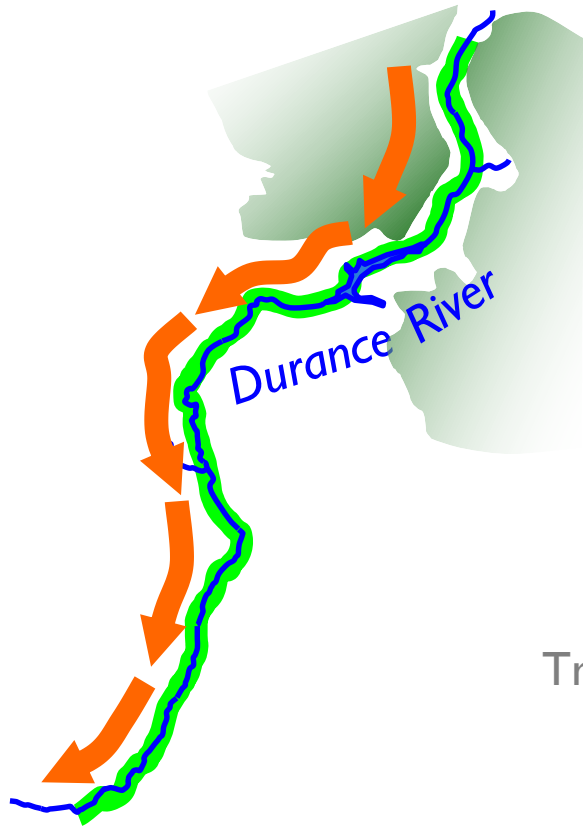


The Durance River valley: a great ecological system to study dispersal



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LabEx ARBRE seminars:
Forest diseases & Global change

INRAE

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INTERACTIONS
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arbre

The biological model: the poplar rust disease



Melampsora larici-populina

Foliar pathogen

Obligate biotrophic fungus

Mixed reproductive mode: Partial clonality

Host alternation between larch and poplar

Annual life cycle:



Sexual
reproduction on
Larch needles

Population expansion

in summer

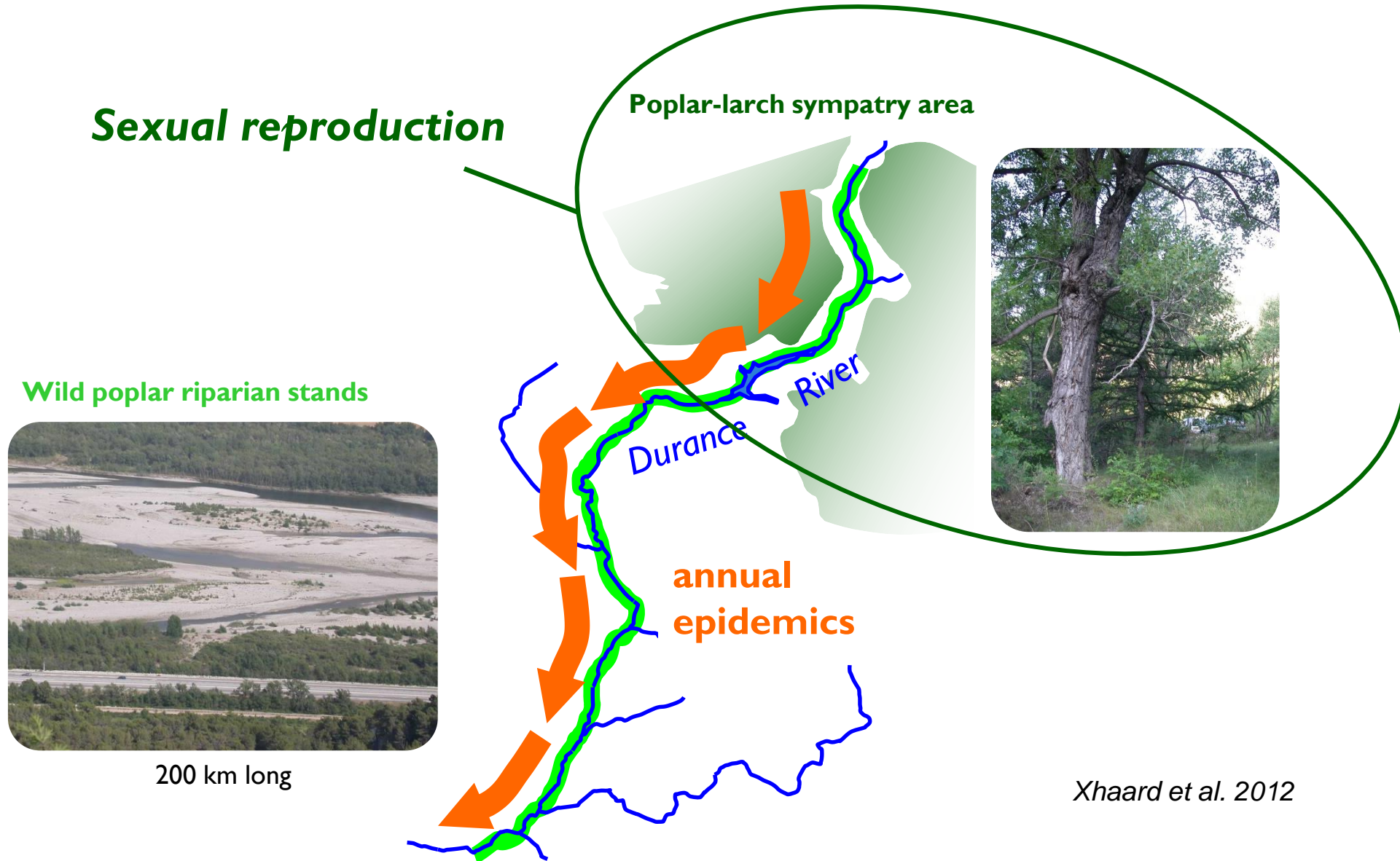
Clonal
multiplication on
Poplar leaves

*Genetic
recombination*

in spring



The Durance River valley: an ideal ecological situation to study the dispersal of poplar rust



Spatio-temporal monitoring of the epidemics

- **7 sampling times** from July to November 2008
- **13 sampling sites**
- **2 sampling scales**
 - ‘Tree’ samples: Percentage of infected trees
 - ‘Twig’ samples: Percentage of infected leaves



Objectives :

1. Description of the epidemics
2. Estimation of the pathogen dispersal

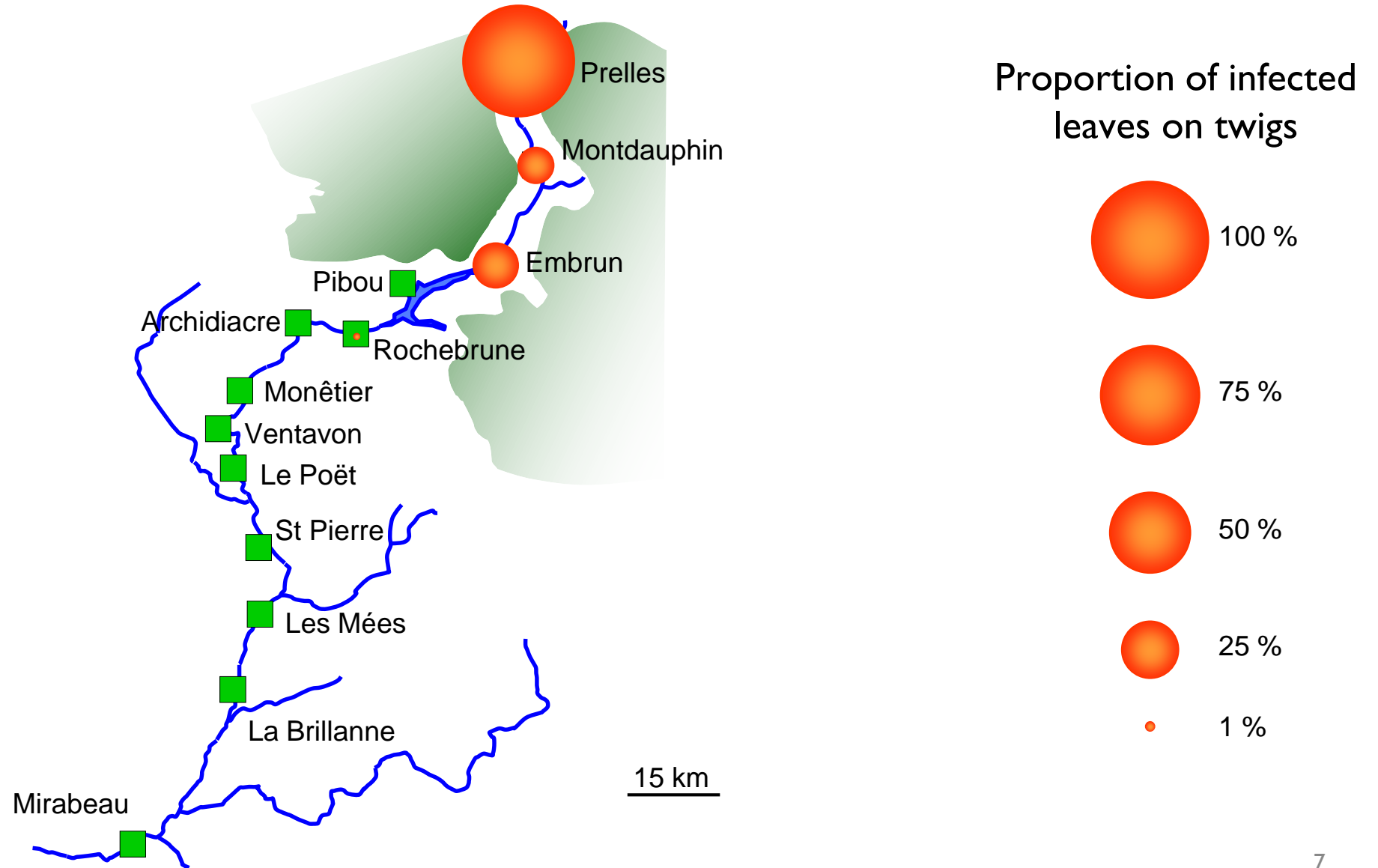
Spatio-temporal monitoring of the epidemics



