While in principle increasing testing frequency has a beneficial effect on the probability of detecting an infected flock, the current results suggest that the effect is unnoticeable if the prevalence is low and several tests during the production period are already being taken. This result agrees with the results of the WHO/FAO (2002) risk assessment in which the effect of sampling frequency was evaluated. Assuming a starting prevalence of 25%, they estimated the effect of either one or three tests during a laying phase over a four year period on consumer *Salmonella* risk from shell eggs. According to their calculation, the one-test protocol reduced the risk of human illness from shell eggs by 70%, while testing three times a year reduced risk by 90%. Thus the cost-benefit ratio was better with the one-test protocol. The starting prevalence of the calculation was relatively high (25%) compared to the Finnish situation, and it is likely that a lower starting prevalence would have reduced the difference between the results of the two testing protocols even further.

We also used our model to assess the effects of higher *Salmonella* prevalence in laying flocks and in shell eggs on consumer health in two scenarios. The first corresponds to the hypothetical situation of a *Salmonella* epidemic in parent flocks, for instance because of contaminated feed (20% of parent flocks infected). Another scenario was a situation where 30% of shell eggs consumed in Finland would have a *Salmonella* prevalence of 0.06%, 0.5% or 1%. This could happen if Finland started to import shell eggs from countries with higher *Salmonella* prevalence or if a large domestic epidemic took place. The percentage (30%) of shell eggs with higher *Salmonella* prevalence was chosen to be the same percentage as Danish shell egg import was in 2001 because we wanted to simulate a realistic scenario of import. The lowest prevalence of contaminated eggs, 0.06%, was chosen to be at the same level as the estimated average prevalence of contaminated eggs in an infected flock based on a re-analysis of literature data (ECFIM-submodel). Hence, if all eggs were from such infected flocks, the prevalence of eggs would be 0.06%. On the other hand, much higher *Salmonella* prevalences in shell eggs have been reported in some European countries (European Commission 2001, 2003a), but it is not very clear what kind of statistical sampling was used or what recognizable subpopulation the resulting sample represents. It is therefore difficult to assess in what sense they represent overall egg production. Considering the results obtained by re-analysing the data in Henzler et al. (1998), a prevalence of *Salmonella* contamination of 1% may seem unrealistically high, but such values and even higher have been continuously reported in European countries. Fortunately, the latest report shows a declining trend (European Commission 2004).

The number of contaminated eggs and also the number of human *Salmonella* cases increased in both scenarios, but the increase was extremely high in the scenario with 30% of production replaced by eggs with higher contamination prevalence. This result suggests that the special guarantees for imported eggs have a consumer protective effect in the current situation, where Finland has much lower *Salmonella* prevalence in flocks of laying hens and in shell eggs than in many other European countries. The result highlights the fundamental importance of a good *Salmonella* situation in primary production.

The number of reported outbreaks caused by shell eggs can also be considered an indication of the *Salmonella* status of egg production in a country. In recent years, Finland has reported very few *Salmonella* outbreaks caused by shell eggs, which

is in agreement with the low apparent *Salmonella* prevalence of laying flocks in the country. However, if the consumption pattern (i.e. frequency of consuming risky egg dishes) would be significantly different in Finland compared to other countries, the rarity of detection of eggborne outbreaks could be partly explained. The surveys conducted during this study on egg consumption patterns in private households and catering establishments showed that even though the majority of consumers only ate safe well-cooked egg dishes, the Finnish population as a whole did not have any particularly safe egg consumption patterns but in fact consumed risky egg dishes as much as reported in other countries (Lievonon et al. 2004; Lievonon & Maijala 2005). These surveys did reveal, however, one particularly interesting detail in egg consumption patterns: the consumption of raw egg dishes decreased with increasing age. Even though the elderly are often mentioned as one of the vulnerable population segments to which special attention should be paid, the results of our survey suggest that, at least in the special case of shell egg consumption, the increasing susceptibility of the elderly might be balanced by their changing food consumption patterns.

During this risk assessment process, we identified many gaps in data. In particular, data on the sensitivity of the testing method, on within-flock prevalence, and the possibility to connect test results with a particular flock would have been beneficial. Although there are data sources available, many gaps still needed to be filled in using other sources of information, e.g. from foreign literature. The validity of such information is always questionable since it does not concern the same recognizable population under assessment. In terms of the model, the exchangeability assumption may not be valid. On the other hand, the situation can only be improved by collecting adequate domestic data, which may be expensive or even impossible to organize. For example, estimating the prevalence of positive eggs produced by an infected flock would require an experiment in which the infected flock is kept only for the purpose of surveillance. Also, we completely lack information about the eventual level of contamination at the time of consumption. One approach to this would be to use predictive microbiological modelling, but the problem is that there are no detailed data about storage, cooking and consumption applicable from the entire retail level to the table, either for private homes or the catering industry. An alternative approach is to assess directly the known records of human cases (as an uncertain censored observation) and the estimated contamination prevalence resulting from primary production, as was done with the CIM. This approach was successfully utilized, for instance, in the previous risk assessment on *Salmonella* in broiler production in Finland (Maijala et al. 2005). Finally, comparison of estimated prevalences from any model with other register data and reports may be problematic if the statistical properties of the sampling are not explicitly known.

This risk assessment model contains uncertainties and hypotheses which are discussed in this report. This quantitative model, however, can be utilized, for instance, when costs of the National *Salmonella* Control Programme are compared with costs of the measures required in the regulations of the European Union or when sampling of the control programme is planned.



## Computational aspects of predictions:

### About the method

In the analysis of surveillance data from production chains, information about prevalence in one part of the chain has effects on other estimates of prevalence along the causal pathway of production. Therefore, Bayesian methods were used to account for different sources of information instead of considering each estimation task separately in an unrelated manner. The observed low apparent prevalence in the breeder flock population is also indirect information about the expected prevalence in production flocks, and vice versa. While the few breeder flocks may be modelled in a fairly detailed fashion, the same cannot be expected for the large number of production flocks. Hence, production flocks were modelled by stationary probabilities of a stochastic process describing the general pattern of production dynamics. Such a model can be further used as a tool for exploring how changes in key parameters alter the stationary distribution. Computationally, this is achieved simply by solving the distribution from the transition probability matrix, with given parameters, instead of heavy simulations of the detailed process. Although a well known concept in stochastic calculus, stationary distributions of Markov chains have not been applied much, or at all, in the probabilistic models of QMRAs. If the main dynamics of the production chain can be captured as a transition probability matrix, this provides a compact model that is readily explored and which can be used both in statistical inference and in summarizing the expected outcome as a stationary distribution, given the estimated (or assigned) parameters.

### Stationarity of the production process

The stationary distribution of the production process is well defined when the sensitivity parameter is greater than zero. If a zero value is assigned, the Markov chain becomes periodic and the stationary distribution cannot be computed. Therefore, computations involving zero sensitivity were performed assuming a value of 0.01. Also, when testing occurs at every second time step, the process becomes periodic regardless of the value of the sensitivity parameter. In this situation, a value of 0.01 was inserted as a probability of detection at an arbitrary time step, given infection.

### Removal of detected positive flocks

The effect was modelled by creating a random process of the production chain which is a replicate of the observed process with data from 2001. If nothing is fixed for the replicate process the distribution of the replicate will be a so-called posterior predictive distribution. This is a conditional distribution based on the observed data of 2001. The replicate process can thus be simulated using the posterior density of the model parameters, i.e. simulating the chain “again” with the estimated parameter distributions. The effect of removing detected positive flocks can be quantified by comparing the predictive distributions (1) under the assumption that the test sensitivity is zero (i.e. fixing this value) and (2) under the assumption that it is the same parameter as for the observed process. Otherwise the joint distribution of the parameters is common for both predictions. For the scenarios, some quantities of the replicate process are given as fixed values. This is explained further below under the section “Scenarios”.

### Alternative testing

The alternative testing strategy concerns production flocks only. Therefore, in the default situation, the predictive distribution is obtained by simulations of the production chain under a stationary distribution defined by a new transition probability matrix concerning the production flocks. The joint distribution of the model parameters

is taken from analysis of the observed year, 2001. In the scenarios, some quantities of the replicate process are given as fixed values. This is explained further below under the section “Scenarios”.

