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TECHNIQUES
AGRICOLES #

2nd model example.

SEIR model of Brown rust disease to help design IPM strategies for future climate.

**Description of Brown rust, Zadoks model, large
scale simulation and practical work with R**

François Brun (ACTA)

IPM CC, October 2016

Brown rust on wheat



Biology, epidemiology et protection solutions

François Brun (ACTA)
(with contributions : Jean-Noël Aubertot, Tito Caffi)
IPM CC, October 2016

Wheat

- One of the oldest cultivated crops (10000 to 12000 years ago)
- *Tri!cum* genus, many cultivated species for many Different Purposes
- Mondial production : ~700 millions of tons by year

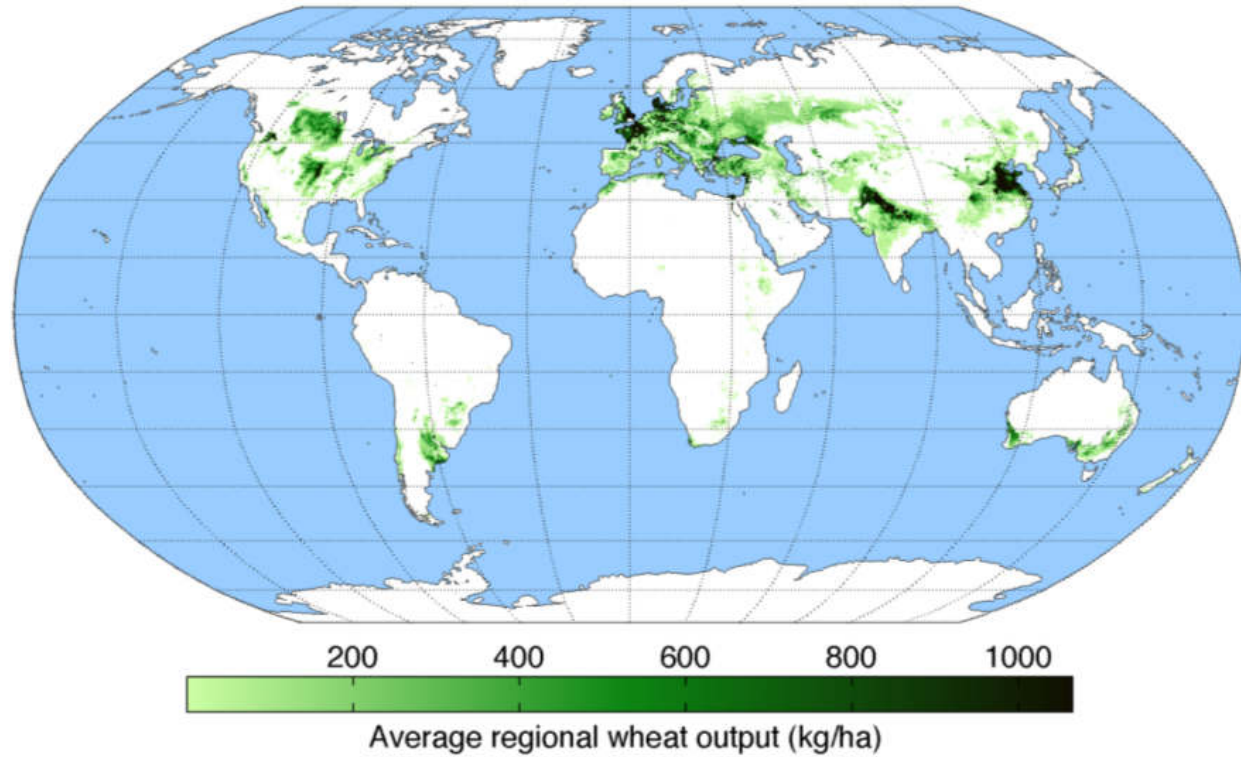


Human alimentation (bread, pasta, beer,...)



Animal alimentation (~15%)

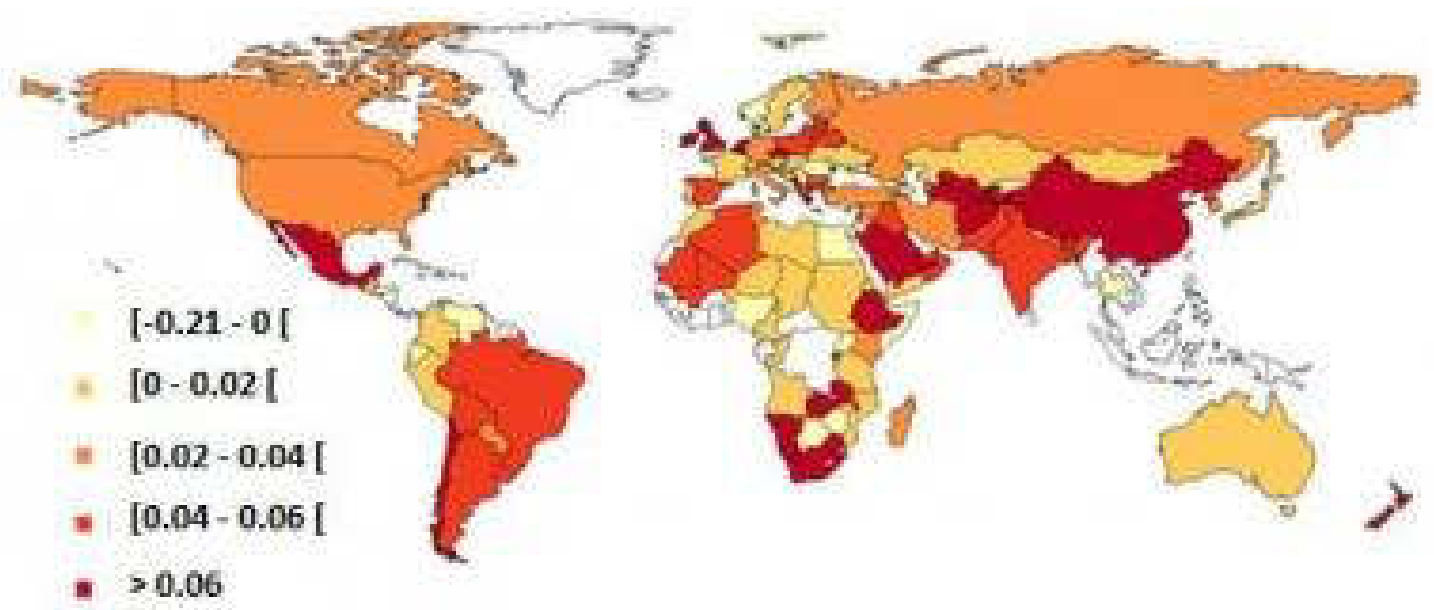
worldwide wheat production (2000)



A global increase of production, but with great variability

Estimated yield increase rates (t ha⁻¹ year⁻¹) for wheat in 2010.

White : countries without data (Michel and Makowski, 2013)



