



# Relationships between in situ genetic diversity of wheat and crop sequences profiles in France between 1980 and 2006

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# RELATIONSHIPS BETWEEN IN SITU GENETIC DIVERSITY OF WHEAT AND CROP SEQUENCES PROFILES IN FRANCE BETWEEN 1980 AND 2006

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# Background and Questions

- ✓ In France, double decrease in bread wheat genetic diversity during the 20<sup>th</sup> century, caused by:
  - ❑ the replacement of landraces by modern pure lines varieties
  - ❑ the diffusion of a reduced number of high yielding semi-dwarf varietiesBonnin et al. 2014
- ✓ During the recent period (1980-2006), changes in genetic diversity seem more complex nationwide, potentially due to a spatial structuration of:
  - ❑ the temporal changes of bread wheat genetic diversity
  - ❑ several determinants of *in situ* crop diversity, such as crop sequences and their changes over the period studiedPerronne et al. in prep, Schott et al. 2010

To what extent the temporal changes in *in situ* crop diversity and crop sequences are both spatially structured and correlated during the period 1980-2006 at the '*département*' scale in France?

# Available datasets (wheat diversity)

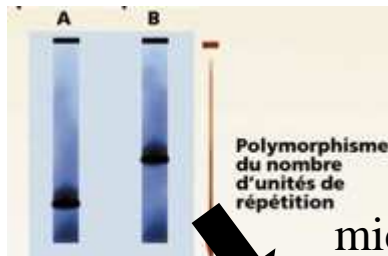
Database “French wheat diversity”:  
 ✓ **acreage of varieties** (55 ‘départements’)  
 ✓ allelic diversity (35 microsatellite markers, ~ 700 genotyped varieties)

statistical services of the  
Wheat Board



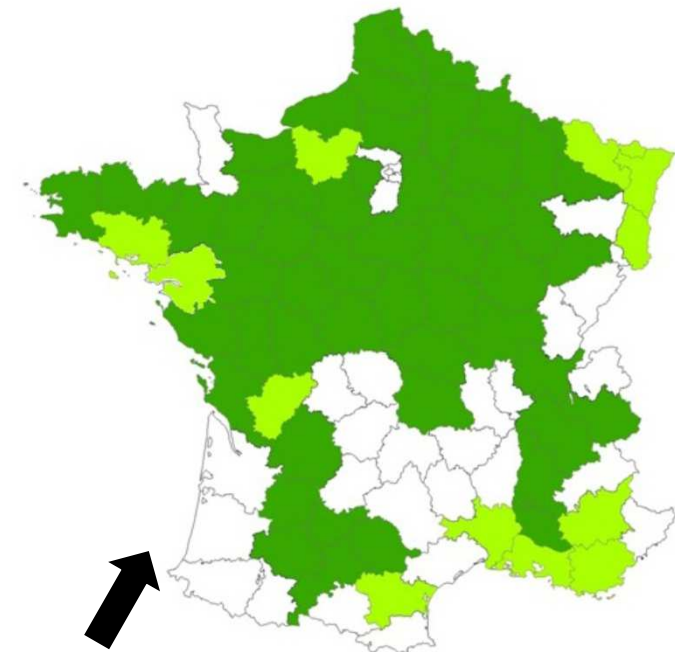
departement	annee	variete	repartition (%)
ain	1980	BLASON	0.180000
ain	1980	CAPELLE DESPREZ	0.270000
ain	1980	CAPITOLE	3.880000
ain	1980	CASTAN	1.300000
ain	1980	CHAMPLEIN	3.940000
ain	1980	CLEMENT	0.040000
ain	1980	COMTAL	0.060000
ain	1980	COURTOT	0.080000
ain	1980	DARIUS	0.100000
ain	1980	ETOILE DE CHOISY	1.690000
ain	1980	HARDI	6.250000

integrating  
within-variety  
diversity



microsatellite markers

TYPE VAR	nom	cfid17h8a	cfid17h8d	gwm11	gwm120	gwm135	gwm149
Lignee pure	ACIENDA	156	188	197	152	139	166
Lignee pure	ACIER	156	212	195	152	139	155
Lignee pure	ADAM	156	194	193	152	196	155
Lignee pure	ADMIRAL	156	206	199	152	139	155
Lignee pure	ADONIS	156	208	205	152	196	155



‘départements’ with acreage of  
varieties surveyed

# Measuring crop varietal and genetic diversity

## ✓ Varietal richness

number of varieties grown in a '*département*' during a year

## ✓ Spatial diversity $N_2$ (Simpson diversity)

measure of spatial evenness of varieties distribution in a '*département*'

Hill (1973)

## ✓ Nei's (1973) gene diversity,

average allelic diversity at all loci for the set of microsatellite markers across the pool of varieties sown in a '*département*' during a year

## ✓ Spatial genetic diversity $H_T^*$ , composite indicator weighted by acreage of varieties

taking into account (i) varietal richness, (ii) varietal diversity and (iii) between-variety allelic diversity

# Available datasets (crop sequences)

‘département 1’	year 1	year 2	year 3	
	wheat	pea	wheat	0.5%
	oil. rape	wheat	barley	7%
	maize	wheat	sunflower	2%



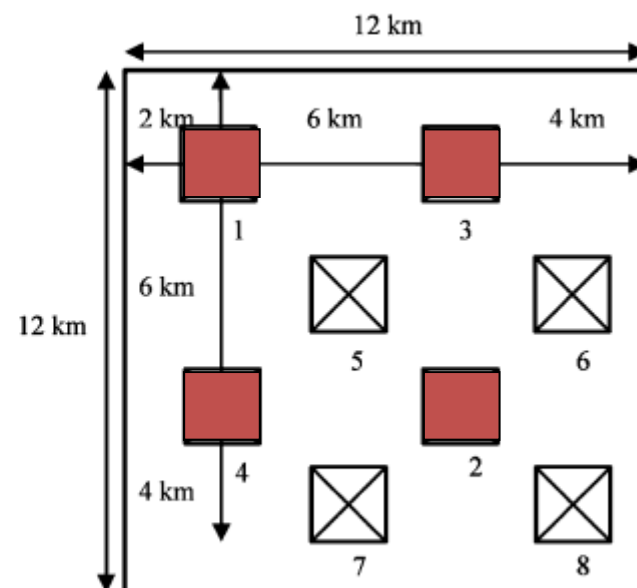
The **Teruti survey** (1981-2004)

two-level systematic sampling method:

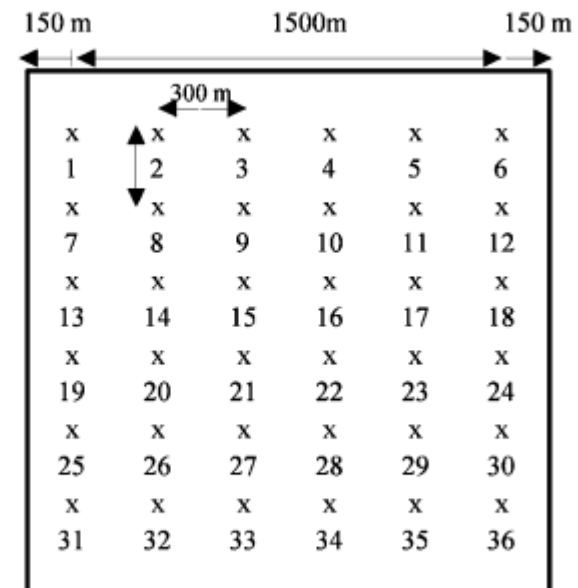
1. France segmented into 4700 grids, with an area of 12 x 12 km per grid, and 4 aerial photos taken (■)
2. Within each aerial photo area, 36 evenly spaced sampling points, i.e. 555,382 sampling points per year
3. Then, extraction of 3-year land-cover subsequences percentages



(a)



(b)



(c)

# 1. Does the temporal changes in genetic diversity and crop sequences appear spatially structured?

## ✓ Description of the statistical methods:

### ☐ Transformation of data

- ☐ Fitting procedure to impute missing data (diversity)

- ☐ Box-Cox transform. to improve the normality of the distribution (CS)

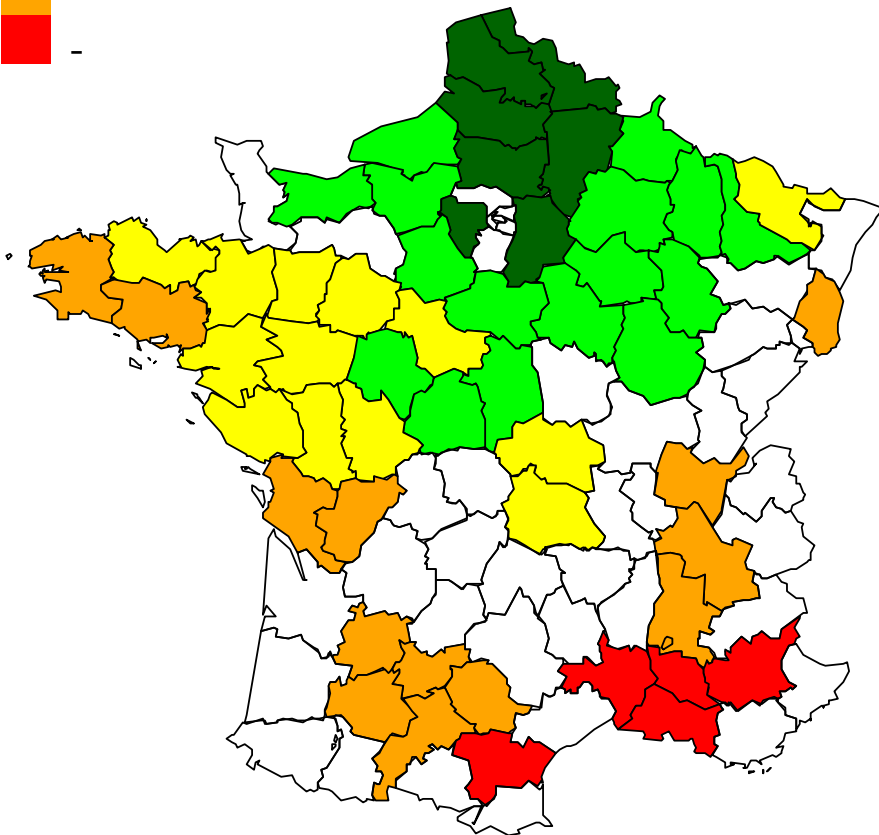
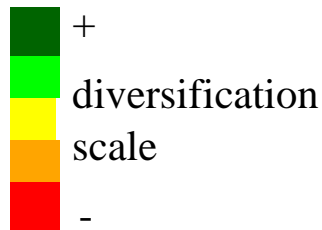
### ☐ Multivariate analysis and clustering (diversity and CS)

- ☐ Principal Component Analysis (PCA)

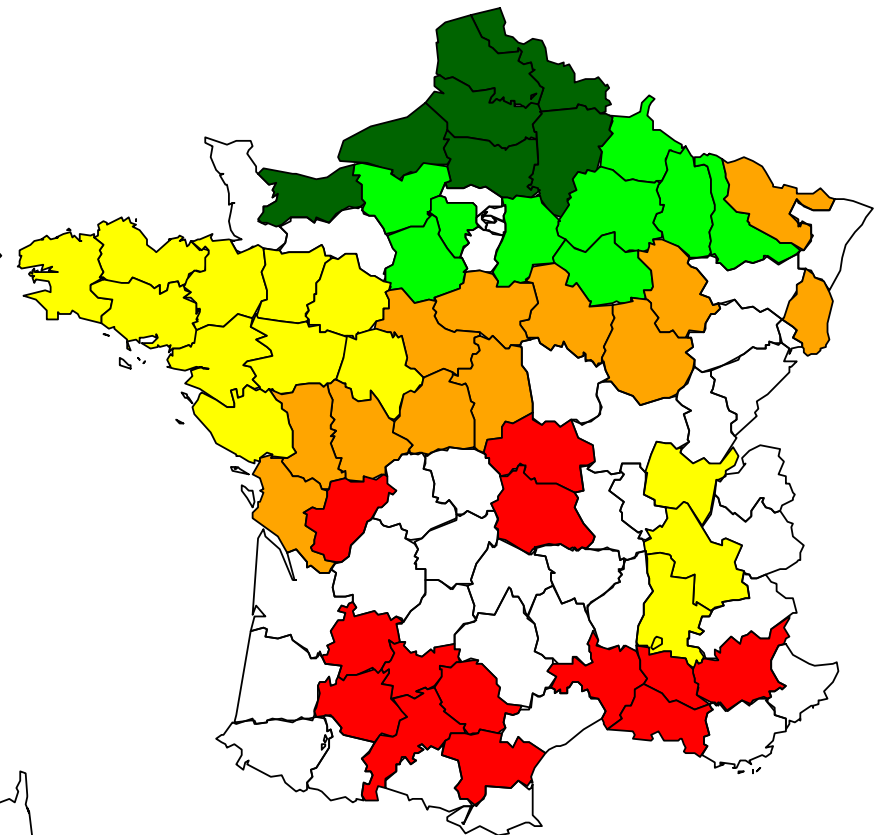
- ☐ K-means clustering algorithm (minimizing the sum of the within-cluster sums-of-squares)