### Scenarios

Under the scenario of approximately 20% infected parent flocks at the beginning of the laying period, 3 out of 13 parent flocks were assigned as “infected” at the 4<sup>th</sup> time step in both production pyramids. Furthermore, they were assigned to be “not removed already” which means that the earliest they would be removed is just before the 5<sup>th</sup> time step. Removal is only possible if such an intervention is simulated. The remaining 10 parent flocks may or may not be infected according to the probability model. The grandparent flocks were assigned to be “not infected” in this scenario. If their infection status were left as “unknown” in this scenario, the model would say they had a very high probability of being infected in such a replicate process because under a low horizontal infection probability, the only possible explanation that fits with the high 20% parent flock infection is that the grandparents must indeed have been infected. In turn, this would amount to a fair number of infections in the remaining 10 parent flocks since their infection status also depends on the same grandparents in the model. The horizontal infection probability is a common parameter for both the scenario replicate and the actual observed process of 2001. The observed data contain no detected infections which forces the estimate of horizontal infection to have a low value. By contrast, when the grandparent flocks are assigned to be “not infected” in the scenario, the only possible explanation of parent flock infection in such replicate process is then horizontal. This causes a higher estimate of the horizontal infection parameter regardless of the observed data in 2001. Hence, the probability that the remaining 10 parent flocks in the pyramid are infected depends on both the vertical and the horizontal infection probability which itself depends on what is given as “fixed values” in the replicate process and the actual observed process. It should be noted that the Bayesian estimates of common parameters are always a compromise between the prior distributions and all assigned data. In these scenarios, the complete data set is the combination of the actual data in 2001 and the “data” of the artificially-created scenario. Concerning a possible joint analysis of several years, it might be reasonable to define year-specific parameters and some dependency structure for them to allow the most recent observations to be the most influential on the prediction, or to capture assumptions of temporal trends, etc. When only one year is taken as observed data, and only one scenario prediction is computed, it is reasonable simply to assume common parameters which cause the predicted parameter values to depend similarly on the actual data and the scenario “data”.

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## **10. Appendix A: Mathematics of the QRA on *Salmonella* in Finnish Egg Production**

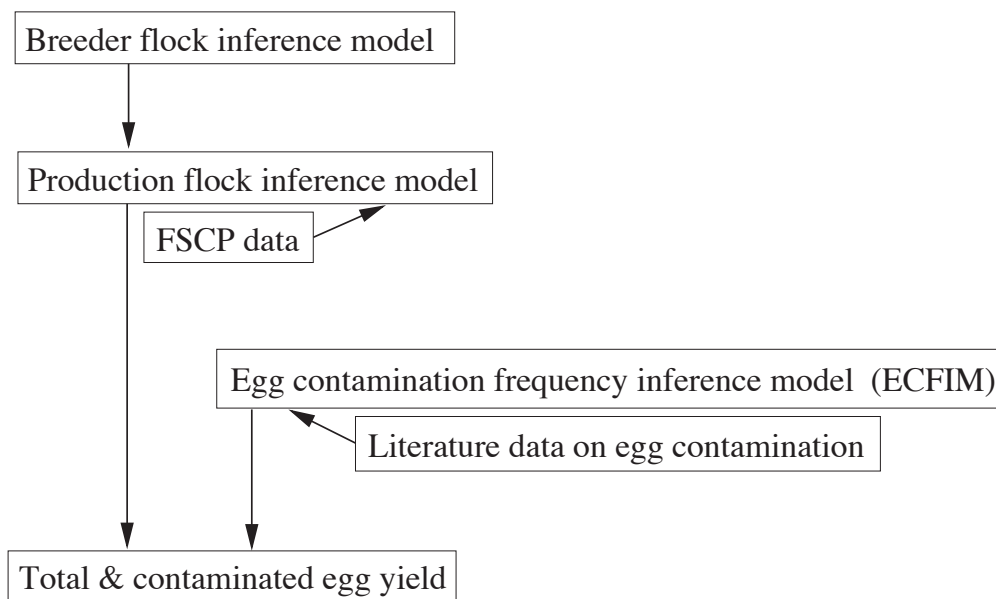
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## Appendix A

# Mathematics of the QRA on Salmonella in Finnish egg production

### A.1 Primary production inference model (PPIM)



For a quantitative risk assessment on salmonella in the production chain, a mathematical model was developed. Primary production can be divided into three levels: grandparent flocks, parent flocks, and production flocks. All production flocks (as well as breeder flocks) are tested regularly for salmonella. According to the FSCP, if a positive test is obtained, the flock is removed from production. Therefore, testing works as a surveillance tool but also as a prerequisite for intervention. Commercial production in Finland can be described by two distinct production pyramids consisting of three flock generations. There are only a few breeder flocks but hundreds of egg laying production flocks. The production flock process was described in terms of stationary distribution [1] of the corresponding Markov chain model.

### A.2 Stationarity in a production process

We assumed regular time steps (8 weeks) to represent possible sampling times of a production flock in a discrete time model. Testing may be done at only some, none, or all of these time steps.

In order to construct a transition probability matrix for a production system, we first need to define the basic elements, or states, of this system and the events that may occur at each given state over a time step. The

model then describes a generic "flock house" which is assumed to hold one flock at a time. The parameters describing the conditional probabilities for each event, given the previous state of the system, jointly define a transition probability matrix which can be used to calculate the stationary, i.e. long run, distribution of the production process.

### A.2.1 Transition probability matrix for flock life history

#### States of the process

A stochastic process was constructed to mimic the egg production process and the occurrence of Salmonella infection together with the testing scheme with intervention. Since each time step represents a period of 8 weeks, a year can be divided into 6 time steps and the entire flock lifetime consists of 9 age steps. In this manner, there are 19 possible states for a generic flock at a generic farm at any randomly chosen testing time, including the empty state during which there is no flock. The flock can be either infected or uninfected, and it can be of a certain age. The ages were numbered according to the 9 steps. Hence, the  $2 \times 9 + 1 = 19$  possible events. The 19 events can be coded as "Break", "0<sub>1</sub>", "0<sub>2</sub>", ..., "0<sub>9</sub>", "1<sub>1</sub>", "1<sub>2</sub>", ..., "1<sub>9</sub>", where each number represents the infectious status ("0"=not infected, "1"=infected) and the subscript number represents the age ("1", ..., "9") for some flock. The empty state is coded "Break" and it is assumed to take one time step.

#### Parameters of the process

In Finland there are currently 2-3 testing visits per egg production flock. According to the FSCP, if a flock is tested and detected to be positive it is removed from the production chain and replaced by a new flock after a short empty period. In the current default situation, the actual testing times are scheduled so that every flock is tested at age step 3 (before the laying period), at age 4 (beginning of the laying period), at age 8, and possibly at the last visit after which the flock is removed anyway. To parameterize the model, we assume that a flock can be infected by horizontal transmission with probability  $h_3$  between any two testing times. Subindex refers to the flock generation, thus  $h_3$  for the 3rd generation, production flocks, see reference [2]. Once the flock is infected, this infection can persist over two testing times with probability  $\eta$ , which was assumed to be the same for all flock generations. If a production flock is infected at some visit, it can be uninfected at the following visit with probability  $s = (1 - \eta)(1 - h_3)$ . When a new production flock is introduced, we assume it to be infected at the first age step with probability  $v_3$  denoting the chance of vertical transmission. If the flock is infected and tested, it can be detected positive with probability  $p$ , i.e. the flock level test sensitivity which is assumed to be the same for all flocks. Specificity of the testing is assumed to be virtually 100%. For short notations we write  $h'_3 = 1 - h_3$ ,  $v'_3 = 1 - v_3$ ,  $p' = 1 - p$  and  $s' = 1 - s$ . These parameters define the following transition probability matrix,  $P$ , of size  $19 \times 19$ :

