The dispersal of sea lice (*Lepeophtheirus salmonis*) genes coding for resistance towards antiparasitic agents – validation of a computer model

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Motivation:

- The increasing sea lice resistance problems in Norwegian salmon farming has become a hindrance for continued expansion of the industry, as staying below the maximum threshold of 0.5 adult female lice per fish has become demanding and expensive. It has also complicated sustainable managing of the industry, and has the potential of compromising the welfare of the salmon in the farms.
- The genetic composition of a population may be influenced by many factors, and even though the general driving forces behind the development and dispersal of resistance are well understood, very few attempts have been made to quantify the relative influence of these.
- Having access to a **reliable** predictive computer model would make it possible to anticipate the spread of resistance alleles, evaluate the strategies that best control lice infections and enable evidence-based decisions.

Aims:

Main: To validate and refine models and other predictive tools for use in describing the spread of drug resistance alleles in sea lice populations under different scenarios.

***Subgoals**:*

1. To establish, test and validate the model with data from laboratory studies on azamethiphos and pyrethroids.
2. To validate the model with field data on the effects of azamethiphos, pyrethroids, hydrogen peroxide, emamectin benzoate, chitin synthesis inhibitors.
3. To complete a broader validation of the model, using combined datasets on both medicinal and non-medicinal control methods.

Methods:

- The models will be based on an individual agent-based model published by McEwan et al. (2015).
- Self-generated datasets describing selection pressure and treatment efficacy for the different compounds under laboratory conditions will be compiled.
- Datasets from field treatments on efficacies, environmental parameters, infection pressures (lice counts in the area) and genotyping data of a representative number of lice collected before and after treatments will be compiled. Other relevant data will also be sought collected for further epidemiological analysis.
- Model validation will be performed in the simulation software AnyLogic®, and results will be analyzed statistically in R.

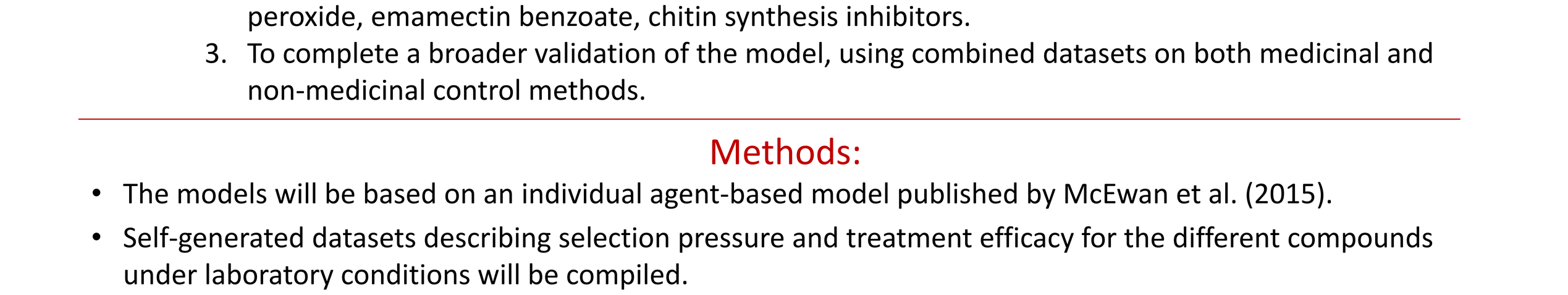

Figure 1. **Example of modelling potential:** The effect of influx of sensitive individuals and alternating treatments on the change in azamethiphos resistance marker distribution (R = resistance alleles) and treatment efficacy (y-axis) after different treatments (x-axis). The starting genotype frequency is equal in a, b and c (presented in a), as is the treatment efficacy of azamethiphos on the different genotypes.

a) Azamethiphos treatment only, **no** influx of sensitive genotypes
b) Azamethiphos treatment only, 22 % influx of sensitive (SS) genotypes after each treatment
c) Azamethiphos and H_2O_2 treatments alternating, 7 % influx of sensitive (SS) genotypes after each treatment

References:

McEwan, G., Groner, M.L., Fast, M.D., Gettinby, G. & Revie, C.W. (2015). Using Agent-Based Modelling to Predict the Role of Wild Refugia in the Evolution of Resistance of Sea Lice to Chemotherapeutants. *PLoS One, 10*(10), e0139128.

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