NDV\_Paper

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## Data

Samples are deemed positive if:

Chicks are positive if one or both (CLO and ON) samples are positive.

Result: No inconsistent ELISA and CT-positive samples

Only CLO is not possible and inconsistent with ELISA

# Material and methods

## Visualization of descriptive data

* Survival plot
* Epidemic curves (number of infectious animals divided by the total) were produced.
* Histogram of infectious period

## Statistical analyses

The infectious period : Parametric survival analyses assuming Normal distribution

The transmission parameter : Generalized linear model with a complementary loglog-link function:

glm(cbind(C, S-C) ~ 1,offset = log(I/N), family = binomial(link = "cloglog"), data = data.set, na.action = na.omit)

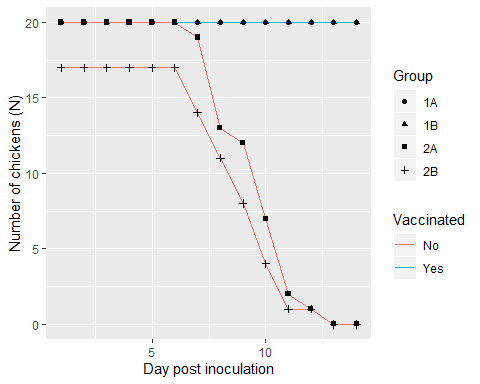
The basic reproduction number The confidence interval is calculated by

Assumes independence between the transmission parameter and the infectious period.

# Results

## Survival curve

survivalplot



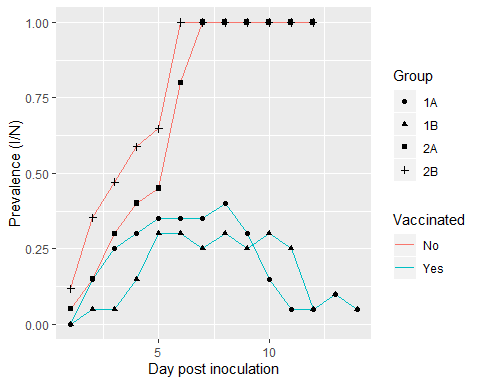
Infection curves

## Epidemic curve SIR and one or both positive

epicurveplot

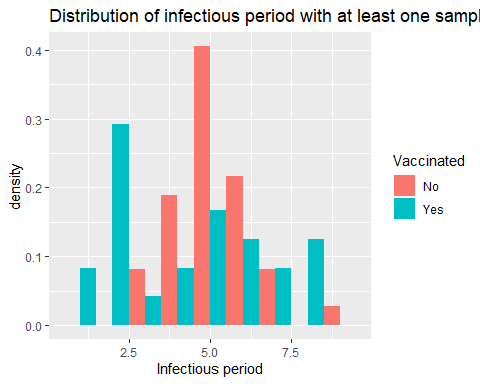
## Warning: Removed 4 rows containing missing values (geom\_path).

## Warning: Removed 4 rows containing missing values (geom\_point).



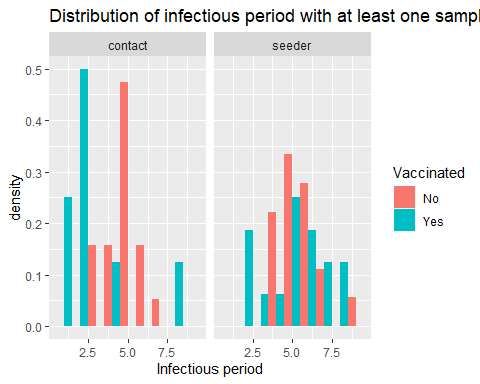
## at least one (CLO or ON) positive sample

hist.one



## at least one (CLO or ON) positive sample

hist.one.chal



## Infectious period

mean.beta.inf.R[, c(1,5,6,7)]

## Vaccinated infper llinfper ulinfper  
## 1 No 4.789474 4.154680 5.424267  
## 2 Yes 3.380799 1.477503 5.284095

p =

signif(pvalueInf,2)

## [1] 0.03

## 

mean.beta.inf.R[, c(1,2,3,4)]

## Vaccinated beta llbeta ulbeta  
## 1 No 0.7123108 0.43678638 1.086711  
## 2 Yes 0.3205199 0.09646276 0.972477

p-value:

signif(pvalueBeta,2)

## [1] 0.023

## 

mean.beta.inf.R[, c(1,11,12,13)]

## Vaccinated R llR ulR  
## 1 No 3.411594 1.29263601 4.198793  
## 2 Yes 1.083613 0.04568178 1.647043

# Conclusion and discussion

## Conclusion

Based on the assumption of one of both samples required to be positive, we find that the transmission parameter is lower, and the mean infectious period in the contact birds is lower, which results in a reproduction number which is smaller, but is not lower than the threshold .