	Break	0 <sub>1</sub>	0 <sub>2</sub>	0 <sub>3</sub>	0 <sub>4</sub>	0 <sub>5</sub>	0 <sub>6</sub>	0 <sub>7</sub>	0 <sub>8</sub>	0 <sub>9</sub>	1 <sub>1</sub>	1 <sub>2</sub>	1 <sub>3</sub>	1 <sub>4</sub>	1 <sub>5</sub>	1 <sub>6</sub>	1 <sub>7</sub>	1 <sub>8</sub>	1 <sub>9</sub>	
Break	0	$v'_3$	0	0	0	0	0	0	0	0	$v_3$	0	0	0	0	0	0	0	0	
0 <sub>1</sub>	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	0	0	0	0	0	
0 <sub>2</sub>	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	0	0	0	0	
0 <sub>3</sub>	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	0	0	0	
0 <sub>4</sub>	0	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	0	0	
0 <sub>5</sub>	0	0	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	0	
0 <sub>6</sub>	0	0	0	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	0	0	
0 <sub>7</sub>	0	0	0	0	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	0	$h_3$	
0 <sub>8</sub>	0	0	0	0	0	0	0	0	0	$h'_3$	0	0	0	0	0	0	0	0	$h_3$	
0 <sub>9</sub>	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1 <sub>1</sub>	0	0	$s$	0	0	0	0	0	0	0	0	$s'$	0	0	0	0	0	0	0	
1 <sub>2</sub>	0	0	0	$s$	0	0	0	0	0	0	0	0	$s'$	0	0	0	0	0	0	
1 <sub>3</sub>	$p$	0	0	0	$sp'$	0	0	0	0	0	0	0	0	$s'p'$	0	0	0	0	0	
1 <sub>4</sub>	$p$	0	0	0	0	$sp'$	0	0	0	0	0	0	0	0	$s'p'$	0	0	0	0	
1 <sub>5</sub>	0	0	0	0	0	0	$s$	0	0	0	0	0	0	0	0	$s'$	0	0	0	
1 <sub>6</sub>	0	0	0	0	0	0	0	$s$	0	0	0	0	0	0	0	0	$s'$	0	0	
1 <sub>7</sub>	0	0	0	0	0	0	0	0	$s$	0	0	0	0	0	0	0	0	0	$s'$	
1 <sub>8</sub>	$p$	0	0	0	0	0	0	0	0	$sp'$	0	0	0	0	0	0	0	0	0	$s'p'$
1 <sub>9</sub>	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

(A.1)

For example, the 13th row of the matrix describes the probabilities of each of the 19 states at a farm, given that at the previous visit there was some flock at its first testing time (age = 3) and it was truly infected (i.e. code "1<sub>3</sub>"). Only 3 of the 19 events are then possible:

probability, given current state is 1 <sub>3</sub>	next state	
$P(\text{detected and removed} \mid 1_3) = p$	Break	(A.2)
$P(\text{not detected, infection ends} \mid 1_3) = s(1 - p)$	0 <sub>4</sub>	
$P(\text{not detected, stays infected} \mid 1_3) = (1 - s)(1 - p)$	1 <sub>4</sub>	

Hence we get the 13th row of the transition probability matrix. The sum of each row must be one.

### Stationary distribution

If the production system is run for a long time, the stochastic process will eventually lead to a so-called stationary distribution (long run distribution) in which the probabilities of the 19 possible states are determined. The stationary distribution does not depend on the position from which the process was started. The stationary probabilities of the 19 possible situations at the farm,  $q^* = (q_1^*, \dots, q_{19}^*)$ , are the solution of the following matrix equation:

$$q^* P = q^*. \quad (\text{A.3})$$

The analytical solution is cumbersome and therefore a numerical computation was used. This was accomplished in Matlab by computing powers of matrix P until stationary probabilities were found. As a result, we obtained stationary probabilities  $q^*$  as a function of parameters  $h_3, v_3, \eta, p$ . The obtained testing results from production flocks can be interpreted as samples from a stationary production process. Hence, the sampling distribution is binomial with probabilities determined by  $q^*$  and  $p$ . The conditional probability of observing  $x_t$  positive and  $n_t - x_t$  negative flocks at the  $t^{\text{th}}$  testing time (age) among  $n_t$  such tests is

$$\begin{aligned} P(x_t \mid n_t, q^*, p) &= \binom{n_t}{x_t} \left( \frac{q_{t+9}^*}{q_t^* + q_{t+9}^*} p \right)^{x_t} \left( \frac{q_t^*}{q_t^* + q_{t+9}^*} + \frac{q_{t+9}^*}{q_t^* + q_{t+9}^*} (1 - p) \right)^{n_t - x_t} \\ &= \text{Binomial} \left( n_t, \frac{q_{t+9}^*}{q_t^* + q_{t+9}^*} p \right). \end{aligned} \quad (\text{A.4})$$

Given the full likelihood with observations  $(x_t, n_t)$  for all recorded testing times  $t \in \{1, \dots, 9\}$  it is possible to compute the posterior density of the parameters, given these data. The posterior density was computed using MCMC sampling with Metropolis-Hastings algorithm in Matlab (200 000 iterations). For the prior distribution we used information from the breeder flock population.

### Prior distribution

The prevalence of infected flocks among production flocks depends not only on the horizontal chance of infection but also on the vertical chance of infection due to possible infections in breeder flocks. Due to the pyramid structure of production, information about breeder flocks (parent and grandparent generation) can be used to derive a prior density of the vertical chance of infections in production flocks,  $v_3$ . With parametric constraint assumptions on all three flock generations some information can also be drawn about the horizontal chance of infection,  $h_3$ , in production flocks.

Concerning the structure of the primary production of eggs and the sampling practice, the situation is closely comparable to the primary production of broilers. Hence, an earlier QRA model of salmonella in Finnish broiler production could be re-used. For details, we refer to [2]. The breeder flock model describes the latent infection status of each flock as a discrete time Markov chain where the time points represent the nine possible testing times of a flock during its lifetime. The infection probabilities are parameterized by vertical and horizontal chances of infection, as well as the probability of sustaining infection over a time step. These parameters are common, or related to the parameters describing similar events for all three generations of

flocks.

To set up the formulation, let us denote the breeder flock data as  $D_{bf}$  and the production flock data as  $D_{pf}$ . Then, the breeder flock model gives the joint posterior distribution as an output, computed with WinBUGS [3]:

$$\pi(h, h_3, \eta, p, v_2, v_3 | D_{bf}). \quad (\text{A.5})$$

This is then taken as a prior distribution in the production flock model leading to an updated distribution, computed with Matlab:

$$\pi(h, h_3, \eta, p, v_3 | D_{pf}, D_{bf}) \propto \pi^*(D_{pf} | h_3, \eta, p, v_3) \pi(h, h_3, \eta, p, v_2, v_3 | D_{bf}), \quad (\text{A.6})$$

where  $\pi^*$  is according to the stationary distribution for the production flock data, as indicated by the equation (A.4). Once the posterior distribution of model parameters is obtained from Matlab, it can be used for calculating predicted stationary probability of infection prevalence in the production flock population, accounting for the parametric uncertainty. The computation was done separately for two different data sets from the two independent production pyramids ISA & SH and LB & LSL.

However, the breeder flock model was computed in WinBUGS whereas the computation with the stationary probabilities could not be done in WinBUGS but in Matlab. Therefore, the resulting distribution taken from the WinBUGS model, as an MCMC sample, was approximated in Matlab by fitted parameter distributions.

### A.3 Total annual production

The total annual egg production is a combination resulting from the two distinct production pyramids ISA & SH and LB & LSL. Since the posterior density of model parameters was derived as an MCMC sample separately for both pyramids, the combined total egg production (and total amount of contaminated eggs) was obtained by summing the two separate and independent predictions. Below, we only describe how to generate such prediction for one production pyramid.

The transition probability model describes the stochastic process of an entire flock life history. However, in the egg production phase, only laying flocks are kept and thus we must conditionalize the stationary distribution to laying states. Whenever a laying flock is removed, it is replaced by a new laying flock after a short empty period. Hence, a new transition probability matrix was defined with only 13 possible states Break, 0<sub>4</sub>, 0<sub>5</sub>, 0<sub>6</sub>, 0<sub>7</sub>, 0<sub>8</sub>, 0<sub>9</sub>, 1<sub>4</sub>, 1<sub>5</sub>, 1<sub>6</sub>, 1<sub>7</sub>, 1<sub>8</sub>, 1<sub>9</sub>, where Break denotes the empty period with no production. In the current default situation, the transition matrix is:

$$P | \text{laying} = \begin{bmatrix} & \text{Break} & 0_4 & 0_5 & 0_6 & 0_7 & 0_8 & 0_9 & 1_4 & 1_5 & 1_6 & 1_7 & 1_8 & 1_9 \\ \text{Break} & 0 & \lambda & 0 & 0 & 0 & 0 & 0 & \lambda' & 0 & 0 & 0 & 0 & 0 \\ 0_4 & 0 & 0 & h'_3 & 0 & 0 & 0 & 0 & 0 & h_3 & 0 & 0 & 0 & 0 \\ 0_5 & 0 & 0 & 0 & h'_3 & 0 & 0 & 0 & 0 & 0 & h_3 & 0 & 0 & 0 \\ 0_6 & 0 & 0 & 0 & 0 & h'_3 & 0 & 0 & 0 & 0 & 0 & h_3 & 0 & 0 \\ 0_7 & 0 & 0 & 0 & 0 & 0 & h'_3 & 0 & 0 & 0 & 0 & 0 & h_3 & 0 \\ 0_8 & 0 & 0 & 0 & 0 & 0 & 0 & h'_3 & 0 & 0 & 0 & 0 & 0 & h_3 \\ 0_9 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1_4 & p & 0 & sp' & 0 & 0 & 0 & 0 & 0 & s'p' & 0 & 0 & 0 & 0 \\ 1_5 & 0 & 0 & 0 & s & 0 & 0 & 0 & 0 & 0 & s' & 0 & 0 & 0 \\ 1_6 & 0 & 0 & 0 & 0 & s & 0 & 0 & 0 & 0 & 0 & s' & 0 & 0 \\ 1_7 & 0 & 0 & 0 & 0 & 0 & s & 0 & 0 & 0 & 0 & 0 & s' & 0 \\ 1_8 & p & 0 & 0 & 0 & 0 & 0 & sp' & 0 & 0 & 0 & 0 & 0 & s'p' \\ 1_9 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}. \quad (\text{A.7})$$

