**Supplementary Material S1**

***animal*. The international journal of animal biosciences.**

**Risk assessment for recrudescence of avian influenza in caged layer houses following depopulation: The effect of cleansing, disinfection and dismantling of equipment.**

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**The source term: Virus loadings in the poultry house**

*Loadings from the three bird matrices, namely feathers, faecal (cloacal), and oropharyngeal secretions*.

Titres of **highly pathogenic avian influenza virus (HPAIV)** are typically reported as **egg infectious dose 50% (EID50)** units. The **total HPAIV infectivity from the three bird matrices namely feathers, faeces and oropharyngeal secretions which goes into the “manure” (*EID50\_manure*)** is calculated from data in Yamamoto *et al.* (2008) and Scottish Government (2016) together with unpublished data from the **Animal and Plant Health Agency (APHA)**. There are few published shedding data for HPAIV in chickens and the risk assessment therefore draws on published data for other bird species. Yamamoto *et al.* (2008) presented H5N1 viral titres in feathers, oropharyngeal swabs and cloacal swabs from three domestic ducks inoculated with H5N1. The titres were not only highest in the feathers (3.8 to 6.9 log10 EID50 /ml) but also were detected for longer periods of time (8 days post infection) compared to in cloacal and oropharyngeal secretions. Although the presence of H5N1 virus in bird feathers is an important consideration, feathers are lost infrequently compared to oropharyngeal and cloacal secretions which are produced daily, and therefore feathers may only make a small contribution to the “manure” in the poultry sheds. Viral titres of H5N1 were higher in oropharyngeal secretions than in cloacal secretions and the data for oropharyngeal secretions are therefore used in this risk assessment. This represents a worst case scenario because much more cloacal secretion is produced than oropharyngeal. According to Yamamoto *et al.* (2008), the highest duck oropharyngeal EID50 was at 4 days post infection at 103.7 EID50/ml. It is assumed that 1 ml equates to 1 g of manure and therefore the viral loading is 103.7 EID50/g manure produced by an infected bird. APHA unpublished data indicate that peak shedding titres for H5N1 clade 2.2 virus in chickens and turkeys are similar at 103.0 to 104.0 EID50/ml.

Manure production data for poultry are used to estimate the amount of solid secretion produced per bird per day. Caged layers (over 17 weeks in age) have been reported to produce 0.84 tonnes of manure per 1 000 birds per week (Scottish Government, 2016). This is equivalent to 120 g per bird per day. The total viral infectivity produced in the poultry house at point of culling from cloacal, oropharyngeal and feathers is calculated as 120 g/bird/day x 64 500 infected birds x 103.7 EID50/g = 3.88 1010 EID50/day. This is in the form of manure, which is removed from the house at a constant rate by the moving manure belt. For example, 129 000 poultry would produce 15.4 tonnes of manure per day, and the poultry house would rapidly fill up with manure if it were not removed. It is assumed that 99.9% of manure is removed from the poultry house each day and that this would have been removed in the 24 hours prior to culling, with 0.1% being left in the poultry house after culling and removal of the infected poultry. Thus 15.4 kg of manure are left each day, representing 3.88 107 EID50 (*EID50\_manure*) in the poultry house at the point of culling and depopulation (Table S1).

*Airborne infectivity which settles as dust*.

