



Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides* spp. wind dispersal

A. Blosse, Davide Martinetti, Giraud Aymeric, Albert Picado de Puig, Karine Chalvet-Monfray, Thibaud Porphyre

► To cite this version:

A. Blosse, Davide Martinetti, Giraud Aymeric, Albert Picado de Puig, Karine Chalvet-Monfray, et al.. Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides* spp. wind dispersal. 2023 SVEPM conference, Mar 2023, Toulouse, France. . hal-04028945v1

HAL Id: hal-04028945

<https://hal.inrae.fr/hal-04028945v1>

Submitted on 14 Mar 2023 (v1), last revised 15 Mar 2023 (v3)

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



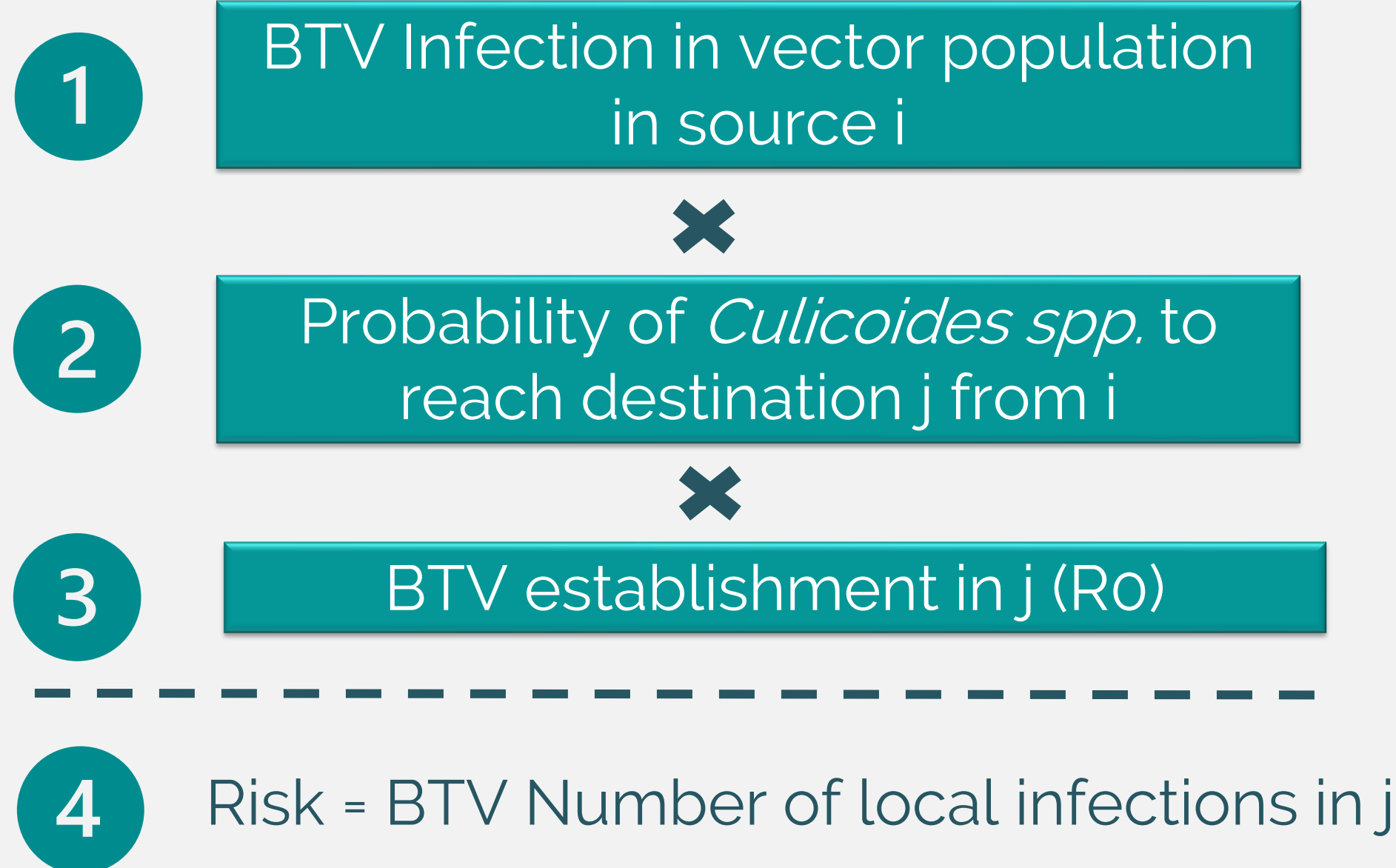
Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides spp.* wind dispersal