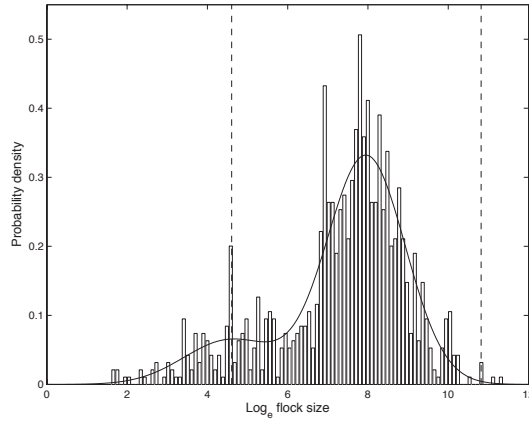
In this matrix,  $\lambda = P(0_4 | q^*, \text{laying, age 4}) = \frac{P^*(0_4 | \text{laying, age 4})}{P^*(0_4 | \text{laying, age 4}) + P^*(1_4 | \text{laying, age 4})}$ , i.e. the probability of no infection at the 4th time step according to the original stationary distribution,  $q^*$ , conditional to laying states. Since a year covers approximately 6 time steps, we need to generate equally many states from the transition matrix

$P$  | laying. The first state is generated from the original stationary distribution after conditioning to laying states. For each production flock house, a series of 6 events is thus generated at each iteration step.

### A.3.1 From flock size to egg yield

For each of the flock houses, i.e. 300 and 700 in the two pyramids, the accommodated flock size  $u_i$  ( $i = 1, \dots, 300$  or  $700$ ) is generated from a fitted distribution representing sizes of all Finnish flock houses, truncated to larger than 100 but smaller than 50000, which then envelops all commercial flock houses:

$$f(\log(u_i)) \sim 0.1898\mathcal{N}(4.5866, 1.1659^2) + 0.8102\mathcal{N}(7.9532, 0.9759^2) \quad , \quad \log(100) < \log(u_i) < \log(50000). \quad (\text{A.8})$$



For each commercial flock house, egg production is then calculated according to the following formula:

$$N_{\text{tot}}(i) = u_i \sum_{\tau=1}^6 \sum_{t=4}^9 56 \times 0.99^{t-3} \alpha_t 1_{\{\text{age } t, \text{ not empty}\}} (\tau \text{th state}), \quad (\text{A.9})$$

which effectively counts only laying states. A factor of 56 describes the number of days within a discrete time step. A factor of 0.99 is the death rate per each age step during laying period, hence the term  $w_t = 0.99^{t-3}$ . Parameter  $\alpha_t$  describes the number of produced eggs per day per chicken. This parameter can be estimated from the known production curves and known annual production data. The estimate used was:

$$\alpha = [0.6839, 0.8934, 0.8705, 0.8332, 0.7873, 0.7308]. \quad (\text{A.10})$$

The number of infected eggs is computed from a similar formula:

$$N(i) = u_i \sum_{\tau=1}^6 \sum_{t=4}^9 56 \times 0.99^{t-3} \alpha_t \beta_{i,t} 1_{\{\text{age } t, \text{ infected, not empty}\}} (\tau \text{th state}), \quad (\text{A.11})$$

where  $\beta_{i,t}$  is a random fraction of internally contaminated eggs from flock  $i$  at age  $t$ . The total egg yield is then the sum of the egg production from all flock houses and 6 time steps covering a year. Likewise, the number of contaminated eggs is summed up. The distribution of the total yield thus results from the parametric uncertainties of the predicted stationary probabilities, and the uncertain state variables of the process, as well as the uncertain egg yield and egg contamination per flock. The total internally-contaminated egg yield ( $N = \sum N(i)$ ) is accommodated as an input in the Egg Distribution Simulation Model (EDSM) describing the number of contaminated servings per year.

The fraction of internally-contaminated eggs produced by an infected flock ( $\beta$ ) was estimated from literature data on observed proportions of *Salmonella* Enteritidis in eggs from infected flocks. For this estimation a separate hierarchical model (egg contamination frequency inference model, ECFIM) was developed.

Total egg yield can be transformed into the weight of total production by using the weight distribution of a single egg. This was estimated by minimizing the following sum of squared errors:

$$\begin{aligned}
& \Phi(0.053, \mu, \sigma^2) - 4.97\%)^2 + \\
& \Phi(0.063, \mu, \sigma^2) - \Phi(0.053, \mu, \sigma^2) - 39.11\%)^2 + \\
& \Phi(0.073, \mu, \sigma^2) - \Phi(0.063, \mu, \sigma^2) - 50.23\%)^2 + \\
& \Phi(1 - (0.073, \mu, \sigma^2) - 5.69\%)^2,
\end{aligned}
\tag{A.12}$$

based on data on shell egg weights received from the National Food Agency Finland. Hence, the estimated distribution was  $N(0.064(kg), 0.006^2)$ . The total weight of e.g.  $N$  eggs is then distributed as  $N(0.064N, 0.006^2 N)$ .

### A.3.2 Egg contamination frequency inference model (ECFIM)

The true fraction of internally-contaminated eggs produced by an infected flock was elicited from literature [4] showing apparent (*Salmonella* Enteritidis) results from  $i = 1, \dots, 60$  infected flocks. The positive counts per flock were  $D = \{ 42 \text{ zeros, } 8 \text{ ones and } 2,2,3,3,4,4,4,6,8,25 \}$ . On average, these resulted from 400 pooled tests per flock, with approximately 10 eggs per pool. The test sensitivity was assumed to be unaffected by pooling. Hence, the model:

$$\begin{aligned}
P(D_i | 10, p_{\text{sen}}, \beta_i) &= \text{Bin}(10, p_{\text{sen}}(1 - (1 - \beta_i)^{10})) \\
P(\beta_i | a, b) &= \text{Beta}(a, b) \\
P(\beta | a, b) &= \text{Beta}(a, b) \quad (\text{predictive}) \\
P(a) &= \text{Exp}(0.001), \quad P(b) = \text{Exp}(0.001) \\
P(p_{\text{sen}}) &= \text{Beta}(12, 12) \quad (\text{expert opinion: } 0.3\text{-}0.7)
\end{aligned}
\tag{A.13}$$

which results in a predictive mean  $E(\beta | D_1, \dots, D_{60}) = 0.06\%$ , and predictive variance  $\text{Var}(\beta | D_1, \dots, D_{60}) = 0.0015^2$ . Based on this, a fitted density of  $\beta \sim \text{Beta}(0.157, 257.8)$  was used in the PPIM.