The **airborne particulate HPAIV infectivity which settles as dust (*EID50\_airborne*)** is calculated from data of Spekreijse et al. (2011). To estimate HPAIV H5N1 loadings from air and dust in the poultry house immediately prior to the point of culling, the number of airborne EID50 produced per infected chicken per day is calculated from the air sampling data of Spekreijse et al. (2011) who collected 20 air samples over 10 days, i.e., two samples per day in each of two rooms with chickens experimentally infected with HPAIV H5N1. Each sample was collected over 10 minutes at a rate of 8 m3/minute and thus represents 1.33 m3. In one room of volume 22 m3, one air sample contained 101.6 EID50 on day 2 and another on day 3 contained 101.3 EID50 (totalling 59.8 EID50 in the two samples combined). The other 18 samples from that room collected over days 1 to 10 were negative. As a worst case scenario only the data from the two positive shedding days (days 2 and 3) are used here. The total volume sampled in that one room over those two days (i.e. four samples) was 4 x 1.33 m3 = 5.33 m3 of air. Thus 13 infected birds produced 59.8 EID50 in 5.33 m3 of air. Assuming this was representative of the 22 m3 volume of the whole room, then 13 infected birds produced 246 EID50 in the room as a whole. The number of airborne EID50 is thus 18.9 per bird in the first room. In the second identical room, however, 56 birds were infected but no airborne infectivity was detected. Combining the results from the two rooms gives 59.8 EID50 in 10.67 m3 (8 air samples over two days) which is 5.6 EID50 per m3. Over 44 m3 (i.e. the two 22 m3 volume rooms), this is 246 EID50 in both rooms from a total of 69 infected birds over two days. The airborne output per infected bird is therefore 3.57 EID50 per infected bird. Since data from two days are used, the estimated airborne infectivity per infected bird per shedding day is 1.78 EID50. For the H5N1 HPAIV infected chickens, the mean infectious period (days of shedding) was 1.3 days (Spekreijse et al., 2011). Assuming 64 500 H5N1-infected birds are present at the time of culling and depopulation then the total airborne loading (*EID50\_airborne*) is 64 500 infected birds x 1.3 days x 1.78 EID50 = 1.5 105 EID50s (Table S1). It is assumed that all of this airborne infectivity has settled as dust within the house at the end of depopulation. Poultry catching normally involves unrest and wing-flapping, which potentially can redistribute the virus load in the poultry house. This together with the generation of aerosols during the cull process is assumed to be included in the estimated loading in cloacal secretions which are based on oropharyngeal titres.

*Table S1. Summary of predicted levels of highly pathogenic avian influenza H5N1 virus (EID50s) in a chicken poultry house at point of depopulation of poultry.*

|  |  |  |
| --- | --- | --- |
| Source | Assumptions | Remaining infectivity at time of culling (EID50) |
| Cloacal, oropharyngeal and feathers (*EID50\_manure*) | 99.9% is removed per day as manure | 3.88 107 |
| Airborne particulate (*EID50\_airborne*) | All settles as dust | 1.5 105 |
| Total | Sum of *EID50\_manure* and *EID50\_airborne* | 3.89 107 |
| Assumes 129 000 birds in the poultry house of which 50% are infected at culling.EID50: Egg infectious dose 50% |

**References**

Scottish Government 2016. Calculating the amount of poultry manure produced. Retrieved on 20 January 2017 from [www.gov.scot/Resource/Doc/278281/0096546.doc](http://www.gov.scot/Resource/Doc/278281/0096546.doc).

Spekreijse D, Bouma A, Koch G and Stegeman JA 2011. Airborne transmission of a highly pathogenic avian influenza virus strain H5N1 between groups of chickens quantified in an experimental setting. Veterinary Microbiology 152, 88-95.

Yamamoto Y, Nakamura K, Okamatsu M, Miyazaki A, Yamada M and Mase M 2008. Detecting avian influenza virus (H5N1) in domestic duck feathers. Emerging Infectious Diseases 14, 1671-1672.

**Supplementary Material S2**

***animal*. The international journal of animal biosciences.**

**Risk assessment for recrudescence of avian influenza in caged layer houses following depopulation: The effect of cleansing, disinfection and dismantling of equipment.**

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**The time period between depopulation of the infected poultry and restocking with the new birds**

The minimum possible **time period between depopulation of the infected poultry and restocking with the new birds (*TbDR*)** is 42 days (EU, 2005). There are typically 2 days between depopulation and preliminary **cleansing and disinfection (C&D)**, 7 days between the first round of cleaning and the second round of cleaning in secondary C&D, and 7 days for secondary C&D. In addition, the re-population of commercial poultry holdings shall not take place for a period of 21 days following the date of completion of the final cleansing and disinfection as provided for in Article 48 the restocking information (EU, 2005). This does not take into account the extra time for decay gained by the practice of dismantling. The expert opinion estimation of *TbDR* is between 40 and 90 days (P. McMullin, personal communication), and these two values were used to define a uniform distribution.

