Determinants of the evolution of genetic diversity of bread wheat in France and their relationships with agricultural practices and production

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Background

The conservation of crop diversity, an option to cope with:

- ✓ climatic instabilities (e.g. drought)
- ✓ emergence of new disease (e.g. new strain of stem rust)
- ✓ the challenge of a more sustainable agriculture

A major crop as biological model, *Triticum aestivum*:

- ✓ an autogamous species with low outcrossing rate
- ✓ sown on approximately 4.5Mha in France



The major points supporting the “modernization bottleneck” hypothesis (i.e. genetic erosion during 20th century, according to van de Wouw et al. 2009):

- ✓ definition of modern pure lines cultivars with zero within-variety genetic diversity based on the DUS criteria
- ✓ extensive use of a few old cultivars crossed with a few new lines containing, for instance, dwarfing genes as the genetic basis of modern pure lines cultivars
- ✓ homogenization and intensification of technical management routes for these modern pure lines cultivars, allowing their sowing on large geographical areas while marginalizing the landraces adapted to specific habitats

H_T*: an indicator of genetic diversity

The development of integrative *in situ* indicators of bread wheat genetic diversity, a requirement considering:

- ✓ the awareness of benefits related to the in-field deployment of agrobiodiversity
- ✓ the need for quantification of evolution in the coming decades

Design of a database “French wheat diversity” including:

- ✓ systematic surveys documenting the acreage of wheat cultivars in ~80 of the French administrative 'départements'
- ✓ ~ 1100 varieties with their genotype at 35 microsatellite markers, evenly distributed along the wheat genome

H_T*: a composite indicator (Bonneuil et al. 2012) taking into account:

- ✓ varietal richness
- ✓ varietal evenness of spatial distribution
- ✓ between-variety genetic diversity (Nei diversity, Nei 1973)
- ✓ within-variety genetic diversity

Major conclusions based on H_T* over the 20th century:

- ✓ First half of the 20th century: drastic decrease due to the replacement of landraces by modern varieties
- ✓ 1990s – 2006, trends of:
  - spatial homogenization between French 'départements'
  - increasing genetic similarities between dominant cultivars

Does the spatiotemporal pattern of genetic diversity highlighted across France have been the same in each ‘département’?

Focus on the 1980-2006 period

Evolution of bread wheat diversity from 1980 to 2006

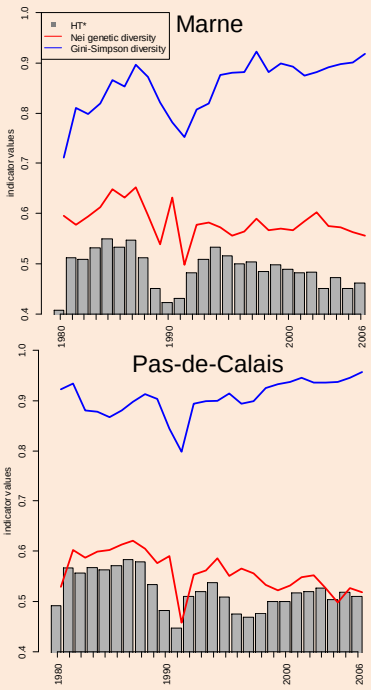

Figure 1: Evolution of three index of wheat diversity in three 'départements' characterized by more than 150,000ha of wheat yearly
H_T*: integrative indicator of genetic diversity
genetic diversity: Nei genetic diversity (Nei 1973)
Gini-Simpson diversity: diversity of spatial distributions of cultivars

Interpretations of key trends (Figure 1):

- ✓ H_T* presents either a slight decrease in ‘Marne’ from 1994 to 2006 or a relative stability in ‘Somme’
- ✓ Nei genetic diversity presents either a slight decrease in ‘Pas-de-Calais’ or a relative stability with inter-annual variability in other 'départements'
- ✓ Gini-Simpson diversity present an increase in the three chosen 'départements', i.e. the five top varieties covered 65.2% of the wheat area in 1980 and 41.4% in 2006 with high differences among 'départements' during the period (i.e. ‘Marne’ was dominated by one cultivar - 46.8% - in 1980, a trend not shared by the two other 'départements')

➡ **Existence of particularities of each 'département' in terms of yearly acreage of different cultivars**

Go beyond: an interdisciplinary research project

Identifying (i) the major determinants of the evolution of wheat genetic diversity over time and (ii) the potential influences of this evolution of wheat genetic diversity on yield, yield stability and disease resistance

- ✓ analysing the trends and inter-annual variability of ***H_T* per French 'département'*** and their relationships with dominant cultivars.
  - ❑ Are there fewer cultivars in 2006 than in 1980?
  - ❑ Are the cultivars more closely related ?
  - ❑ Does the 'départements' show a greater homogenization?
- ✓ studying the influence of intensification of technical management routes on the evolution of ***H_T**
- ✓ studying the relationships between ***H_T**** and (i) yield production and stability and (ii) pathogen dynamic

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