### ☐ Mapping of identified groups

# 1. Temporal changes in varietal richness and diversity are spatially structured

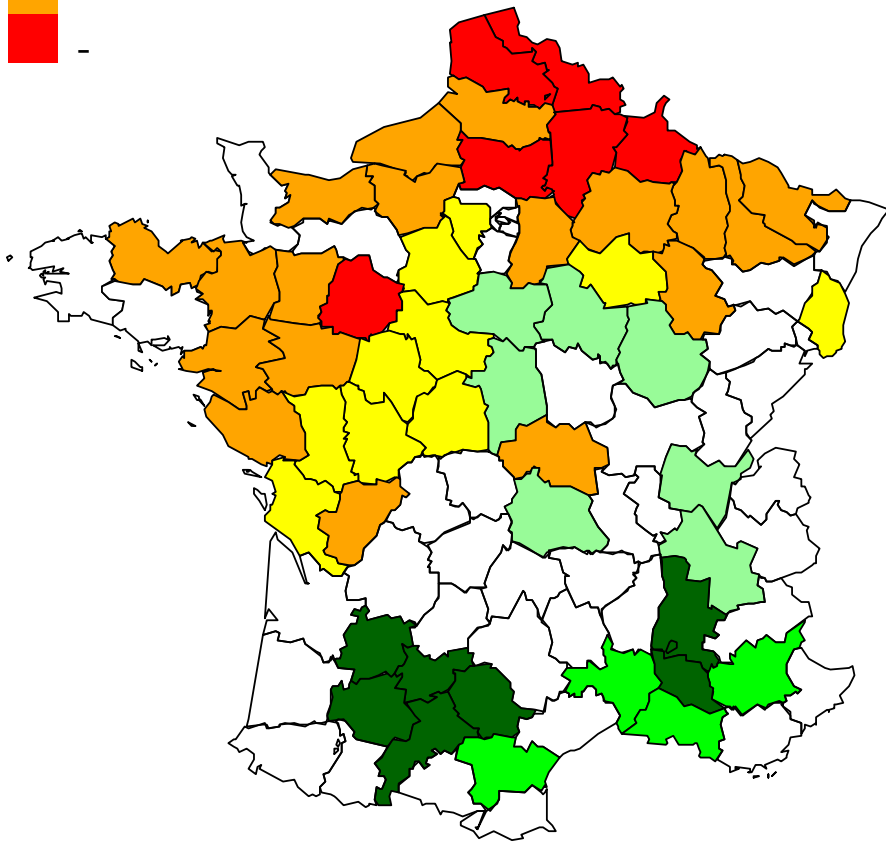
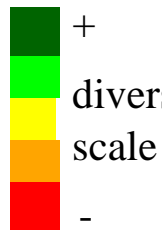


