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

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06/10/2015
Background and Questions

✓ In France, double decrease in bread wheat genetic diversity during the 20th century, caused by:
  - the replacement of landraces by modern pure lines varieties
  - the diffusion of a reduced number of high yielding semi-dwarf varieties

✓ 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 studied

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?

Bonnin et al. 2014
Perronne et al. in prep, Schott et al. 2010
Available datasets (wheat diversity)

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

statistical services of the Wheat Board

integrating within-variety diversity

microsatellite markers

‘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’

✓ 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)

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

<table>
<thead>
<tr>
<th>'département 1'</th>
<th>year 1</th>
<th>year 2</th>
<th>year 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>wheat</td>
<td>pea</td>
<td>wheat</td>
<td></td>
</tr>
<tr>
<td>oil. rape</td>
<td>wheat</td>
<td>barley</td>
<td></td>
</tr>
<tr>
<td>maize</td>
<td>wheat</td>
<td>sunflower</td>
<td></td>
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</tbody>
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| Source: Agreste |

(a) France map
(b) Sampling grid
(c) Sampling points

0.5% 7% 2%
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)

- **1981-1990 period**
  - Winter wheat/beet system with potato

- **1991-2003 period**
  - Livestock system based on forage maize + temporary grasslands + cereals
  - Mainly maize in monoculture system

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

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<tbody>
<tr>
<td>number cultivars</td>
<td>65.55</td>
<td>102.01</td>
<td>66.68</td>
<td>103.20</td>
<td>150.27</td>
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<tr>
<td>N2</td>
<td>82.53</td>
<td>51.92</td>
<td>104.53</td>
<td>145.27</td>
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<tr>
<td>Nei</td>
<td>60.38</td>
<td>150.09</td>
<td>190.97</td>
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<td></td>
</tr>
<tr>
<td>$H_T^*$</td>
<td>78.50</td>
<td>72.71</td>
<td>273.22</td>
<td></td>
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<tr>
<td>CS 1981-1990</td>
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</tbody>
</table>

$\chi^2$ 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

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<tbody>
<tr>
<td>number cultivars</td>
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<td>0.2499</td>
<td>0.3121</td>
<td>0.5049</td>
<td>0.5439</td>
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<tr>
<td>$N_2$</td>
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<td>0.5395</td>
<td>0.5466</td>
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<tr>
<td>Nei</td>
<td>0.2772</td>
<td></td>
<td>0.2954</td>
<td>0.2301</td>
<td>0.2970</td>
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<tr>
<td>$H_T^*$</td>
<td></td>
<td>0.3690</td>
<td></td>
<td>0.2012</td>
<td>0.3196</td>
</tr>
<tr>
<td>CS 1981-1990</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.8435</td>
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- 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

evolution de la diversité génétique HT*

la diversité génétique évolue distinctement selon le département

- tendance à l’augmentation ou la diminution
- patron ± complexe (avec maximum local ou non)
- gamme de variation de la diversité génétique ± 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