**Estimating the fraction of pathogen surviving in the properly cleansed and disinfectant-treated bulk phase portion**

Virkon S is a disinfectant officially authorised for C&D in the UK. At 21°C, a 1-log10 inactivation of **highly pathogenic avian influenza virus (HPAIV)** H5N1 sprayed onto fomite surfaces (plastic, metal and wood) requires 3.0 - 3.5 minutes when treated immediately with 1% (w/v) Virkon S disinfectant (C. Warren, personal communication) confirming that this disinfectant rapidly inactivates HPAIV. However, there is no information on whether the inactivation is log-linear and over how many logs. Furthermore in the poultry house environment, the virus will be physically sequestered in an organic matrix (feed, debris, faeces, poultry litter and other secretions) which would not only buffer the pH but also protect the virus through inactivating the residual disinfectant (Lucyckx et al., 2015). Thus dried faecal pats, accumulated dust, layering of faecal material and matted feathers on the muck belts are the areas to be considered not only in terms of HPAIV loading, but also in terms of the matrix for decay and inactivation (R. Davies, personal communication). To address this, total aerobic bacteria count data presented by Lucyckx et al. (2015) for C&D of an operational poultry house are used as the data source for the degree of inactivation by C&D. 1% Virkon S is effective against bacteria and viruses (Hernndez et al. 2000) and the total aerobic bacteria counts recorded by Lucyckx et al. (2015) before and after C&D are used to calculate the **fraction of pathogen surviving C&D in those parts of the poultry house that can be reached by C&D (*γ*)** (i.e. in the properly cleansed and disinfectant-treated bulk phase portion). These values are presented in Table 1 and represent the values of *γ* used in Equation 2 for the different streams.

**Estimating the fraction of debris that by-passes the bulk phase**

The **fractions of debris and organic material (and hence associated viruses) in those parts within each stream where C&D cannot reach with and without dismantling and which therefore by-pass the bulk phase and effective C&D (*fbypass*)** are set out in Table 2 and define the *fbypass* parameter for each stream in Equation 2. There are no experimental data for the amount of material which does not receive effective C&D. These values are therefore determined from estimations made by visiting a chicken layer farm. The approach used was to estimate lower and upper values for a uniform distribution. For example, it was estimated that between 10% and 40% of virus in material on the manure belt could survive preliminary disinfection.

In effect, *fbypass* reflects the efficiency of C&D at operational scale, the smaller *fbypass*, the greater the efficiency as less of the virus-contaminated material avoids C&D. The preliminary C&D is considered not to be as efficient as secondary C&D. After preliminary C&D, a considerable amount of organic matter is still present and it is assumed for example that 25% remains on the manure belt (Table 2). During preliminary C&D, dead birds and the litter are cleared out, however there is no degreasing or scrubbing. There is only drenching with disinfectant. Thus preliminary C&D is assumed to be of relatively low efficiency (Table 2) depending on the stream. For example, it is assumed that the manure belt is least effectively cleansed, with 10 to 40% of material not being cleansed/disinfected properly. In contrast, it is assumed that only 1 to 10% of the floor is not cleansed in preliminary C&D. While the physical disturbance of preliminary C&D may produce aerosols these are negligible compared to the proportions of material assumed to be remaining overall.

In contrast to preliminary C&D, secondary C&D is much more thorough with power washes and fine brushes through greater workforce deployment to maximise removal of organic material. Degreasing and disinfection are undertaken and then repeated after 7 days. This is reflected in the smaller fractions of material that by-pass the process in secondary C&D (Table 2) compared to preliminary C&D. Dismantling further reduces *fbypass* compared to not dismantling for the equipment streams. Again the fractions for by-pass are based on expert opinion of what is achievable in practice rather than experimental data. Two secondary C&D scenarios are considered, namely without and with dismantling. Higher percentage by-pass is assumed without dismantling (Table 2).

**Exposure through inhalation of dust and ingestion by the restocked poultry**

As for the by-pass fractions, the **fractions of the infective material remaining after C&D that are inhaled (*finhale*) and ingested (*fingest*) by the restocked poultry** as out in Table 1 for each of the streams are based on expert opinion and assumptions in the absence of data. Although there is considerable uncertainty in these estimates, it is considered they are worst case assumptions. It is assumed that moving parts convert 10% of any remaining infectivity into dust which is inhaled by the restocked of birds. Similarly 10% of any material remaining on the floor is suspended into the air through the disturbance by people walking through the poultry house. It is assumed that only 0.01% of any material left in the metal troughs is actually inhaled by the birds. It is assumed that 50% of any material left in the metal troughs, moving hoppers and chains is ingested by the birds, while the birds have no access to any material on the floors and only limited access to the waste streams.

