

# Genetic parameters of tick-infestation on lambs of the Norwegian White Sheep

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10<sup>th</sup> World Congress on  
Genetics Applied to  
Livestock Production

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## Abstract

Sheep farmers in Norway experienced an increase in lamb loss on range pasture. One reason for is tick-borne fever (TBF) caused by *A. phagocytophilum* infection transmitted by the tick *Ixodes ricinus*.

Within breed variation in response to an *A.ph.* infection suggest that genetic variation is present.

Here genetic parameters of tick-count on lambs are estimated using data on 555 lambs of the Norwegian White Sheep breed from 6 different farms and a 10-generation pedigree.

Results suggest that heritability for tick-count among Norwegian White Sheep was moderate to high and that tick-load may be reduced by selective breeding.

## Objective

- to identify possible within-breed genetic variation in tick-counts in lambs

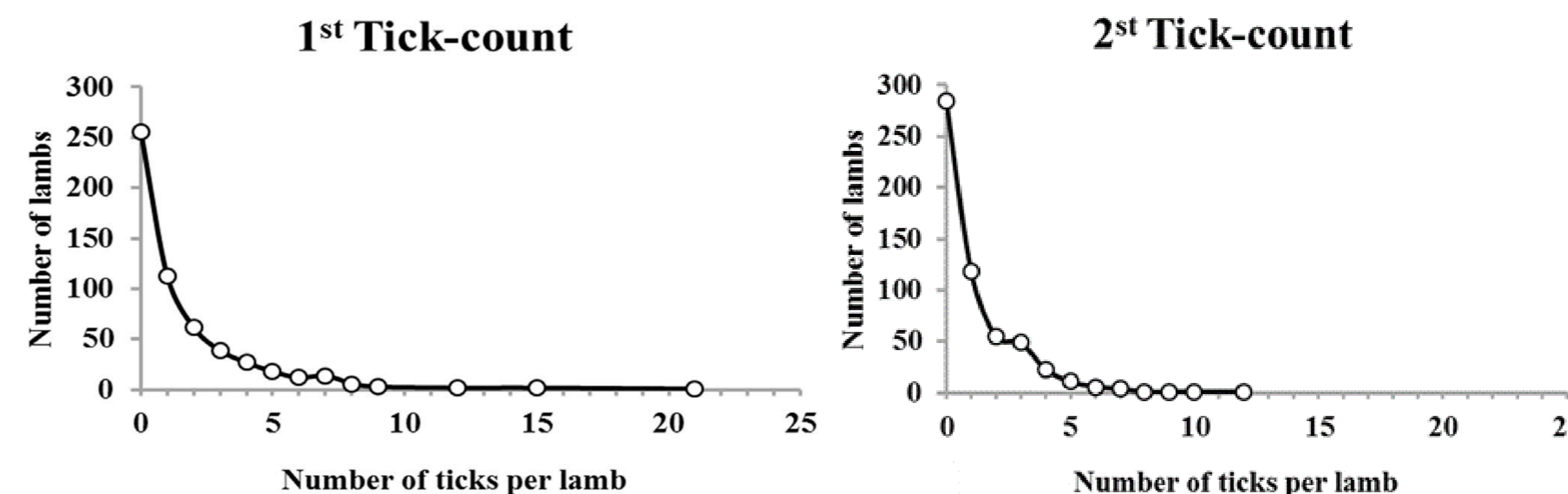


## Methods

- (Co)variance components estimated using maximum likelihood algorithm in ASReml
- three alternative sire-dam mixed models; linear models on observed tick-count, linear model on natural logarithm [observed tick-count + 1] and Poisson model.

## Results

**Distribution of the first and second tick-count per lam.**



**Estimates of heritability ( $h^2$ ), repeatability ( $r$ ) and common environmental effect ( $c^2$ ) of tick-count by three alternative models.**

Model	$h^2$	$r$	$c^2$
Linear [observed]	0.37 <sup>0.09</sup>	0.39 <sup>0.08</sup>	0.00 <sup>0.00</sup>
Linear [ln(observed+1)]	0.32 <sup>0.09</sup>	0.37 <sup>0.07</sup>	0.00 <sup>0.00</sup>
Poisson	0.59 <sup>0.10</sup>	0.69 <sup>0.09</sup>	0.00 <sup>0.00</sup>

Superscript is a standard error of the estimate.

## Conclusions

- moderate to high heritability for tick-count among Norwegian White Sheep
- tick-load may be reduced by selective breeding, but heritability estimates may be biased upwards.
- more studies are needed to accurately estimate the heritability for tick-count.

## References

- Stuen, S. (2003). PhD Thesis: Norwegian School of Veterinary Science, Norway.
- Granquist, E.G., Stuen, S., Crosby, L. et al. (2010). Vet. Immunol. Immunopathol. 133:117-124.
- Stuen, S., Grøva, L., Granquist E.G. et al. (2011). Acta Vet. Scand. 53:8
- Gilmour, A.R., Gogel, B.J., Cullis, B.R. et al. (2009). VSN international Ltd. UK.