



Evaluation of the Diversity in cultivated Lettuce (*Lactuca sativa* L.), Contribution of Wild Accessions and Old Varieties

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Introduction

The aim of this study is to evaluate the diversity present in *Lactuca sativa* L. species and to measure its evolution during the last 60 years

Materials and methods

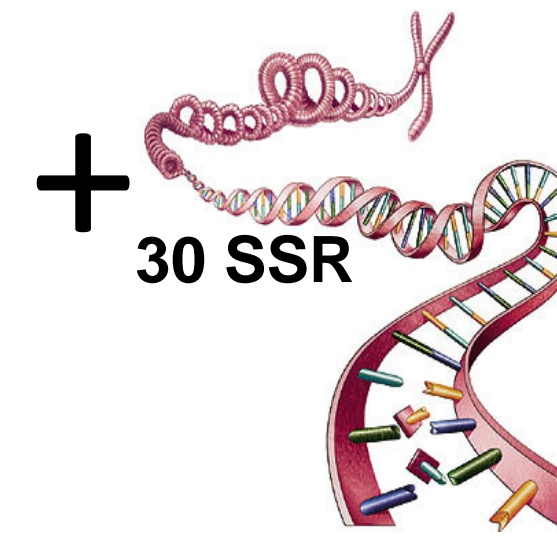
500 varieties listed in the EU Catalog



issued from

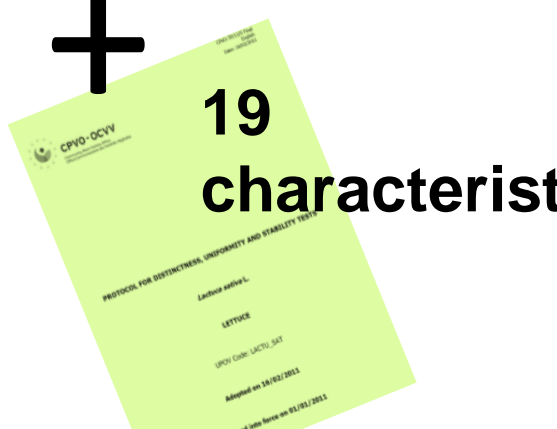
6 growth types : AC, BE, BA, BI, RO, GR

4 periods : <1970, 1970-1985, 1985-2000, >2000



GENOTYPING

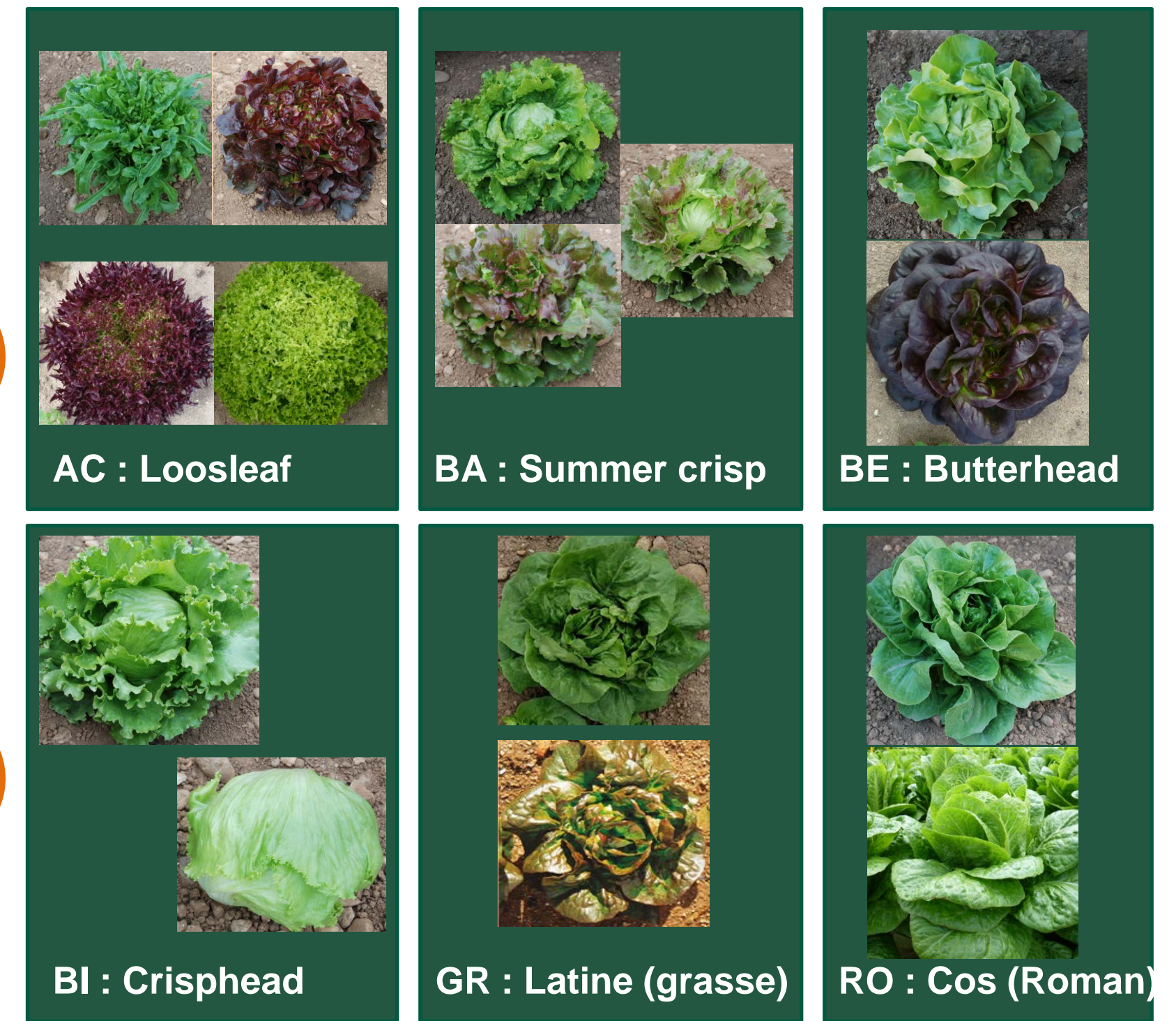
Molecular data



CARACTERISATION

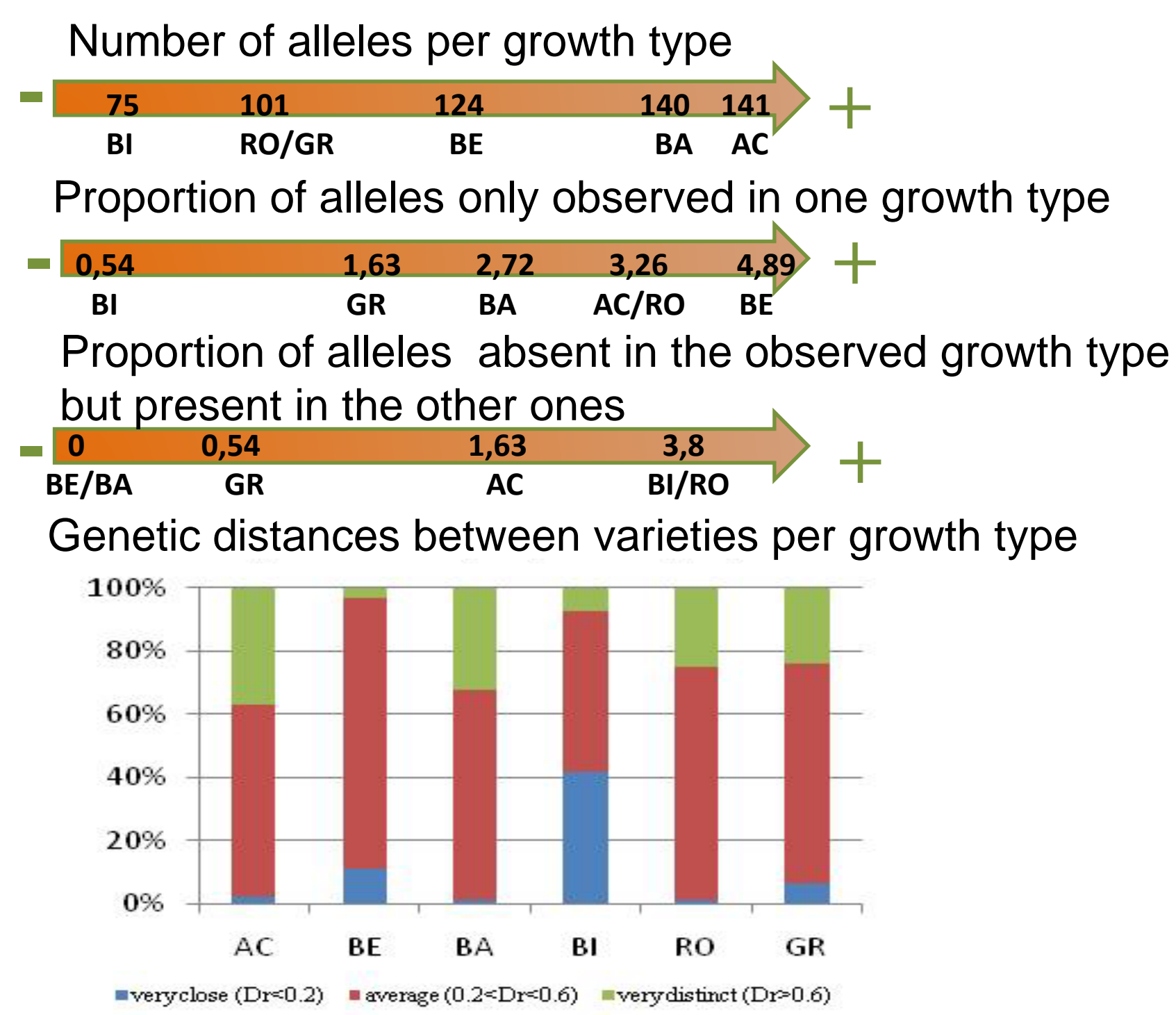
Morphological data

13 morphological & 6 pathological



Results

Allelic diversity per growth type



Since the middle of 80's the allelic diversities has increased but is uneven according to the observed growth type and the periods chosen.

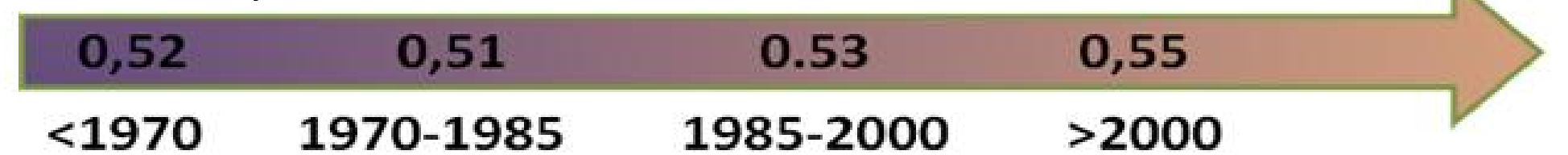
The introduction of new alleles is not uniform overtime.