**Calculation of exposures to restocked poultry**

The **infectivity ingested by the restocked poultry through each stream (*EID50\_ingest\_stream*)** was calculated as

$$EID\_{50\\_ingest\\_stream}=EID\_{50\\_source\\_stream}×10^{-\frac{TbDR}{D\_{t}}}×f\_{survive\\_stream}×f\_{ingest}$$

where ***EID50\_source\_stream* is the source term infectivity in a given stream immediately after depopulation of the infected poultry** as calculated by Equation 1 and ***fsurvive\_stream* is the fraction of input pathogen surviving C&D for each stream** as calculated by Equation 2. Similarly the **infectivity inhaled by the restocked poultry through each stream (*EID50\_inhale\_stream*)** was calculated as

$$EID\_{50\\_inhale\\_stream}=EID\_{50\\_source\\_stream}×10^{-\frac{TbDR}{D\_{t}}}×f\_{survive\\_stream}×f\_{inhale}$$

It should be noted that infective material present in the manure source term in Equation 1 may be converted to dust during the operation of equipment in the restocked poultry house and hence inhaled and thus it is appropriate to calculate *EID50\_inhale\_stream* from *EID50\_source\_stream* from Equation 1.

The **total poultry exposure (*Exposure\_EID50*)** was calculated for each of the three C&D scenarios as.

$$Exposure\\_EID\_{50}=\sum\_{All streams}^{}EID\_{50\\_ingest\\_stream}+\sum\_{All streams}^{}EID\_{50\\_inhale\\_stream}$$

**Receptor term: Using dose-response to estimate risk of infection for highly pathogenic avian influenza virus H5N1**

While the EID50 is a useful assay to measure levels of live virus in manure components and airborne particulate, a dose-response is required to convert EID50 units into live chicken ID50 units, where one chicken ID50 is the amount of infectious virus which when given to a single chicken has a 50% probability of infecting that chicken. According to Aldous et al. (2010) there are 103.4 EID50 units per chicken ID50 for H5N1 HPAIV (A/turkey/Turkey/1/05) in live chickens on challenge through both the intraocular (0.1 ml) and intranasal (0.1 ml) routes. Since H7N1 HPAIV is less infectious to chickens than H5N1 HPAIV with an ID50 of 104.6 EID50 (Aldous et al., 2010), the H5N1 data are used here. Thus it is assumed that there are 103.4 EID50/chicken ID50 and the **number of chicken ID50s ingested by the chicken flock as a whole within the poultry shed (*NChicken\_ID50*)** is given by

$N\_{Chicken\\_ID50}=\frac{Exposure\\_EID\_{50}}{10^{3.4}}$.

**References**

Aldous EW, Seekings JM, McNally A, Nili H, Fuller CM, Irvine RM, Alexander DJ and Brown IH 2010. Infection dynamics of highly pathogenic avian influenza and virulent avian paramyxovirus type 1 viruses in chickens, turkeys and ducks. Avian Pathology 39, 265-273.

EU 2005. EU Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC Article 49. Retrieved on 20 January 2017 from<http://eur-lex.europa.eu/legal-content/EN/ALL/?uri=CELEX:32005L0094>.

Hernandez A, Martro E, Matas L, Martin M and Ausina V 2000. Assessment of in-vitro efficacy of 1% VirkonS against bacteria, fungi, viruses and spores by means of AFNOR guidelines. Journal of Hospital Infection 46, 203-209.

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**Supplementary Material S3**

***animal*. The international journal of animal biosciences.**

**Risk assessment for recrudescence of avian influenza in caged layer houses following depopulation: The effect of cleansing, disinfection and dismantling of equipment.**

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*R code*

#---

# run: "R-studio desktop"

# written: "R version 3.4.1"

#---

### Model ----

Risk\_Calc <- function(Mass, EID50, Number\_Birds, p\_Remain, days\_of\_shedding,

 Scenario, Parameters1, Parameters2,

 ns, min, max, min\_TbDR, max\_TbDR,

 Parameters4, Parameters5,

 EID50\_oralID50, CV)

 {

 Source\_term\_calculation <-function(Mass, EID50, Number\_Birds, p\_Remain, days\_of\_shedding)

 {

 Cloacal=Mass\*EID50[1]\*Number\_Birds\*0.5\*p\_Remain

 GAL=EID50[2]\*Number\_Birds\*0.5\*days\_of\_shedding

 I=cbind(Cloacal,GAL)

 rownames(I)="Infectivity"

 return(Source\_term\_calculation=I)