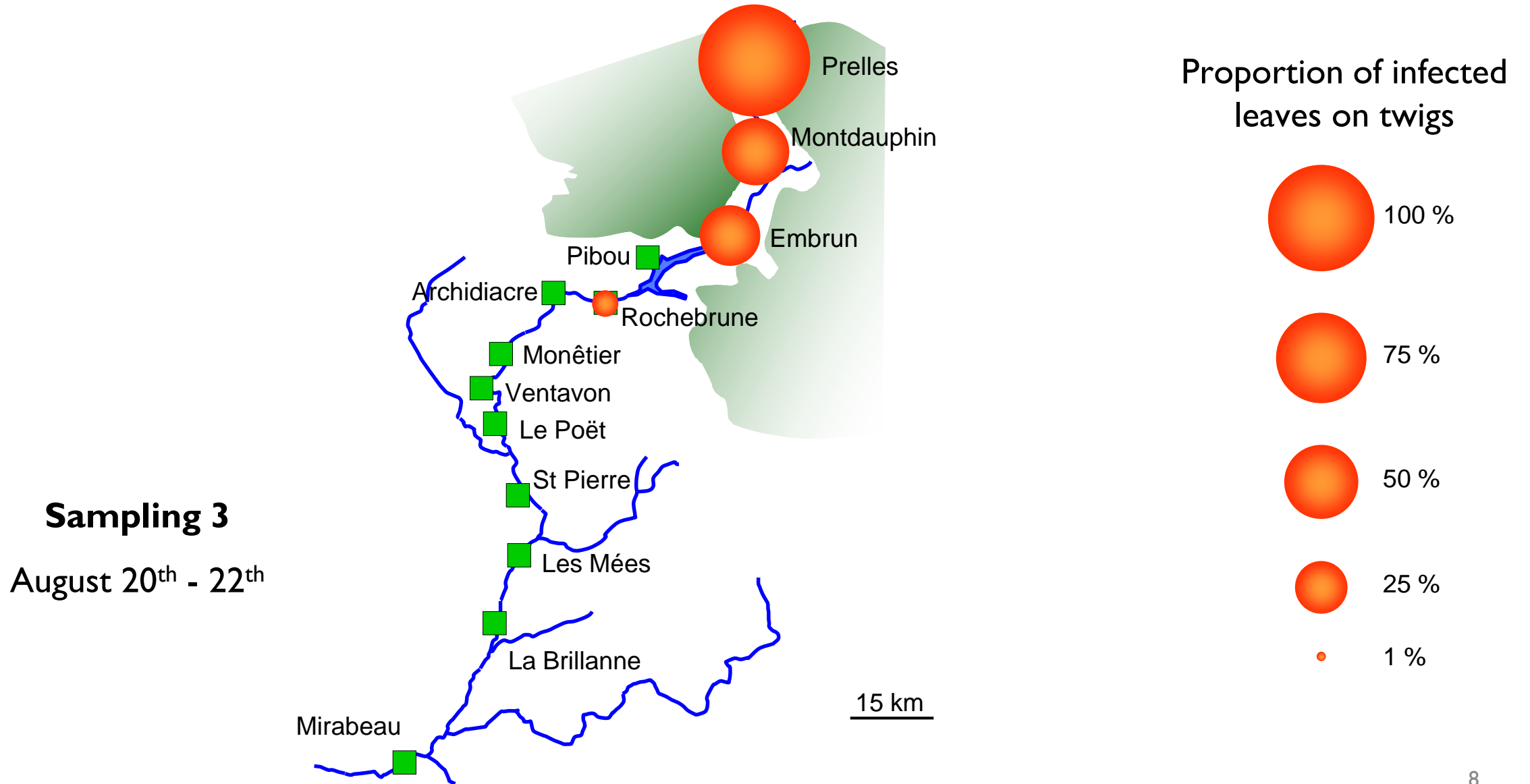
Spatio-temporal monitoring of the epidemics

Sampling 2

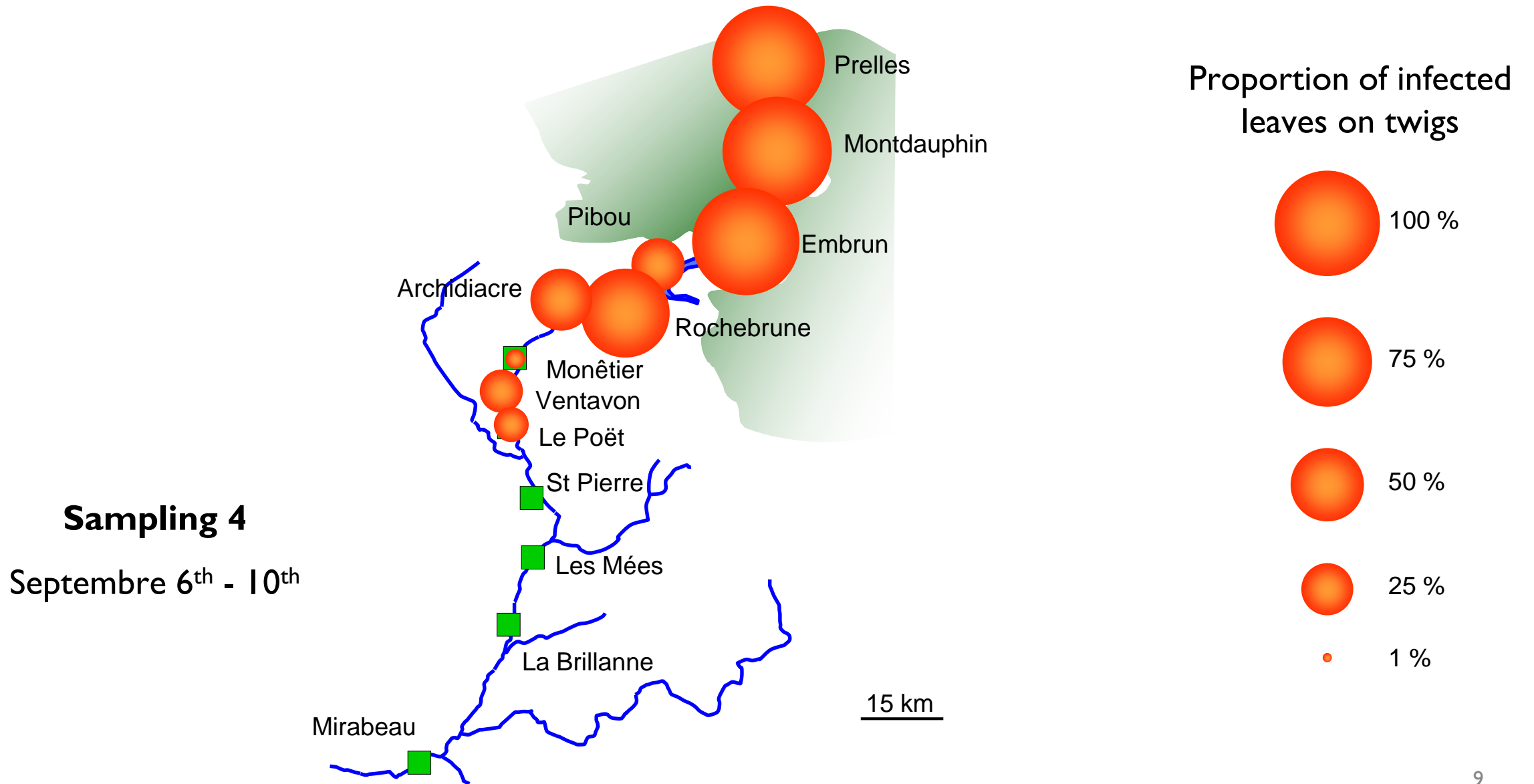
July 28th - 30th



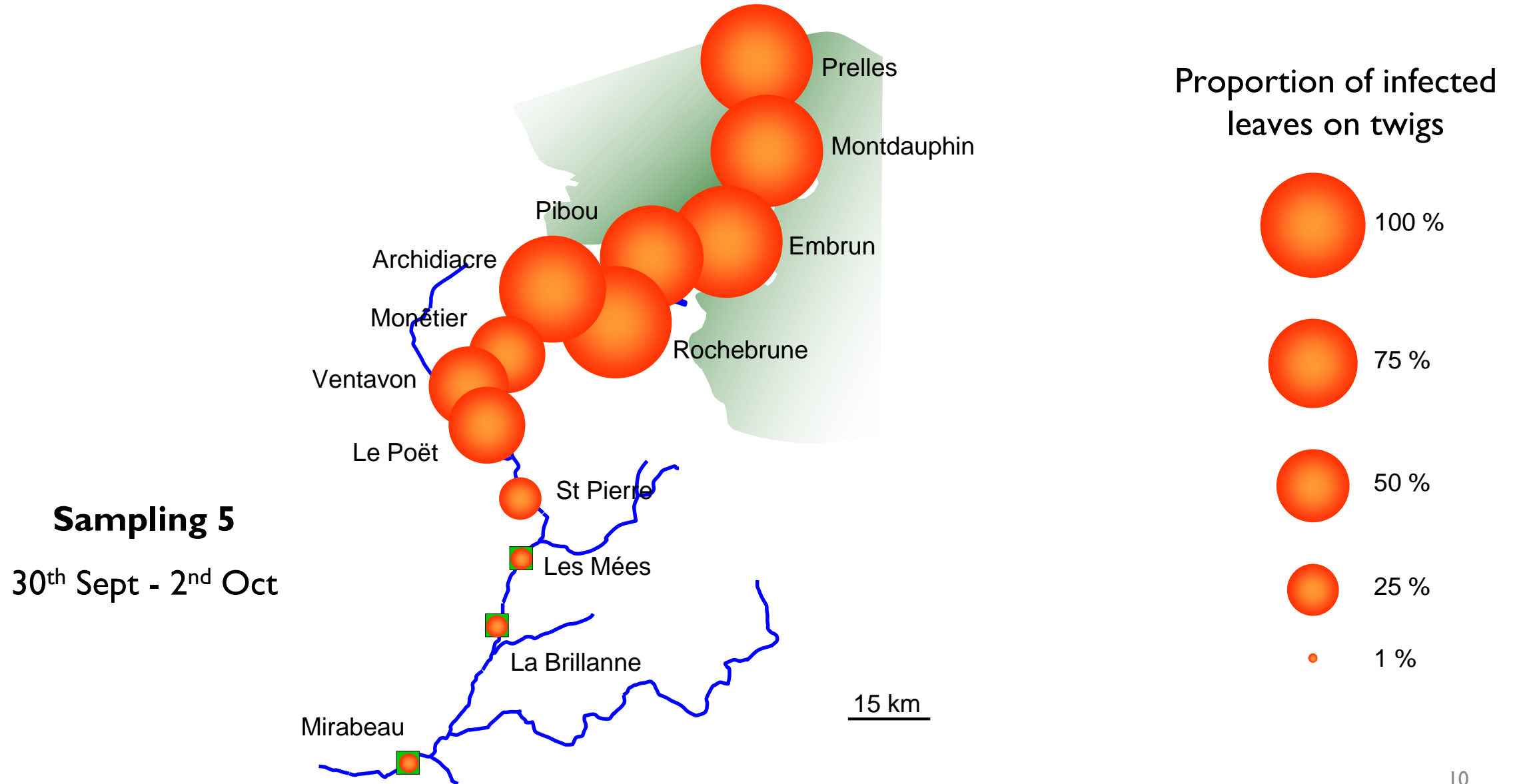
Spatio-temporal monitoring of the epidemics