Varietal richness

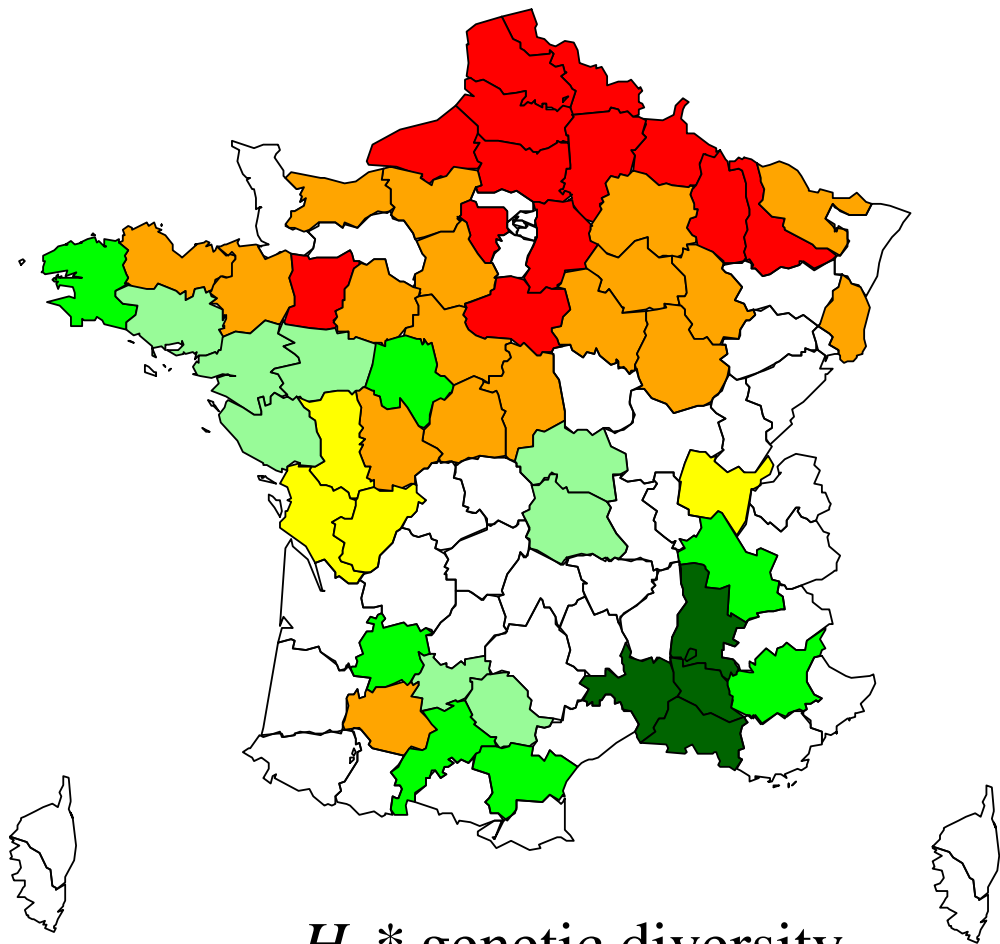


Spatial diversity

# 1. Temporal changes in genetic diversity are spatially structured

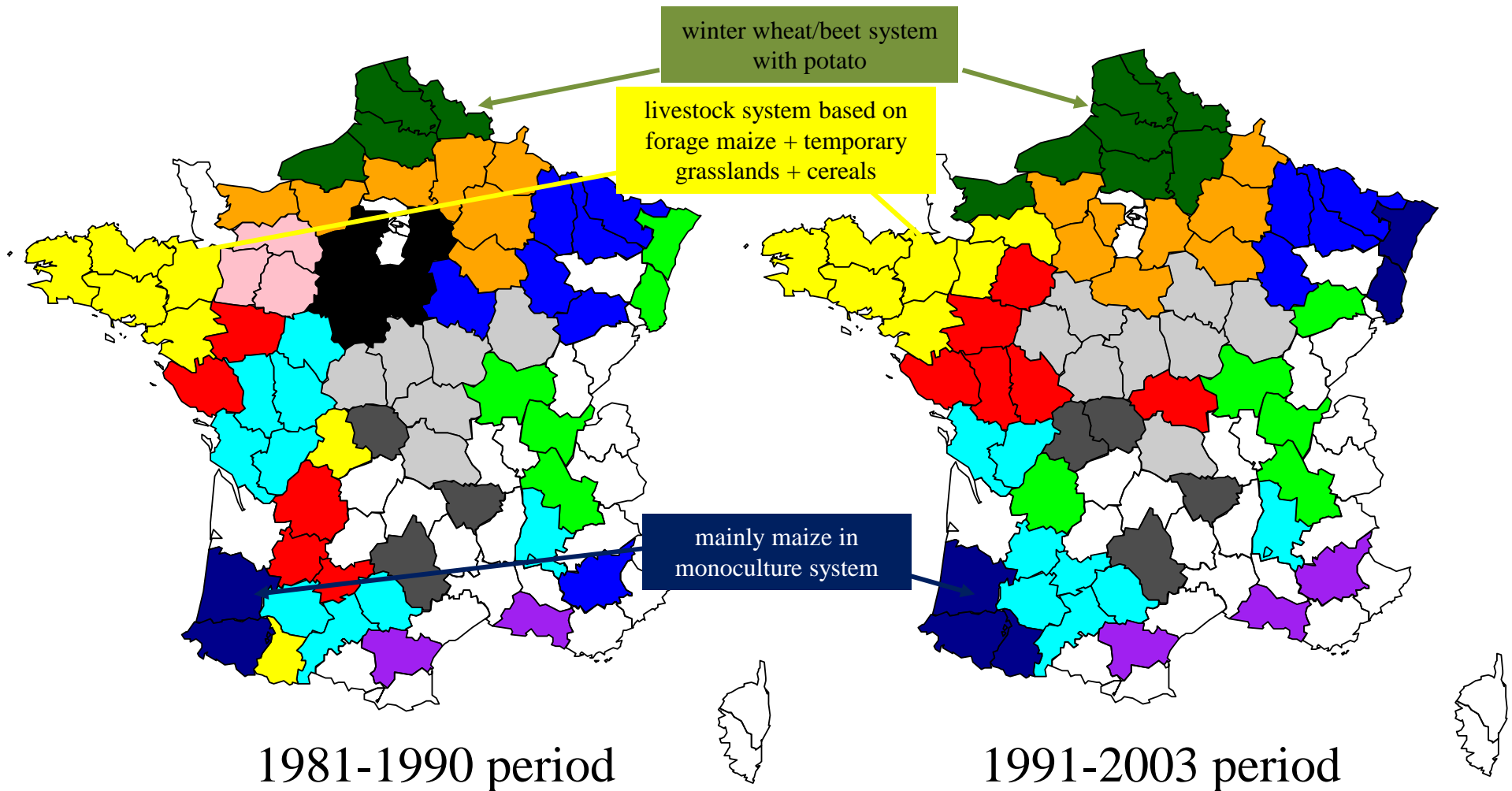


Nei's gene diversity  
(unweighted by acreages)



$H_T^*$  genetic diversity  
(weighted by acreages)

# 1. Crop sequences are spatially structured during two distinct periods (1981-1990 and 1991-2003)



colors are not related to diversification of crop sequences  
two subperiods are due to different sampling procedures

## 2. Are the temporal changes in genetic diversity and crop sequences correlated?

- ✓ Are the groups identified for both diversity indicators and crop sequences on two periods similar ?

□  $\chi^2$  test, sequential Bonferroni–Holm adjustment for multiple comparisons

	$N_2$	Nei	$H_T^*$	CS 1981-1990	CS 1991-2003
number cultivars	65.55	102.01	66.68	103.20	150.27
$N_2$		82.53	51.92	104.53	145.27
Nei			60.38	150.09	190.97
$H_T^*$				78.50	72.71
CS 1981-1990					273.22

$\chi^2$  statistic

- ✓ all variables are **significantly correlated**, with **higher correlations between diversity indicators and crop sequences**
- ✓ CS profiles were **highly conserved between two periods**
- ✓ **CS 1991-2003 period** was **more correlated with diversity changes**

## 2. Are the temporal changes in genetic diversity and crop sequences correlated?

- ✓ Are patterns of changes and CS profiles identified correlated (using quantitative differences)?