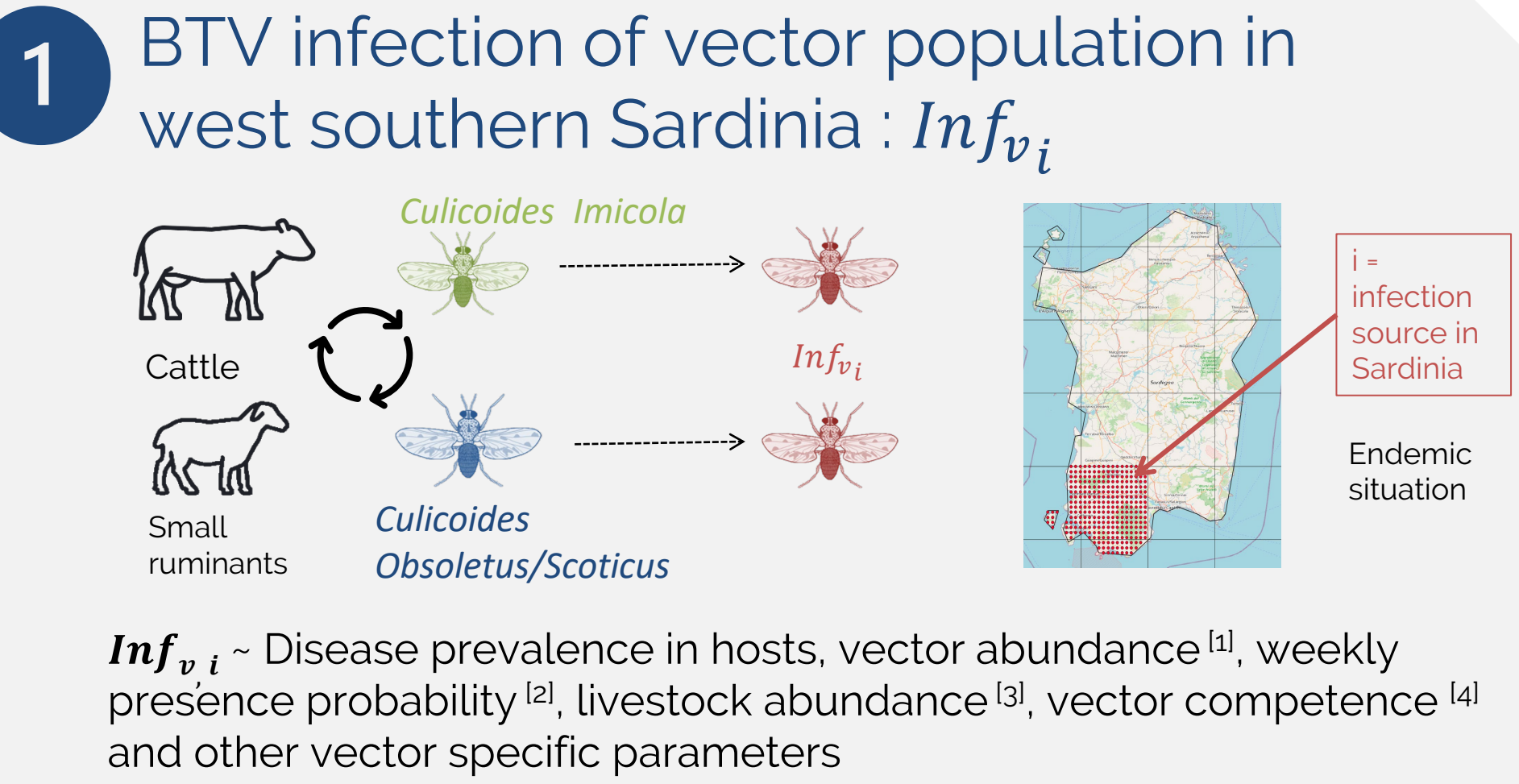
Sardinia island (Italy) experiences regular **orbiviruses incursions** like serotype 3 of **BlueTongue Virus (BTV)** in 2018, or Epizootic Hemorrhagic Disease Virus (EHDV) in 2022. Once the disease is established in Sardinia, what is the risk of introduction for the other regions in Europe?