Different diseases – *Puccinia* genus



Stem rust
Puccinia graminis

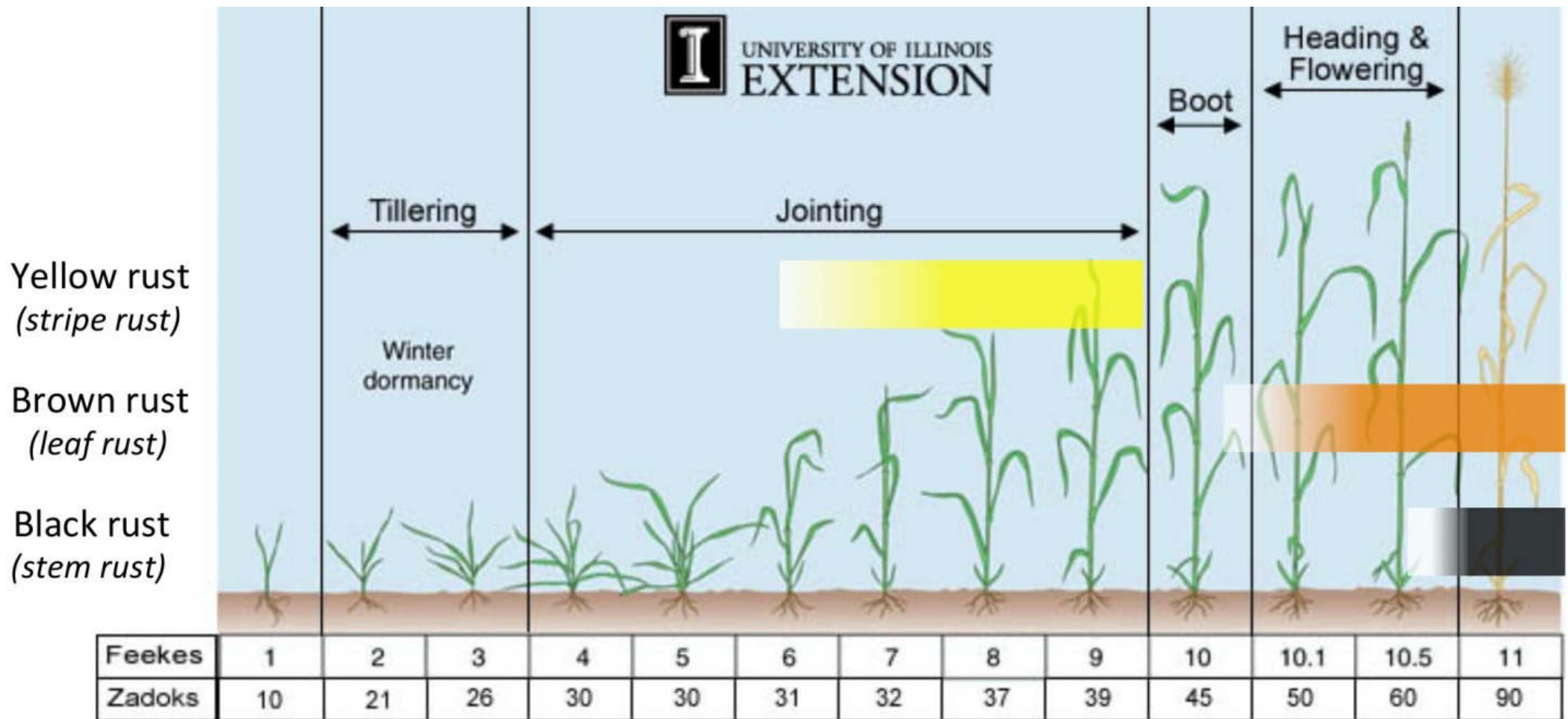


Stripe rust
P. striiformis



Leaf rust
P. triticina
P. recondita f.sp. *tritici*

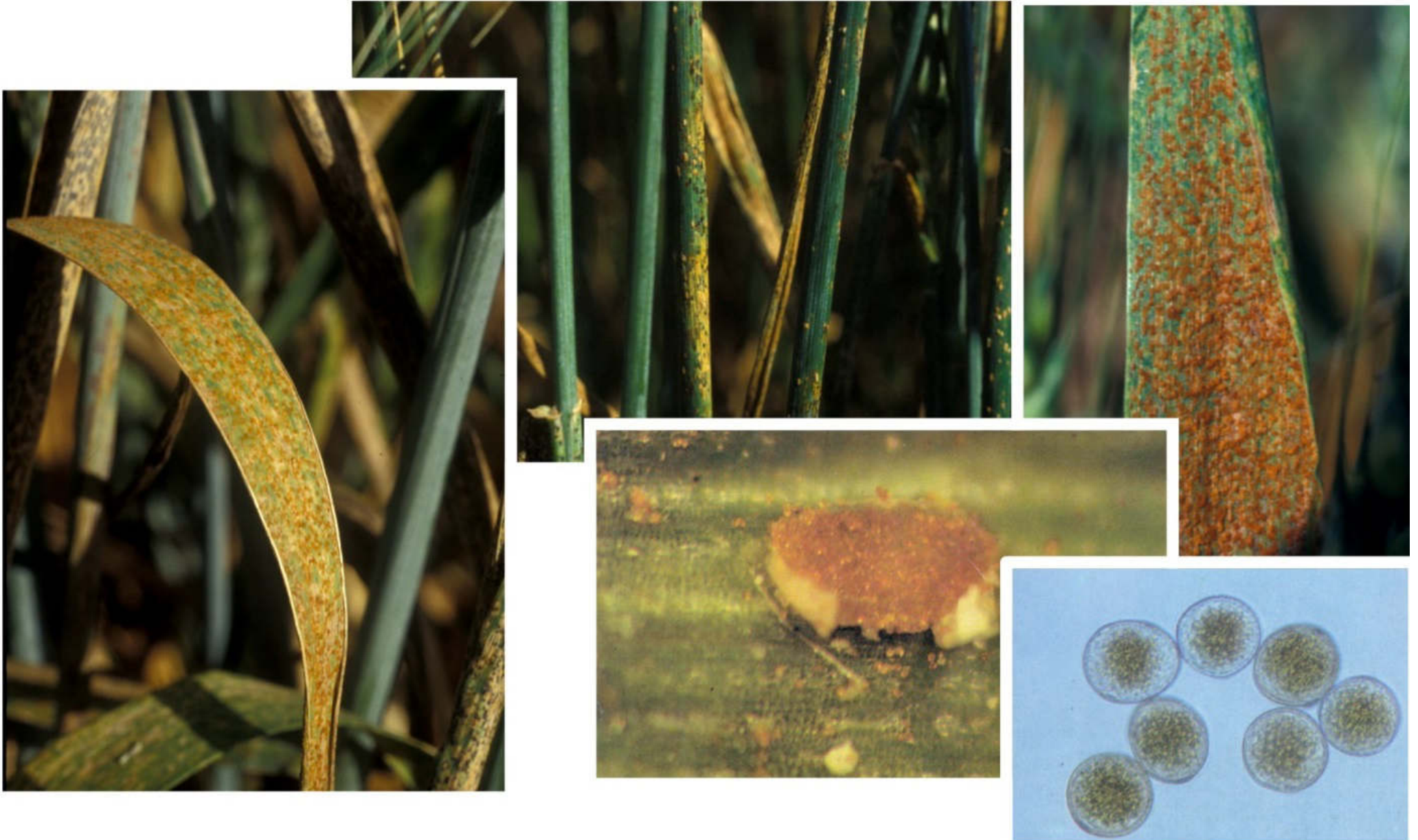
Wheat phenology and rusts



Brown rust = Leaf rust

- Maladie importante en France
- Important disease at mondial scale
- Early infection can cause 42--94% yield loss. Mostly due to less grains in heads
- Pustules with orange--red spores cover leaves and some stem => less photosynthesis
- Resistant varieties exist and are effective for control

