ENV
NANTES

How herd structure influences the within-herd spread of bovine viral diarrhoea virus (BVDV)

P. Ezanno*, C. Fourichon, H. Seegers

*Corresponding author: Unit of Animal Health Management, ENVN, INRA, BP 40706, F-44307 Nantes, France
Ph. +33 240 687 854; Fax +33 240 687 768; Email ezanno@vet-nantes.fr

INTRODUCTION

In structured populations, groups may have contrasted risks of spreading pathogens in relation to the infectiousness of infected individuals in each group and to the contact rate within- and between-group. In models of within-herd BVDV spread, typical cattle herds were modelled for which parameters of the herd dynamics could be estimated. Herd structure was rarely modelled, whereas the between-group BVDV transmission rate for persistently-infected (PI) animals has been shown to highly influence BVDV spread. Moreover, various herd structures are encountered in the field due to variations in the number of groups per herd, group types and between-group relationships. The objective was to model BVDV spread in a dairy herd for different within-herd contact structures in order to identify at-risk scenarios in terms of BVDV spread.

MODEL & SCENARIOS

Model of within-herd BVDV spread.

A stochastic compartmental model in discrete time (time step = 14 days) represented the BVDV spread in a typical Holstein dairy herd (Tab. 1) of medium size (45 cows, 20 heifers and the associated young-stock). Between-group transitions depended on sex, age or reproductive status. In each group, animals were susceptible (*S*), transiently-infected (*T*), immune (*R*), protected by maternal antibodies (*M*) or PI (*P*). *T* animals were infectious for 14 days. Half the *P* animals died before one year of age. Initially, all animals were susceptible. BVDV was introduced once in the herd by the purchase of an immune heifer carrying a PI fœtus.

Group	Definition
c	calves
H_1	young heifers
H_2	older heifers
LC	lactating cows
DC	dry cows

Tab. 1: Herd consisted in 5 groups

Pairs
c + LC
c + H_1
$H_1 + H_2$
H_2 *+ DC*
LC + DC

Tab. 2: Pairs of groups

Scenarios of herd structure.

A between-group transmission parameter was specified per pair of groups. In the reference scenario, between-group transmission was 0.10 for all pairs. Group isolation corresponded to no between-group transmission for a given group. Merging groups g_1 and g_2 (Tab. 2) led to the following function of transmission, with *a* denoting for groups other than g_1 or g_2; $\beta^X{}_w$ the within-group transmission rate for animals in infectious status *X* (*P* or *T*); $\beta^P{}_{b\text{-}g1,a}$ the transmission rate between groups g_1-g_2 and *a* for *P* animals; $P_x(t)$ and $T_x(t)$ the number of *P* and *T* animals, and $N_x(t)$ the total number of animals in group *x* at time *t*.

$$p_{\text{inf}}(g_1,g_2,t)=\beta_w^P\frac{P_{g_1}(t)+P_{g_2}(t)}{N_{g_1}(t)+N_{g_2}(t)}+\beta_w^T\frac{T_{g_1}(t)+T_{g_2}(t)}{N_{g_1}(t)+N_{g_2}(t)}+\sum_{a\neq g_1,g_2}\beta_{b-g_1,a}^P\frac{P_a(t)}{N_a(t)\left(N_{g_1}(t)+N_{g_2}(t)\right)}$$

Output	Definition
Per_80pc	time needed to reach 80% of infection extinction
EpSizP	cumulative # of P animals
NbP	mean # of *P* animals / infected herd
NbPF	mean # of females carrying a *P* foetus / infected herd
NbT	mean # of *T* animals / infected herd

Tab. 3: Model outputs definitions

RESULTS

Isolating groups.

Isolating all groups simultaneously globally decreased model outputs (Fig. 1), the effect being especially due to isolating group *LC*. Isolating group *c* decreased infection persistence and the mean number of immune dams carrying a PI foetus, but increased the mean number of PI animals in infected herds. Isolating groups H_1, H_2 or *DC* had globally a lower if any effect. The number of *T* animals in infected herds was not very sensitive to isolating a group.

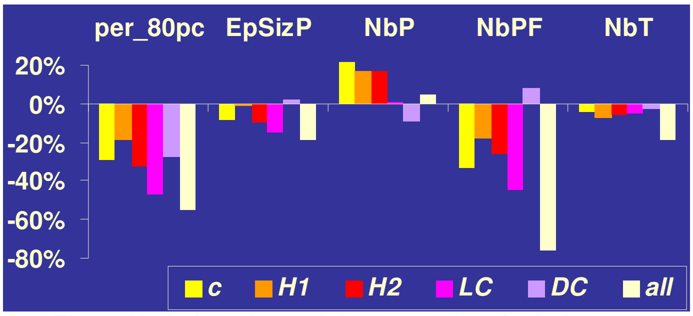

Fig. 1: Variations in model outputs after isolating groups

Merging groups.

Merging all groups increased all model outputs, the effect being especially due to merging *c* and *LC*. Merging H_1 and H_2 also increased model outputs with a lower effect. Both merging H_2 and *DC* or *c* and H_1 barely decreased BVDV spread. Merging *LC* and *DC* had no effect on BVDV spread.

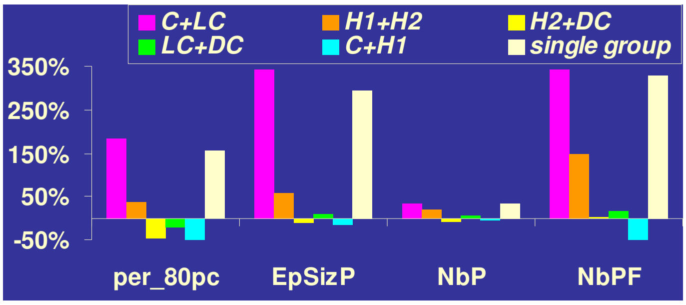

Fig. 2: Variations in model outputs after merging groups

CONCLUSION

Within-herd BVDV persistence after a single introduction of the virus in a fully susceptible herd is reduced if lactating cows are isolated from other groups, especially from calves, and if young animals are raised in a single group.