Supplementary material

Modelling contamination of trucks used in the shipment of pigs infected with porcine reproductive and respiratory syndrome virus

Krishna K Thakur*, Crawford W. Revie*, Daniel Hurnik*, Javier Sanchez*; thakurvet@gmail.com
* Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PEI, Canada

Data Description (Estimation of values/parameters)

Truck use

The proportion of trucks used ($Tr.use_i$) for two, three and four or more "j" farm visits on a given day and the proportion of trucks with more than the minimum number of shipped animals (Min_{ani}) for each of three "k" production types were obtained from the pilot pig traceability data.

Shipment size and travel time

The number of infectious animals in a given shipment, and the travel time were estimated as described below:

Prevalence of shedding animals on a truck

The prevalence of shedding animals (Shed.prev.k) was adjusted by the within-farm prevalence of PRRS (A.Prev.k). Expert judgement suggested that the proportion of animals shedding the virus (Shed.anim.k) varied according to the growth stage of the pigs being transported and it was suggested that 20%, 50% and 70% of weaned piglets, nursery pigs, and finishing pigs, respectively, would typically be shedding the virus. However, in doing so, we might have underestimated the risk by not accounting for those animals there were not seropositive yet but were still shedding the virus.

Several studies have reported very high within-farm prevalence of PRRS virus ranging from 80 -100% (Dee and Joo, 1994; Maes, 1997; Nodelijk et al., 2003). For this study, we used an animal-level prevalence (A.Prev.k) of 80% and evaluated the impact of this variable on the model outcome by carrying out sensitivity analysis.

Minimum number of shedding animals in a shipment

PRRS virus is excreted through urine, faeces and oral fluids of infected animals in addition to several other bodily secretions (Wills et al., 1997c; Bierk et al., 2001), though the dynamics of these shedding patterns is not well documented. Therefore, it was difficult to quantify the amount of PRRS virus likely to be present on any given shipment truck. We were interested in estimating the infectious potential of the trucks such that the virus could be transmitted to naive animals. We therefore assessed whether or not the trucks would likely have sufficient viral load to infect susceptible pigs. Dee and colleagues (2004b) demonstrated that the presence of two infectious pigs on a truck trailer for two hours was sufficient to transmit the virus to naive pigs on the subsequent introduction of these animals to the truck. Using these guidelines as a cut-off value, we categorized trucks as having sufficient infectious virus or not to transmit PRRS virus to naïve pigs (i.e. they must have transported at least two infectious animals and have had a travel time of at least two hours).

Minimum number of animals (Minani.k) on a truck to have at least two infectious animals

We used the hypergeometric distribution to estimate the minimum number of shedding animals needed in a shipment (Minani.k) for each production type, in order to have two infectious animals (Nani) on a truck that were shedding the virus. We used 95th percentile of shipment size (Shipsize.k), as recorded in the pilot pig traceability data, for each of the three production types as 'N', and the number of shedding animals, which was based on Shed.prev.k, as the 'm' parameter of the hypergeometric process. For psi, we used one, as the odds of drawing a shedding animal from the shipment was similar to that of drawing an animal that was not shedding the virus. Psi is the odds of drawing shedding vs not shedding animal from the sample using hypergeometric distribution.

Shipment size (Shipsize) and Minimum shipment size (Minship.k)

The shipment size was simulated as a triangular distribution with 5th and 95th percentile of the shipment size recoded in the pilot pig traceability dataset for each of the three production types as minimum and maximum of the distribution. Based on this distribution for shipment size, the probability that a truck had minimum shipment size (Minship.k) or more animals than Minani.k was estimated using the step function available in OpenBUGS.

Infective Dose (Inf.dose)

Finally, we estimated the probability that a truck has an infective dose of PRRS virus (Inf.dose) if it shipped at least Minani and had a travel time (Travel) of at least two hours.