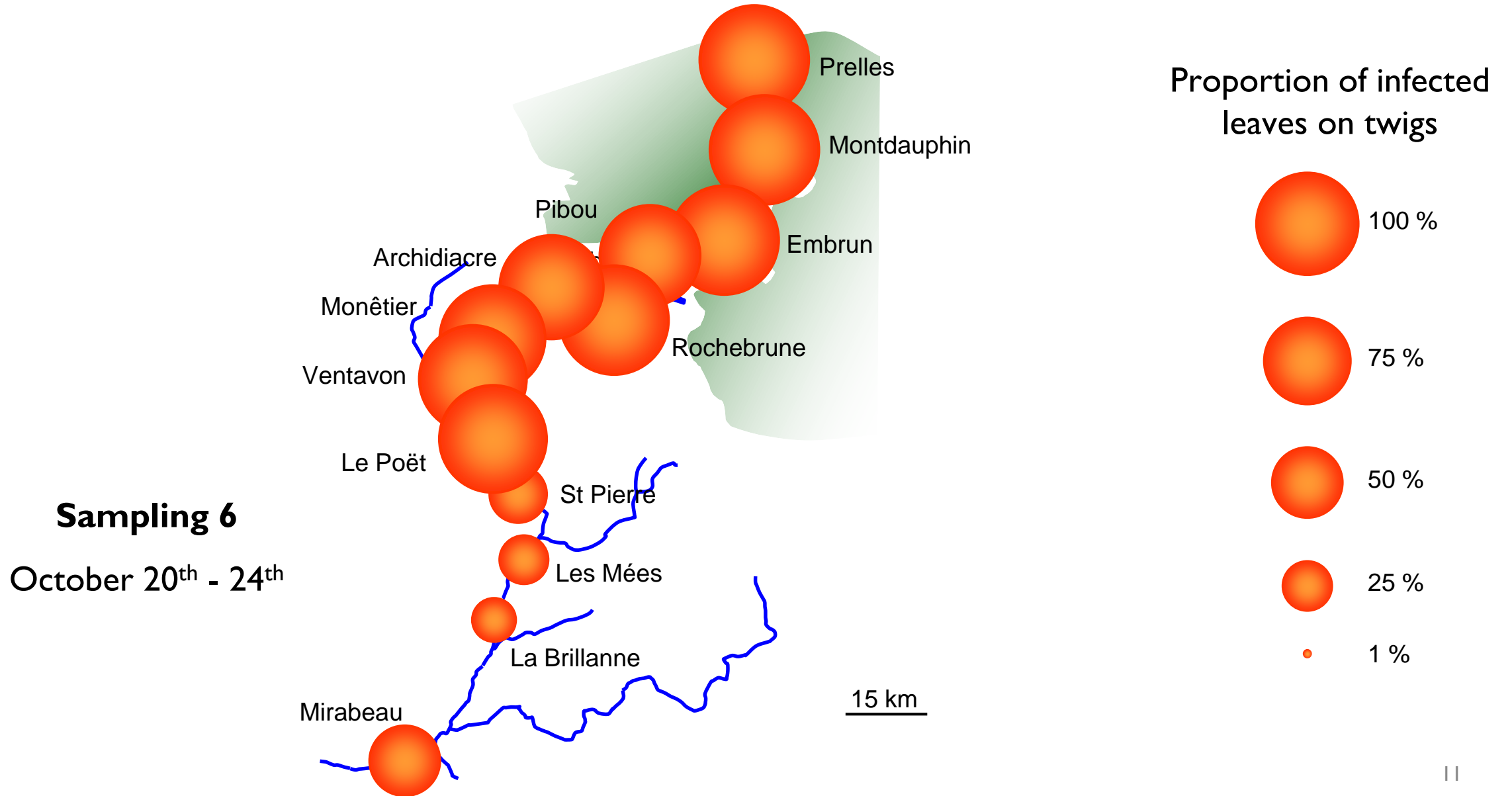
Spatio-temporal monitoring of the epidemics



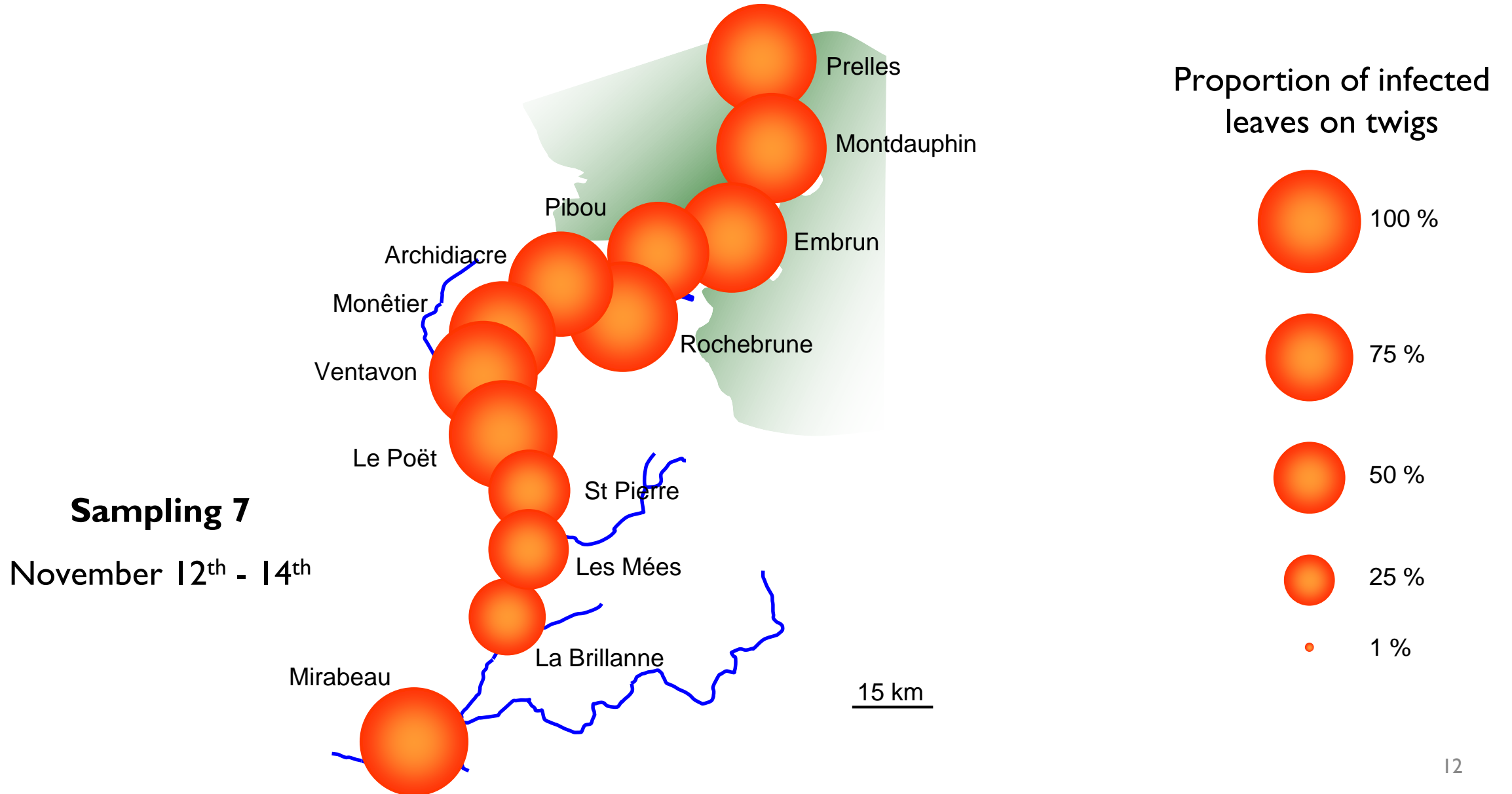
Spatio-temporal monitoring of the epidemics



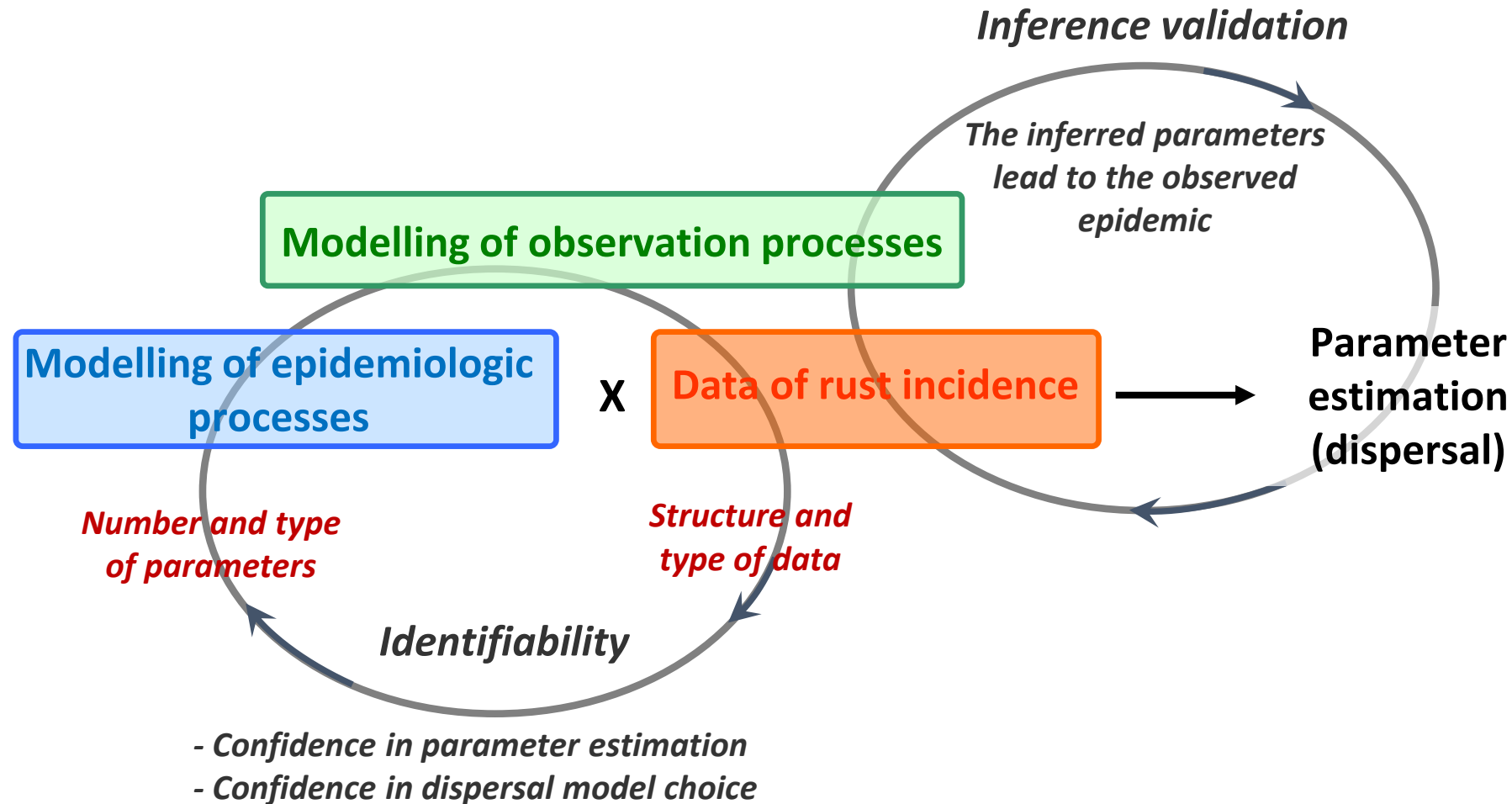
Spatio-temporal monitoring of the epidemics



Spatio-temporal monitoring of the epidemics



Estimation of the parameters with a mechanistic-statistical approach



The mechanistic model

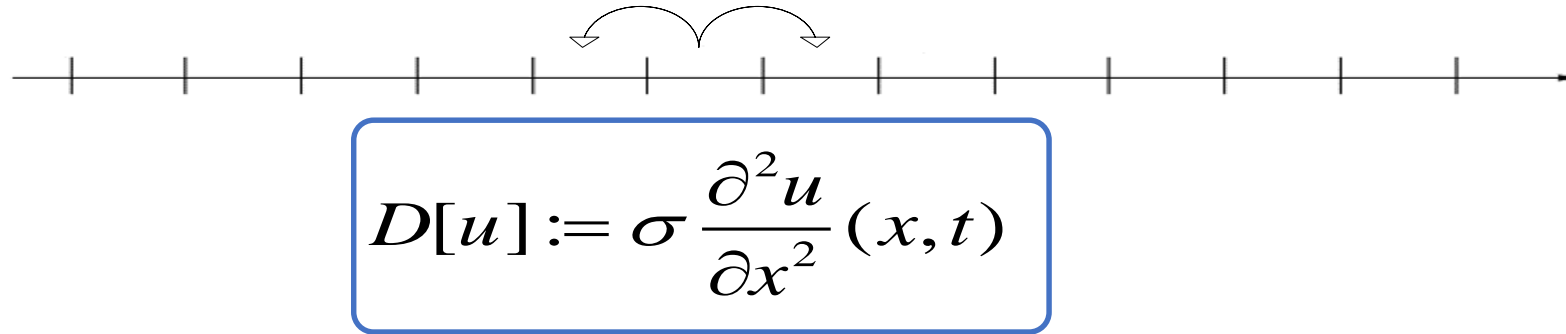
Representation of epidemiological processes with a deterministic model

$$\partial_t u(x, t) = \underbrace{D[u](x, t)}_{\text{Movement}} + \underbrace{ru(K - u)}_{\text{Local growth}}$$