Long-distance dispersal of the *Culicoides* vectors through the wind is a major disease **introduction pathway** but remains rarely considered in quantitative risk assessment models. However, combination of epidemiological and meteorological models can provide useful insights on risk estimations. A methodological framework and its first application for Sardinia as the infection source, are hereby presented.

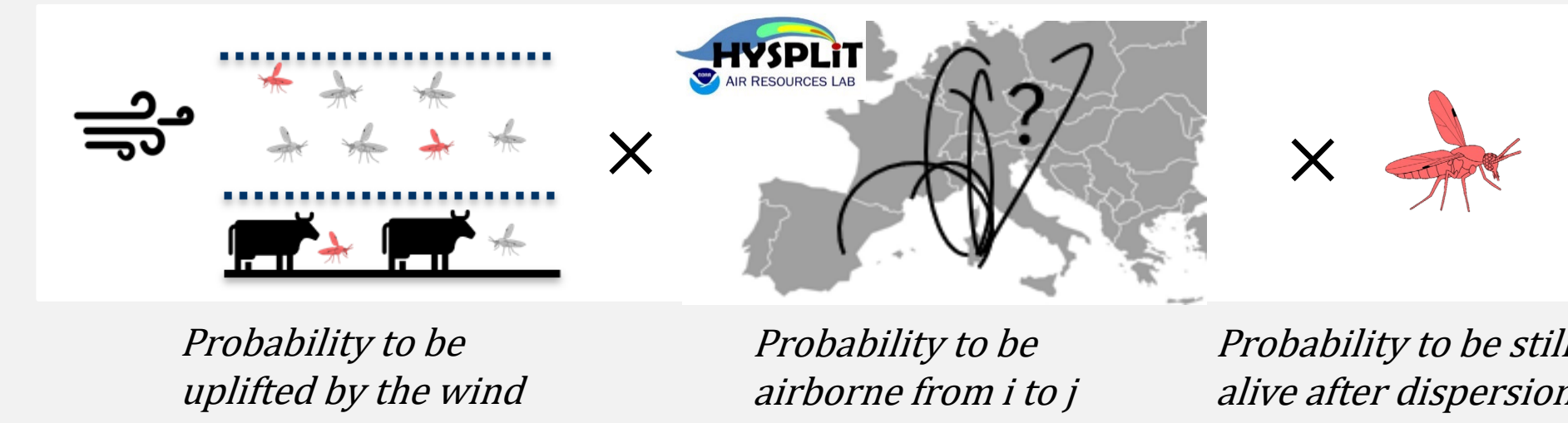
Model Framework



Method



- 2** Probability of long-distance dispersal : P_{LDWDj}
1. Simulate HYSPLIT® aerial trajectories from source area (i) to destination cells (j) :
 - daily from Week 11 (mid March) to Week 46 (mid November), named « study period »
 - at sunrise & sunset
 2. Filter trajectories according to **survival conditions** of the *Culicoides*.
 - o Max duration of aerial transport : scenarios for 24, 48 and 72 hours
 - o Trajectory below planetary boundary layer
 - o Temperature >10°C
 3. Calculate **frequency of trajectories reaching j** as a proxy for the probability to be dispersed from i to destination j by the wind
 4. Calculate **probability of long distance dispersal** considering ecology & biology of the *Culicoides spp.*