 }

# Estimating the uniform distributions for the fraction by-passing the bulk phase

 simul<-function(ns, min, max, min\_TbDR, max\_TbDR)

 {

 l1=as.numeric(dim(min)[1])

 l2=as.numeric(dim(min)[2])

 y<-array(dim=c(l1,l2,ns))

 y1<-c()

 y2<-array(dim=c(l1+1,l2,ns))

 for (j in 1:ns){

 for (i in 1:l1){

 for (k in 1:l2){

 y[i,k,j]<-runif(1, min[i,k], max[i,k])

 }#k

 }#i

 y1<-runif(1, min\_TbDR, max\_TbDR)

 y2[,,j]<-array(rbind(y[,,j],y1))

 }#j

 return(Parameters3=y2)

 }#fun

 Source\_term<-Source\_term\_calculation (Mass, EID50, Number\_Birds,

 p\_Remain, days\_of\_shedding)

# Initial infection on Equipment

 DIF=array(dim=c(7,2))

 dimnames(DIF)<-list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

 for (i in 1:length(Source\_term)) {

 DIF[,i]=Source\_term[i]\*(Parameters1[,i])

 }

# Decay Rate as a costant

 Parameters3<-simul(ns, min, max, min\_TbDR, max\_TbDR)

 nc=as.numeric(dim(Parameters3)[2])

 nit=as.numeric(dim(Parameters3)[3])

 nr=as.numeric(dim(Parameters3)[1])-1

 eff\_decay<-array(dim=c(7,2))

 if (Scenario==1) {

 DIF4=array(dim=c(1,nit))

 mod="Preliminary disinfection"

 } else if (Scenario==2)

 {

 DIF4=array(dim=c(nit,nit))

 mod="Secondary: By-pass rate without dismantling"

 } else if (Scenario==3)

 {

 DIF4=array(dim=c(nit,nit))

 mod="Secondary: By-pass rate with dismantling"

 }

 for(ii in 1:nit){

 # print (ii)

 eff\_decay<-DIF/10^((Parameters3[nr+1,1,ii])/10)

# Effect of C&D

# Viral loadings after cleansing and disinfection

 By\_pass\_preliminary=array(dim=c(7,2))

 By\_pass\_secondary\_without\_dismantling=array(dim=c(7,2))

 By\_pass\_secondary\_with\_dismantling=array(dim=c(7,2))

 dimnames(By\_pass\_preliminary)=list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

 By\_pass\_preliminary=(1-Parameters3[-(nr+1),1,ii])\*Parameters2+Parameters3[-(nr+1),1,ii]

 DIF1=eff\_decay\*By\_pass\_preliminary

# Different scenarios

 if (Scenario==1) {

 DIF2=DIF1

 DIF3=array(dim=c(7,2))

 dimnames(DIF3)=list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

 for (j in 1:2) {

 DIF3[,j]=DIF2[,j]\*(Parameters4[,j]+Parameters5[,j])

 }

 DIF4[1,ii]=sum(DIF3, na.rm=TRUE)

 } else if (Scenario==2)

 {

 for (jj in 1:nit) {

 By\_pass\_secondary\_without\_dismantling=(1-Parameters3[-(nr+1),2,jj])\*

 Parameters2+Parameters3[-(nr+1),2,jj]

 DIF2=DIF1\*By\_pass\_secondary\_without\_dismantling

 DIF3=array(dim=c(7,2,nit))

 dimnames(DIF3)=list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

 for (j in 1:2) {

 DIF3[,j,jj]=DIF2[,j]\*(Parameters4[,j]+Parameters5[,j])

 }

 DIF4[jj,ii]=sum(DIF3, na.rm=TRUE)

 }

 } else if (Scenario==3)

 {

 for (jjj in 1:nit) {

 By\_pass\_secondary\_with\_dismantling=(1-Parameters3[-(nr+1),3,jjj])\*

 Parameters2+Parameters3[-(nr+1),3,jjj]

 DIF2=DIF1\*By\_pass\_secondary\_with\_dismantling

 DIF3=array(dim=c(7,2,nit))

 dimnames(DIF3)=list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

 for (j in 1:2) {

 DIF3[,j,jjj]=DIF2[,j]\*(Parameters4[,j]+Parameters5[,j])

 }

 DIF4[jjj,ii]=sum(DIF3, na.rm=TRUE)