#### ECFIM WinBUGS model code

The model was computed using WinBUGS version 1.4. After a burn-in period of 1000, a further 100,000 MCMC iterations were computed.

```

model{
for (i in 1:60){
pt[i] ~ dbeta(alpha,beta)      #trueprevalence in flock i
true[i] ~ dbin(pt[i],4000)    #true positives in a sample of eggs, flock i
apparent[i] ~ dbin(ps,true[i]) #detected positives in a sample of eggs, flock i
# replace above 2 lines as follows, if assume any number of positive eggs in a pos pool:
# pt10[i] <- 1-pow(1-pt[i],10) #probability that there is at least one infected egg among 10
# psen10[i] <- pt10[i]*ps #probability of detecting and that there is at least one among 10
# apparent[i] ~ dbin(psen10[i],400) }
alpha ~ dexp(0.001)
beta ~ dexp(0.001)
prep ~ dbeta(a,b)      #posterior predictive distribution for the forthcoming flock
  lo <- 0.3 #eggtest sensitivity lower bound (~95%)
  up <- 0.7 #eggtest sensitivity upper bound (~95%)
  ms <- (lo+up)/2
  vars <- ((up-lo)/4)*((up-lo)/4)
  alpha_s <- -ms*(ms*ms-ms+vars)/vars #parameters for beta-prior density
  beta_s <- (ms*ms-ms+vars)*(ms-1)/vars
  ps ~ dbeta(alpha_s,beta_s)
}

```

## A.4 Egg distribution simulation model (EDSM)

### A.4.1 From total eggs to eggs used for undercooked servings

Given the total number of contaminated eggs,  $N$ , and the known percentages of different consumption categories  $\rho_1, \dots, \rho_n$ , the number of contaminated eggs falling into each category is Multinomial:

$$x \sim \mathbf{M}(N, \rho) \quad (\text{A.14})$$

The relevant categories were (1) private households, (2) catering industry, (3) food industry and (4) other. The probabilities (relative proportions) of these categories were  $\rho = (0.6239, 0.1028, 0.0257, 0.2476)$ . It was assumed that only the first two categories can produce servings which may be contaminated. Hence, the further computations depend only on  $x_1$  and  $x_2$ . The proportion of undercooked servings in private households was estimated from a survey study [5]. As a result, the proportion  $r_1$  was modeled as  $r_1 = r_{11} + r_{12}$  where  $r_{11} \sim \mathbf{N}(\mu_{h,1} = 0.117, \sigma_{h,1}^2 = 0.009^2)$  and  $r_{12} \sim \mathbf{N}(\mu_{h,2} = 0.0387, \sigma_{h,2}^2 = 0.0052^2)$ . The number of eggs used in undercooked servings in private households is then binomially distributed  $\text{Bin}(x_1, r_1)$ . The catering industry was further divided into 3 groups of establishments according to the size of establishment. The proportion of production in each group (within the catering industry) was estimated as  $c = (0.4465, 0.4959, 0.0576)$ . The proportions of undercooked servings were then estimated in each category, based on survey data. According to the survey, some establishments produce no undercooked servings at all. Hence, the fraction of undercooked servings in each establishment type was modeled as a mixture density with a probability  $p_0$  of zero and  $1 - p_0$  of nonzero values:

$$\begin{aligned} r_{2i} &= (1 - I_i)z_i \\ I_i &\sim \text{Bern}(p_{0,i}) \\ \text{logit}(z_i) &\sim \mathbf{N}(\mu_{c,i}, \sigma_{c,i}^2) \end{aligned} \quad (\text{A.15})$$

Given the proportions of undercooked servings in each establishment type  $r_{21}, r_{22}, r_{23}$ , the total proportion of undercooked servings in the catering industry was computed as a weighted average:  $r_2 = \sum r_{2i}c_i$ . In the survey, there were data from 54, 59, and 28 establishments. The numbers of establishments with no undercooked servings were 28, 28, and 21, respectively. The rest had reported a positive fraction  $\boxed{z_{i,k_i}}$  with  $k_1 \in [1, \dots, 26]$ ,  $k_2 \in [1, \dots, 31]$  and  $k_3 \in [1, \dots, 7]$ . Using these data, the posterior predictive distribution of proportions  $r_{2i}$  was computed with WinBUGS (see code below). The total number of eggs used for undercooked servings in private households and in the catering industry is then a sum of two binomially distributed variables, i.e.  $y_1 \sim \text{Bin}(x_1, r_1)$  and  $y_2 \sim \text{Bin}(x_2, r_2)$ .

#### Catering industry WinBUGS model code

```
model{
  for (i in 1:3){ #for each group of establishments
    p_zero[i] ~ dunif(0,1) #true fraction of well cooked servings in group i
    # realized well cooked servings in sample n[i](DATA: n[],zeros[]):
    zeros[i] ~ dbin(p_zero[i],n[i])
    # priors for each group (for the nonzero proportions):
    mu[i] ~ dnorm(0.0,0.001)
    tau[i] <- 1/(sig[i]*sig[i])
    sig[i] ~ dunif(0,10)
    # predicted value for a generic member in each group:
    # generate the predicted value if it is nonzero:
    pred[i] ~ dnorm(mu[i],tau[i])
    predp[i] <- exp(pred[i])/(1+exp(pred[i]))
    # generate the predicted status (zero/nonzero):
    zero[i] ~ dbern(p_zero[i])
    # generate the predicted final value (r21,r22,r23)
    # as a mixture of zeros and nonzero proportions:
```

```

r2[i] <- (1-zero[i])*predp[i] }
# group specific models for the nonzero proportions (DATA: propo1[], propo2[], propo3[]):
for (j1 in 1:ncater[1]){
  proportion1[j1] <- logit(propo1[j1])
  proportion1[j1] ~ dnorm(mu[1],tau[1]) }
for(j2 in 1:ncater[2]){
  proportion2[j2] <- logit(propo2[j2])
  proportion2[j2] ~ dnorm(mu[2],tau[2]) }
for(j3 in 1:ncater[3]){
  proportion3[j3] <- logit(propo3[j3])
  proportion3[j3] ~ dnorm(mu[3],tau[3]) }}

```

The model was computed using WinBUGS version 1.4. After a burn-in period of 1000, a further 100,000 MCMC iterations were computed.

#### A.4.2 From eggs to servings

Each egg will result in some number of servings. According to recipes, the **servings per egg** (spe) can vary from values below one to almost ten. Most often, there is only one serving per egg, however. Serving data were obtained separately from private households and the catering industry and from typical recipes of meals made. In private households the servings per egg in different meal types were 0.4, 1, 1.2, 2, 3.17, 4.62, and 9.55. The corresponding percentages of these meals were 4.357, 87.9330, 0.741, 1.582, 3.137, 0.381, 0.745. In the catering industry, these data were 0.4, 1, 2, 3.17, 4.61 and 9.55. The percentages were 9.0830, 56.4200, 2.3630, 6.2540, 0.4210 and 25.4590, corresponding to different meal types. To envelop the estimated continuous densities, maximum and minimum value were also specified as 0.2 and 57.6 which correspond to 5 eggs in one serving and one egg of  $0.9 \times 64 = 57.6\text{g}$  distributed into servings each containing a gram of egg. All reasonable values should fall between these boundaries. The majority of servings containing egg have exactly one egg per serving. The proportion of such servings was used to describe the probability of the event that an egg will result in exactly one serving. Otherwise, the number of servings was described as a distribution derived from the percentages and values excluding ones. After normalizing for values not equal to one, these were:

home, spe	0.2	0.4	1.2	2	3.17	4.62	9.55	57.6
home, proportion	0	0.3982	0.0677	0.1446	0.2867	0.0348	0.068	0
catering, spe	0.2	0.4	2	3.17	4.61	9.55	57.6	
catering, proportion	0	0.2084	0.0542	0.1435	0.0097	0.5842	0	

Based on these data, a continuous probability function was estimated to describe values that are not equal to one. Thus the "servings per egg" (spe) variable was defined as:

$$\begin{aligned}
 \text{spe} &= I_1 + (1 - I_1)s \\
 I_1 &\sim \text{Bern}(p_1) \\
 \log(s) &\sim F,
 \end{aligned} \tag{A.16}$$

where  $P(\text{spe}=1) = p_1$  takes a different value for home and catering, as well as the distribution  $F$ . The fitted parameters of density  $F$  for spe-values not equal to one were obtained by minimizing the squared errors of a cumulative mixture distribution  $\alpha N(\eta_1, \gamma_1^2) + (1 - \alpha)N(\eta_2, \gamma_2^2)$ . However, the cumulative percentages cannot be uniquely determined from the discrete probability data. Hence, the discrete probabilities were interpreted either as lower intervals (below the corresponding value) or upper intervals (over the corresponding value). This leads to two estimated cumulative densities  $F_-$  and  $F^-$ . The final fitted density  $F$  was taken as an average of these. The computation was performed using *fminsearch* function in Matlab. For private households, the parameter estimates were:

$$\begin{array}{l}
 F_- \quad \left| \begin{array}{l} \hat{\eta}_1 = -1.0419 \quad \hat{\eta}_2 = 0.8711 \quad \hat{\gamma}_1 = 0.0979 \quad \hat{\gamma}_2 = 0.3824 \quad \hat{\alpha}_- = 0.4423 \\ \hat{\eta}_1^- = 0.0949 \quad \hat{\eta}_2^- = 1.3058 \quad \hat{\gamma}_1^- = 0.0798 \quad \hat{\gamma}_2^- = 0.2563 \quad \hat{\alpha}^- = 0.4613, \end{array} \right.
 \end{array}$$