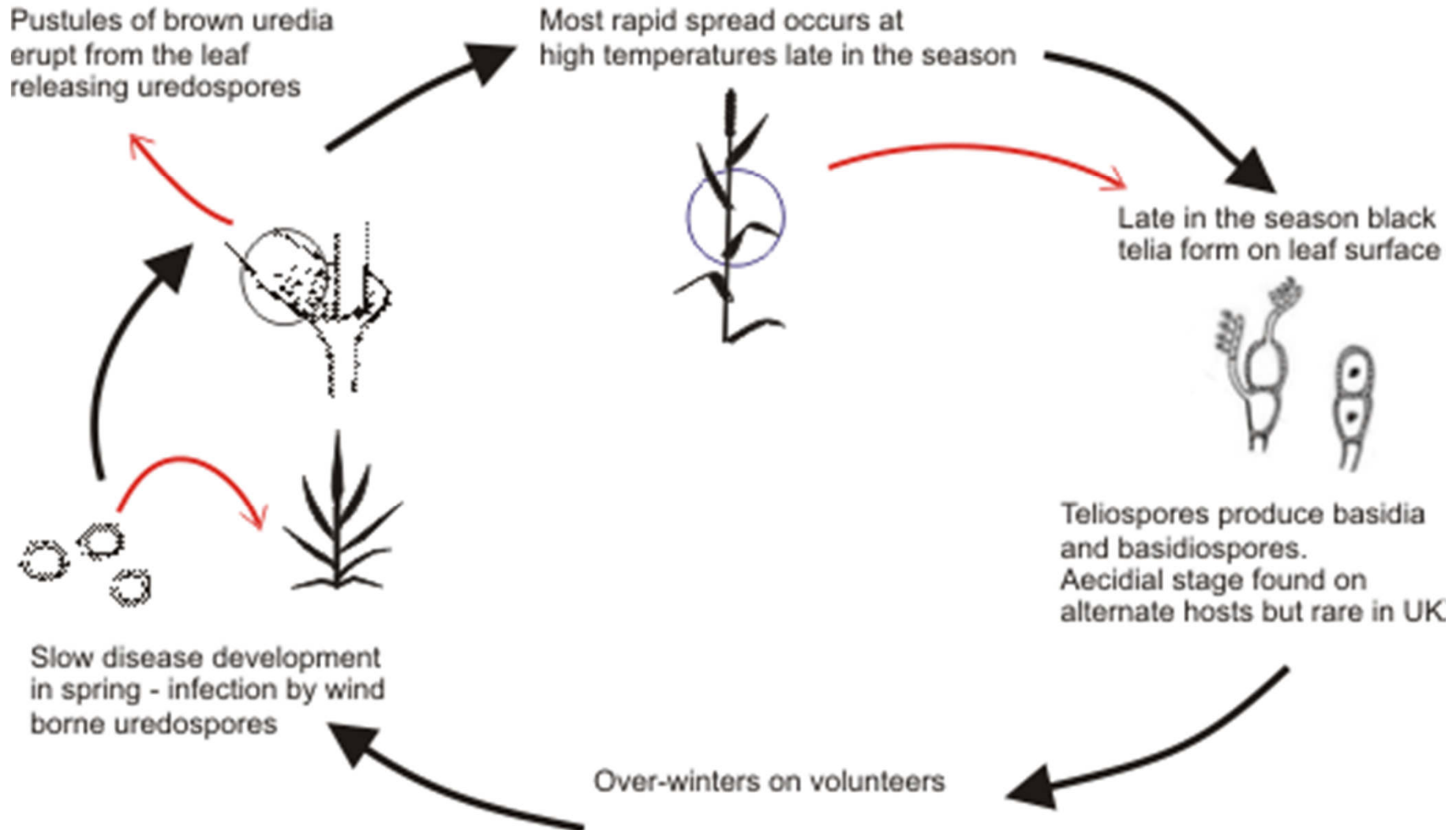
Leaf rust --- symptoms



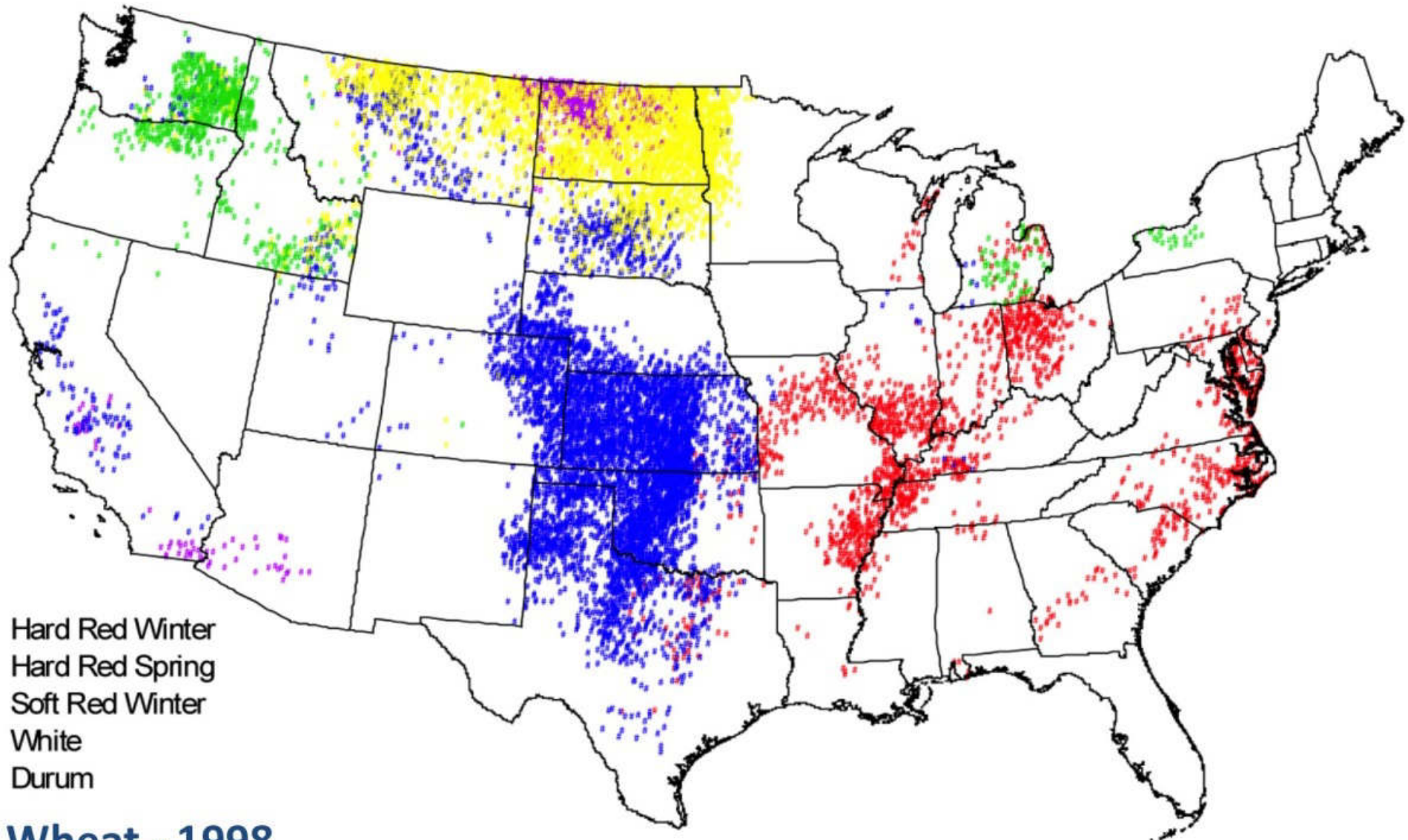
Orange/brown uredia with uredospores

Rust - life cycle

Brown rust *Puccinia triticina*



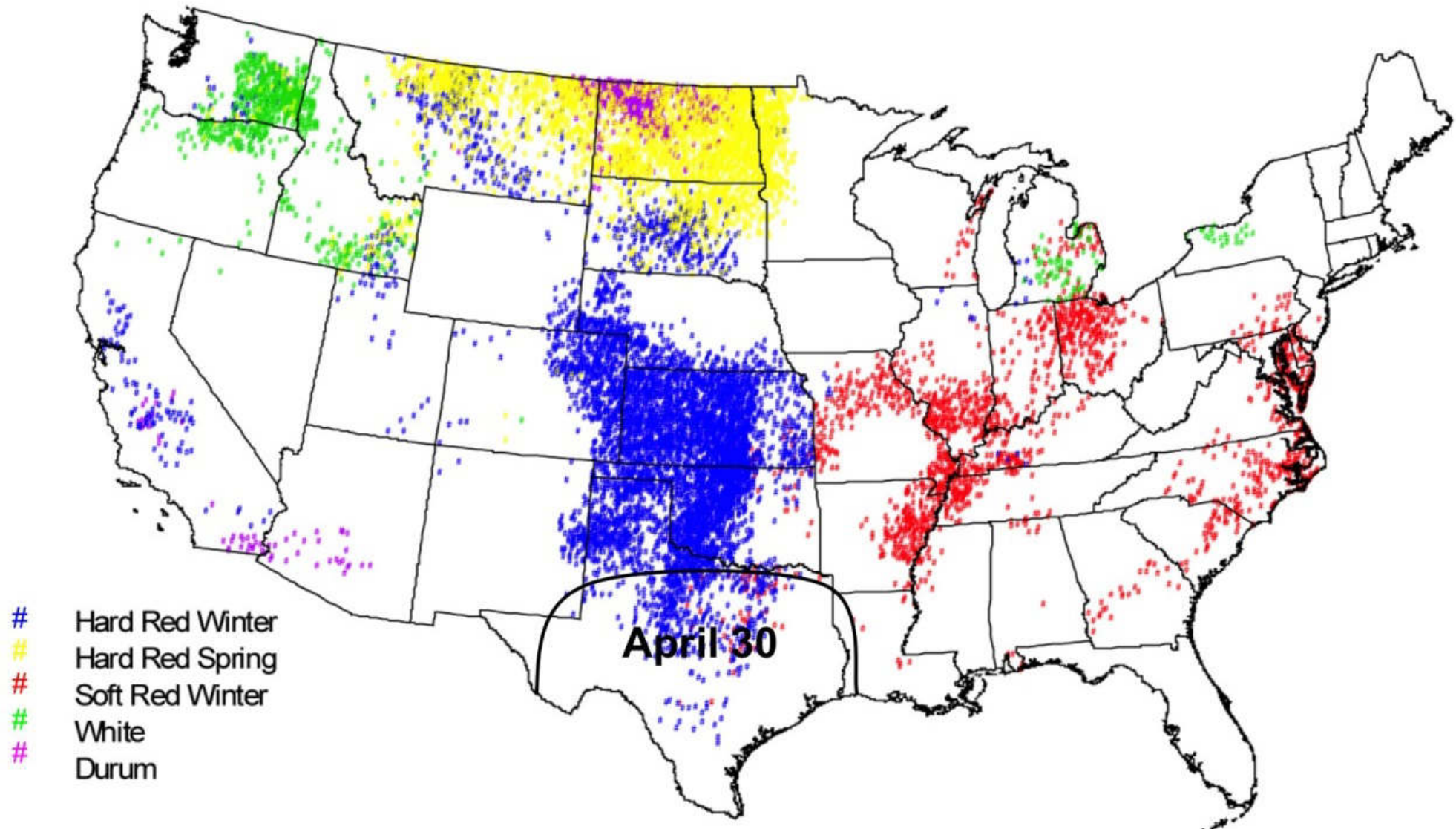
Epidemiology at large scale



U.S. Wheat - 1998

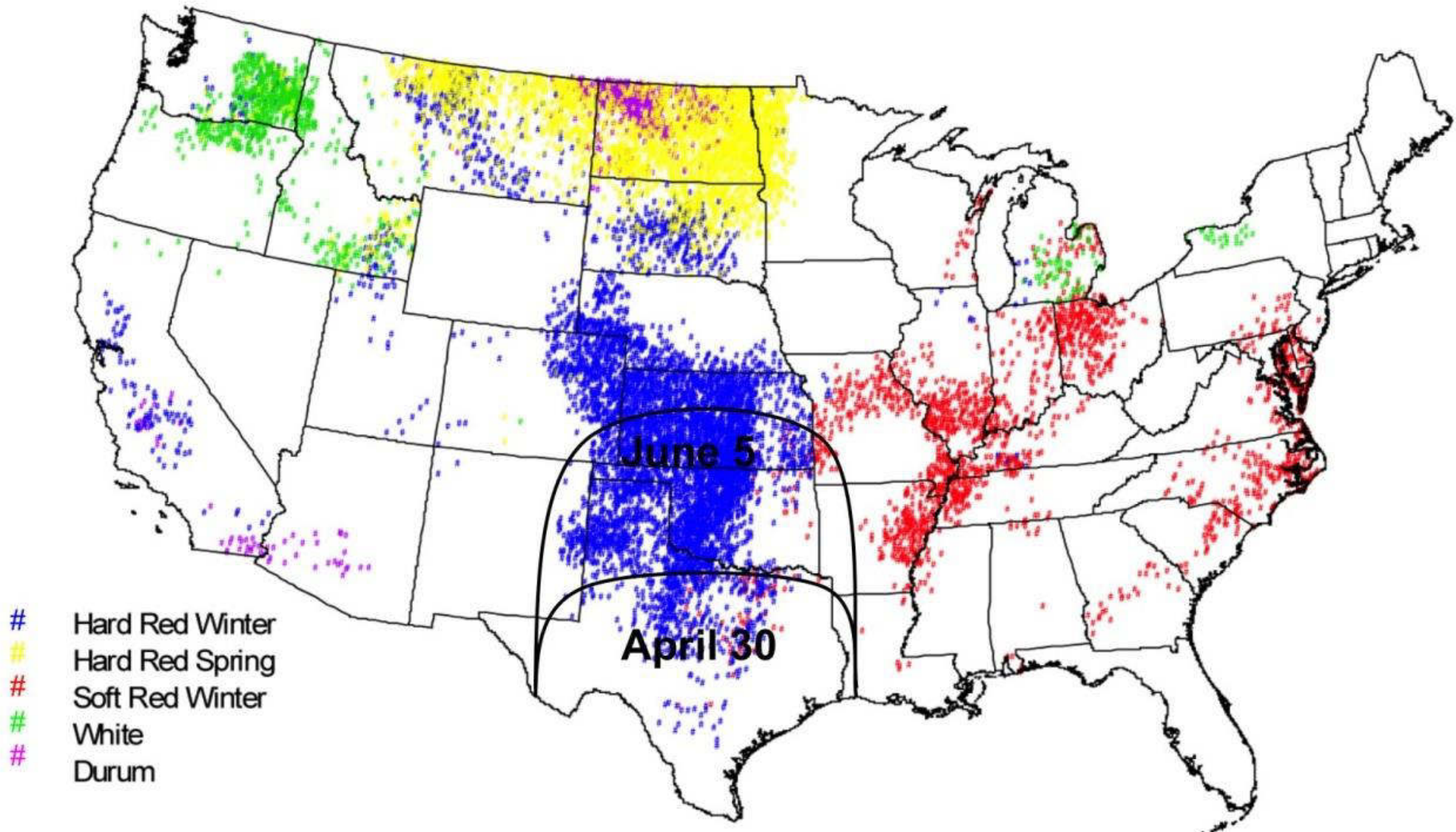
Epidemiology at large scale

Mean date of first Infection



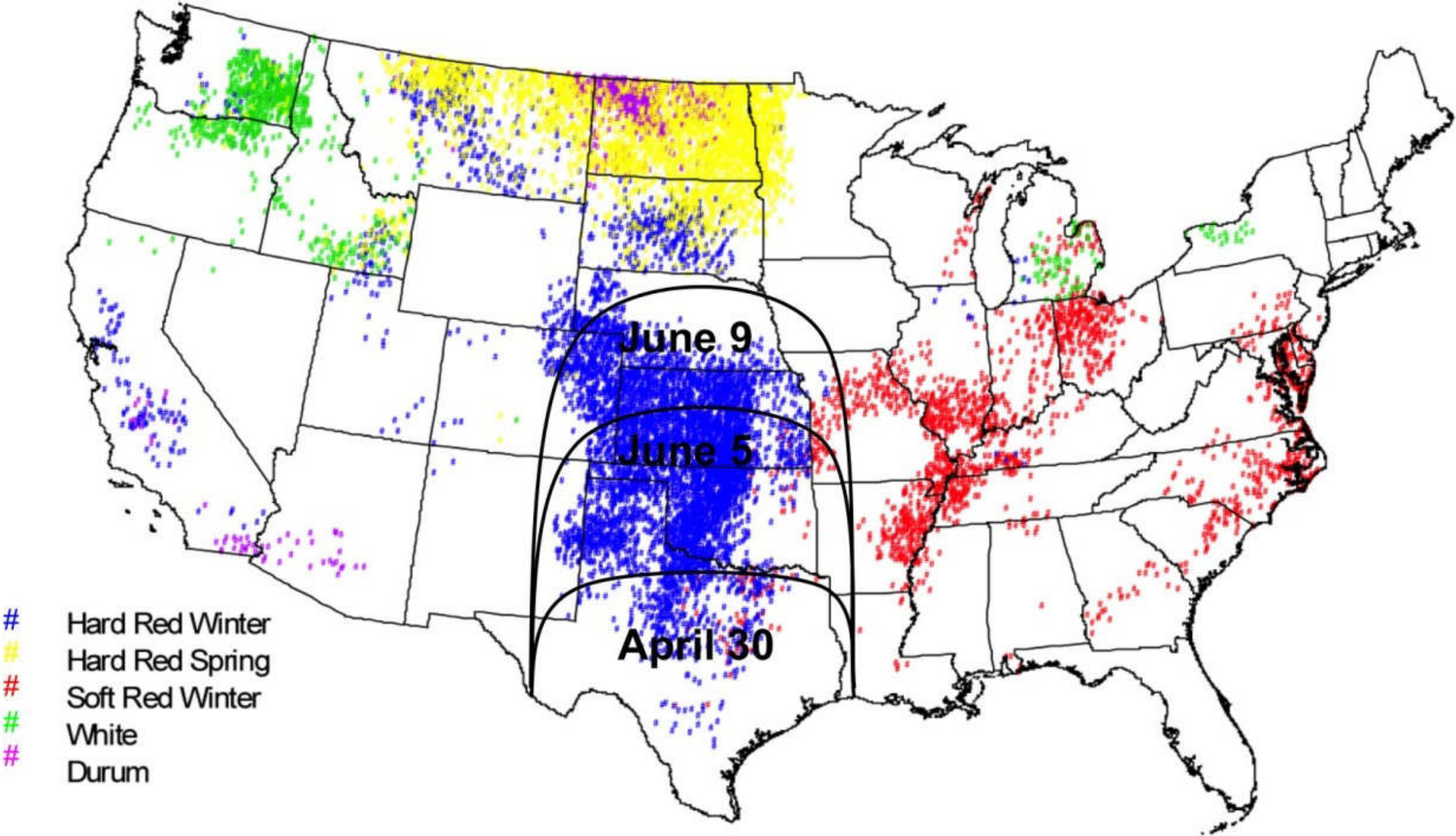
