How to estimate the *Culicoides imicola* vectorial capacity for Bluetongue virus: benefit of the Bayesian approach

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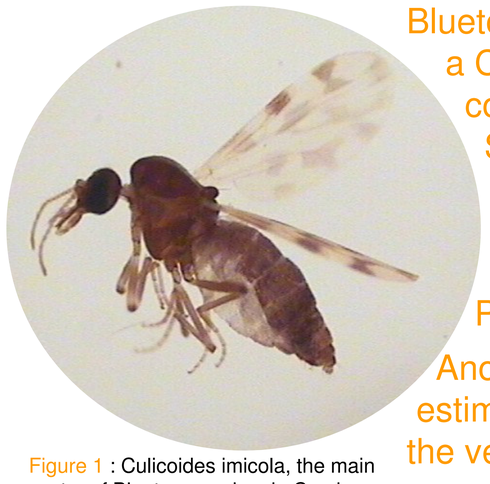

Figure 1 : Culicoides imicola, the main vector of Bluetongue virus in Corsica.
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Bluetongue (BT) is a viral disease transmitted in the old World by *Culicoides imicola*, a Ceratopogonidae Diptera (figure 1). It is a major disease that could lead serious economic consequences if the virus is introduced into naïve ovine populations as European ones.

Since 1998, several outbreaks have occurred in the Mediterranean region involving different serotypes. In 2004, the virus has still circulated in most of these areas (Corsica, Italy, Sicily, Sardinia, Spain, Greece) [Purse, B. V. *et al.*, 2005].In that context, predictive models have been developed to estimate the distribution of this vector in relation to satellite-derived climate variables [Baylis, M. *et al.*, 1999, Purse, B. V. *et al.*, 2004, Tatem, A. J. *et al.*, 2003].

Another way to approach the risk of disease spread is to estimate the potential of virus transmission in an area using the vectorial capacity (VC) of *Culicoides imicola* (box 1).

Box 1

Vectorial capacity represents " the number of infections the population of a given vector would distribute per case per day at a given place and time, assuming conditions of non-immunity" [Garrett-Jones, C., 1964].

Objective

- construct a model to estimate the vectorial capacity of *Culicoides imicola* population present in the southern France. It shall integrate relevant environmental factors that may influence it (temperature/humidity, host density; animal species, *imicola* abundance, etc. - figure 2).
- map this predictive vectorial capacity in the French Mediterranean basin.

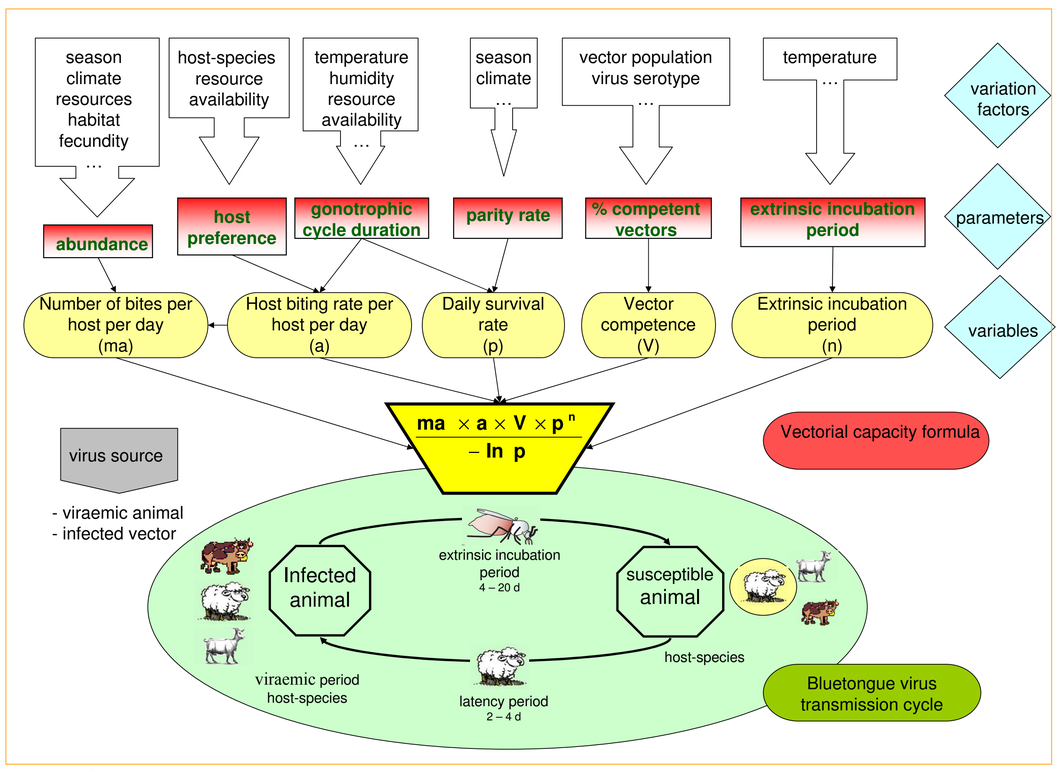

Figure 2 : Schematic representation of environmental factors that may influence entomological components of the *Culicoides imicola* vectorial capacity.