For the catering industry, the estimates became:



$$\begin{array}{l} F_- \mid \hat{\eta}_1 = 1.7701 \quad \hat{\eta}_2 = -0.9540 \quad \hat{\gamma}_1 = 0.2150 \quad \hat{\gamma}_2 = 0.1159 \quad \hat{\alpha}_- = 0.6678 \\ F^- \mid \hat{\eta}_1 = 3.5741 \quad \hat{\eta}_2 = 0.7912 \quad \hat{\gamma}_1 = 0.0657 \quad \hat{\gamma}_2 = 0.7064 \quad \hat{\alpha}^- = 0.5657, \end{array}$$

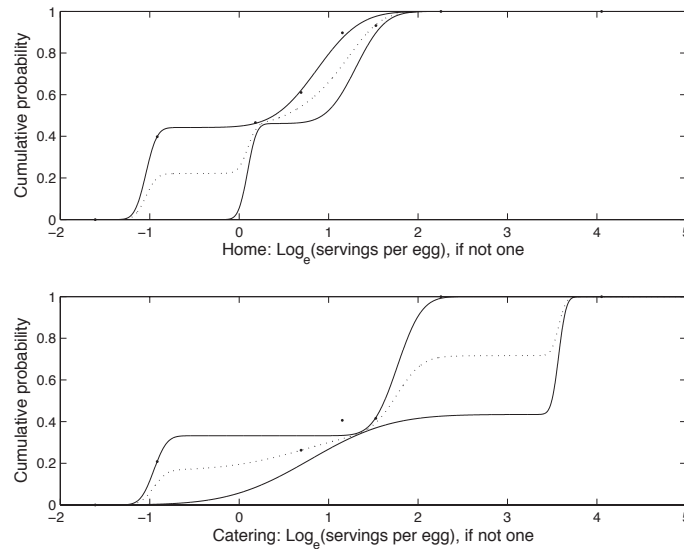
with  $P(\text{spe}=1) = p_1^{\text{catering}} = 0.5642$ . The resulting serving size from an egg (spe) is thus generated as described in equation (A.16), and draws from density  $F$  can be simulated as

$$\begin{aligned} I_d &\sim \text{Bern}(0.5) \\ \log(s) &= I_d \log(s_-) + (1 - I_d) \log(s^-) \\ \log(s_-) &\sim F_- \\ \log(s^-) &\sim F^-. \end{aligned} \tag{A.17}$$

The procedure for generating the number of servings (home & catering) is then:

$$\begin{aligned} \text{ones}_1 &\sim \text{Bin}(y_1, p_1^{\text{home}}) \\ \text{ones}_2 &\sim \text{Bin}(y_2, p_1^{\text{catering}}) \\ \text{spe}_1(i) &\sim F^{\text{home}}, \quad i = 1, \dots, y_1 - \text{ones}_1 \\ \text{spe}_2(i) &\sim F^{\text{catering}}, \quad i = 1, \dots, y_2 - \text{ones}_2, \end{aligned} \tag{A.18}$$

from which the total number of servings will be derived as:  $\text{ser} = \text{ones}_1 + \text{ones}_2 + \sum_i \text{spe}_1(i) + \sum_i \text{spe}_2(i)$ , rounded to the nearest integer. Since the number of eggs is large, the law of large numbers was used by sampling the total sum from a normal distribution, after computing the expected number (home: 1.13, catering: 6.14) and variance (home: 0.40, catering: 127.11) of spe for a single egg. The average serving size was computed as  $0.9 \times 64 \times (y_1 + y_2) / \text{ser}$ , where  $0.9 \times 64$  is the average weight of egg (grams), excluding egg shell.



## A.5 Scenarios and interventions

By *scenario*, we mean a hypothetical situation specified by hypothetical observations under which the prediction is required. For example, a scenario might be that a certain prevalence is assumed in a specified population. This prevalence information is then treated as observed data, which leads to revised parameter estimates according to the Bayes formula. I.e., the posterior distribution depends not only on the original actual data, but also on the assigned scenario data. For example, if we assume that 20% of production flocks are infected whereas the infection status of the remaining 80% is unknown under the scenario, the predictive distribution for the unspecified flocks is

$$P(\text{outcomes from unspecified flocks} \mid \text{data, scenario data}) \tag{A.19}$$

whereas the prediction for the specified infected flocks is

$$P(\text{outcomes from specified flocks} \mid \text{data, scenario data, status of the specified flocks}) \quad (\text{A.20})$$

By *intervention*, we mean a hypothetical action, which has a causal effect [6] on the variables to be predicted (child nodes in a DAG), but has no effect on the parameter estimates (parent nodes in a DAG). For example, not removing detected positive flocks can be described in the model by setting flock test sensitivity to  $p = 0$ . Then, instead of computing the predictive distribution

$$P(\text{outcome} \mid \text{data}) = \int P(\text{outcome} \mid h, h_3, \eta, p, v_3) P(h, h_3, \eta, p, v_3 \mid \text{data}) \quad (\text{A.21})$$

we compute the modified predictive distribution

$$P(\text{outcome} \mid \text{data}, p = 0) = \int P(\text{outcome} \mid h, h_3, \eta, p = 0, v_3) P(h, h_3, \eta, p, v_3 \mid \text{data}) \quad (\text{A.22})$$

However, setting arbitrary parameter values for the transition probability matrix may lead to nonexistence of the stationary distribution. This occurs if  $p = 0$ . Hence, the computations were performed by setting  $p = 0.01$  which approximates the situation without flock removal. All interventions of interest may not be possible to express by assigning parameter values. For example, changes in the temporal allocation of testing times lead to a different structure of the transition probability matrix. If the proposed intervention is that flocks are tested every second time step, the stationary distribution does not exist regardless of the value of  $p$ . Therefore, we assigned a value of  $0.01 = P(\text{detected} \mid 1_4)$  for an arbitrary even time step, which was sufficient to compute the approximating stationary distribution. An intervention may also be expressed by functionals of the original parameters, for example, by multiplication of a certain parameter, before computing the predictive distribution.

### A.5.1 Algorithm for scenario prediction: parent flock infections

Steps to compute the scenario prediction when 20% of laying parent flocks are infected in the beginning of the laying period, starting a calendar year, and when the remaining 80% of laying parent flocks are unspecified, and all grandparent flocks are assumed uninfected:

1. Compute posterior  $P(\text{parameters} \mid D_{\text{bf}}, 20\% \text{ parent replicates inf, grandparent replicates not inf})$ , using WinBUGS model of the breeder flocks.
2. Compute posterior  $P(\text{parameters} \mid D_{\text{pf}}, D_{\text{bf}}, 20\% \text{ parent replicates inf, grandparent replicates not inf})$  using the above posterior as prior in the stationary model of production flocks, using Matlab.
3. Simulate, in Matlab, the primary production replicate process under parameters obtained from the previous posterior, but assign 20% parent replicates as infected. Obtain  $v_3$  as predictive scenario distribution.
4. Compute stationary distribution for the replicate process under the above parameter distribution including parameter  $v_3$ , using Matlab.
5. Simulate annual total egg yield and internally-contaminated eggs based on the above stationary probabilities of the replicate process, using Matlab.
6. Simulate the number of eggs (and contaminated eggs) that are used for undercooked servings, in Matlab.
7. Simulate the number of resulting contaminated servings, in Matlab.

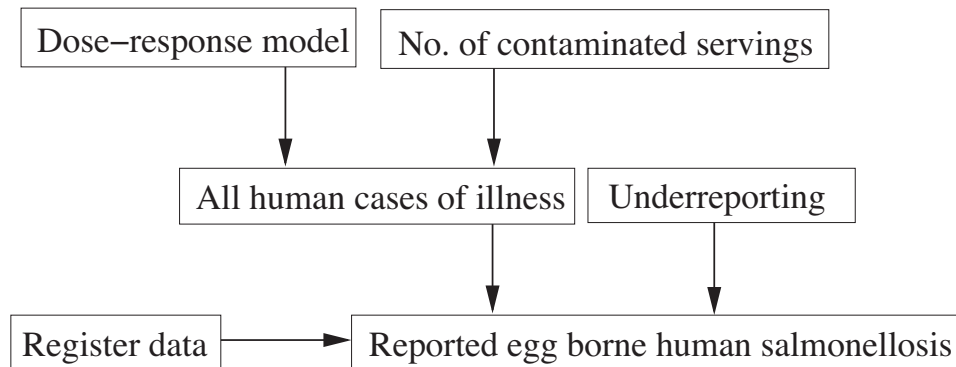
Note: in step 1, the condition is "3 p-flocks are inf and laying at 4th visit, and their parent flocks (gp-flocks) have existed for at least one laying step regardless of removal intervention, and they are assigned not infected".