Spore density at time t and point x

The dispersal models

I Diffusion

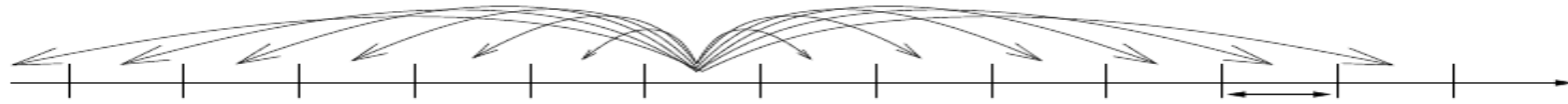

$$D[u] := \sigma \frac{\partial^2 u}{\partial x^2} (x, t)$$

Parameter: diffusion coefficient σ

- **Advantages :**
 - Mathematic theory ell described
 - Numerically 'easy' and fast
- **Drawbacks :**
 - Modelling of flows and not unit movements
 - A single dispersal function available

The dispersal models

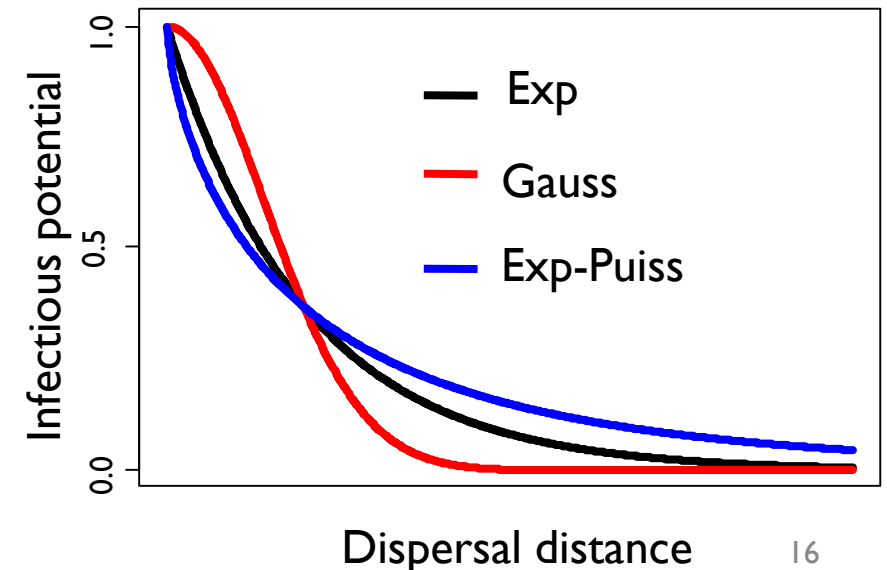
3 Dispersal kernels



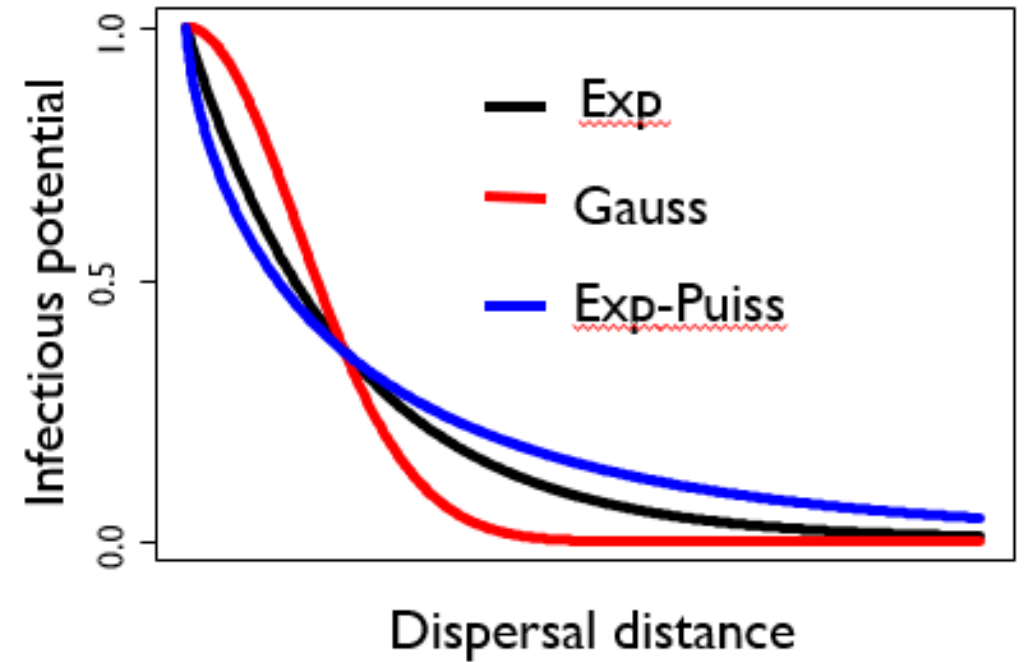
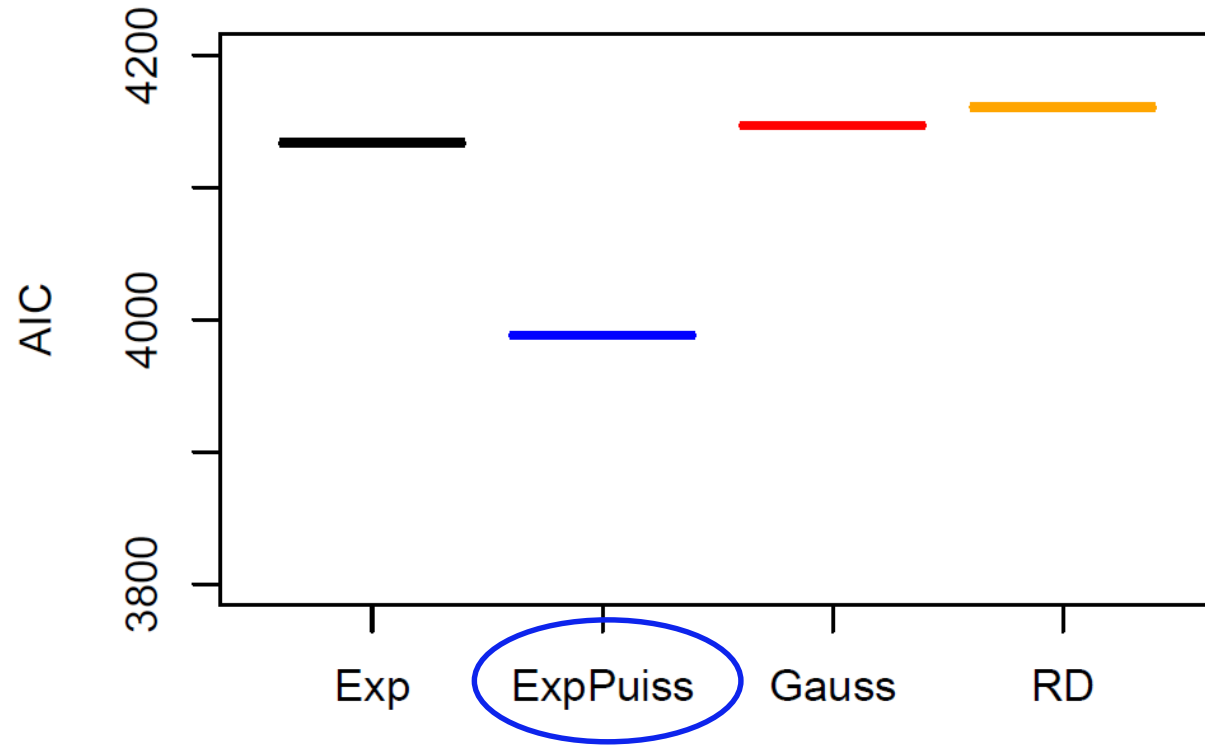
$$D[u](x,t) := \int k_{\lambda}(y-x) [u(y,t) - u(x,t)] dy$$

Dispersal kernel k_{λ} with parameter λ

- **Advantages :**
 - Redistribution of individuals density: representative of individual movements
 - Different forms of dispersal available
- **Drawbacks :**
 - Numerically 'costly'
 - Few theoretical descriptions



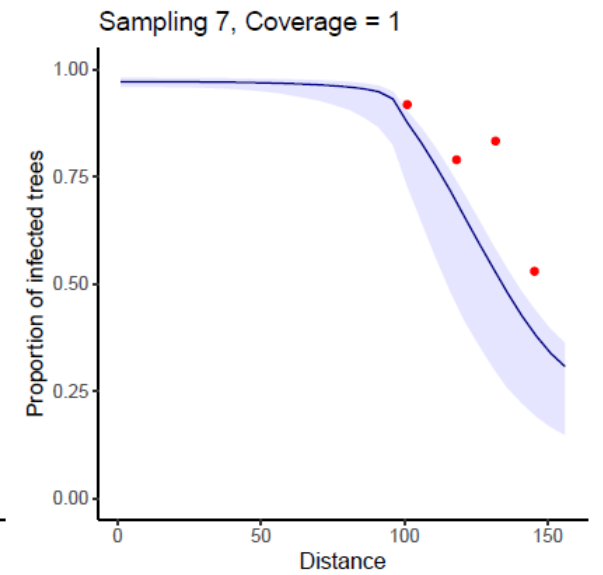
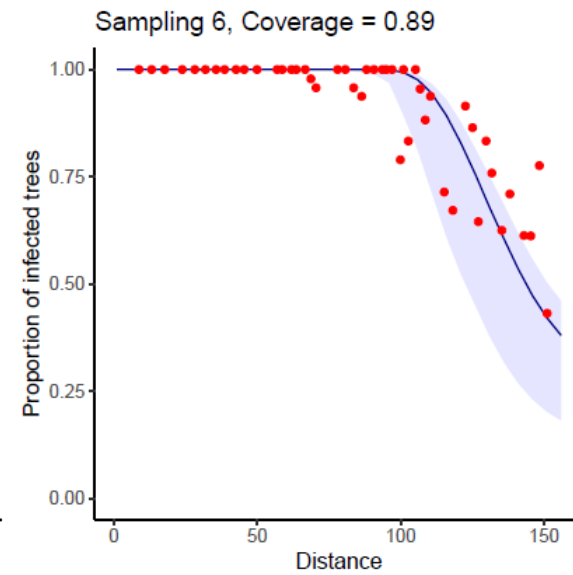
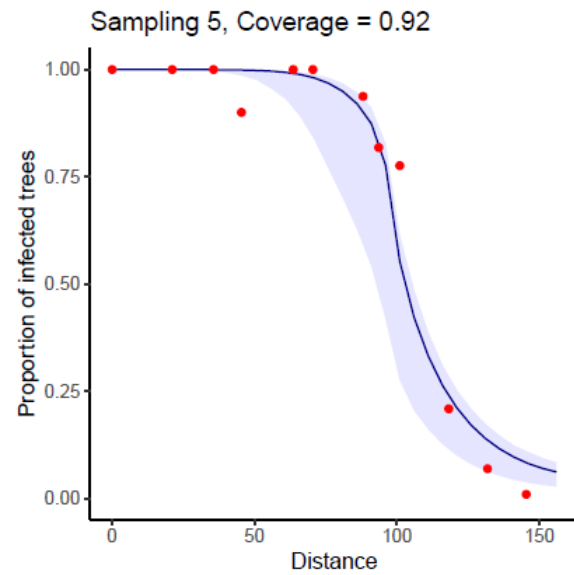
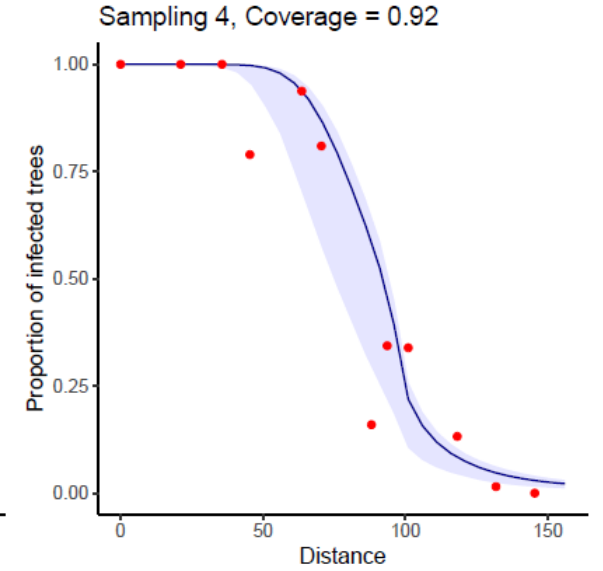
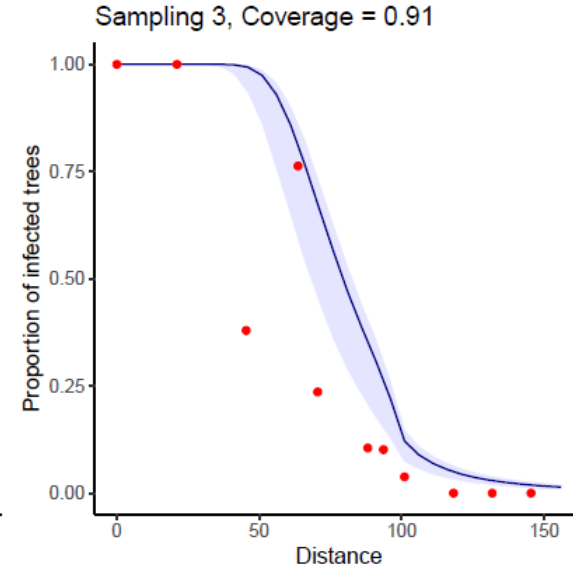
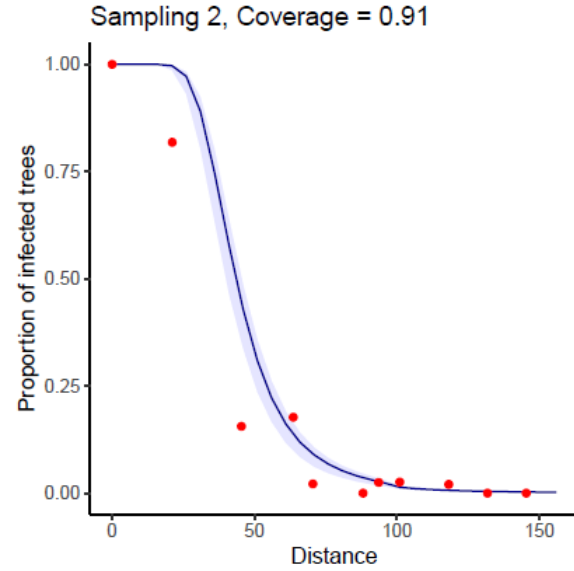
Best dispersal model