Epidemiology at large scale

Mean date of first Infection



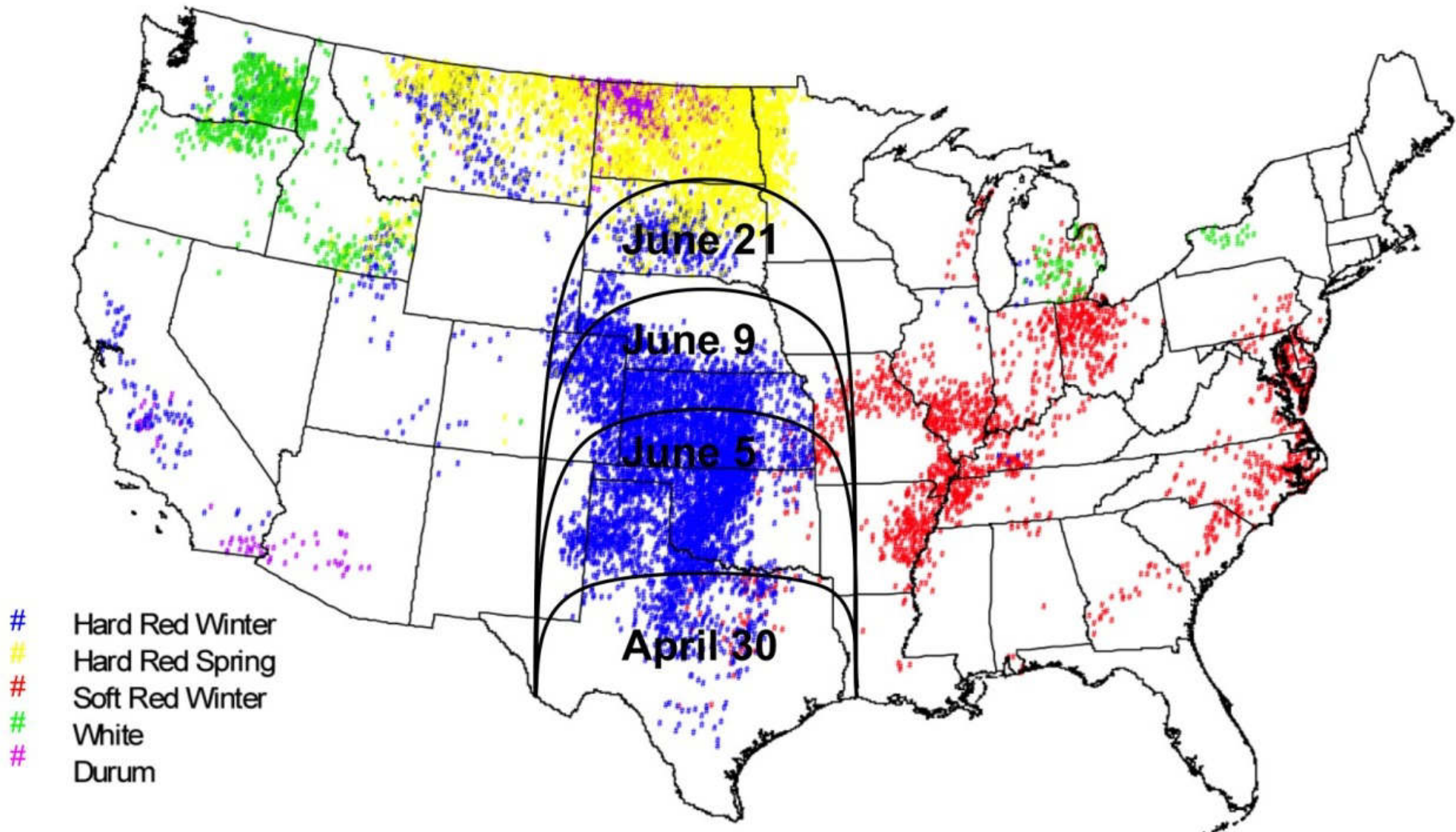
Epidemiology at large scale

Mean date of first Infection



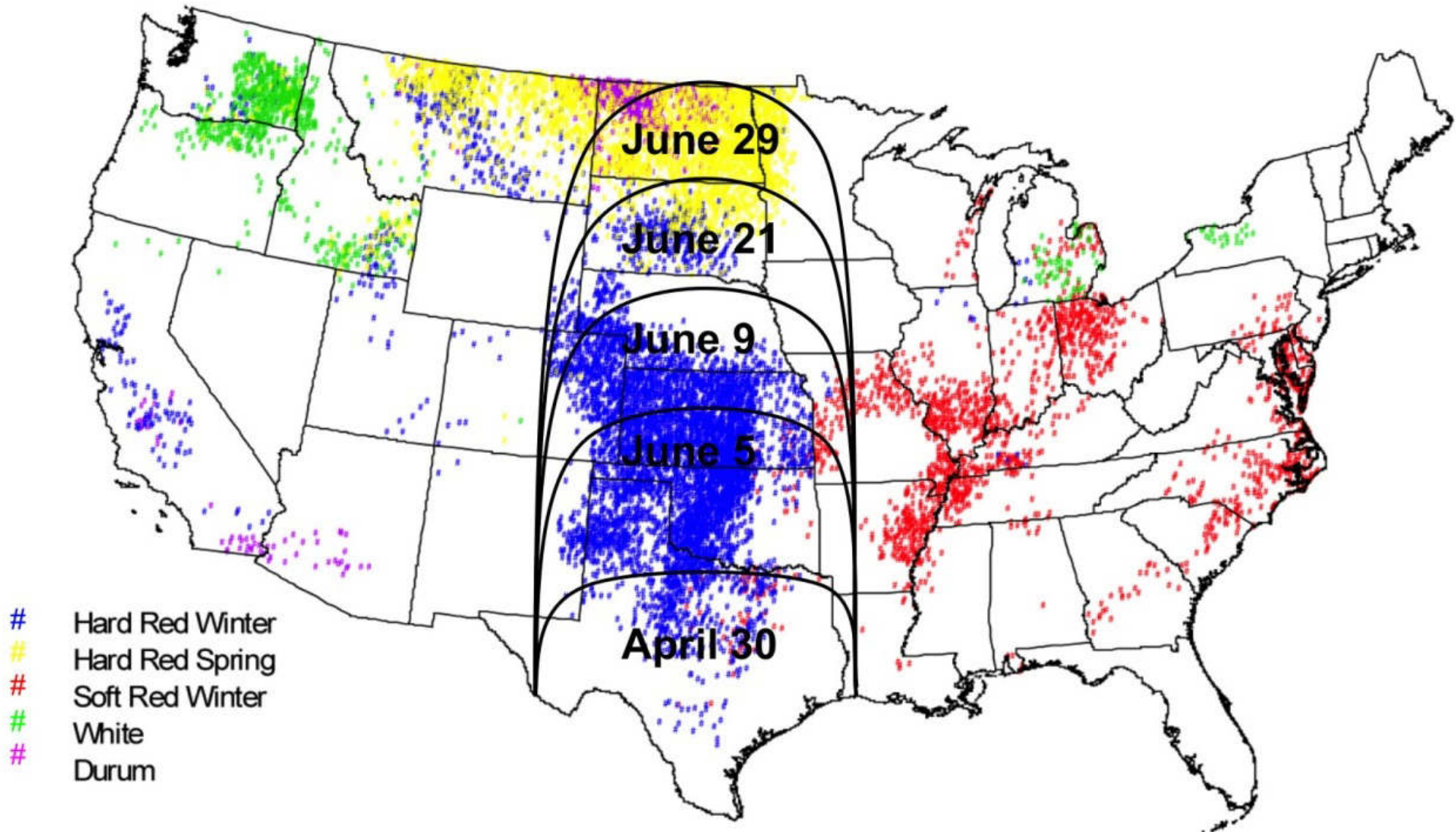
Epidemiology at large scale

Mean date of first Infection



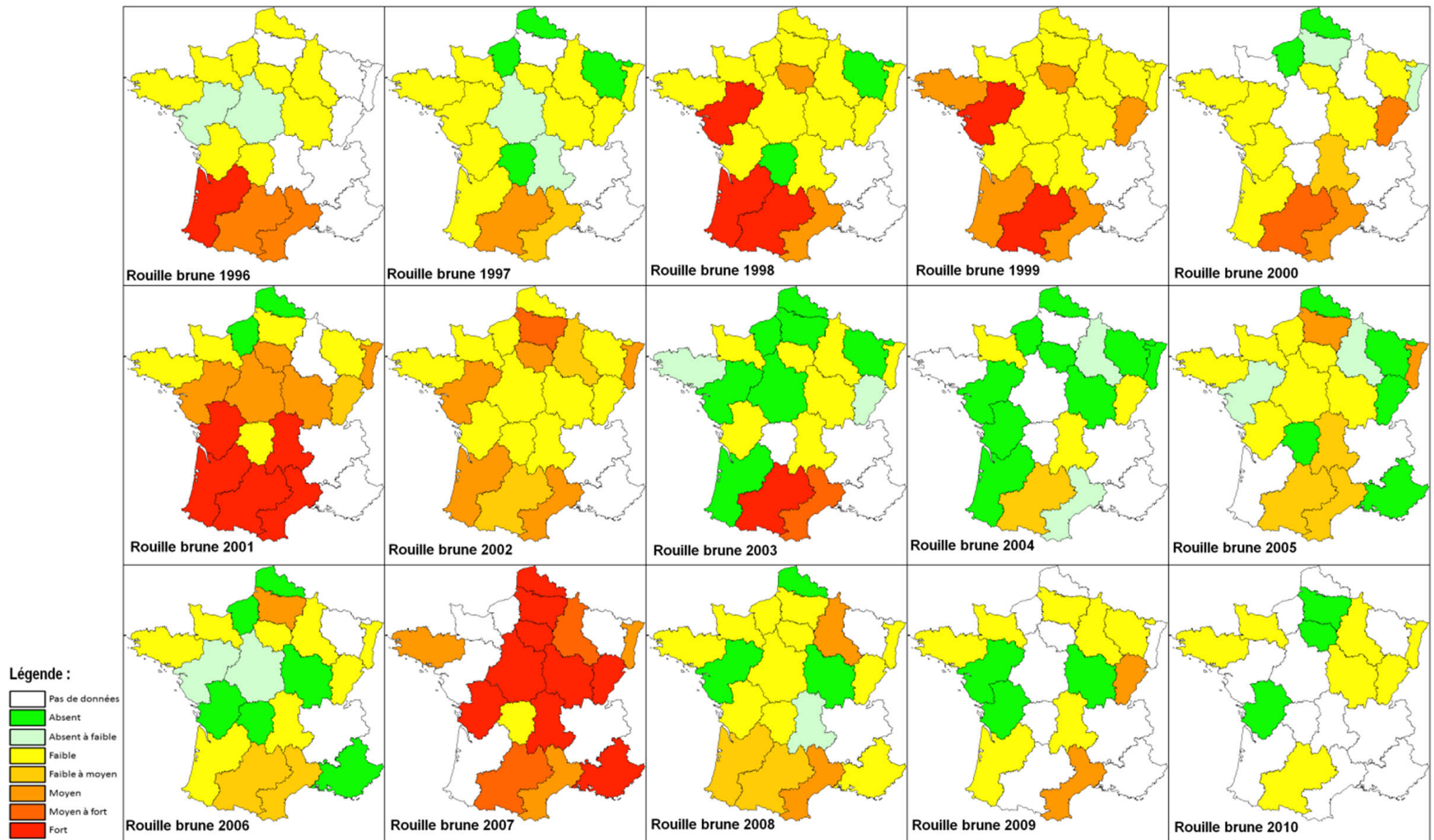
Epidemiology at large scale

Mean date of first Infection



Potential severity of leaf rust in France