□ Mantel test, sequential Bonferroni–Holm adjustment for m. comparisons

	$N_2$	Nei	$H_T^*$	CS 1981-1990	CS 1991-2003
number cultivars	0.7122	0.2499	0.3121	0.5049	0.5439
$N_2$		0.2772	0.2954	0.5395	0.5466
Nei			0.3690	0.2301	0.2970
$H_T^*$				0.2012	0.3196
CS 1981-1990					0.8435

Mantel statistic

- ✓ all variables are **significantly correlated** at the ‘département’ scale, with **higher correlations between varietal diversity indicators and crop sequences** than between **genetic diversity indicators and crop sequences**

# Take-home messages

- ✓ Temporal changes in *in situ* crop diversity and crop sequences on two periods were correlated:

‘*départements*’ showing a comparable temporal change in their diversity were usually characterized by comparable crop sequences

⇒ suggest that crop sequences could be a determinant of *in situ* crop diversity

- ✓ Temporal changes in varietal diversity were more correlated with crop sequences than temporal changes in genetic diversity:

⇒ suggest that crop sequences could further influence the number of varieties and their relative spatial distribution at the landscape-scale

# Relationships between crop sequences and genetic diversity of bread wheat: hypotheses

- ✓ Crop sequences as proxies of agroclimatic conditions related to production situations and diseases pressures. These spatially structured explanatory factors condition varietal choice by agricultural cooperatives, based on disease resistance of available varieties and targeted markets
- ✓ Crop sequences as proxies of types of farming and cropping systems, conditioning varietal choice
- ✓ Crop sequences as direct drivers of varietal choice, due to preceding crop of wheat, taking into account soil-borne diseases and weeds

# Perspectives

- ✓ Identifying the major determinants of spatio-temporal evolution of *in situ* crop diversity of bread wheat
- ✓ Studying different scenarios of direct and indirect causal links between these determinants
- ✓ Studying the relationship between *in situ* crop diversity and yield, taking into account these determinants

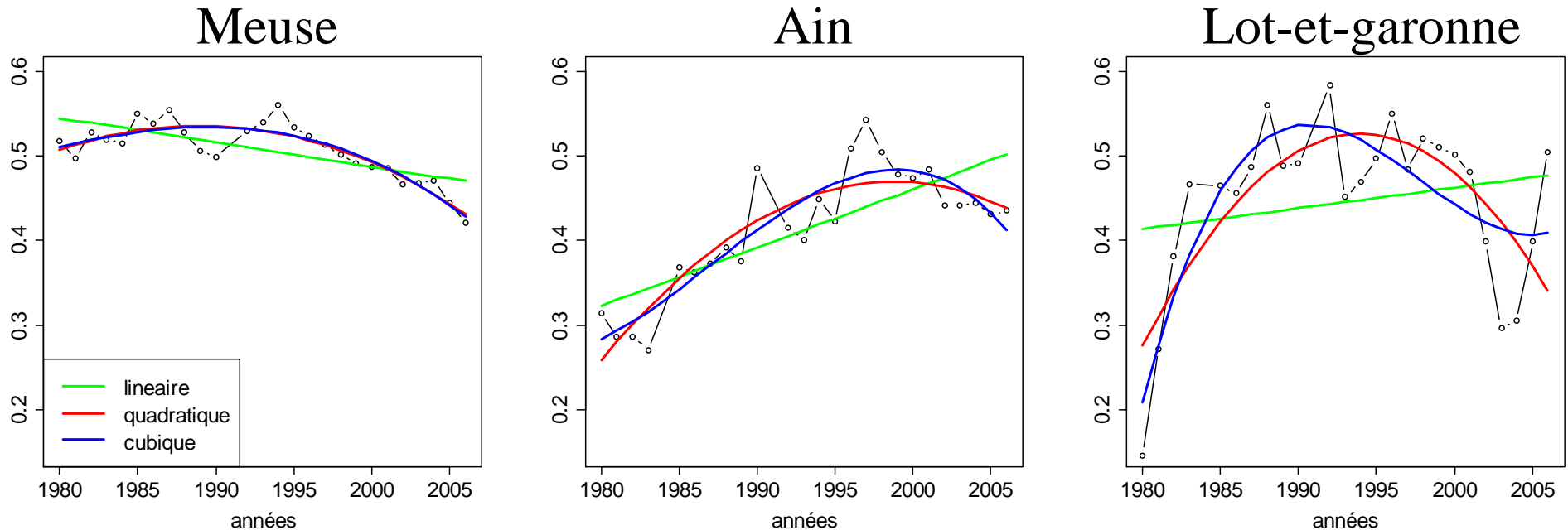


Thank you for your attention

We thank David Makowski, Robin Goffaux, Pierre Montalent and Jérôme Enjalbert for fruitful discussions on the part related to the analysis of bread wheat diversity. We thank Claire Hamon, Isabelle Bonnin and Christophe Bonneuil for previous work on bread wheat diversity. The postdoctoral fellowship is funded by Labex BASC

# Une évolution temporelle complexe, dépendant du département étudié

évolution de la diversité génétique HT\*

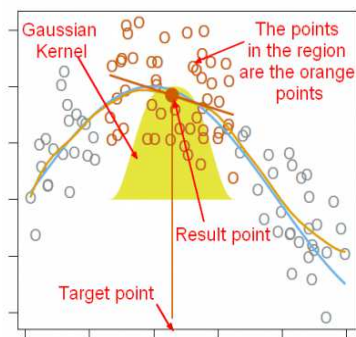


➡ la diversité génétique évolue distinctement selon le département

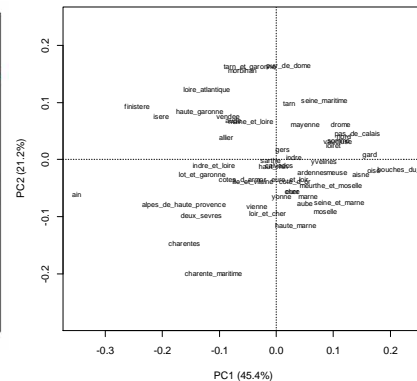
- ☐ tendance à l'**augmentation** ou la **diminution**
- ☐ patron  $\pm$  complexe (avec **maximum local** ou **non**)
- ☐ **gamme de variation** de la diversité génétique  $\pm$  importante