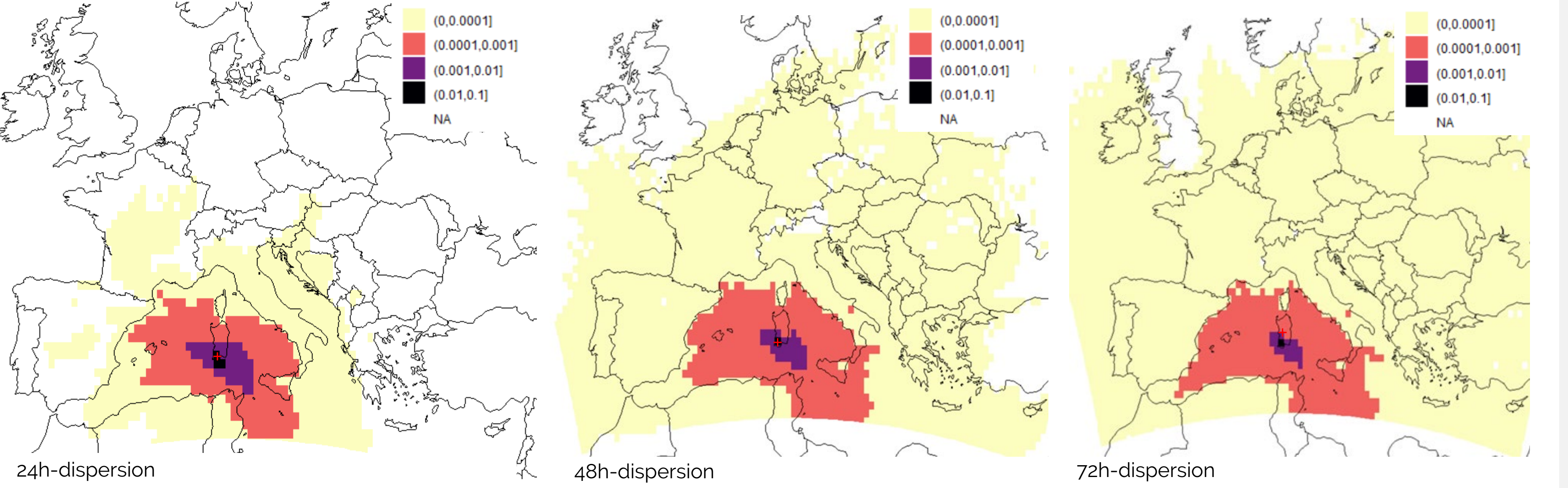
- 3** First local establishment at destination : R_0j
- R_0 = Basic Reproduction Number
- R_0 = Average number of secondary infections in destination produced by one exogenous infected vector
- Disease can be established at destination only if $R_0 > 1$
- R_0 formula from Turner et al.^[5] consider :
- different hosts populations and vectors populations
 - potential cross infections between vector populations

- 4** Introduction Risk
- Introduction risk in j is a combination of the 3 previous steps
- Risk = Number of local infections in destination j per unit of time