 }

 }

 }

# Predicted Risk

 PI=(DIF4/EID50\_oralID50)\*CV

 return(list(Scenario=mod,

 Infect=Source\_term,

 PredictedRisk=PI,

 Infectivity=DIF4,

 Exposure\_median=median(DIF4),

 Exposure\_CI\_low=quantile(DIF4, 0.025),

 Exposure\_CI\_high=quantile(DIF4, 0.975),

 Probability\_CI\_low=quantile(PI, 0.025),

 Probability\_CI\_high=quantile(PI, 0.975),

 Probability\_median=median(PI)

 ))

}

### Defining parameters ----

# Mass

Mass <- 120

# EID\_50

EID50<-c(Cloacal=5011.8723362727,

 GeneralAirborneLoading=1.7864041909)

# Number of birds

Number\_Birds <- 129000

# Minimum and maximum values used to define the uniform distributiions by-passing

# the "bulk" phase (f\_bypass)

min\_preliminary<-c(0.05, 0.01,0.01,0.10,0.01,0.01,0.01)

max\_preliminary<-c(0.20, 0.10,0.10,0.40,0.10,0.10,0.10)

min\_secondary\_without<-c(0.005, 0.005,0.01,0.025,0.005,0.005,0.005)

max\_secondary\_without<-c(0.02, 0.02,0.04,0.10,0.02,0.02,0.02)

min\_secondary\_with<-c(0.00025, 0.00025,0.005,0.005,0.00025,0.00025,0.005)

max\_secondary\_with<-c(0.01, 0.01,0.02,0.02,0.01,0.01,0.02)

min<-cbind(min\_preliminary,min\_secondary\_without,min\_secondary\_with)

max=cbind(max\_preliminary,max\_secondary\_without,max\_secondary\_with)

# Defining the time minimum and maximum values of the

# period between depopulation of infected poultry and

# restocking with the new birds

min\_TbDR<-40

max\_TbDR<-90

# Defining Number of simulation ----

ns <- 1000

# p\_remain

p\_remain <- 0.001

# Defining number of days of shedding

days\_of\_shedding <- 1.3

# Defining scenario:

# Preliminary disinfection = 1

# Secondary: By-pass rate without dismantling = 2

# Secondary: By-pass rate with dismantling = 3

scenario <- c(1:3)

### Defining Parameters1 = Fractions of infectivity entering the different streams ----

X=c(0.001, 0.001, 0.001, 0.897, 0.05, 0.05, NA,

 0.01, 0.01, 0.01, 0.2, 0.1, 0.05, 0.62)

Parameters1<-array(X, dim=c(7,2))

dimnames(Parameters1)<-list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

### Defining Parameters2 = Fractions of infectivity surviving C&D through the different streams ----

Y=c(0.0003162278, 7.94328234724282E-05, 7.94328234724282E-05, 2.51188643150958E-05, 7.94328234724282E-05, 6.30957344480193E-05, 7.94328234724282E-05,

 0.0003162278, 7.94328234724282E-05, 7.94328234724282E-05, 2.51188643150958E-05, 7.94328234724282E-05, 6.30957344480193E-05, 7.94328234724282E-05)

Parameters2<-array(Y, dim=c(7,2))

dimnames(Parameters2)<-list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

### Defining Parameters4 = Fractions of infectivity inhaled through the different streams ----

K=c(0.0001, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1,

 0.0001, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1)

Parameters4<-array(K, dim=c(7,2))

dimnames(Parameters4)<-list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

### Defining Parameters5 = Fractions of infectivity ingested through the different streams ----

M<- c(0.5, 0.5, 0.5, 0.01, 0.01, 0.1, 0,

 0.5, 0.5, 0.5, 0.01, 0.01, 0.1, 0)

Parameters5=array(M, dim=c(7,2))

dimnames(Parameters5)<-list(c("Metal trough","Moving hopper", "Moving chain",

 "Manure belt", "Cross conveyer", "Air drying eqp",

 "Floor"),

 c("Manure","Airborne particulate"))

### Running the model ----

for (s in 1:(length(scenario))) {

results[[s]] <-Risk\_Calc(Mass, EID50, Number\_Birds, p\_remain,

 days\_of\_shedding, s, Parameters1, Parameters2,

 ns,min,max,min\_TbDR, max\_TbDR, Parameters4, Parameters5,

 10^3.4, 0.69)