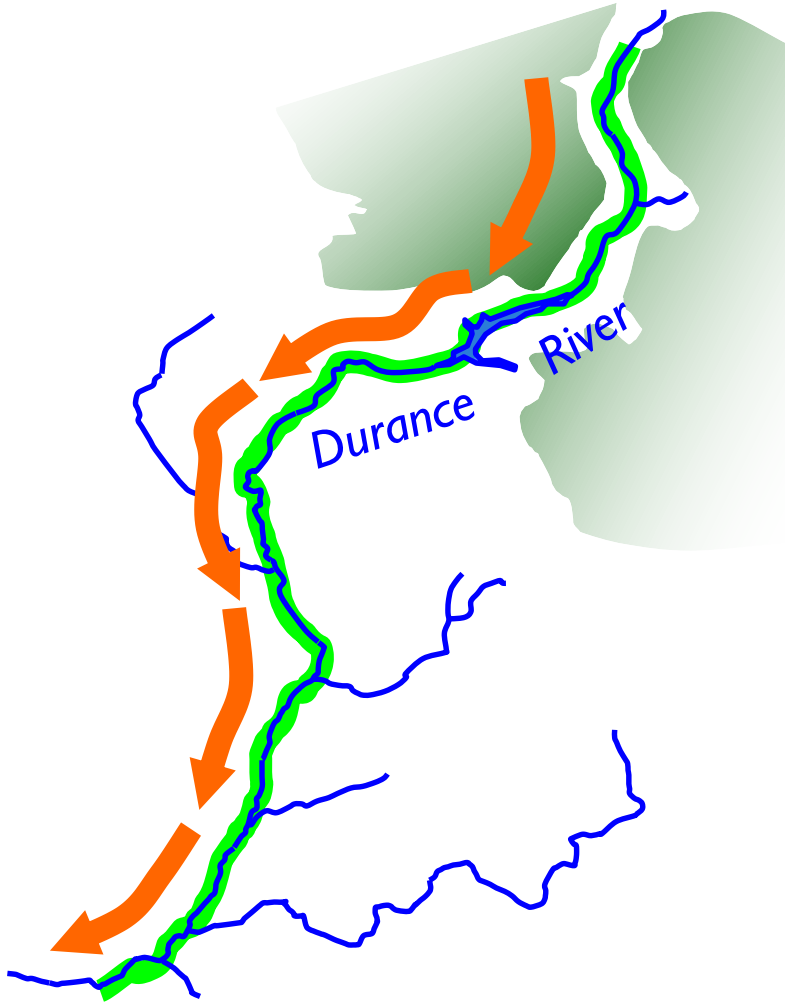
→ The estimated dispersal model is the fat-tailed kernel ExpPuiss with frequent long distance dispersal events

Comparison of the estimated and the observed epidemics

Parameter	Estimation
r_1	0.03 (<0.001)
r_2	0.09 (0.002)
γ	3.23 (0.4)
λ	0.92 (0.003)
τ	0.21 (<0.001)
σ^2	1.16 (0.004)



Population genetic consequences of poplar rust dispersal?



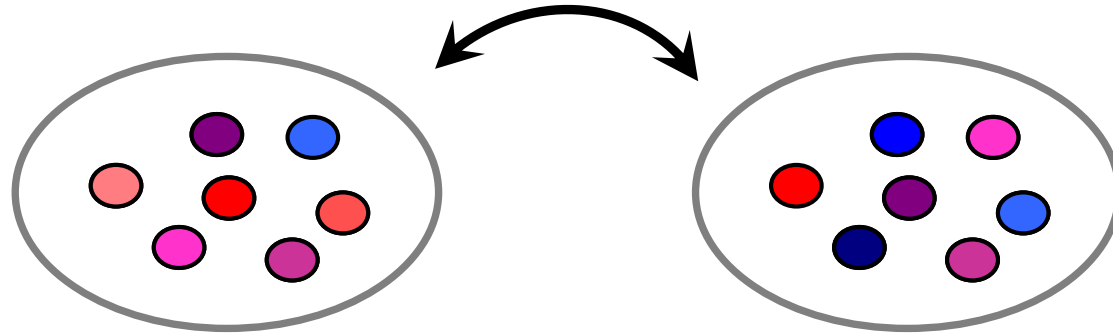
- **What are the genetic signals of this range expansion?**
- **Is it repeatable?**

Genetic consequences of dispersal

Twofold action

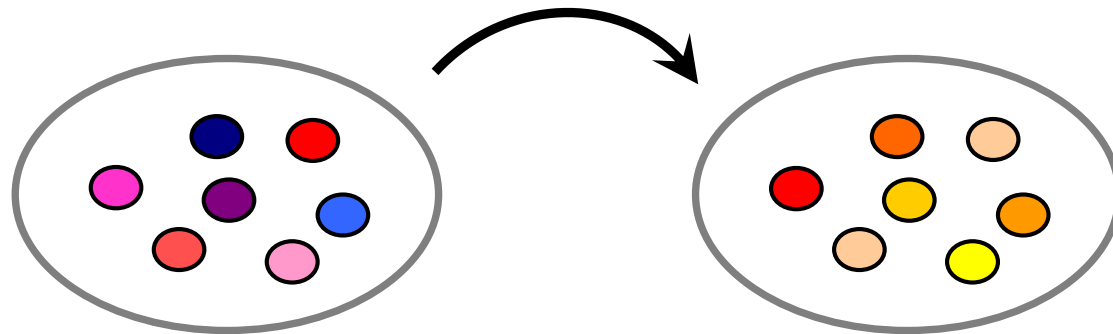
1- Constraining force

Erase
genetic differentiation
and impede local adaptation



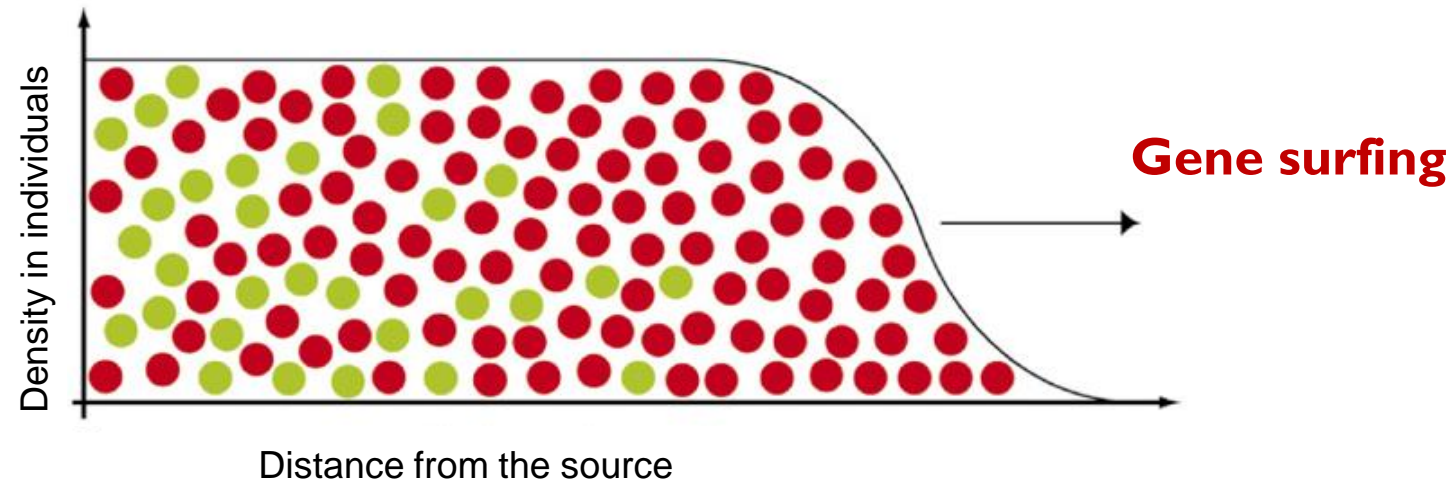
2- Creating force

Generate
genetic differentiation
Spread of beneficial alleles



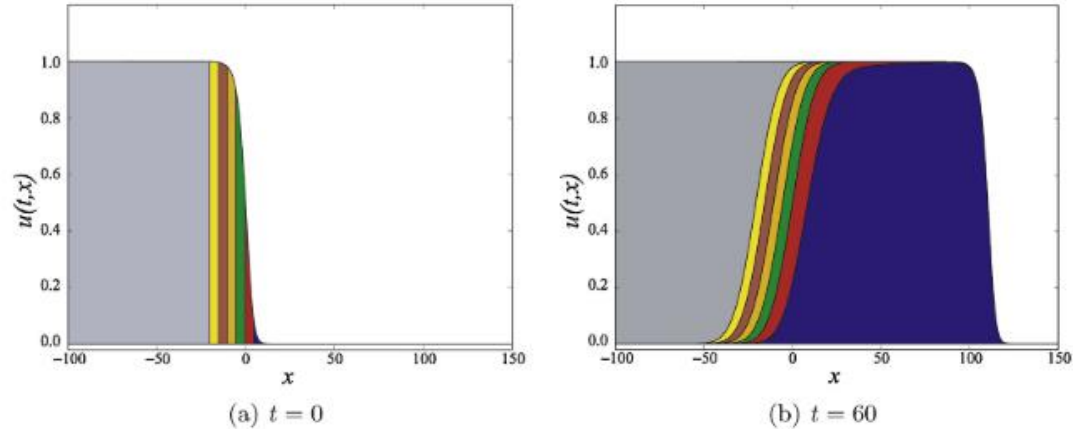
Change in population genetic structure along range expansion