## 2 & 3. La diversité variétale et génétique est-elle spatialement structurée?

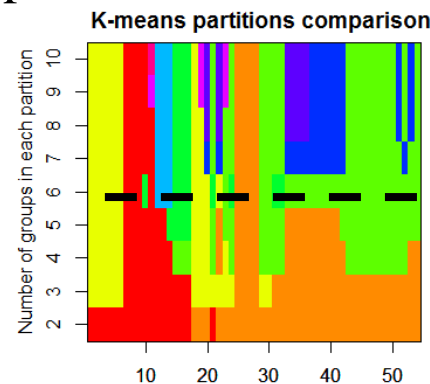
- ✓ approche statistique: approche multivariée et clustering
  - lissage des données: ré-estimation des valeurs manquantes
  - identification de groupes de départements à évolution temporelle similaire: Discriminant Analysis of Principal Components
    - Analyse en Composantes Principales (ACP): axes majeurs de variation
    - groupement des K-means sur axes: évolution temporelle similaire
    - Analyse Discriminante (AD) sur axes: influence des différentes années sur l'identification des patrons d'évolution temporelle distinct



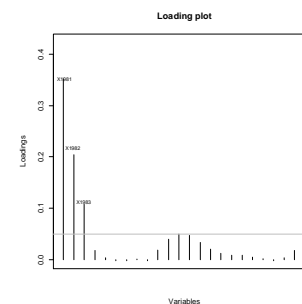
lissage



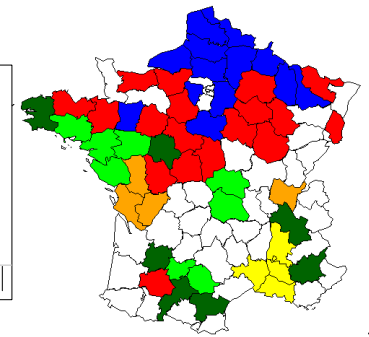
ACP: sélection axes



groupement

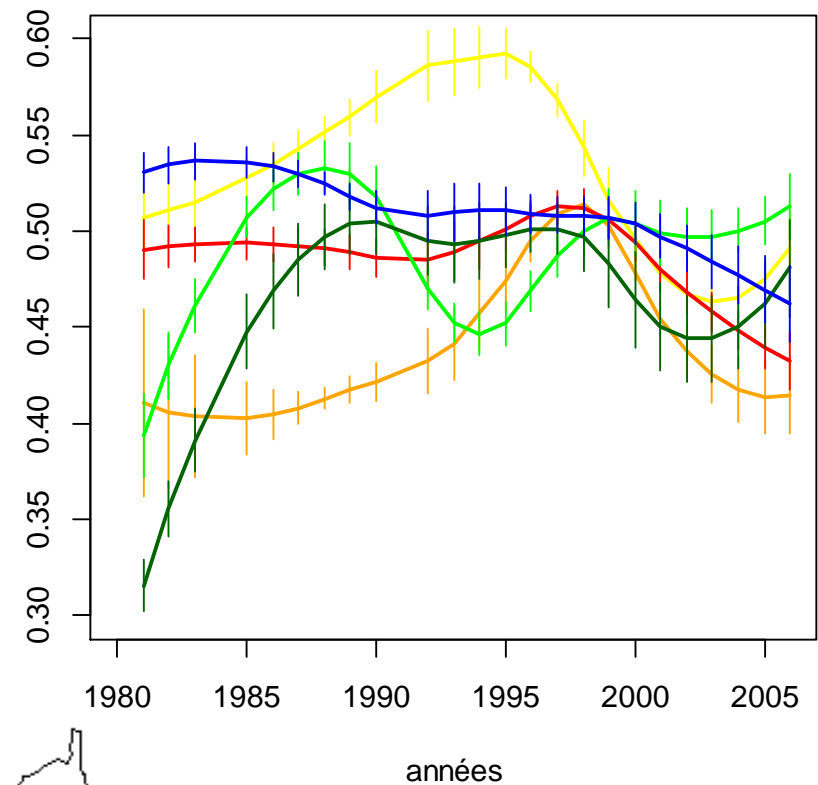
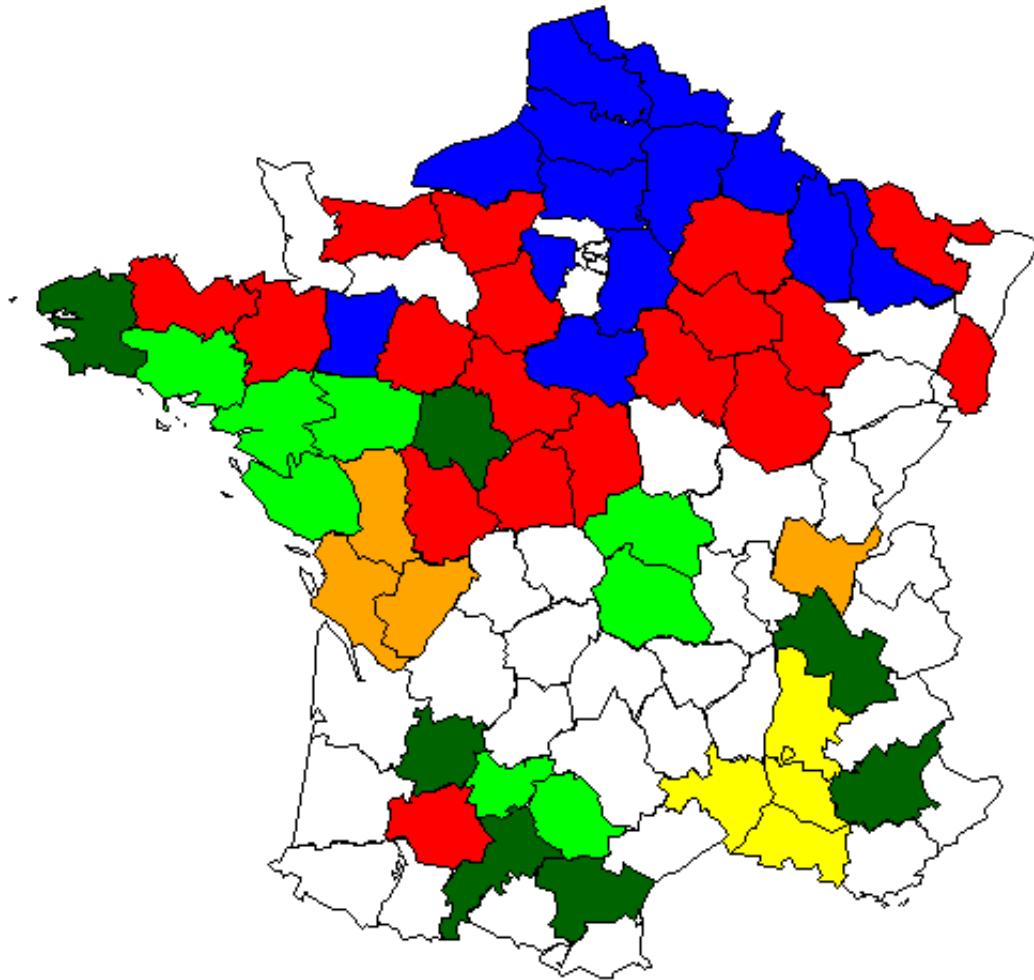