Additionally, since the infectious dose is related to the environmental conditions, we calculated the infective dose (Inf.dose) for warm and cold seasons. PRRS virus has been described as having a median infectious half-life of 14.6 hours (95% CI = 12.6 - 17.2) in pig manure at an ambient temperature of 220°C (Linhares et al., 2012). The PRRS virus has a comparatively longer half-life of 112.6 hours (95% CI = 103.2 - 123.8) in pig manure at an ambient temperature of 40°C (Linhares et al., 2012). We were guided by this information to extend the model to incorporate viral decay in order to quantify the risk that trucks would still be contaminated with PRRS virus on subsequent days in either warm and cold months.

For warmer months, we assumed that at least one infectious dose of virus would be present

on trucks that have at least two infectious animals, that had been kept on the truck for at least two hours. So, based on viral decay with an assumed half-life of 15 hours, for at least one infectious dose of virus to be present during the 15 hours subsequent to the truck being used on Day 1, would require that at least four infectious animals (this is analogous to having two infectious doses of virus on Day 1) were present on the truck, and similarly for the truck to be infectious for the next 30 hours that at least eight infectious animals would need to have been present. On the other hand, for colder months we assumed that trucks with at least two infected animals could be considered to be infective for around five days, as the half-life of the virus is much longer (112.6 hrs at 40°C), and thus we did not attempt to quantify the likelihood for time points beyond a one week duration from which the truck initially became infected.

Travel time

In order to estimate the amount of virus shed during transportation, the travel time was first estimated and then the probability that a given shipment was longer than two or more hours was computed. It was assumed that the most likely travel time in Ontario, Canada was around two hours, which corresponds to the travel time estimated by Dee et al. (2004b) for swine operations in Minnesota and was likely to vary between a minimum of half an hour and a maximum of six hours. We used this information to parameterise a triangular (min, max) distribution in OpenBUGS. First, two similar uniform distributions were computed for travel time (min/2, max/2) and these distributions were summed together that yielded a triangular distribution. These equations provided a travel time distribution with mean and median of 3.25 hours.

The probability that a given shipment lasted for at least two hours was estimated using the step function to the distribution of travel time. The step function provided the probability of travel time equal to 1 if the travel time was more than two hours.

Table S1: Summary posterior distribution of nodes and scenarios used in the Bayesian model simulated to evaluate the probability that a truck will be contaminated with PRRS virus at the end of a working day.

Nodes	Median	95% CrI*	Mean	SD!
F.pos.2	1	0-2	0.994	0.71
F.pos.3	2	0-3	1.50	0.87
F.pos.4	2	0-4	2.00	1.0
F.inf.2	1	0-1	0.753	0.43
F.inf.3	1	0-1	0.873	0.33
F.inf.4	1	0-1	0.938	0.24
Comb.prob	1	0-1	0.831	0.25
Minani.Fa	16	4-39	17.00	8.94
Minani.Nu	6	2-15	6.50	3.35
Minani.Fi	4	2-9	4.31	2.00
Minship.Fa	1	0-1	0.678	0.47
Minship.Nu	1	0-1	0.701	0.45
Minship.Fi	1	1-1	0.711	0.46
Nani.Fa1	2	0-8	2.7	2.09
Nani.Nu1	2	0-7	2.58	1.81
Nani.Fi1	2	0-6	2.42	1.51
Nani.Fa1.step	1	0-1	0.688	0.46
Nani.Nu1.step	1	0-1	0.702	0.46
Nani.Fi1.step	1	0-1	0.711	0.45
Travel.time	3.25	1.13-5.39	3.25	1.12
Travel	1	0-1	0..851	0.355
W.efficacy	0.010	0.005-0.115	0.024	0.032
Wd.efficacy	0.588	0.308-0.831	0.590	0.14
Wdd.efficacy	0.978	0.782-1	0.955	0.06
Scenarios	**Median**	**95% CrI***	**Mean**	**SD!**
2.fa	0	0-1	0.429	0.49
2.nu	0	0-1	0.445	0.50
2.fi	0	0-1	0.450	0.50
3.fa	1	0-1	0.505	0.5
3.nu	1	0-1	0.524	0.49
3.fi	1	0-1	0.531	0.49
4.fa	1	0-1	0.540	0.4
4.nu	1	0-1	0.560	0.50
4.fi	1	0-1	0.568	0.50

Table S1 continued on page 4

Table S1 continued: Summary posterior distribution of nodes and scenarios used in the Bayesian model simulated to evaluate the probability that a truck will be contaminated with PRRS virus at the end of a working day.