Joint action of drift and dispersal → **Regular increase in genetic differentiation and reduction of genetic diversity**

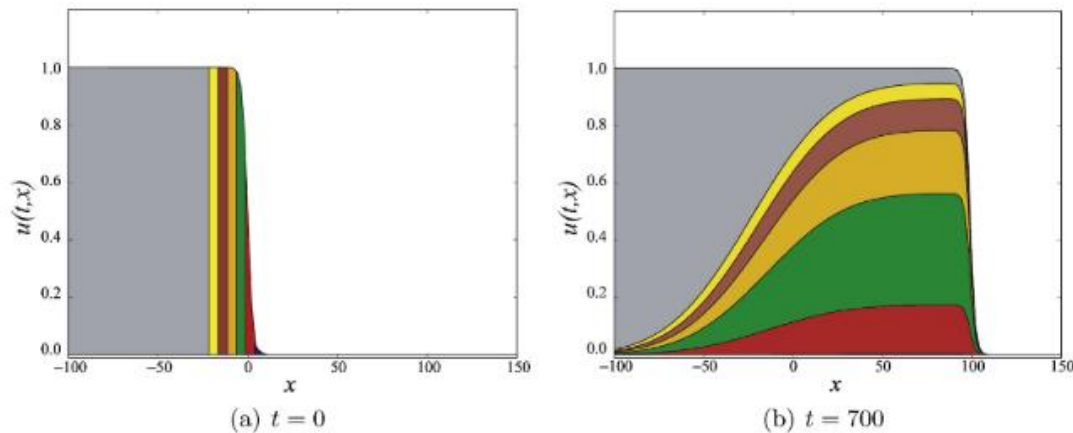


The genetic structure depends on dispersal regimes

Pulled wave: Erosion of genetic diversity

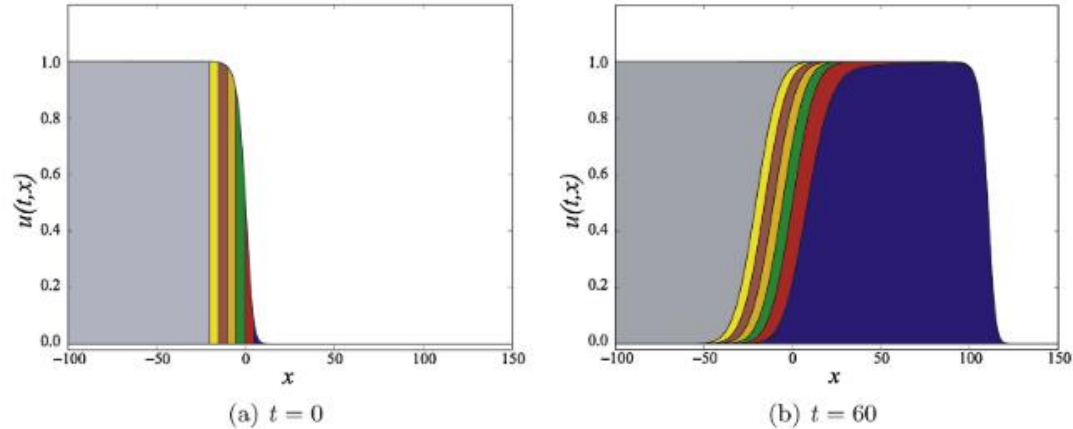


Pushed wave: Conservation of genetic diversity

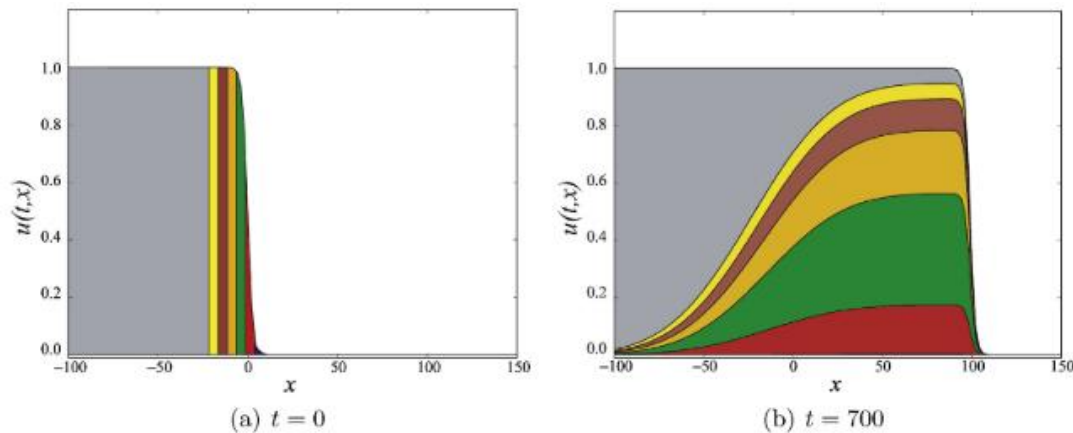


The genetic structure depends on dispersal regimes

Pulled wave: Erosion of genetic diversity



Pushed wave: Conservation of genetic diversity



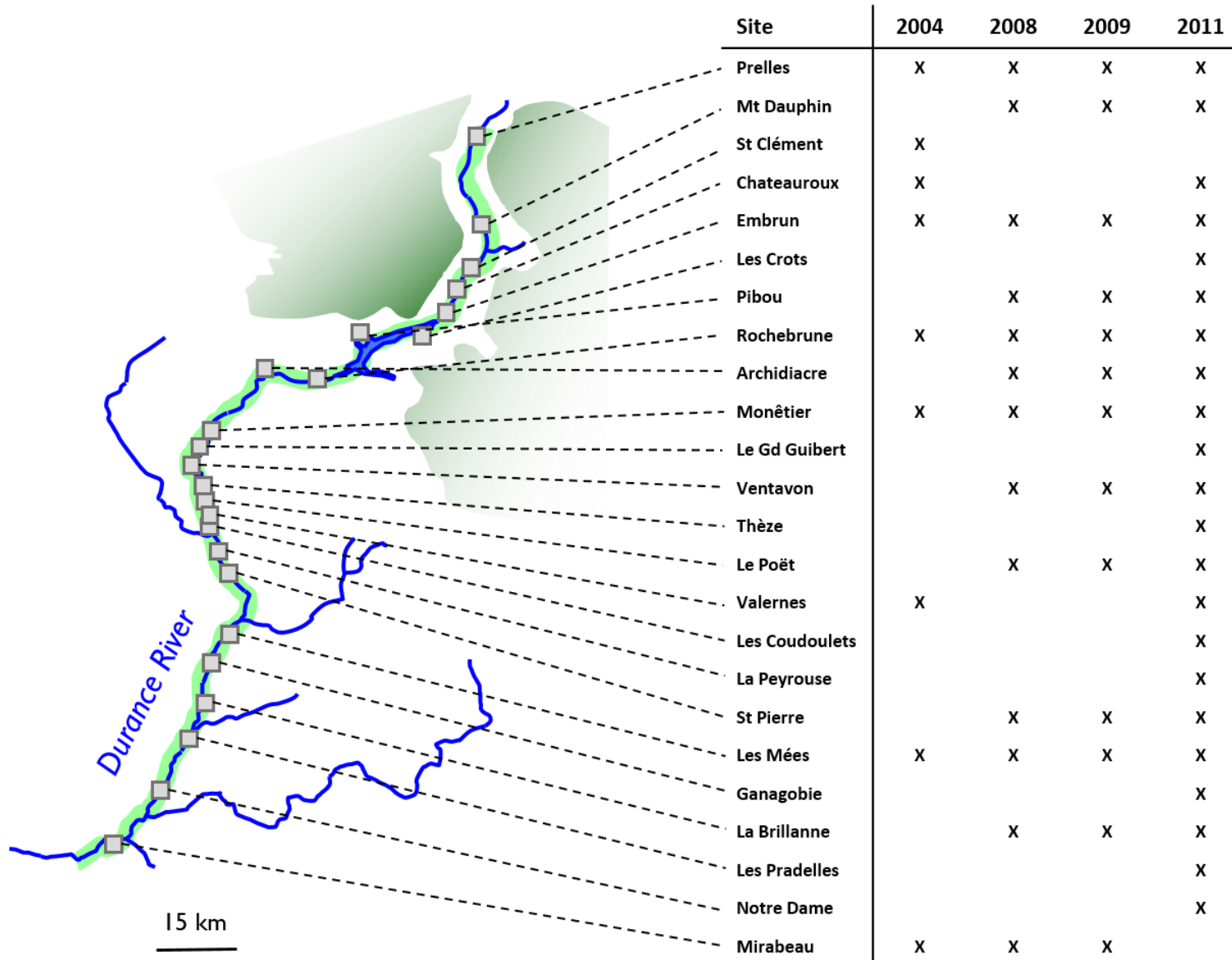
Biological invasions offer the opportunity to test these hypotheses

Main limitations are :

- **Knowing the starting point**
- **Monitoring the colonization**
- **Having replicates**

Poplar rust colonization along the Durance River is an ideal system

Annual samplings at the end of the epidemic



Contrasted epidemics:

weak intensity in 2004

VS

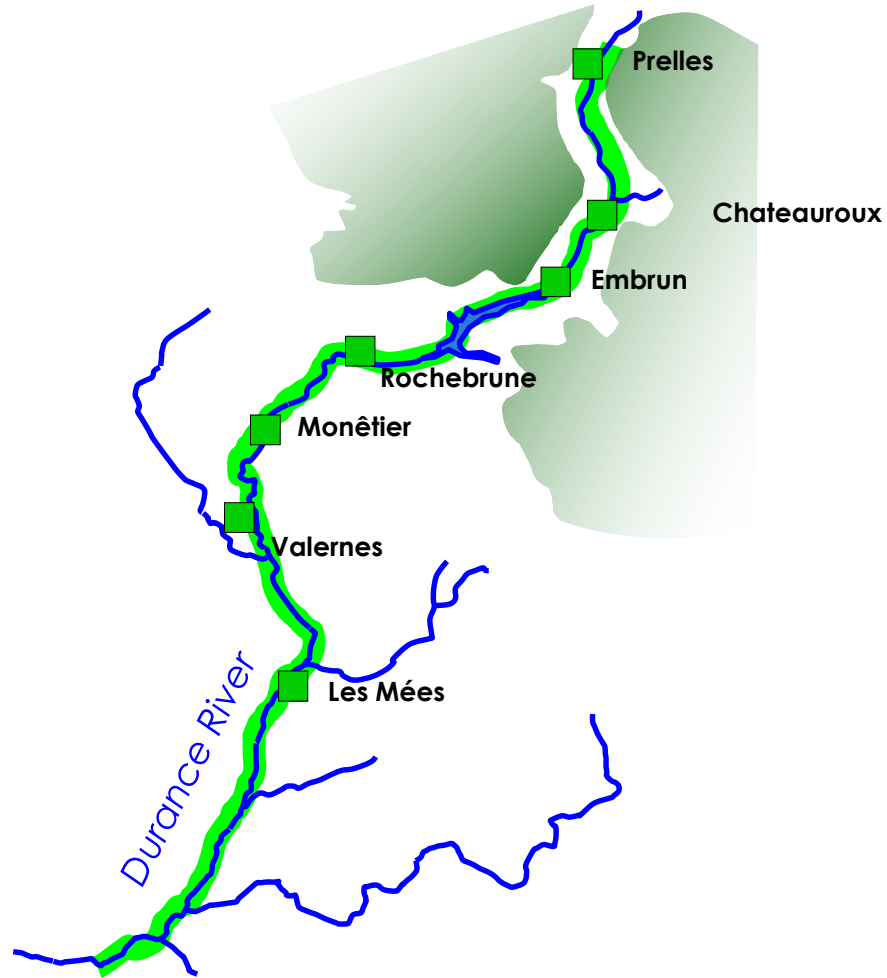
high intensity in 2008

Genotyping effort:

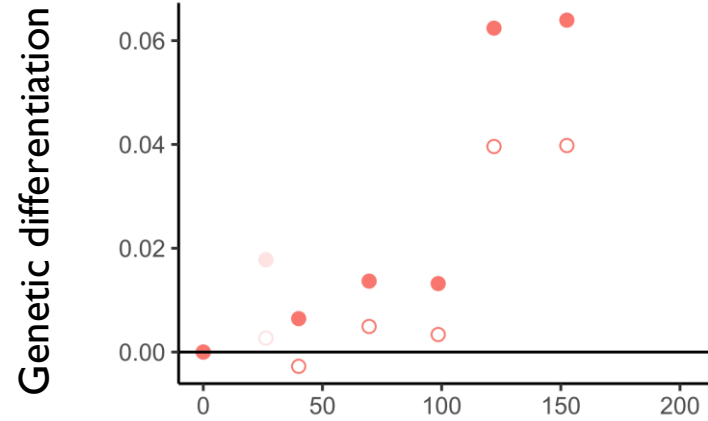
~ 3000 individuals typed
with 20 microsatellite
markers

The genetic consequences of the Durance River colonization

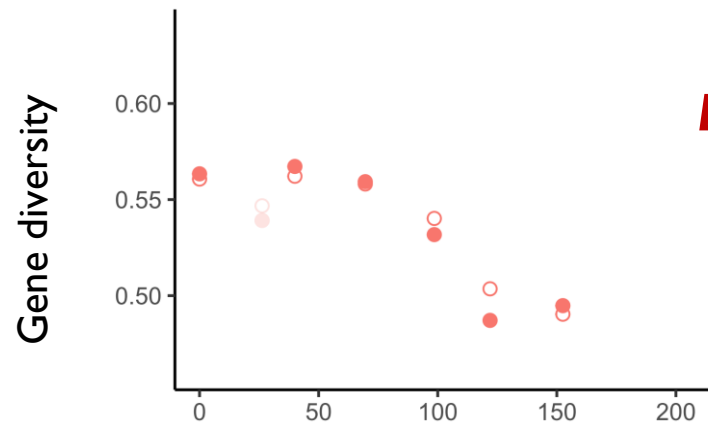
year 2004



Becheler et al. 2016, Saubin et al. in prep.



Genetic signal of recurrent founder events



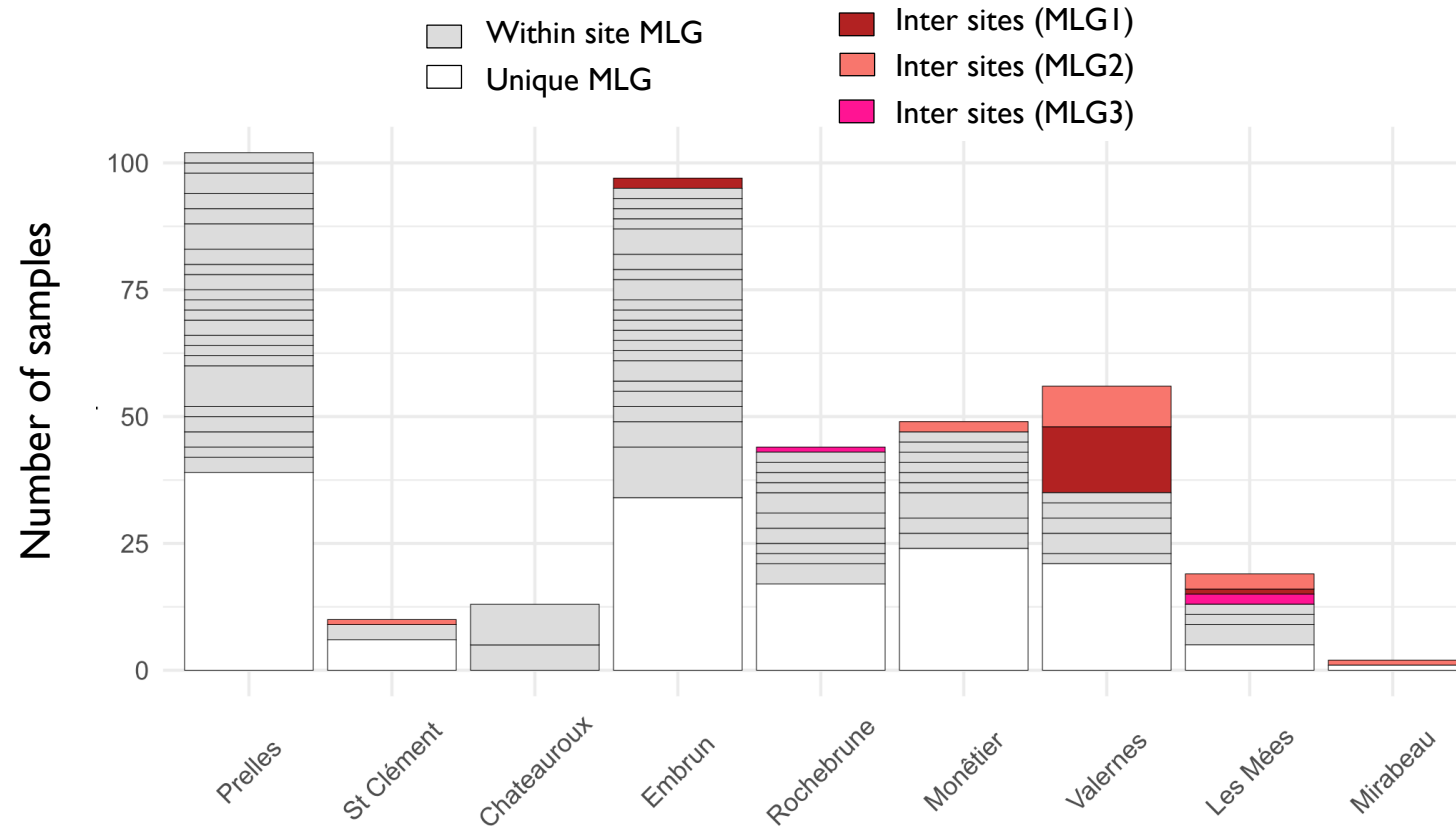
Evidence for gene surfing?

- with clonal replicates
- without clonal replicates

Distance from upstream (km)

Clones do not surf but play leapfrog

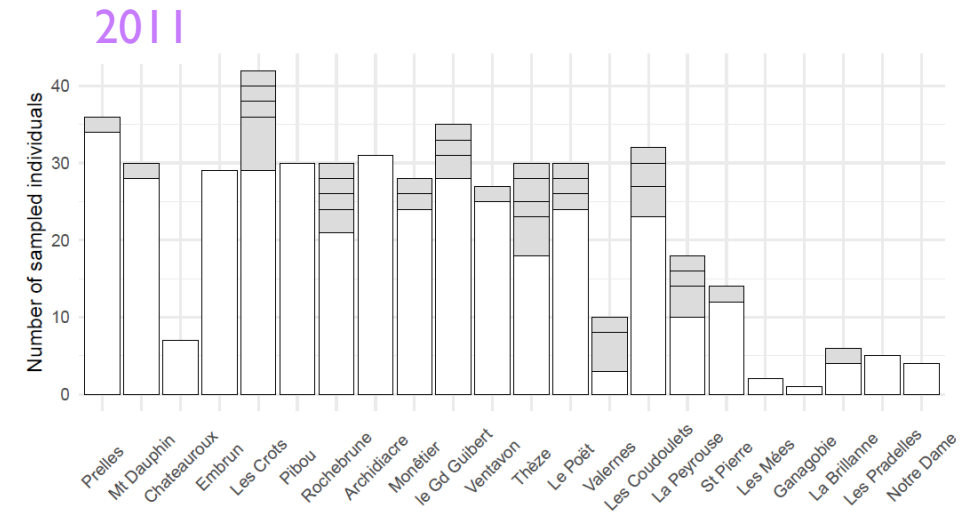
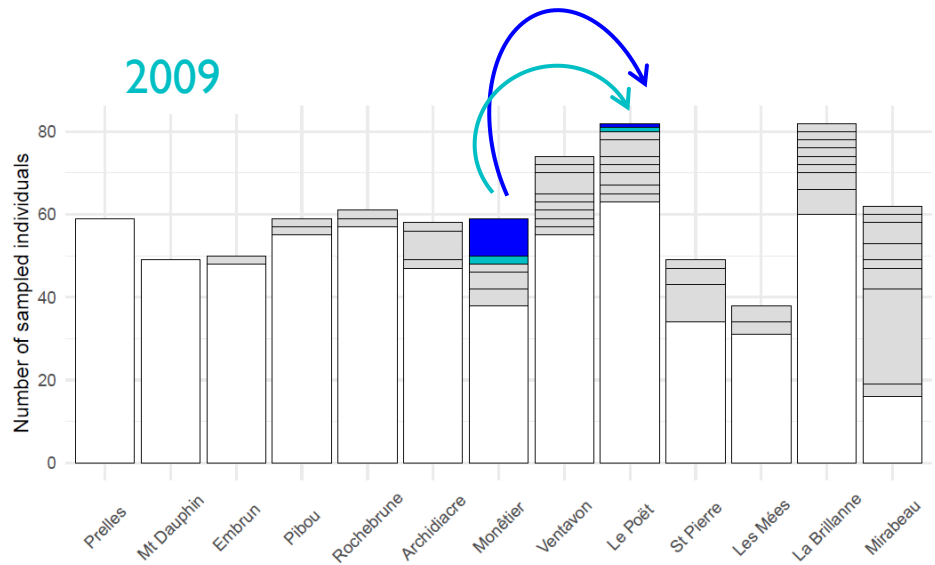
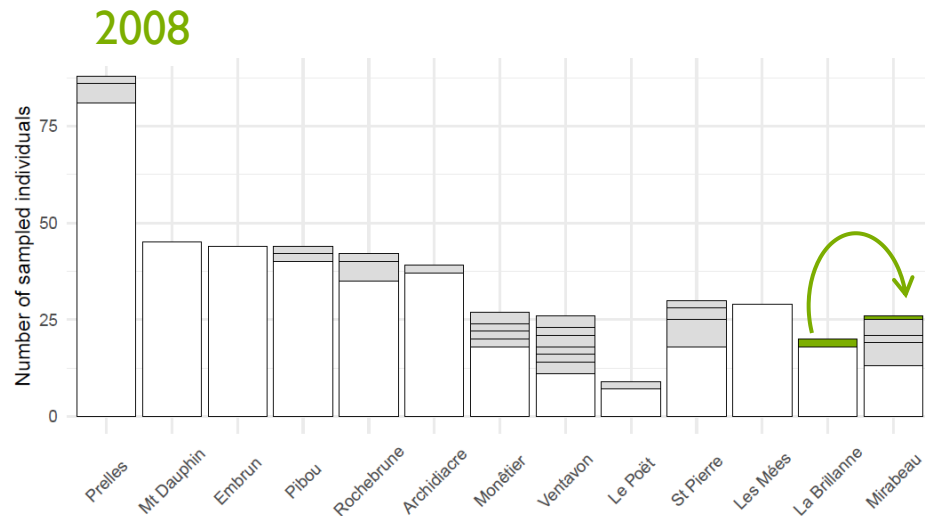
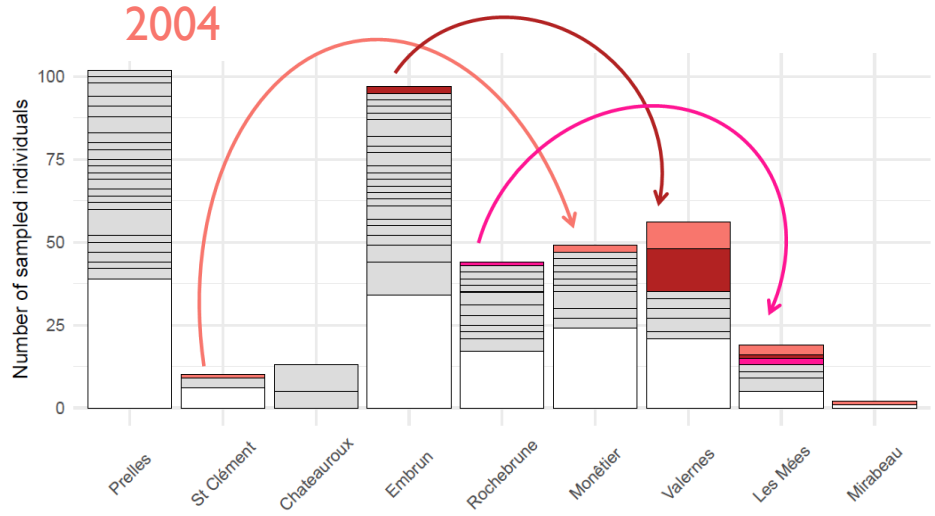
Distribution of clonal lineages (MLG)