AD: pondération

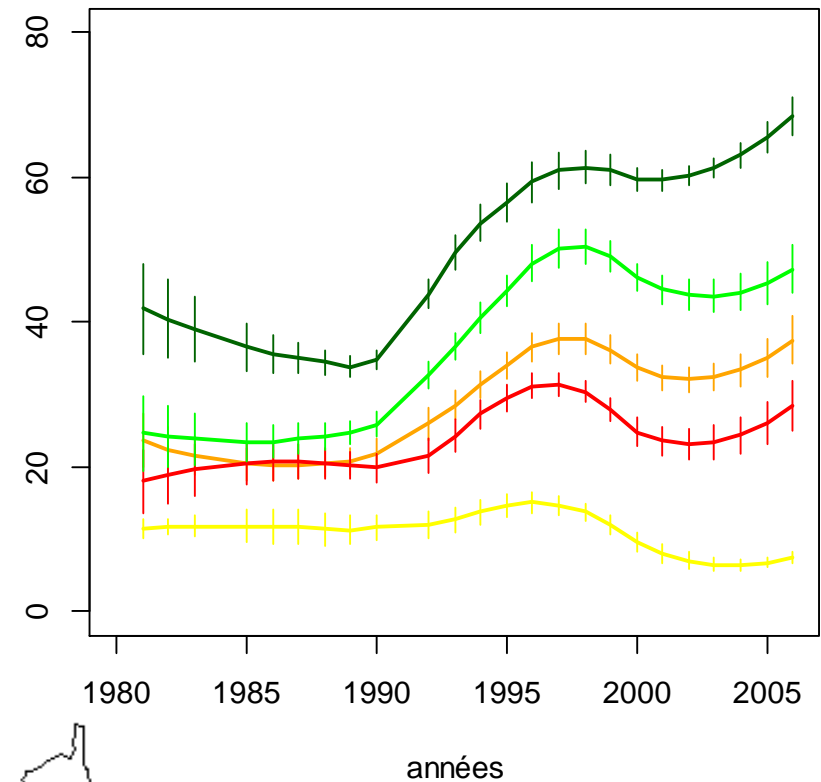
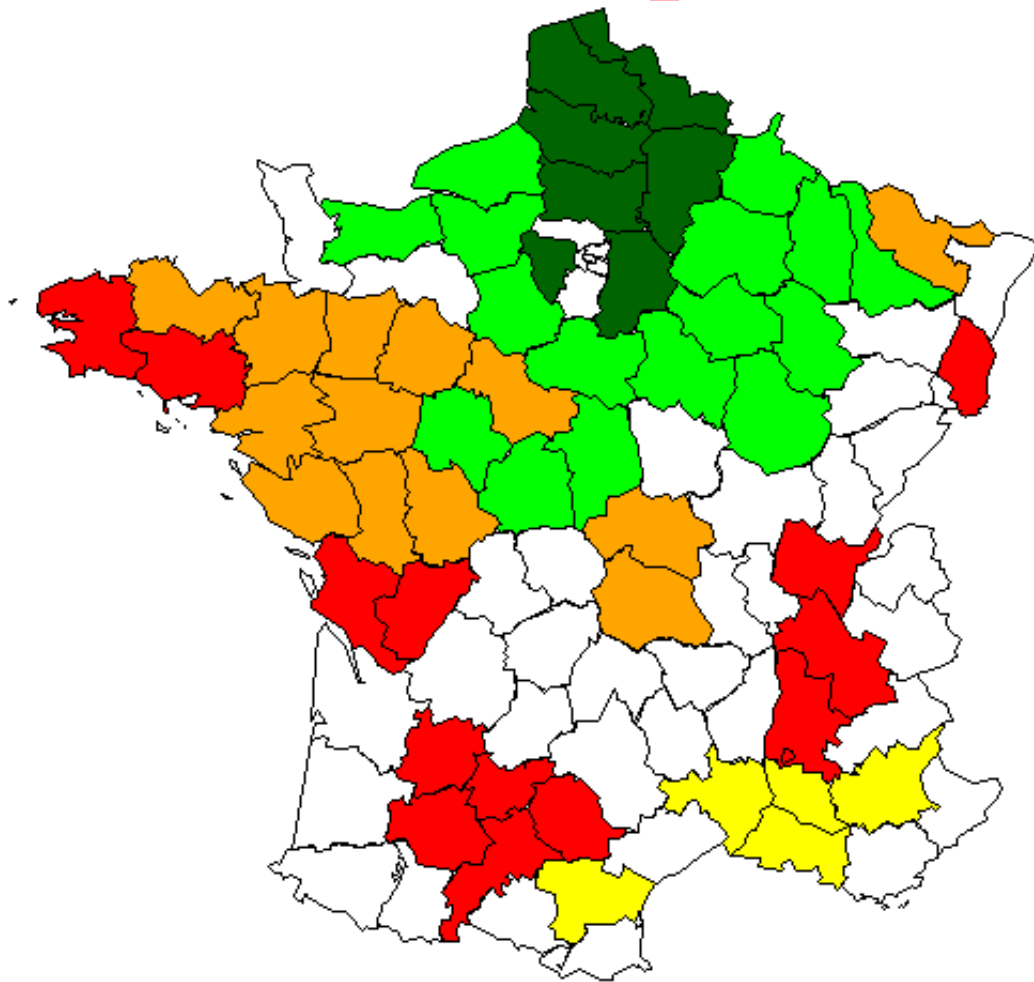