# Additional assessment

## Compare CT value

For those that were defined positive

signif(summary(lm(valueP ~ ci + Sample + Vaccinated, data= melt.ct.data))$coefficients,2)

## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 26.00 0.49 52.0 8.1e-124  
## ciseeder -1.90 0.53 -3.7 3.0e-04  
## SampleON swab -0.56 0.55 -1.0 3.1e-01  
## VaccinatedYes 8.40 0.59 14.0 3.7e-33

summary(lm(valueP ~ ci, data= melt.ct.data[melt.ct.data$Vaccinated=="Yes"& melt.ct.data$Sample=="ON swab",]))

##   
## Call:  
## lm(formula = valueP ~ ci, data = melt.ct.data[melt.ct.data$Vaccinated ==   
## "Yes" & melt.ct.data$Sample == "ON swab", ])  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -5.5151 -1.8651 0.9407 2.1549 4.6607   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 30.869 0.720 42.87 <2e-16 \*\*\*  
## ciseeder 1.476 0.829 1.78 0.0806 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.694 on 55 degrees of freedom  
## (503 observations deleted due to missingness)  
## Multiple R-squared: 0.05449, Adjusted R-squared: 0.03729   
## F-statistic: 3.169 on 1 and 55 DF, p-value: 0.08055

summary(lm(valueP ~ ci, data= melt.ct.data[melt.ct.data$Vaccinated=="No"& melt.ct.data$Sample=="ON swab",]))

##   
## Call:  
## lm(formula = valueP ~ ci, data = melt.ct.data[melt.ct.data$Vaccinated ==   
## "No" & melt.ct.data$Sample == "ON swab", ])  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -7.4628 -2.4659 -0.5778 2.4695 10.1472   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 25.833 0.589 43.862 < 2e-16 \*\*\*  
## ciseeder -3.649 0.917 -3.979 0.000154 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.038 on 78 degrees of freedom  
## (438 observations deleted due to missingness)  
## Multiple R-squared: 0.1688, Adjusted R-squared: 0.1581   
## F-statistic: 15.84 on 1 and 78 DF, p-value: 0.0001537

## Seeder acted as contact

Two seeder bird #817 and #818 in unvaccinated were positive slower. These were transfered to the contact group.

## INfectious period

#  
mean.beta.inf.R[, c(1,5,6,7)]

## Vaccinated infper llinfper ulinfper  
## 1 No 4.789474 4.154680 5.424267  
## 2 Yes 3.380799 1.477503 5.284095

pvalueInf

## [1] 0.02951464

## Transmision parameter

mean.beta.inf.R[, c(1,2,3,4)]

## Vaccinated beta llbeta ulbeta  
## 1 No 0.7123108 0.43678638 1.086711  
## 2 Yes 0.3205199 0.09646276 0.972477

pvalueBeta

## [1] 0.02274817

## Reproduction number

mean.beta.inf.R[, c(1,11,12,13)]

## Vaccinated R llR ulR  
## 1 No 3.411594 1.29263601 4.198793  
## 2 Yes 1.083613 0.04568178 1.647043

## Information on versions

sessionInfo()

## R version 3.6.0 (2019-04-26)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 17763)  
##   
## Matrix products: default  
##   
## locale:  
## [1] LC\_COLLATE=Dutch\_Netherlands.1252 LC\_CTYPE=Dutch\_Netherlands.1252   
## [3] LC\_MONETARY=Dutch\_Netherlands.1252 LC\_NUMERIC=C   
## [5] LC\_TIME=Dutch\_Netherlands.1252   
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## other attached packages:  
## [1] survival\_3.1-8 lme4\_1.1-21 Matrix\_1.2-18 ggplot2\_3.2.1 openxlsx\_4.1.4  
##   
## loaded via a namespace (and not attached):  
## [1] zip\_2.0.4 Rcpp\_1.0.3 plyr\_1.8.5 highr\_0.8   
## [5] nloptr\_1.2.1 pillar\_1.4.3 compiler\_3.6.0 tools\_3.6.0   
## [9] boot\_1.3-24 digest\_0.6.23 nlme\_3.1-143 evaluate\_0.14   
## [13] lifecycle\_0.1.0 tibble\_2.1.3 gtable\_0.3.0 lattice\_0.20-38   
## [17] pkgconfig\_2.0.3 rlang\_0.4.4 yaml\_2.2.1 xfun\_0.12   
## [21] withr\_2.1.2 stringr\_1.4.0 dplyr\_0.8.4 knitr\_1.27   
## [25] grid\_3.6.0 tidyselect\_1.0.0 glue\_1.3.1 R6\_2.4.1   
## [29] rmarkdown\_2.1 minqa\_1.2.4 reshape2\_1.4.3 farver\_2.0.3   
## [33] purrr\_0.3.3 magrittr\_1.5 MASS\_7.3-51.5 splines\_3.6.0   
## [37] scales\_1.1.0 htmltools\_0.4.0 assertthat\_0.2.1 colorspace\_1.4-1  
## [41] labeling\_0.3 stringi\_1.4.4 lazyeval\_0.2.2 munsell\_0.5.0   
## [45] crayon\_1.3.4