



BMT/13/12 Add.

ORIGINAL: English

DATE: December 8, 2011

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

**WORKING GROUP ON BIOCHEMICAL AND MOLECULAR
TECHNIQUES, AND DNA-PROFILING IN PARTICULAR**


Thirteenth Session
Brasilia, November 22 to 24, 2011

ADDENDUM

THE USE OF MOLECULAR MARKERS FOR THE LETTUCE SPECIES


Document prepared by experts from France

Groupe d'Étude et de contrôle
des Variétés Et des Semences




THE USE OF MOLECULAR MARKERS FOR THE LETTUCE SPECIES

→ *Assessment of genetic diversity and species structure*
→ *New tool of managements of the lettuce reference collection*

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A study with a double aim :

1. Evaluation of the **diversity** of *Lactuca sativa* L. species and measure of its evolution overtime
2. Proposition of a **new tool** for the management of reference collection in the DUS context

Lettuce = Species with **many morphological variations** → **Cultigroup**

Introduction / Background

Aim 1-Diversity


- ☛ Butterhead (BH)

Aim 2-A new tool ?


- ☛ Looseleaf (LL)
- ☛ Summer crisp (SC)

Conclusion

- ☛ Crisphead (CH)
- ☛ Romaines (RO)
- ☛ Latines (LA)
- ☛ Chinese lettuce



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In this first part, has been studied the allelic diversity :

- present un each cultigroup
- existing at the moment M
- introduced per period

Materials and methods

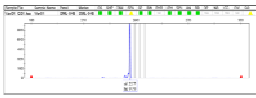
500 EU varieties



LL, BH, SC, CH, RO, LA
<1970, 1970-1985,
1985-2000, >2000

Molecular profile realisation

30 SSR Markers



Results analyse with the GeneMapper software


Introduction / Background

Aim 1-Diversity


Aim 2-A new tool ?

Conclusion

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Summary of results

- 500 lettuce varieties → 184 alleles put in evidence by the 30 SSR markers
- 4 to 17 allèles per locus

Allelic diversity per cultigroup

		Put in evidence alleles number					
	75	101	124	140	141	+	
Aim 1-Diversity	CH	RO/LA	BH	SC	LL		
		Subservient to one cultigroup alleles proportion					
	0,54	1,63	2,72	3,26	4,89	+	
Aim 2-A new tool ?	CH	LA	SC	LL/RO	BH		
		Absent allele from one cultigroup proportion					
	0	0,54	1,63			+	
Conclusion	BH/SC	LA	LL				
				3,8	CH/RO		


