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## Abstract:

Classical scrapie is a transmissible spongiform encephalopathy that affects small ruminants. Due to potential health risks, it is submitted to eradication measures. It is characterised in sheep by a genetic factor based on the PrP major susceptibility gene. Therefore, control strategies partly rely on selective breeding. Our aim was to study the impact of such strategies on the disease spread within a flock. To achieve this goal, an epidemiological dynamic model was coupled to the optimal outputs of a genetic model. The resulting model was applied to French dairy flocks exhibiting contrasting PrP genotype frequencies. Several breeding strategies, corresponding to various levels of genetic loss, were compared. They had a strong impact on the disease outbreak and are therefore an efficient tool to control scrapie. However, their efficacy in terms of disease eradication strongly depended on the scrapie introduction scenarios (e.g. one initial infected ewe vs. one per year). The robustness of the results was tested by a sensitivity analysis.