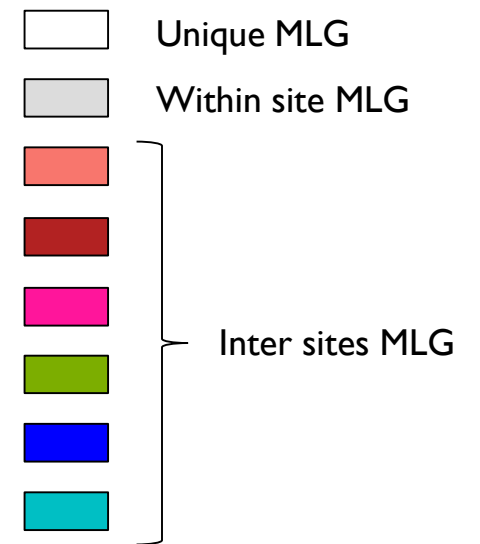
Becheler et al. 2016

This “patchy” distribution is in accordance with frequent LDD events

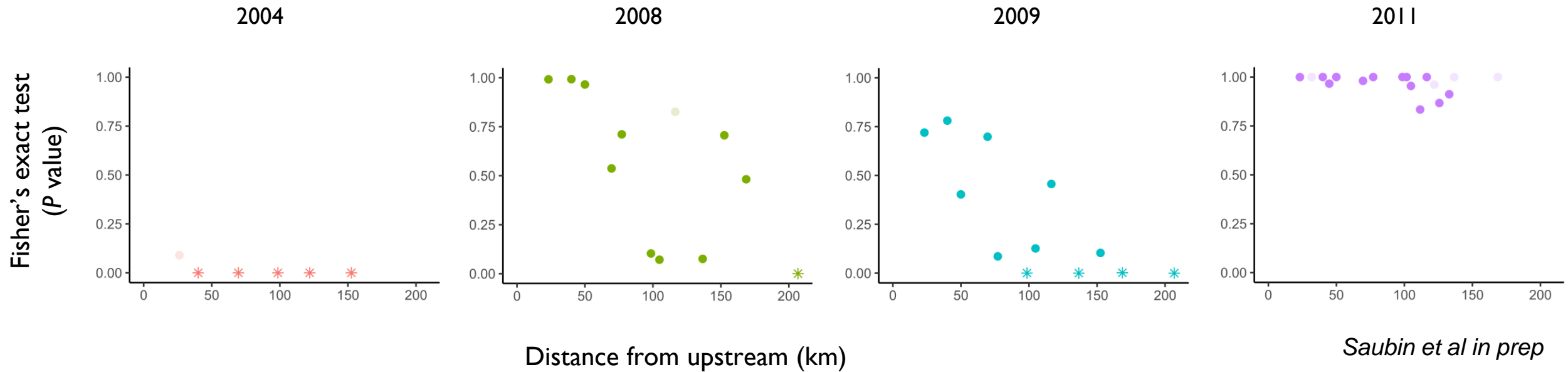
Different frequencies of leapfrog events across years



Distribution of clonal lineages (MLG)



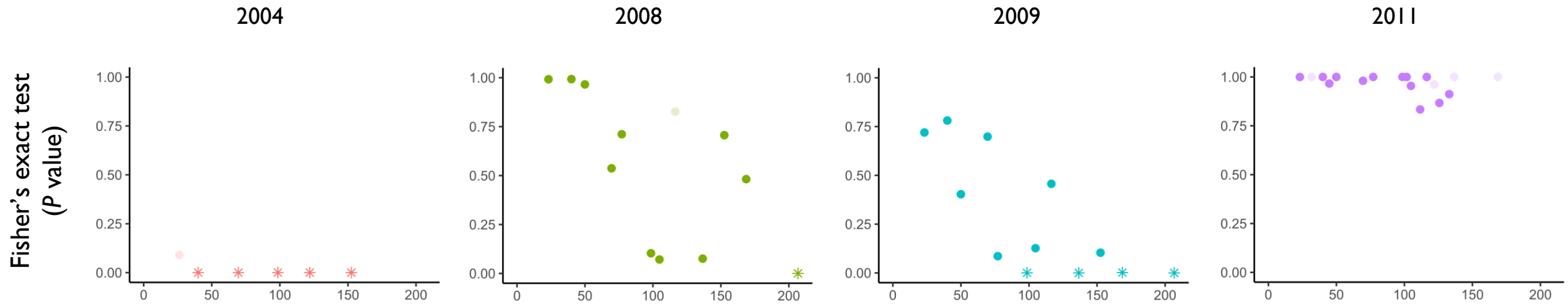
Test of genetic conservation along the invaded domain



Saubin et al in prep

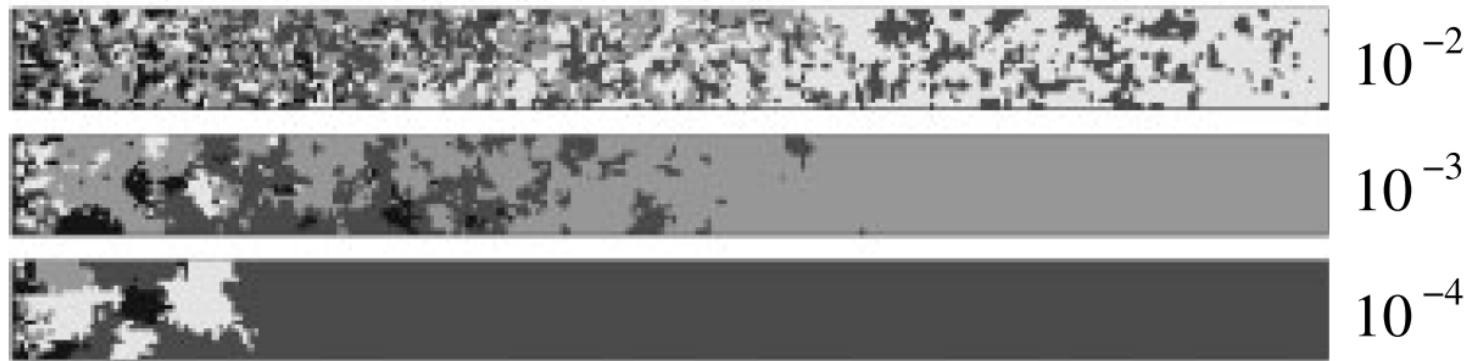
Large inter-annual variation: from no conservation at all across the domain in 2004 to strict conservation of genotypes in 2011.

Test of genetic conservation along the invaded domain



Saubin et al in prep

Inter-annual variation may indicate differences in dispersal regime

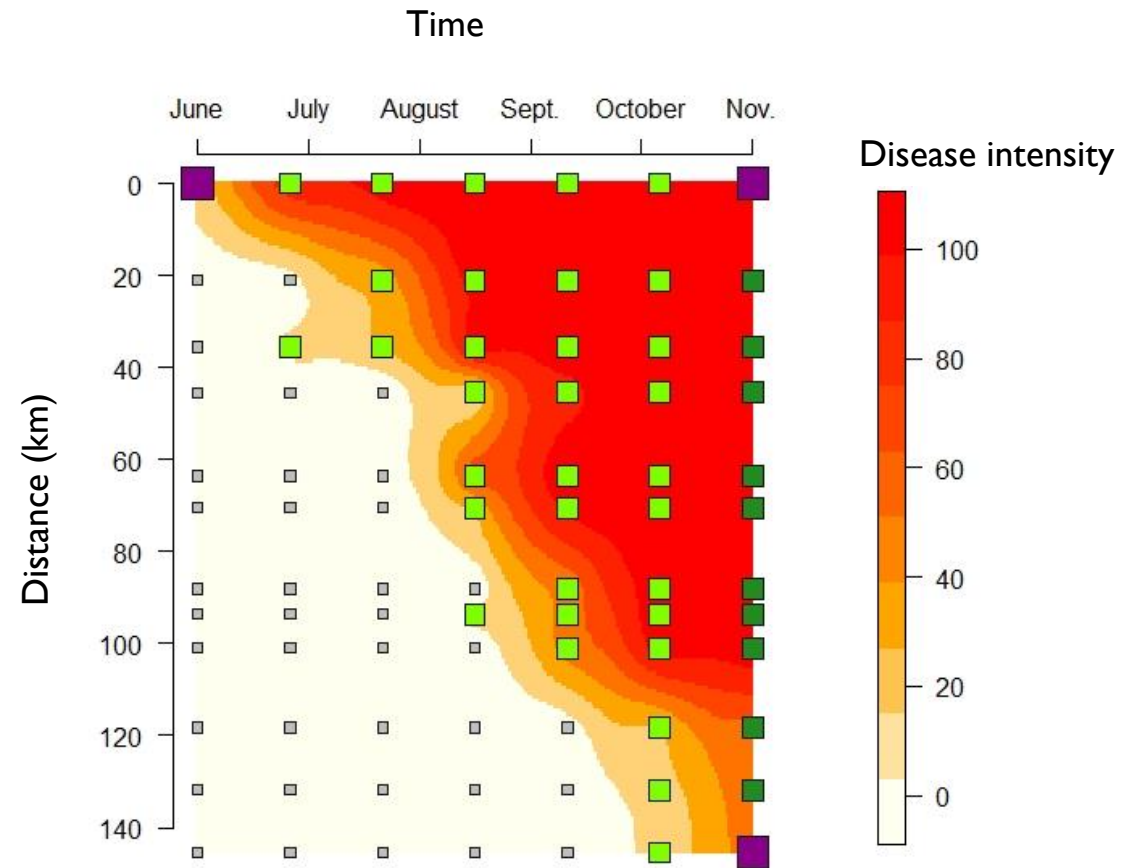


Bialozyt et al. 2006

Frequency of LDD

Perspective: coupling demography and population genetics analyses

Spatio-temporal analysis of epidemiology and population structure



Acknowledgements

Main Contributors:

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Pascal Frey