Scenarios	Median	95% CrI*	Mean	SD!
fa	0.499	0-1	0.482	0.45
nu	0.522	0-1	0.490	0.45
fi	0.529	0-1	0.501	0.45
fa.w	0.486	0-0.996	0.471	0.44
nu.w	0.511	0-0.996	0.488	0.44
fi.w	0.517	0-0.996	0.495	0.44
fa.wd	0.164	0-0.636	0.197	0.21
nu.wd	0.181	0-0.639	0.205	0.21
fi.wd	0.185	0-0.643	0.207	0.21
fa.wdd	0.001	0-0.159	0.022	0.05
nu.wdd	0.001	0-0.159	0.023	0.05
fi.wdd	0.001	0-0.160	0.023	0.05

* 95% credible Interval
! Standard deviation

Table S2: Sensitivity analysis for the probability that a truck used by swine farms will be contaminated with PRRS virus at the end of a working day.

		Parameter						
Scenarios	Notations	Nani	F. Prev	A.Prev	Shed.ani	±% change in input parameter	Median probability	±% change in median probability
fi	1344	2	50	80	70	NA	0.517	Baseline scenario
Change in Nani to 4	2344	4	50	80	70	100%	0.474	-9.71
Change in Nani to 8	3344	8	50	80	70	200%	0.318	-39.43
Change in farm level prevalence to 10%	1144	2	10	80	70	-80	0.000	-100.00
Change in farm level prevalence to 30%	1244	2	30	80	70	-40	0.311	-40.76
Change in farm level prevalence to 70%	1444	2	70	80	70	40	1.0	90.48
Change in animal level prevalence to 10%	1314	2	50	10	70	-87.5	0.000	-100.00
Change in animal level prevalence to 30%	1324	2	50	30	70	-62.5	0.458	-12.76
Change in animal level prevalence to 50%	1334	2	50	50	70	-37.5	0.515	-1.90
Change in animal level prevalence to 100%	1354	2	50	100	70	25	0.551	4.95
Change in shedding animal (Shed.ani) to 10%	1341	2	50	80	10	-85.7	0.000	-100.00
Change in shedding animal (Shed.ani) to 30%	1342	2	50	80	30	-57	0.485	-7.62
Change in shedding animal (Shed.ani) to 50%	1343	2	50	80	50	-28.6	0.516	-1.71
Change in shedding animal (Shed.ani) to 90%	1345	2	50	80	90	28.6	0.555	5.71

