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**

<table>
<thead>
<tr>
<th>Model</th>
<th>$h^2$</th>
<th>$r$</th>
<th>$c^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linear [observed]</td>
<td>0.37</td>
<td>0.39</td>
<td>0.00</td>
</tr>
<tr>
<td>Linear [ln(observed+1)]</td>
<td>0.32</td>
<td>0.37</td>
<td>0.00</td>
</tr>
<tr>
<td>Poisson</td>
<td>0.59</td>
<td>0.69</td>
<td>0.00</td>
</tr>
</tbody>
</table>

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**