représentation

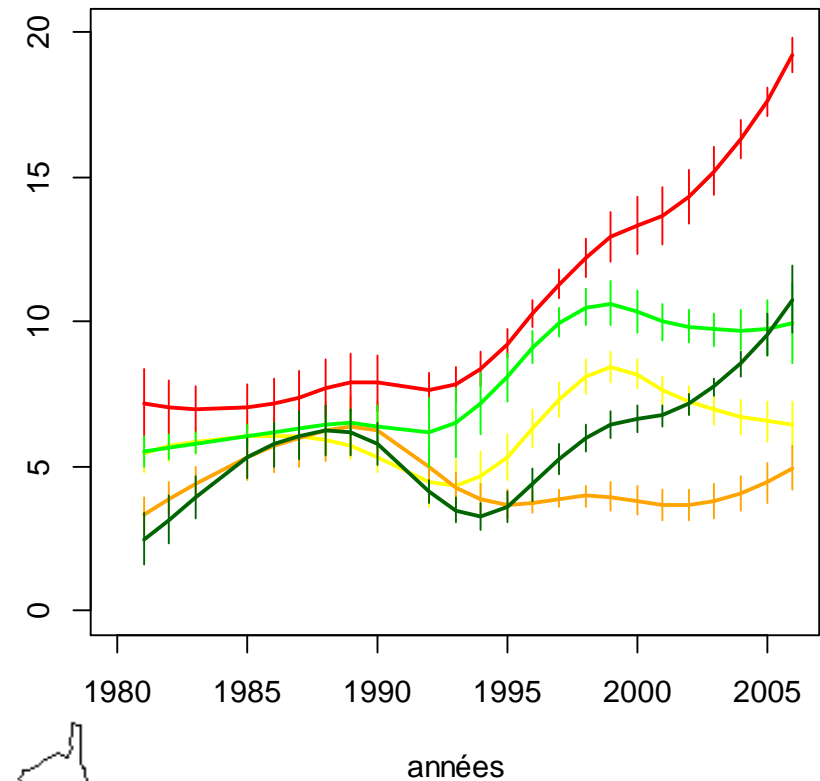
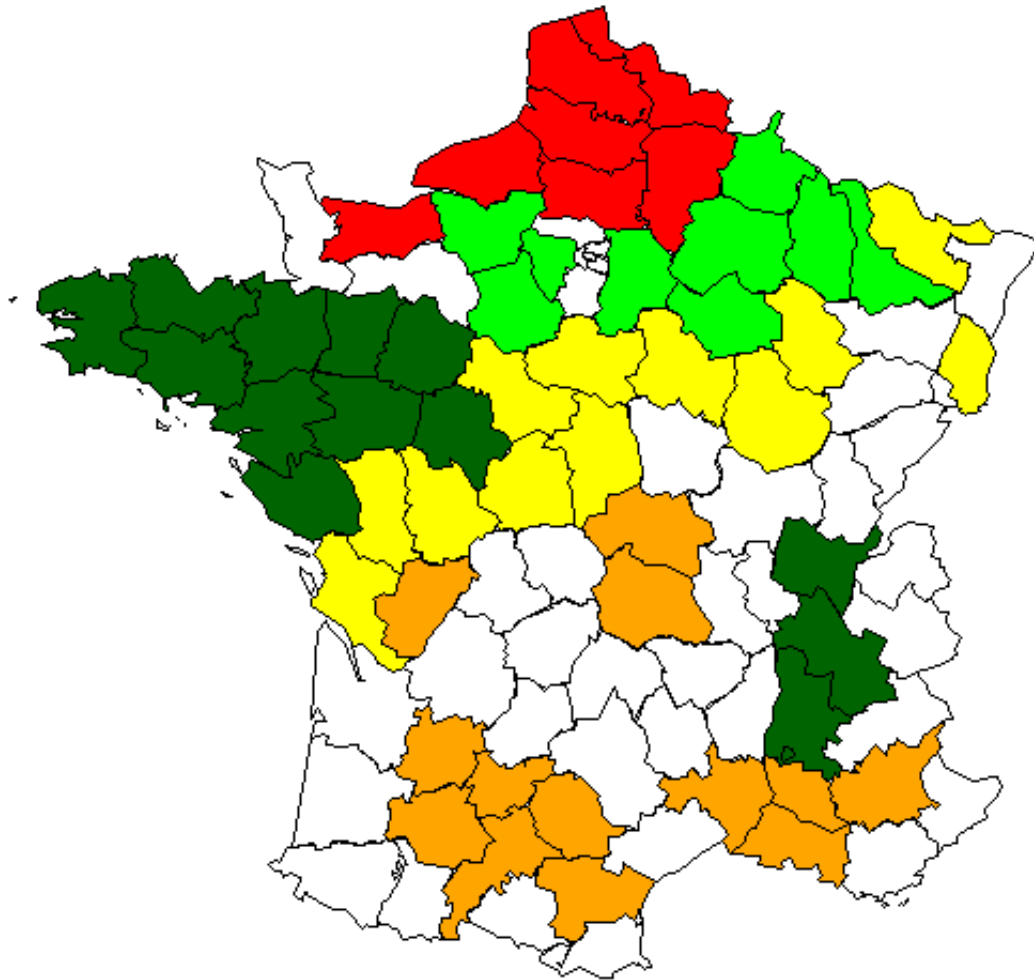
# Une évolution temporelle de la **diversité génétique HT\*** spatialement structurée



# Une évolution temporelle de la **richesse** **variétale spatialement structurée**



# Une évolution temporelle de la **diversité variétale spatialement structurée**



# Une évolution temporelle de la **diversité génétique de Nei spatialement structurée**