#CODES FOR THE MODEL

#A. Codes for OpenBugs

```
Model {

tr.use[1:3] ~dmulti(p.truse[], 100)
p.truse[1:3]~ddirch(alpha[])
for(k in 1:3){ alpha[k]<-1}

#Truck used by
#tr.use2 ~ dbin(p.truse2, n)
#tr.use3 ~ dbin(p.truse3, n)
#tr.use4 ~ dbin(p.truse4, n)

#P that atleast one farm is infected
farm.pos2 ~ dbin(farm.prev, 2)
F.inf.2<- step(farm.pos2-0.5)

farm.pos3 ~ dbin(farm.prev, 3)
F.inf.3<- step(farm.pos3-0.5)

farm.pos4 ~ dbin(farm.prev, 4)
F.inf.4<- step(farm.pos4-0.5)

comb.prob <-F.inf.2*p.truse[1]+F.inf.3*p.truse[2]+F.inf.4*p.
truse[3]

#P that the truck has more than Minimum infected animals

Nani.fa~dhyper(Minani.fa, m.fa, N.fa, 1)
n1.fa~dunif(1,50)
Minani.fa<-round(n1.fa)
shipsize.fa1~dunif(5, 175)
shipsize.fa2~dunif(5, 175)
shipsize.fa<-(shipsize.fa1+shipsize.fa2)

Nani.fa1~dhyper(Minani.fa,m.fa, N.fa, 1)
Nani.fa1.step<- step(Nani.fa1-2)

Minship.Fa <- step(shipsize.fa-Minani.fa)*Nani.fa1.step

Nani.nu~dhyper(Minani.nu, m.nu, N.nu, 1)
n1.nu~dunif(1,30)
Minani.nu<-round(n1.nu)
shipsize.nu1~dunif(6, 350)
shipsize.nu2~dunif(6, 350)
shipsize.nu<-(shipsize.nu1+shipsize.nu2)

Nani.nu1~dhyper(Minani.nu,m.nu, N.nu, 1)

Nani.nu1.step<- step(Nani.nu1-2)

Minship.Nu <- step(shipsize.nu-Minani.nu)*Nani.nu1.step
Nani.fi~dhyper(Minani.fi, m.fi, N.fi, 1)
n1.fi~dunif(1,20)
Minani.fi<-round(n1.fi)
shipsize.fi1~dunif(3, 150)
shipsize.fi2~dunif(3, 150)
shipsize.fi<-(shipsize.fi1+shipsize.fi2)

Nani.fi1~dhyper(Minani.fi,m.fi, N.fi, 1)
Nani.fi1.step<- step(Nani.fi1-2)

Minship.Fi <- step(shipsize.fi-Minani.fi)*Nani.fi1.step

#P that the travel time was more than two hours
travel.time1~dunif(0.25, 3)
travel.time2~dunif(0.25, 3)
travel.time<-(travel.time1+travel.time2)

##travel.time~dbeta(alpha.t, beta.t)
#mean<-(min.t+lambda*mode.t+max.t)/(lambda+2)
#alpha.t<-(mean-min.t)*(2*mode.t-min.t-max.t)/((mode.t-
  mean)*(max.t-min.t))
#beta.t<-(alpha.t*(max.t-mean))/(mean-min.t)
#lambda~dgamma(alpha1, beta1)

#travel.time ~ dnorm(mean, prec)C(0,)
#mean <-(0.5+4*2+6)/6
#sd<-(6-0.5)/6
#prec<-1/pow(sd, 2)
Travel <- step(travel.time-2)

#Evaluation of cleaning and disinfection protocols

#Truck_wash_protection node
N.W.Prot ~ dbin(W.efficacy, N.W)

#Tr_washndisinfection_protection node
N.Wd.Prot ~ dbin(Wd.efficacy, N.Wd)

#Tr_washndisinfectionndry_protection node
N.Wdd.Prot ~ dbin(Wdd.efficacy, N.Wdd)

# Prior distribns for efficacy - 50%
W.efficacy ~ dbeta(0.5,0.5)
Wd.efficacy ~ dbeta(0.5,0.5)
Wdd.efficacy ~ dbeta(0.5,0.5)

#p.truse2 ~ dbeta(0.5,0.5)
#p.truse3 ~ dbeta(0.5,0.5)
#p.truse4 ~ dbeta(0.5,0.5)

#Prior for travel time
#alpha1<-0.0001
#beta1<-0.0001

#Scenarios
#Scenarios without cleaning
S.2.fa <- F.inf.2*Minship.Fa*Travel
S.2.nu <- F.inf.2*Minship.Nu*Travel
S.2.fi <- F.inf.2*Minship.Fi*Travel
S.3.fa<- F.inf.3*Minship.Fa*Travel
S.3.nu <- F.inf.3*Minship.Nu*Travel
S.3.fi<- F.inf.3*Minship.Fi*Travel
S.4.fa <- F.inf.4*Minship.Fa*Travel
S.4.nu <- F.inf.4*Minship.Nu*Travel