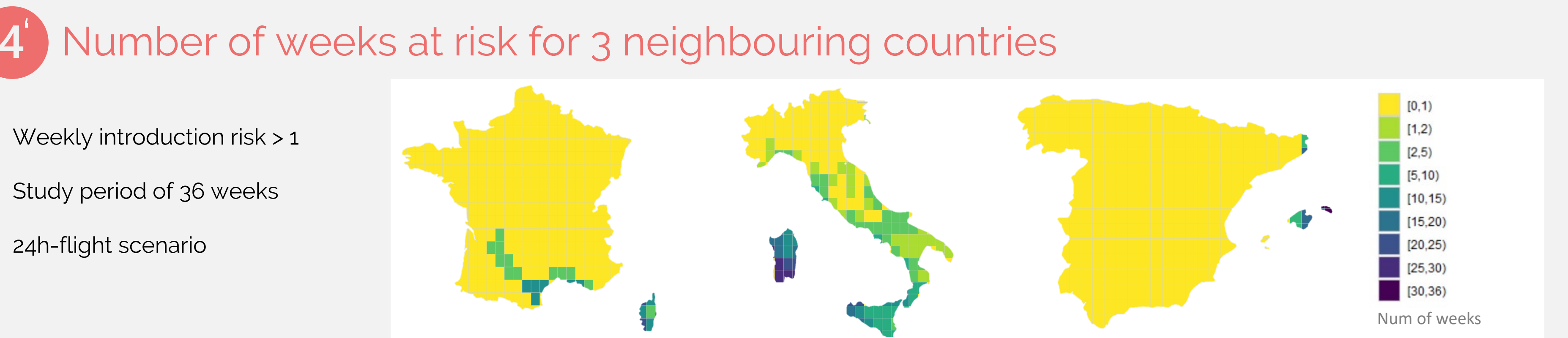
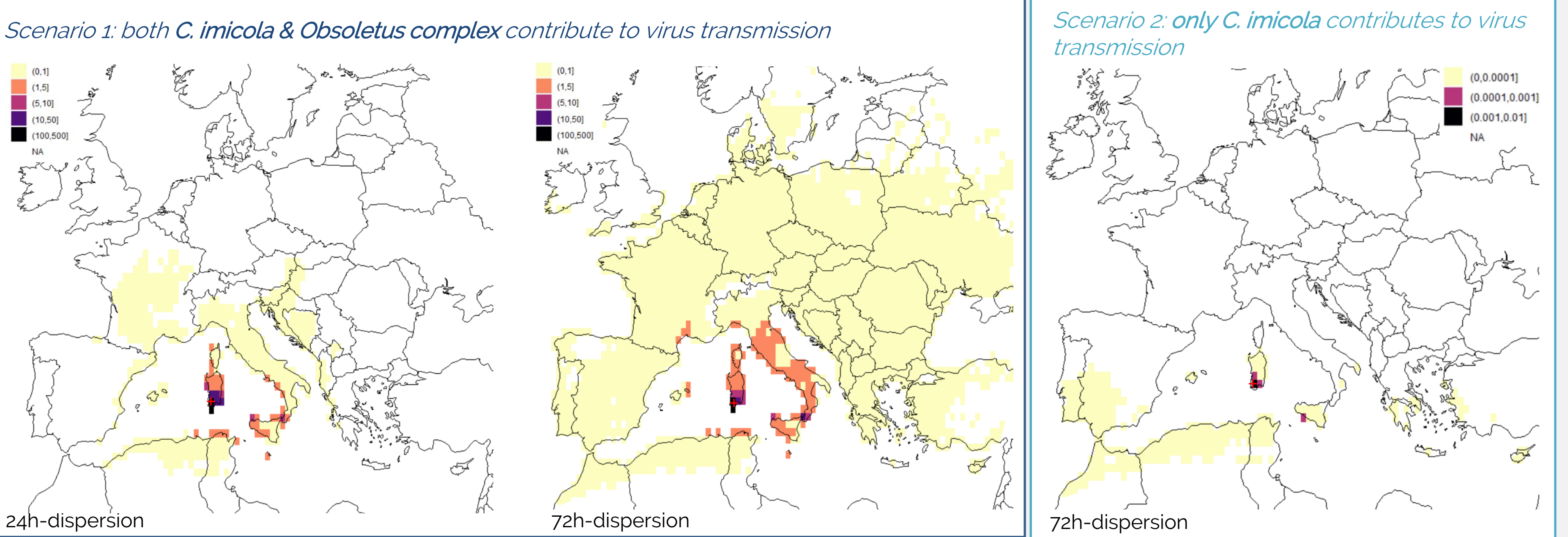
Results

- 1** Infection in i
- Prevalence arbitrary set in source:
50 cattle cases $\Leftrightarrow prev_c = 0.66\%$
200 small ruminant cases $\Leftrightarrow prev_s = 0.06\%$
- Vector infection starts end of April and ends mid of November
C. imicola: [0,5 - 1,9] infected midges / week
C. obsoletus/scoticus: [45 - 2500] infected midges / week

- 2** Long distance dispersal to destination j by wind
- Mean of weekly probabilities for long distance dispersal from source area i (*) according to 3 scenarios of maximal duration of aerial transport (1, 2 or 3 days)



- 4** Yearly risk of introduction at destination
- Mean of weekly secondary infections at destination according to vector contribution to transmission



- The vector dispersion halo from Sardinia mostly points to the **southeastern direction**. It **expands to the west** as the vector flight duration increases but very rarely to the north.
- Risk of new introduction remains mostly **limited to Sicily, continental Italy and Corsica**. Annual risk for continental France (southwest) and Spain (Balears islands) was only evidenced considering 72h of flight and **competence of both vector types**.
- If only *C. imicola* contributes to the disease transmission, there is no significant risk of further introduction to neighbouring countries.
- Mediterranean islands are exposed almost the entire period whereas continental areas are **exposed during only few weeks, at most 3 months**.

- Next steps:**
- Finetune estimations of vectors abundance data
 - Perform sensitivity analysis
 - Make the model generic for any combination of source and destination

References: ^[1] <https://doi.org/10.5334/ohd.33> ; ^[2] <https://doi.org/10.1046/j.1439-0450.2003.00632.x> ; ^[3] <https://doi.org/10.1038/sdata.2018.227> ; ^[4] <https://doi.org/10.1038/s41597-020-00587-y> ; ^[5] [0.1371/journal.pone.0053128](https://doi.org/10.1371/journal.pone.0053128) ;