Niveau d'attaque régional pour la rouille brune de 1996 à 2010 (source : bilans nationaux des services de la protection des végétaux)

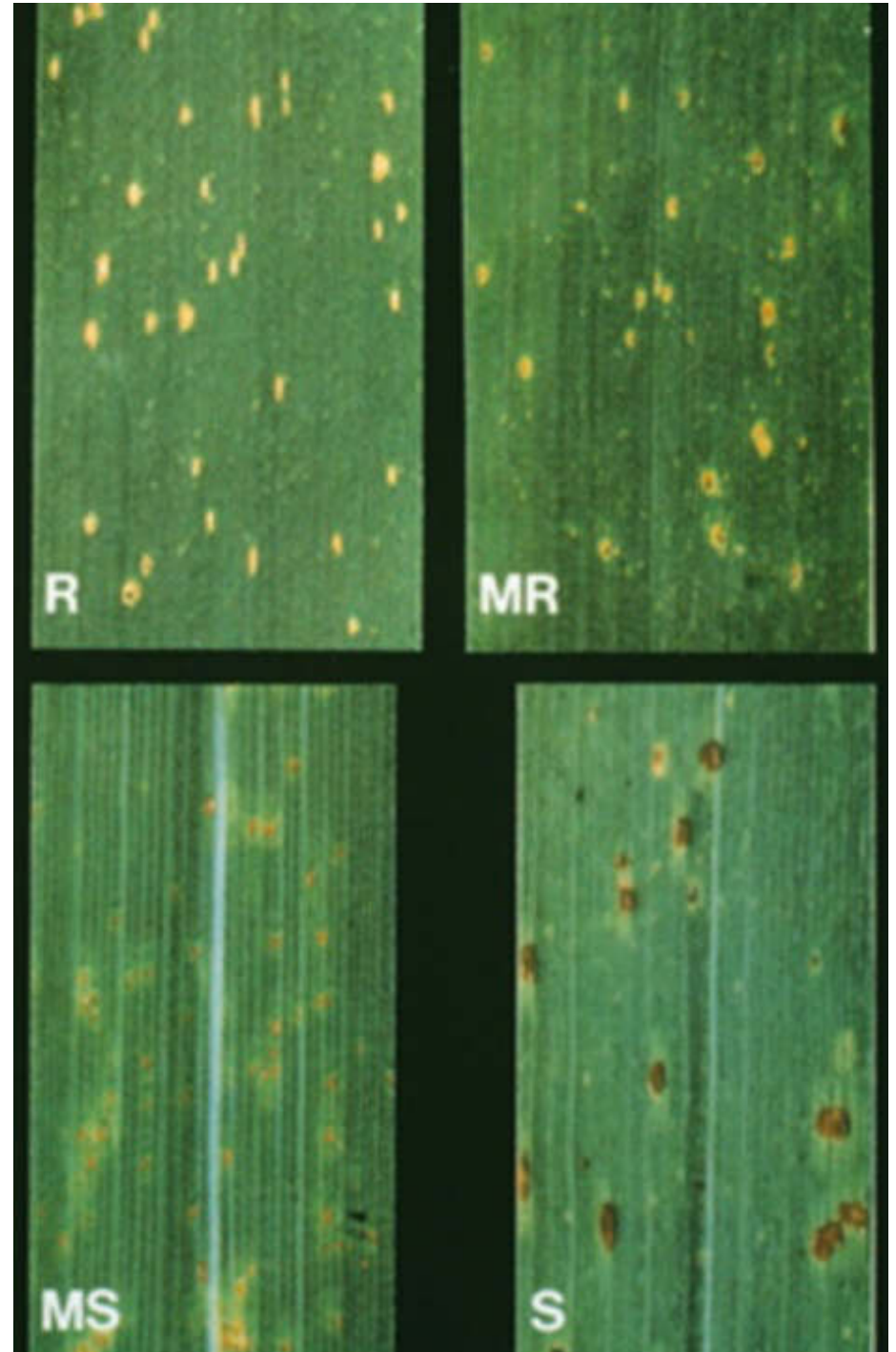


Regional monitoring reports available on www.pestobserver.eu

(Data from SRPV, DGAL, 1996-2010)

Leaf rust - control : Resistance

- Good resistance for varieties of Spring wheat
- Resistance for the varieties of Winter wheat but rapid genetic evolution
- A slowdown in the progress of the epidemic
- Less infections
 - Longer latency duration
 - less spores
 - Shorter sporulation duration



Leaf rust - Chemical control

- Fungicides available: several families
- effectiveness in prevention (before infection)
- Curatively on infected culture, may also stop the disease for 3 to 5 weeks depending on the fungicide, the dose and conditions