### A.5.2 Import scenario

In this scenario, it was assumed that 30% of the domestic production is replaced by imported eggs with a given prevalence,  $p_{\text{im}}$ . The total number of contaminated eggs is then calculated based on the MCMC sample of the number of internally-contaminated eggs  $N$  and the total number of eggs  $N_{\text{tot}}$  under the default situation:

$$0.7N + 0.3N_{\text{tot}}p_{\text{im}} \quad (\text{A.23})$$

## A.6 Consumption Inference Model (CIM)



The uncertain number of undercooked contaminated servings was described as a gamma-density, fitted to the posterior predictive distribution resulting from the EDSM. This distribution was then used as a prior density in the Consumption Inference Model (CIM) utilizing data on actual reported domestic cases (years 1995-2001) that could be linked to egg consumption. The conditional distributions and priors in this model were:

$$\begin{aligned}
 n_o &\sim \text{Bin}(p_{\text{sel}}, n_t) I_{\{0,44\}}(n_o) \\
 n_t &\sim \text{Bin}(p, n_{\text{ser}}) \\
 p_{\text{sel}} &\sim \text{Beta}(20, 80) \\
 n_{\text{ser}} &\sim \Gamma(0.8953, 0.0034) \\
 p &= 1 - (1 + \text{cfu} \times \text{size}/21.159)^{-0.2767} \\
 \text{cfu} &\sim \text{N}^+(0, \sigma^2) \\
 \text{size} &\sim \text{N}(42.8670, 8.8775^2)
 \end{aligned}
 \tag{A.24}$$

The observed reported cases  $n_o$  were given as censored observation between 0-44, based on the public health statistics and serotyping of salmonella cases and the salmonella types found in egg production over recent years. Parameter  $p_{\text{sel}}$  denotes the chance of becoming a reported case (underreporting factor) for each of the  $n_t$  true cases of illness. The chance of illness,  $p$ , is given by a fixed dose-response model, where  $\text{cfu}/(\text{g})$  denotes the average level of contamination at the time of consumption and  $\text{size}$  is the average size (grams of egg) per serving. The prior for the average  $\text{cfu}$ -level per contaminated undercooked serving was chosen as a normal density  $\text{N}(0, \sigma^2)$ , restricted to the positive axis. The median of this half-normal density was specified as 1 (default), 10, or 10000 for the sake of sensitivity analysis. We also computed a model version without the dose-response model, i.e. by assigning a uniform prior for parameter  $p$  directly. The model was implemented in WinBUGS.

### A.6.1 Scenarios and interventions with CIM

All scenarios and interventions ultimately concerned the variable  $n_{\text{ser}}$ , i.e. contaminated servings. In the default situation, this was first quantified by a prior distribution obtained from EDSM, and a joint posterior density was computed from the CIM. When the causal effects were quantified, a distribution was assigned for  $n_{\text{ser}}$ . In order to still utilize the information of the posterior distribution obtained from CIM, the causal predictions were computed on the basis of the joint posterior density by replacing every sampled value of  $n_{\text{ser}}$  by the corresponding value from the causal distribution so that these two are stochastically point-wise coupled. This means that each sampled point  $a$  from the marginal posterior density  $\pi(n_{\text{ser}} | \text{data})$  is replaced by a point  $b$  from  $\pi_{\text{causal}}(n_{\text{ser}})$  with the same percentile point. To compare the scenarios and interventions, all causal predictions were computed using stochastic point-wise coupling with the marginal posterior density, including the default situation where the causal distribution is equal to the original prior.

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## 11. Appendix B: Summary Tables

**Table 12.** Summary of the Egg Contamination Frequency Inference Model (ECFIM). Codes are included only when applicable.

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
	Number of infected flocks studied	60	Henzler et al. (1998)	Henzler et al. (1998) report data from a voluntary <i>Salmonella</i> Enteritidis prevention project in the USA from April 1992 to October 1994. We assume that their results are applicable for modelling <i>Salmonella</i> prevalence in shell eggs produced in Finland in 2001.
	Number of tested eggs in each infected flock	4,000	Henzler et al. (1998)	From every positive holdings 4000 eggs were collected.
$D_i$	Number of apparent positive eggs from flock $i$ .	0 - 25 per 4,000 tested eggs per flock	Henzler et al. (1998)	
$p_{sen}$	Sensitivity of the laboratory culture technique	Beta(12,12)	Gast (1993b); Valentin-Bon et al. (2003)	The laboratory culture methods used by Henzler et al. (1998) was considered at least as sensitive as a method used by Gast (1993b) but not more sensitive than a method used by Valentin-Bon et al. (2003).
$a, b$	Hyper parameters for the chance of contamination per egg from an infected flock	Exp(0.001)	Conditional hyper priors leading to uniform prior for the chance of contamination.	

Table 13. Summary and data sources of the Primary Production Inference Model (PPIM). Codes are included only when applicable.

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
	The number of imported grandparent chicks (LSL hybrid) in 2001	1,440	The Association for Animal Disease Prevention in Finland	
	The number of grandparent flocks (LSL hybrid) in 2001	1	Industry information	One imported lot is one flock.
	The number of imported grandparent chicks (Isabrown and Shaver) in 2001	1,000 (Shaver) and 1,000 (Isabrown)	The Association for Animal Disease Prevention in Finland	
	The number of grandparent flocks (Isabrown and Shaver) in 2001	2	Industry information	One imported lot is one flock.
	The length of rearing period of grandparent flock (all hybrids)	16 - 18 weeks	Expert opinion	An average, differences between hybrids are not taken into account.
	The length of production period of grandparent flock (all hybrids)	38 - 43 weeks	Expert opinion	An average, differences between hybrids are not taken into account.
	The number of imported parent chicks (LB hybrid) in 2001	2,500	The Association for Animal Disease Prevention in Finland	
	The number of parent flocks (LSL and LB hybrids) in 2001	13	Industry information	
	The number of parent flocks (Isabrown and Shaver) in 2001	13	Industry information	
	The length of rearing period of parent flock (all hybrids)	16 - 18 weeks	Expert opinion	An average, differences between hybrids are not taken into account.
	The length of production period of parent flock (all hybrids)	45 - 50 weeks	Expert opinion	An average, differences between hybrids are not taken into account.
	Total number of layer flocks	1,000	National Food Agency Finland	One farm equals one flock. Only farms delivering eggs into egg packing plants are included.
	The number of LSL and LB layer flocks	700	Joensuu (2002); Finlands' Poultry Association	We assume that LSL and LB hybrids had a 70% market share in 2001.
	The number of Isabrown and Shaver layer flocks	300	Joensuu (2002); Finlands' Poultry Association	We assume that Isabrown and Shaver hybrids had a 30% market share in 2001.
	The length of rearing period of layer flocks (all hybrids)	14 - 18 weeks	Expert opinion	An average, differences between hybrids are not taken into account.
	The length of production period of layer flocks (all hybrids)	50 - 54 weeks	Expert opinion	An average, differences between hybrids are not taken into account.

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
	The average length of a production break between layer flocks	9 weeks	Uusitalo (2003)	We assume that all farmers included in the model have a production break between layer flocks.
	The number of samples for <i>Salmonella</i> control during grandparent and parent rearing period	290	FSCP / EVI-EELA-MMM Publications 1/2003	Sampling three times during rearing period
	The number of positive <i>Salmonella</i> control samples during grandparent and parent rearing period	0	FSCP / EVI-EELA-MMM Publications 1/2003	
	The number of samples for <i>Salmonella</i> control during grandparent and parent production period	144	FSCP / EVI-EELA-MMM Publications 1/2003	Sampling every eight weeks
	The number of positive <i>Salmonella</i> control samples during grandparent and parent production period	0	FSCP / EVI-EELA-MMM Publications 1/2003	
	The number of samples for <i>Salmonella</i> control during layer rearing period	77	FSCP / EVI-EELA-MMM Publications 1/2003	Sampling once during layer rearing period
	The number of positive <i>Salmonella</i> control samples during layer rearing period	0	FSCP / EVI-EELA-MMM Publications 1/2003	
	The number of samples for <i>Salmonella</i> control during layer production period	1,728	FSCP / EVI-EELA-MMM Publications 1/2003	Sampling 3 times during production period
	The number of positive <i>Salmonella</i> control samples during layer production period	0	FSCP / EVI-EELA-MMM Publications 1/2003	
	The number of the LSL and LB layer flocks of which 3 <i>Salmonella</i> control samples are taken during production period	577		We assume that 1000 layer flocks belonged to the FSCP in 2001 and the holding period for a flock was 67 weeks.
	The number of the LSL and LB layer flocks of which 2 <i>Salmonella</i> control samples are taken during production period	123		We assume that 1000 layer flocks belonged to the FSCP in 2001 and the holding period for a flock was 67 weeks.
	The number of the Isabrown and Shaver layer flocks of which 3 <i>Salmonella</i> control samples are taken during production period	247		We assume that 1000 layer flocks belonged to the FSCP in 2001 and the holding period for a flock was 67 weeks.