S.4.fi <- F.inf.4*Minship.Fi*Travel
S.fa <- comb.prob*Minship.Fa*Travel
S.nu <- comb.prob*Minship.Nu*Travel
S.fi <- comb.prob*Minship.Fi*Travel

#Scenarios with cleaning
S.fa.w <- (1-W.efficacy)*comb.prob*Minship.Fa*Travel
S.fa.wd <- (1-Wd.efficacy)*comb.prob*Minship.Fa*Travel
S.fa.wdd <- (1-Wdd.efficacy)*comb.prob*Minship.Fa*Travel
S.nu.w <- (1-W.efficacy)*comb.prob*Minship.Nu*Travel
S.nu.wd <- (1-Wd.efficacy)*comb.prob*Minship.Nu*Travel
S.nu.wdd <- (1-Wdd.efficacy)*comb.prob*Minship.Nu*Travel
S.fi.w <- (1-W.efficacy)*comb.prob*Minship.Fi*Travel
S.fi.wd <- (1-Wd.efficacy)*comb.prob*Minship.Fi*Travel
S.fi.wdd <- (1-Wdd.efficacy)*comb.prob*Minship.Fi*Travel
}
```

```
#B.  Codes for R for combined outputs and for running the
   CODA package
#Truck risk Model

library(R2OpenBUGS)

setwd("C:\\Users\\Risk_paper")

#Data
#Truck used by
tr.use= c(49, 19, 32)

#travel time

N.W.Prot=0
N.W=20
N.Wd.Prot=6
N.Wd=10
N.Wdd.Prot=10
N.Wdd=10
Nani.fa=2
Nani.nu=2
Nani.fi=2

#Now these parameters can easily be changed for the sensitivity
            analysis
farm.prev=0.5

shed.prop.fa=0.2
shed.prop.nu=0.5
shed.prop.fi=0.7

ani.prev=1

N.fa=351
m.fa=round(ani.prev*shed.prop.fa*N.fa); m.fa

N.nu=700
m.nu=round(ani.prev*shed.prop.nu*N.nu); m.nu

N.fi=250
m.fi=round(ani.prev*shed.prop.fi*N.fi); m.fi

data.b <- c("tr.use", "N.W.Prot", "N.W", "N.Wd", "N.Wd.Prot",
"N.Wdd.Prot", "N.Wdd", "Nani.fa", "Nani.nu", "Nani.fi", "m.fa",  "N.fa",

        "m.nu", "N.nu", "m.fi", "N.fi", "farm.prev" )

par.b <- c("farm.pos2", "farm.pos3", "farm.pos4", "comb.prob",
  "Minani.fa",

      "Minani.nu", "Minani.fi", "Minship.Fa", "Minship.Nu",
  "Minship.Fi",

      "Nani.fa1", "Nani.nu1", "Nani.fi1", "Nani.fa1.step",
  "Nannu1.step", "Nani.fi1.step",

      "travel.time", "Travel", "W.efficacy", "Wd.efficacy",
  "Wdd.efficacy",

      #Scenarios

      "S.2.fa", "S.2.nu", "S.2.fi", "S.3.fa", "S.3.nu", "S.3.fi", "S.4.fa",
      "S.4.nu", "S.4.fi", "S.fa", "S.nu", "S.fi",

      #Scenarios with cleaning

      "S.fa.w", "S.fa.wd", "S.fa.wdd", "S.nu.w", "S.nu.wd",
        "S.nu.wdd",
      "S.fi.w" , "S.fi.wd", "S.fi.wdd"

)
#par.c<-c("S.4.fi")

inits.2<- list(list( W.efficacy=0, Wd.efficacy=1, Wdd.efficacy=0.1),
#shipsize.fa=5,

          list( W.efficacy=0.05, Wd.efficacy=0.5, Wdd.efficacy=1),
           #shipsize.fa=50,

          list( W.efficacy=1, Wd.efficacy=0.5, Wdd.efficacy=0.1))
           #shipsize.fa=100,

tr.risk <- bugs(data.b, inits=inits.2 , parameters=par.b,
  "Risk_model_openbugs_May19.txt",

          n.chains = 3, n.burnin=10000, n.iter = 50000, n.thin=1,
codaPkg=F,

          working.directory = getwd(), clearWD=F, debug=F,
           DIC=F)

print(tr.risk, digits=4)

#analysis convergence
library(coda)
tr.out=as.mcmc.list(tr.risk)
codamenu()
2
tr.out
#after this need to use interactive coda menu
gelman.plot(tr.out, bin.width = 10, max.bins = 50)
```