⇒ **Importance of treatment positioning to maximize efficiency**

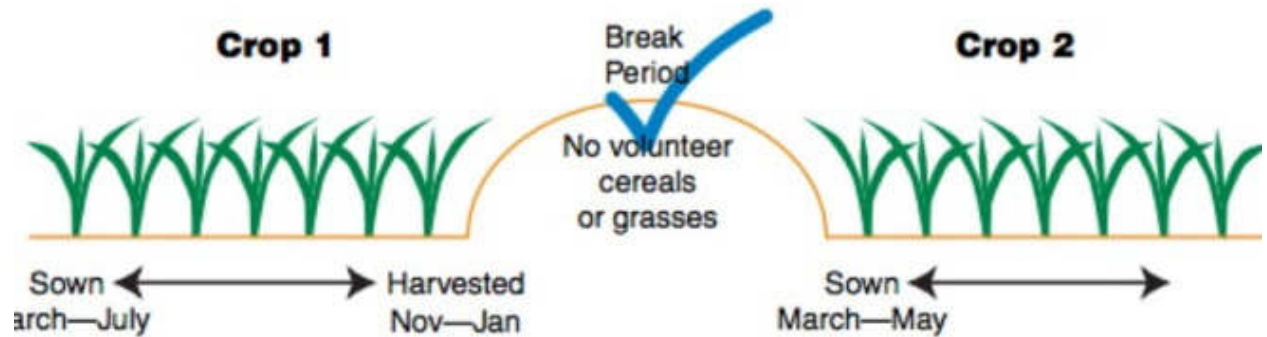
Leaf rust - cultural practices

Date of sown, fertilization, intercultural

- Volunteer cereals can be a host of leaf rust
 - Intercultural management
 - Weeds management (mechanical or chemical)
- *But relative effect, because if Spring conditions are very favorable, then even small remaining quantities are sufficient...*

How Rust infections can 'bridge' two cropping seasons*

DO



DON'T



*Moist conditions are essential for germination and infection by rust spores. Germination takes 12—24 hours.

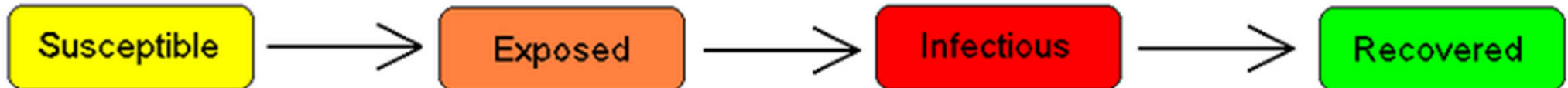
SEIR Model of Brown rust on Wheat

- Part 1. presentation and practical work**
- Part 2. possibility to use it for the projects**

SEIR model

- Susceptible-Exposed-Infectious-Removed (SEIR) model.
- Compartmental models widely used in epidemiology (human, animal, vegetal)

From http://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology



- For infections with significant period of time during which the individual has been infected but is not yet infectious themselves. During this latent period the individual is in compartment Exposed
- Based on the epidemiological concepts “latent period”, “infectious period”, and “multiplication factor”.

Original publication

- Zadoks (1971). Systems Analysis and the dynamics of Epidemics. *Phytopathology*, 61:441-598

Systems Analysis and the Dynamics of Epidemics

J. C. Zadoks

Laboratory of Phytopathology, Agricultural University, Wageningen, The Netherlands.

I thank C. T. De Wit for technical advice, and Mrs. F. M. Daendels for linguistic assistance.

A system is a limited section of the real world. The limits are chosen in such a way that the environment of the system does not materially influence the system. Within a system, the variables show a variety of mutual interactions. In botanical epidemiology, the main components of the system are the host crop, the parasite (sometimes also the vector), and the microclimate.

Systems analysis is a method by which complex situations can be understood and described quantitatively. A systems analysis contains some of the following elements: measurement, analysis, and simulation. The variables of the system must be measured. The quantitative relations between the variables must be analyzed. Prior to or during the measurement and

analysis phases, the basic concepts evolve which are to be applied in a model that embraces all variables and their interrelationships. Simulation is the construction of the model and the study of its behavior.

The aim of systems analysis is to describe a system as a whole, the holistic approach. Advances have been made in the fields of business administration research (4), ecology (1, 16), and recently in phytopathology (15). The present contribution is mainly inspired by the author's studies on cereal rusts.

Systems analysis.—Measurement and analysis.—This paper is a theoretical study. It is not concerned with the techniques of measuring. The measurements referred to are taken from the literature. Only two

PHYTOPATHOLOGY for May (61:441-598) was issued 19 May 1971

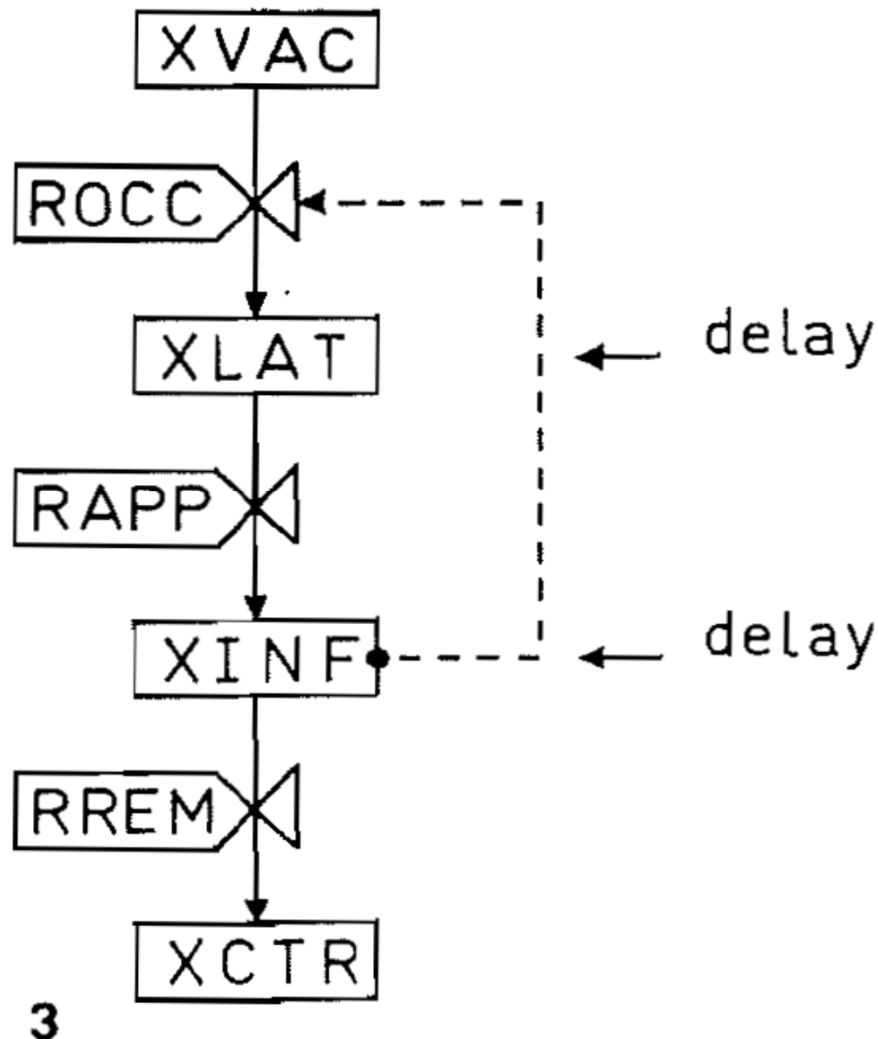
Objectives

- **Objectives:**
 - **Understand an existing simple SEIR model from literature.**
 - **Write the simulator for this model in R.**
 - **Use the model for different objectives (Projects).**

Description of the model

4 state variables

- **XVAC** : vacant (healthy) sites
- **XLAT** for latent site
- **XINF** for infectant sites
- **XCTR** for the cumulative total of removal (post infectious) sites



Fluxes (rates)

- **rocc**: rate of occupation
- **rapp**: rate of apparition
- **rrem**: rate of removal

More detailed (and different versions in the paper)