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
	The number of the Isabrown and Shaver layer flocks of which 2 <i>Salmonella</i> control samples are taken during production period	53		We assume that 1000 layer flocks belonged to the FSCP in 2001 and the holding period for a flock was 67 weeks.
p	Sensitivity of <i>Salmonella</i> laboratory culture method	Beta(55.5,18.5)	Prior distribution elicited from expert opinion	We assume that the test sensitivity for a pooled sample was not greatly affected by dilution effects of pooling due to enrichment methods used.
	Specificity of <i>Salmonella</i> laboratory analysis	100 %	Expert opinion	
log(u <sub>1</sub> )	Log-size of an egg laying flock (natural log).	$0.1898 \cdot N(4.5866, 1.1659^2) + 0.8102 \cdot N(7.9532, 0.9759^2)$ , truncated between log(100) and log(50000)	Information Centre of the Ministry of Agriculture and Forestry	
	Egg production per hen per day	71.5 - 93.4%	Management guides of Lohmann, Shaver and Isabrown hybrids	Average curve of egg production of different hybrids was divided into six gradual production period. This stepwise curve was used.
	Egg production per hen in 2001 in Finland	17.2 kg	MMMTIKE 2002	
	Death rate of laying hens during the production period	4 - 6% / production period	Expert opinion	According to the expert, the average death rate amongst flocks of laying hens in Finland varies between 4 to 6% during the production period. Therefore, during each stepwise part of the production period, the death rate of 1% was taken in account.
h	Chance of horizontal infection between two consecutive sampling times in breeder flocks	U(0,1)		No reliable data exist.
h <sub>3</sub>	Chance of horizontal infection before sampling in layer flocks	U(0,1) <sub>(h=h3)</sub>	Expert opinion	Since safety measures are higher in breeder than in production flocks, h <sub>3</sub> was estimated to be at least equal or higher than h.
η	Chance of ongoing infection to prevail in the grandparent and parent flocks between two consecutive sampling times	Beta(9,1)		In a flock becomes infected by <i>Salmonella</i> , it is difficult to cure. Therefore, a high prior probability was assigned for the event that an infection remains in an infected flock.



**Table 14.** Summary and data sources of the Egg Distribution Simulation Model (EDSM). Codes are included only when applicable.

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
N	Number of contaminated eggs	1,800 in 2001 with 95% credible interval of [0,7,400]	The Primary Production Inference Model	
w	Weight of shell eggs	$N(0.064 \text{ (kg)}, 0.0005^2)$	National Food Agency Finland	
	Annual shell egg production in 2001	56.5 million kg	MMMTIKE (2002)	
	Consumption of shell eggs on farms	0.5 million kg	MMMTIKE (2002)	
	Direct sale of shell eggs on farms	1.7 million kg	MMMTIKE (2002)	
	Amount of shell eggs delivered to the packing plants	54.5 million kg	MMMTIKE (2002)	
	Amount of shell eggs for hatching and animal feed	0.4 million kg	MMMTIKE (2002)	
	Export of shell eggs and egg products	7.1 million kg	Foreign Trade Statistics of the National Board of Customs	
	Import of egg products	0.3 million kg	Foreign Trade Statistics of the National Board of Customs	
	Consumption of egg products	6.8 million kg	Food and Farm Facts, Ltd	
	Consumption of shell eggs by private households	34 million kg	Expert opinion	
	Consumption of shell eggs by catering sector	5.6 million kg	The AONJensen Catering Purchase 1999 Survey and the Finnish Hotel and Restaurant Association	The value (year 1999) was calculated by dividing the amount of money spent on purchasing shell eggs by the catering sector with the average price of shell eggs at the wholesale level. We assume that estimates obtained in 1999 are also adequate in 2001.
$p_1, p_2, p_3, p_4$	Proportions of egg consumption in private households, catering industry, food industry and other.	$(0.6239, 0.1028, 0.0257, 0.2476)$	Proportions are calculated using the values mentioned in the preceding rows of this table.	The proportions can be used as probabilities for an egg to end up in each category.
$f_1$	Fraction of risky egg dishes in private households	$f_1 = f_{11} + f_{12}$ , where $f_{11} \sim N(0.117, 0.009^2)$ , $f_{12} \sim N(0.0387, 0.0052^2)$	Primary data of the survey reported by Lievonen & Majjala (2005)	
$f_{11}, f_{12}$	Proportion of two meal types containing undercooked or raw egg		Primary data of the survey reported by Lievonen & Majjala (2005)	
$c_1, c_2, c_3$	Proportions of consumption in three types of establishments in the catering industry	$(0.4465, 0.4959, 0.0576)$	Primary data of the survey reported by Lievonen & Majjala (2005)	
$f_{21}, f_{22}, f_{23}$	Proportion of risky egg dishes in three types of establishments in the catering industry	Estimated from data as posterior predictive distributions	Primary data of the survey reported by Lievonen & Majjala (2005)	
$f_2$	Fraction of risky egg dishes in the catering sector	$f_2 = f_{21} \cdot c_1 + f_{22} \cdot c_2 + f_{23} \cdot c_3$	Primary data of the survey reported by Lievonen & Majjala (2005)	Weighted ( $c_i$ ) proportions ( $f_{11}, f_{21}, f_{22}, f_{23}$ ) of establishment types, estimated from survey data.
spe	Servings per egg	$1 + (1 - i)_s$ $i \sim \text{Bern}(p_i)$ $\log(s) \sim F$	Serving sizes of different dishes were taken from cookery books and percentages of consumption were from the postal surveys to private households and catering establishments (Lievonen et al. 2004; Lievonen & Majjala 2005)	
F	Probability distribution for number of servings resulting from an egg, if not exactly one.	Mixture density estimated from data (Separately for private households and catering industry)	Serving sizes of different dishes were taken from cookery books and percentages of consumption were from the postal surveys to private households and catering establishments (Lievonen et al. 2004; Lievonen & Majjala 2005)	Maximum serving consists of 5 eggs, and minimum serving consists of 1g of egg.
$p_i$	Probability that one egg results into exactly one serving	$p_1 = 0.8793$ (private households), $p_2 = 0.5642$ (catering industry)	Serving sizes of different dishes were taken from cookery books and percentages of consumption were from the postal surveys to private households and catering establishments (Lievonen et al. 2004; Lievonen & Majjala 2005)	

**Table 15.** Summary of the inputs of the Consumption Inference Model (CIM).

Code	Meaning	Distribution / Formula / Value	Source of information	Assumption
$n_{ser}$	Number of contaminated servings	$\Gamma(0.8953, 0.0034)$	Fitted prior distribution from the output of the simulation model (EDSM)	
size	Average size of a serving (g)	$N(42.9, 8.9^2)$	Fitted prior distribution from the output of the simulation model (EDSM)	
cfu	Average contamination (cfu/g) at the time of consumption	$N^+(0, \sigma^2)$	Uninformative prior density over a wide range of (positive) values expressing vague prior knowledge	Median = 1. (In sensitivity analysis, also values of 10 and 10000)
$n_o$	Estimated number of reported human cases due to <i>Salmonella</i> from shell eggs	censored observation in 0-44	Zoonoses in Finland 1995 - 1999; MMM(2000)	Assumed to be between 0-44 based on the serovars and phagetypes of isolated strains from humans, poultry and eggs in 1999 (worst case since 1995).
$\alpha, \beta$	Parameters of the dose response model	$\alpha=21.159, \beta=0.2767$	WHO/FAO (2002) report	The model used is applicable also for Finnish total population.
$p_{sel}$	Probability of a case of illness being diagnosed and reported (underreporting)	Beta(20,80)	Wheeler et al. (1999); STM (1997)	Most probable values should be in the range 0.1-0.3

## EELAn julkaisusarja

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Luentokokoelma/Föreläsningsserie

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Riskiprofiili

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Luentokokoelma/Föreläsningsserie

03/2005  
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