Introduction / Background

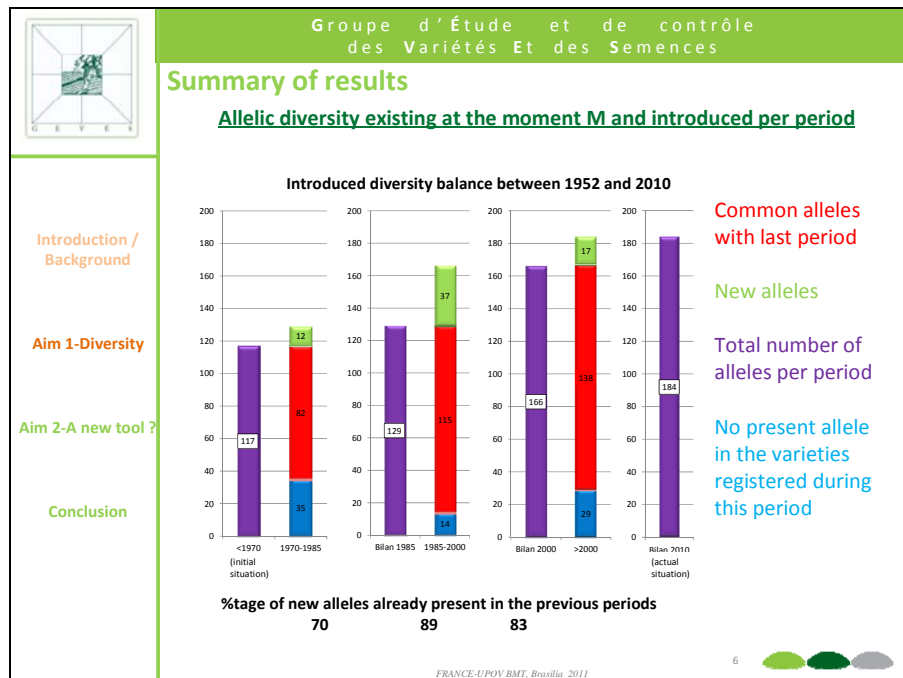
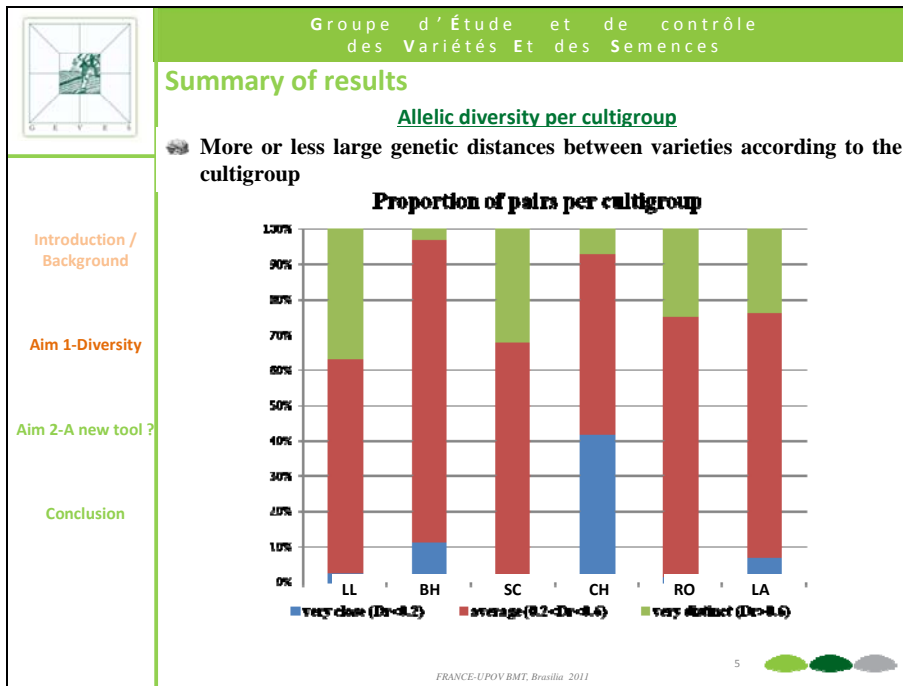
Aim 1-Diversity