604

PHYTOPATHOLOGY

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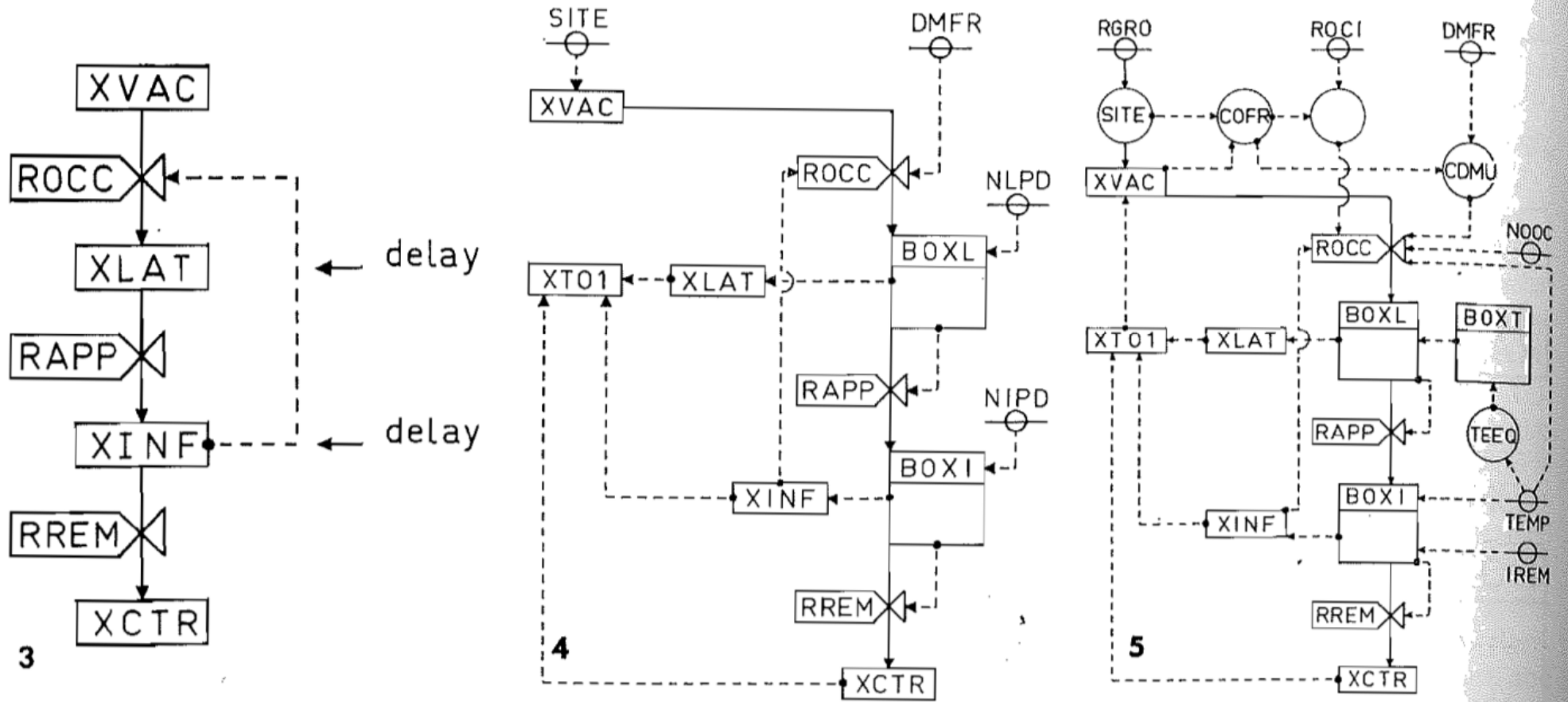


Fig. 3-5. Models of epidemics: 3) a simple model, elementary flow diagram; 4) a simple model, detailed flow diagram; and 5) advanced model, detailed flow diagram.

Equations of the SEIR model for plant disease of Zadoks (1971)

Definition of the model structure as difference equations.

$$XVAC(\text{day}+1) = XVAC(\text{day}) - \text{rocc}$$

$$XLAT(\text{day} + 1) = XLAT(\text{day}) + \text{rocc} - \text{rapp}$$

$$XINF(\text{day}+1) = XINF(\text{day}) + \text{rapp} - \text{rrem}$$

$$XCTR(\text{day}+1) = XCTR(\text{day}) + \text{rrem}$$

Delays for latency and infectiousness

In order to represent the delay processes of latency and infectiousness, both XLAT and XINF state variables are defined as boxcar trains BOXL (latent) and BOXI (infectant). For example, the structure BOXL stores information on each cohort, ie number of sites that enter latency on each day, and determines when the cohort finishes the latency period (nlpd).

Definition of rates

rocc: rate of occupation : nb of sites Vacant=>Latent

$$\text{rocc} = \text{cofr} * \text{DMFR} * \text{XINF}$$

$$\text{with } \text{cofr} = \max\left(\frac{XVAC(\text{day})}{\text{SITE0}} ; 0\right)$$

rapp: rate of apparition : nb of sites Latent=>Infectant

$$\text{rapp} = \text{outflow}(XLAT) = \text{outflow}(BOXL)$$

rrem: rate of removal : nb of sites Infectant=>removed

$$\text{rrem} = \text{outflow}(XINF) = \text{outflow}(BOXI)$$

Additional auxillary variables of interest are :

$$XTO1 = XLAT + XINF + XCTR$$

$$XSEV = XINF + XCTR$$

$$\text{severity} = \frac{XSEV}{XLAT + XINF + XCTR + XVAC}$$

To begin with, a simplest version

- A supplementary hypothesis:
 - no delay function, but continuous rate with equivalent time constant

(a little more simple to program and sufficient to understand the major aspect of SEIR dynamic model)

Equations of the **simplified** SEIR model.

Definition of the model structure as difference equations.

$$XVAC(\text{day}+1) = XVAC(\text{day}) - \text{rocc}$$

$$XLAT(\text{day} + 1) = XLAT(\text{day}) + \text{rocc} - \text{rapp}$$

$$XINF(\text{day}+1) = XINF(\text{day}) + \text{rapp} - \text{rrem}$$

$$XCTR(\text{day}+1) = XCTR(\text{day}) + \text{rrem}$$

Definition of rates

Note that you need to add rules to avoid having negative state variables and the order of calculation is important.

rocc: rate of occupation : nb of sites Vacant=>Latent

$$\text{rocc} = \min(\text{cofr} * \text{dmfr} * XINF(\text{day}), XVAC(\text{day}))$$

$$\text{with } \text{cofr} = \max\left(\frac{XVAC(\text{day})}{SITE0}; 0\right)$$

rapp: rate of apparition : nb of sites Latent=>Infectant

$$\text{rapp} = \min(XLAT[\text{day}] * 1 / \text{nlpd}, XLAT[\text{day}] + \text{rocc})$$

$$\text{rapp} = \min\left(\frac{XLAT(\text{day})}{\text{nlpd}}, XLAT(\text{day}) + \text{rocc}\right)$$

rrem: rate of removal : nb of sites Infectant=>removed

rrem: rate of removal : nb of sites Infectant=>removed

$$\text{rrem} = \min\left(\frac{XINF(\text{day})}{\text{nipd}}, XINF(\text{day}) + \text{rapp}\right)$$

Additional auxillary variables of interest are :

$$XTO1 = XLAT + XINF + XCTR$$

$$XSEV = XINF + XCTR$$

$$\text{severity} = \frac{XSEV}{XLAT + XINF + XCTR + XVAC}$$

Lets start in R

Proposition of a common structure : an empty model function. Copy the following lines in a new script.

```
zakoks.simple.model = function (nlpd=4,nipd=1,dmfr=16,SITE0 =  
5*10^9,weather=NULL, sdate = 1, ldate = 140) {
```

```
# here you will write the core of the model
```

```
return(list(sim=data.frame(day = sdate:ldate, XVAC = XVAC[sdate:ldate],  
XLAT = XLAT[sdate:ldate], XINF = XINF[sdate:ldate],XCTR =  
XCTR[sdate:ldate],XTO1=XTO1[sdate:ldate], XSEV= XSEV[sdate:ldate],  
severity=severity[sdate:ldate]),  
param=c(nlpd=nlpd,nipd=nipd,dmfr=dmfr,SITE0 = SITE0)))  
} # end of model
```

How to structure the code ?

- creation of state variable as vector
- initialization of state variable
- Simulation loop
 - Calculate rates of change of state variables (dTT, dB, dLAI)
 - Update state variables *
- End simulation loop
- Return results

First Simulations

Name	Value	Description	Unit
nlpd	8	Duration for latency period	day
nipd	30	Duration for infectious period	day
dmfr	16	Coefficient of multiplication	-
XVAC0	1e+10	Initial number of vacant sites	sites
XLAT0	1	Initial number of latent sites (first contamination)	sites