Modelling of strategies for genetic control of scrapie in sheep: the importance of population structure

T.J. Hagenaars, M.B. Melchior, J.J. Windig, A. Bossers, A. Davidse, F.G. van Zijderveld

Background

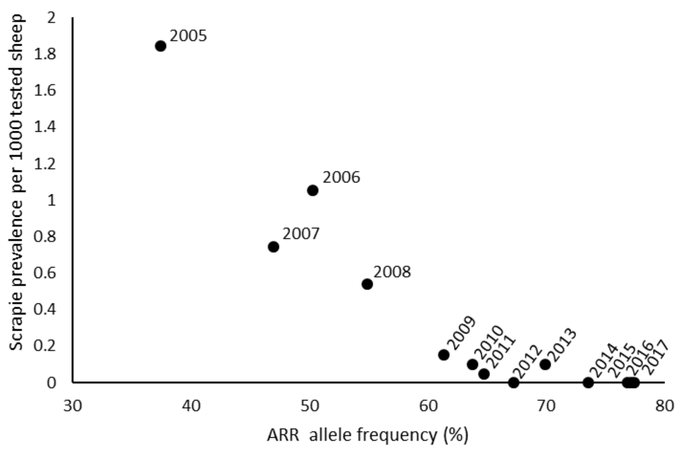
- Scrapie is a TSE in sheep and an example of a disease that may be controlled through breeding for disease resistance.
- EU member states have introduced strategies for breeding against scrapie based on selection of genetically resistant breeding rams.
- The strategy in The Netherlands consisted of selecting resistant rams for breeding throughout both breeding and production sectors.

Objectives

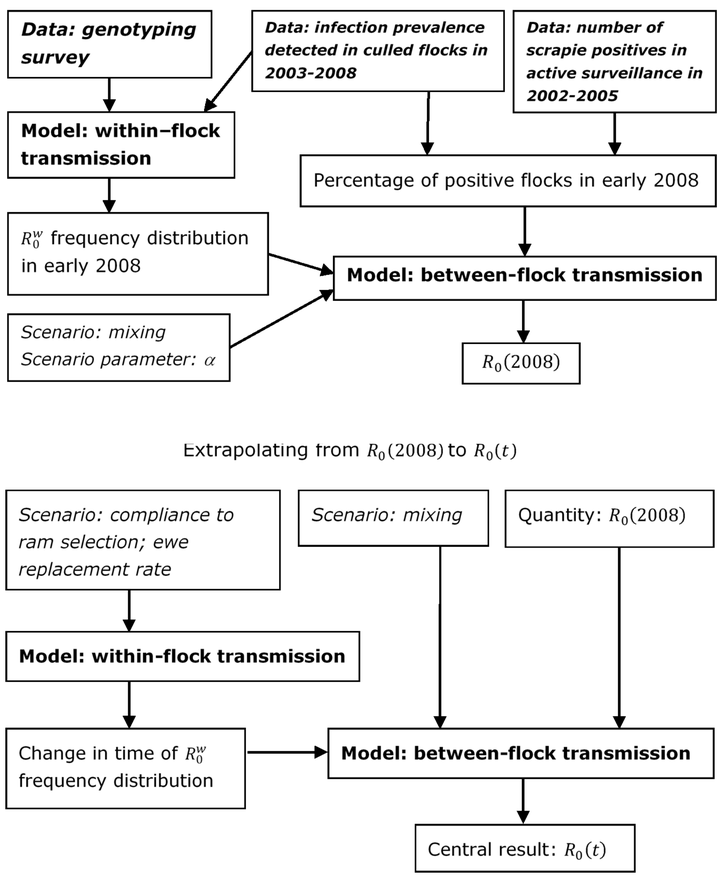
- Mathematical modelling the effect of a breeding program on the spreading capacity of scrapie in a national flock
- Using this model to assess how long a breeding strategy needs to be maintained to achieve disease control.

Method

- Development of a model applied to the Dutch context, using data:
  - on the genetic content of the Dutch sheep population;
  - on scrapie occurrence in this population.