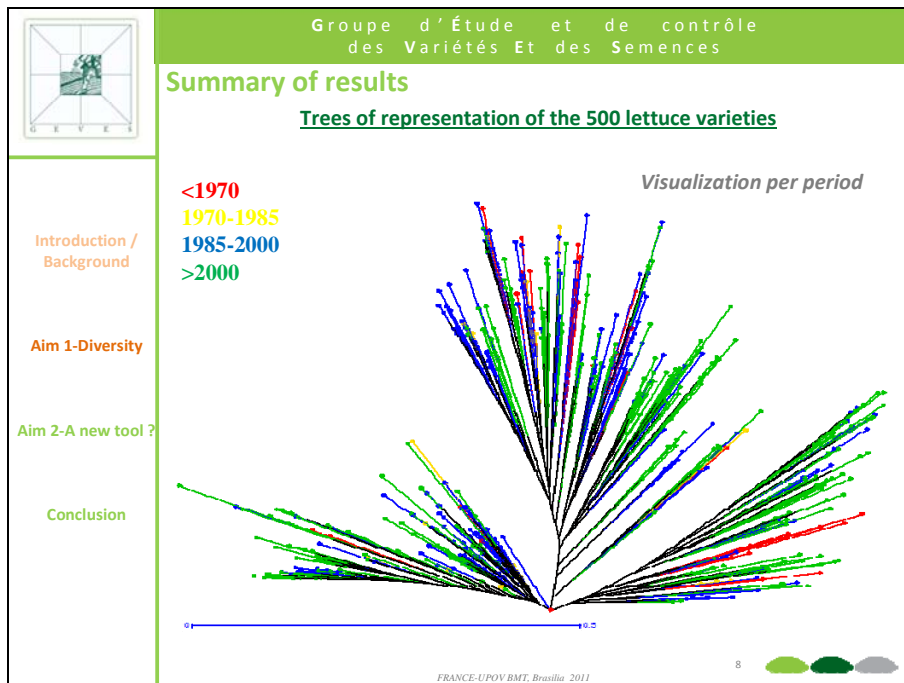
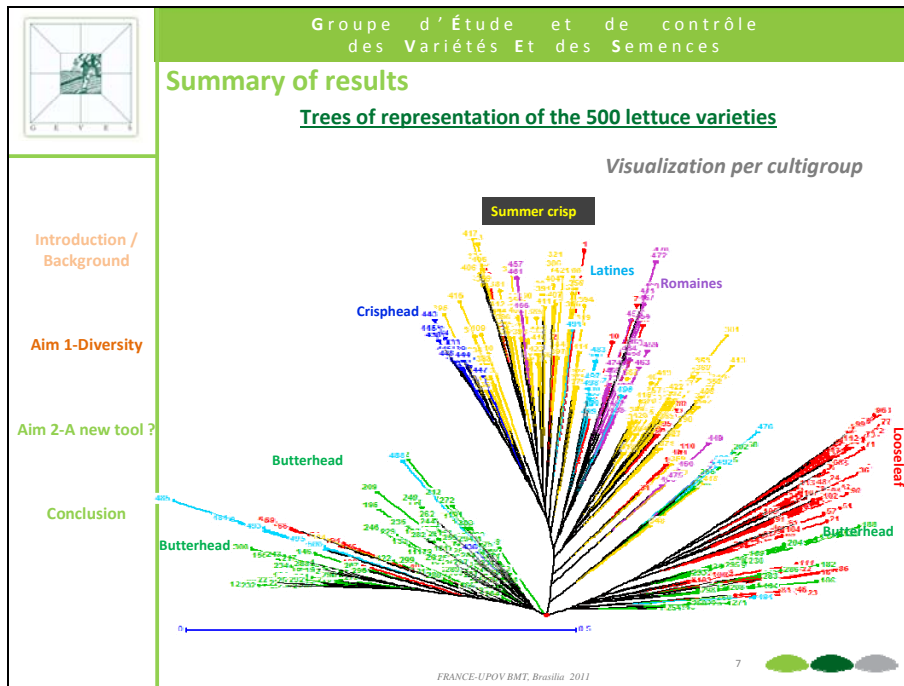
Aim 2-A new tool ?

Conclusion

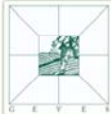
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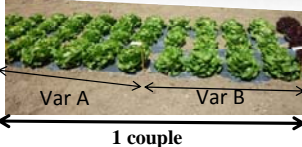


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In this second part, the tested approach concerns the association of molecular data to phenotypic data to structure the lettuce reference collection

Materials and methods

Crop experts were asked to observe different pairs of varieties grown side by side and to give a note using the following scale :

- 0 – the 2 varieties are similar or very close
- 1 – the 2 varieties are close but distinct
- 2 – the comparison is useful, but the varieties are clearly distinct
- 3 – the comparison could have been avoided, as the varieties are different
- 4 – the comparison should be avoided, as the varieties are very different

The obtained notes have been associated with the Rogers' distances and the phenotypic distances* of each pair.

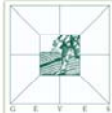
This approach allows us to obtain 2 thresholds:

- the molecular one
- the phenotypic one for "Distinct plus" varieties.

**Phenotypic distances have been obtained with the GAIA software after configuration of a lettuce application based on matrix of 8 points to declare distinct varieties*

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Summary of results

Distinction of pairs based on molecular and phenotypic distances

Conclusion

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<p>Introduction / Background</p>	<p>In conclusion...</p> <ul style="list-style-type: none">☛ Lettuce species structuring based on the cultigroup☛ Since 1985, increase of the allelic diversity☛ ...but uneven according to the observed cultigroup☛ Despite this increase in diversity, varieties have relatively close genetic distances between them
<p>Aim 1-Diversity</p>	<ul style="list-style-type: none">☛ 0,4 molecular threshold → no immediate construction of a new management tool
<p>Aim 2-A new tool ?</p>	<p>However...</p>
<p>Conclusion</p>	<ul style="list-style-type: none">☛ 27% of the varieties included in french reference collection have been characterized☛ Molecular data = useful for identify varieties<ul style="list-style-type: none">→ for infringement procedures→ in procedure to investigate essential derivation
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<p>Thank you</p>	
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