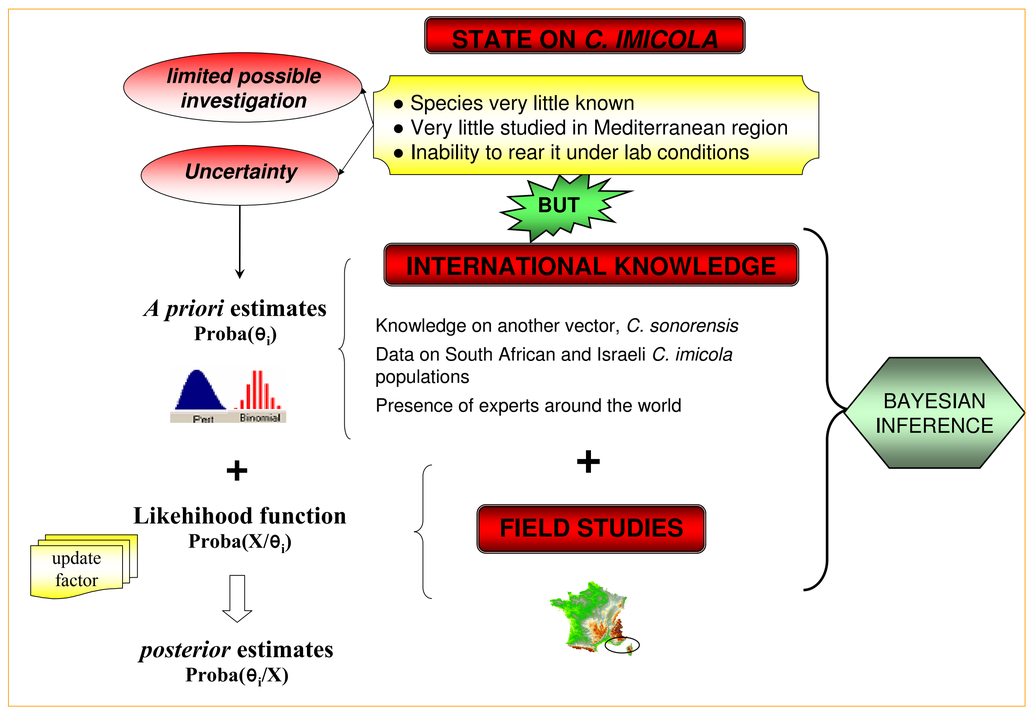

Figure 3 : Benefit of the bayesian approach

Steps

- Choice of probabilistic distributions modelling parameters of the CV formula: *a priori* distribution should fit with international knowledge and expert opinions.
- Monte Carlo simulation and sensitivity analysis (@risk software)
  - ➥ This step enabled to focus studies on parameters that mainly affect the outcome.
- Collecting data to improve the model:
  - ➥ Survey on *Culicoides imicola* in Var (France) to study *C. imicola* dynamics and its factors
  - ➥ *C. imicola* competence study by experimental oral infection (BTV 2 +/- 16)
- Posterior distributions of the VC parameters – model development - validation

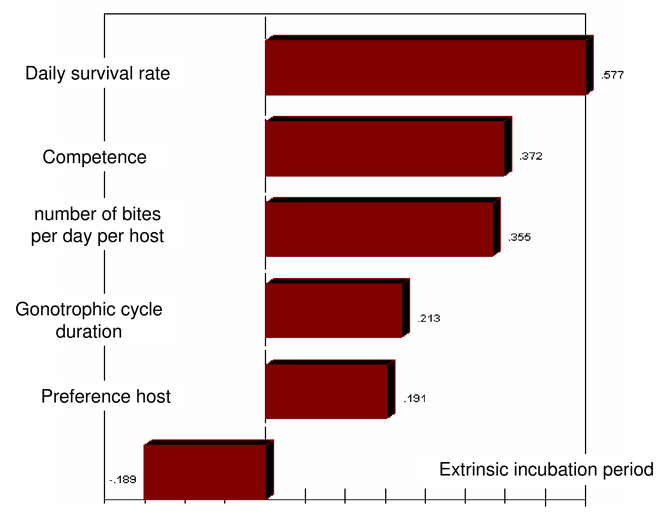

Figure 4 : Sensitivity analysis of the model parameters using international knowledge : a first step to direct studies

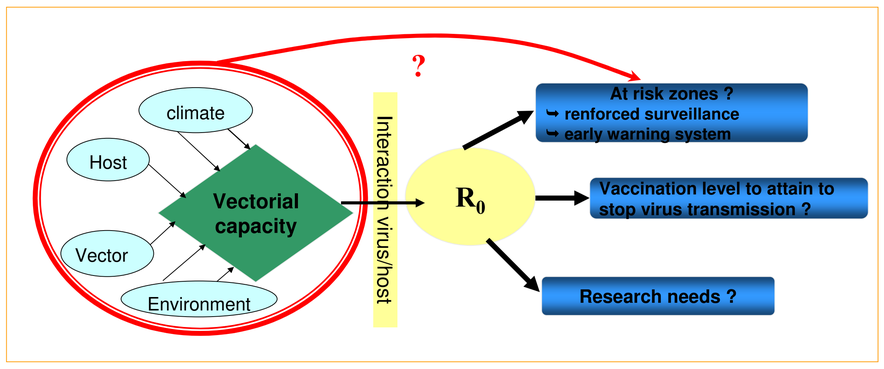

Figure 5 : "Understanding vector capacity is the key to understanding disease dynamics", Mullens (1995)

Perspectives

The establishment of such a BTV map risk based on vectorial capacity estimates should help decision makers to answer questions about BT management as :

- Which vaccination level is it critical to attain to stop the BT transmission?
- Where are the BT risk zones? And when?

This study should also permit to detect pertinent indicators that can be integrated in an early warning system (figure 5).

Centre de coopération internationale en recherche agronomique pour le développement

Design and production: CIRAD, Innovation and Communication Office
Fax: +33 4 67 61 55 13 - March 2005

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