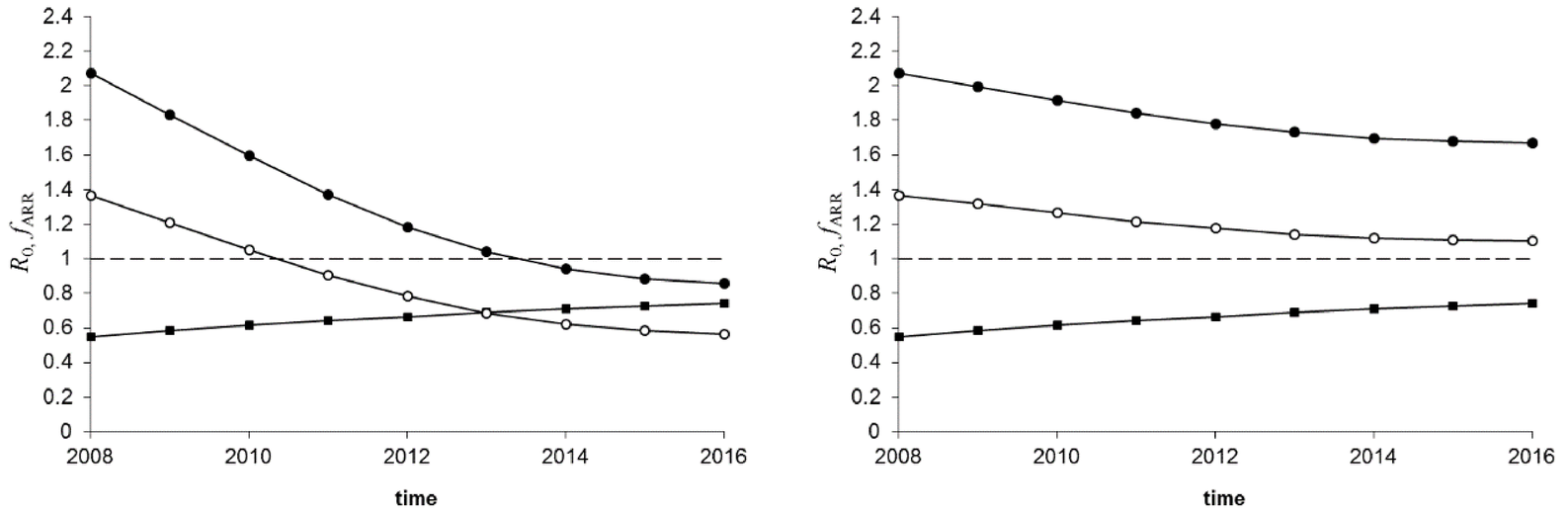
Data informing the model for calculating of the quantity $R_0(2008)$



References

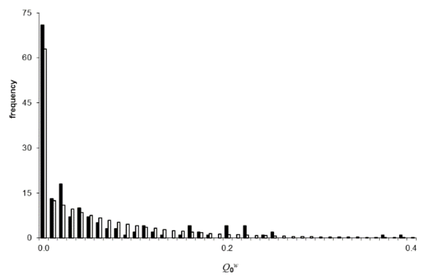
1. Hagenaars T.J., Windig J.J. PLoS ONE 2015; 10(10): e0139436.
2. Hagenaars TJ, Melchior MB, Windig JJ, Bossers A, Davidse A, van Zijderveld FG (2018) PLoS ONE 13(3): e0195009.

Results

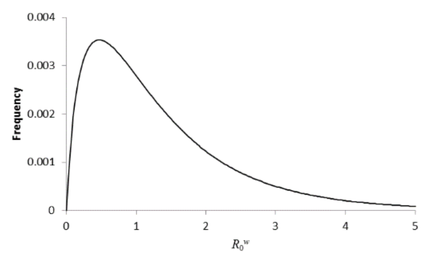


Predicted effect of breeding program. Predicted R_0 between Dutch flocks (circles) and ARR allele frequency f_{ARR} (squares) as a function of time; assumed is a yearly replacement rate of 20% (r = 20%). The line with open (closed) circles corresponds to moderate (strong) mixing heterogeneity between flocks. The dashed line indicates the critical value R_0 = 1. Left panel: Compliance to ram selection of 75%; Right panel: Compliance to ram selection of 35%.

Model details



Weighted flock genotype frequencies: histogram of R^w_0/β. Black bars: calculated using the within-flock model of Ref. [1] from the genotyping survey results in 168 flocks. White bars: model distribution.



Model distribution of within-flock R_0.

Conclusions

- The time needed for obtaining scrapie control depends crucially on two parameters measuring sheep population structure:
  - the between-flock heterogeneity in genotype frequencies,
  - the heterogeneity of mixing (contact rates) between sheep flocks.
- Estimating the first parameter from Dutch genetic survey data and assuming scenario values for the second one, enables model prediction of the time needed to achieve scrapie control in The Netherlands.

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Wageningen University & Research
P.O. Box 123, 6700 AB Wageningen
Contact: thomas.hagenaars@wur.nl
T + 31 (0)320 238398
www.wur.nl/en/Research-Results/Research-Institutes/Bioveterinary-Research