Allelic diversity existing at the moment M

	<1970	1970-1985	1985-2000	>2000
Number of varieties	28	48	244	497
Number of alleles put in evidence in the period	116	129	166	184
Allelic richness	3.90	4.30	5.53	6.13
% of varieties couple with $Dr^* \leq 0.2$	0.26	2.04	3.19	1.93
% of varieties couple with $Dr^* > 0.6$	39.68	39.72	41.10	40.38

*Dr = Rogers distance

Nei Diversity Index



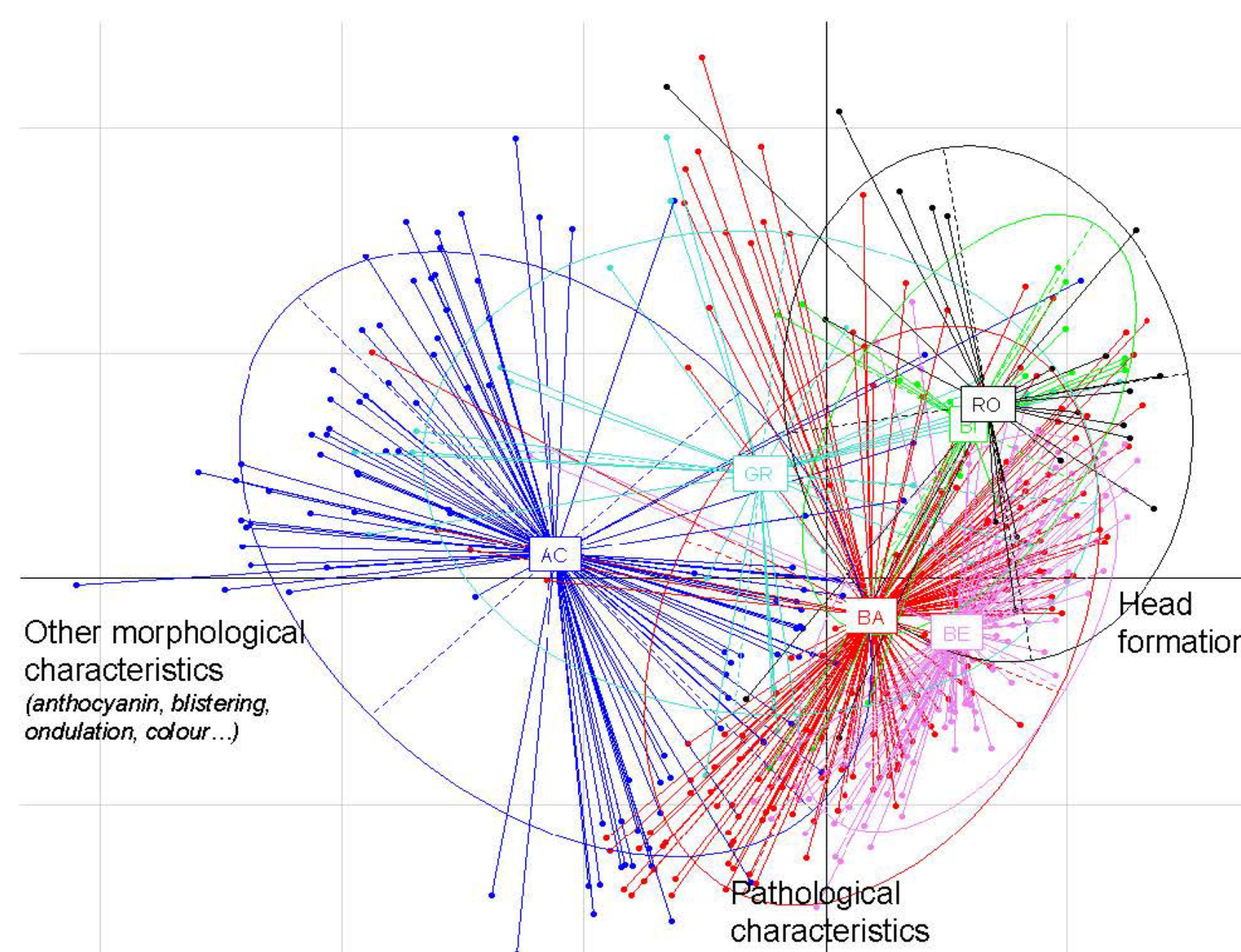
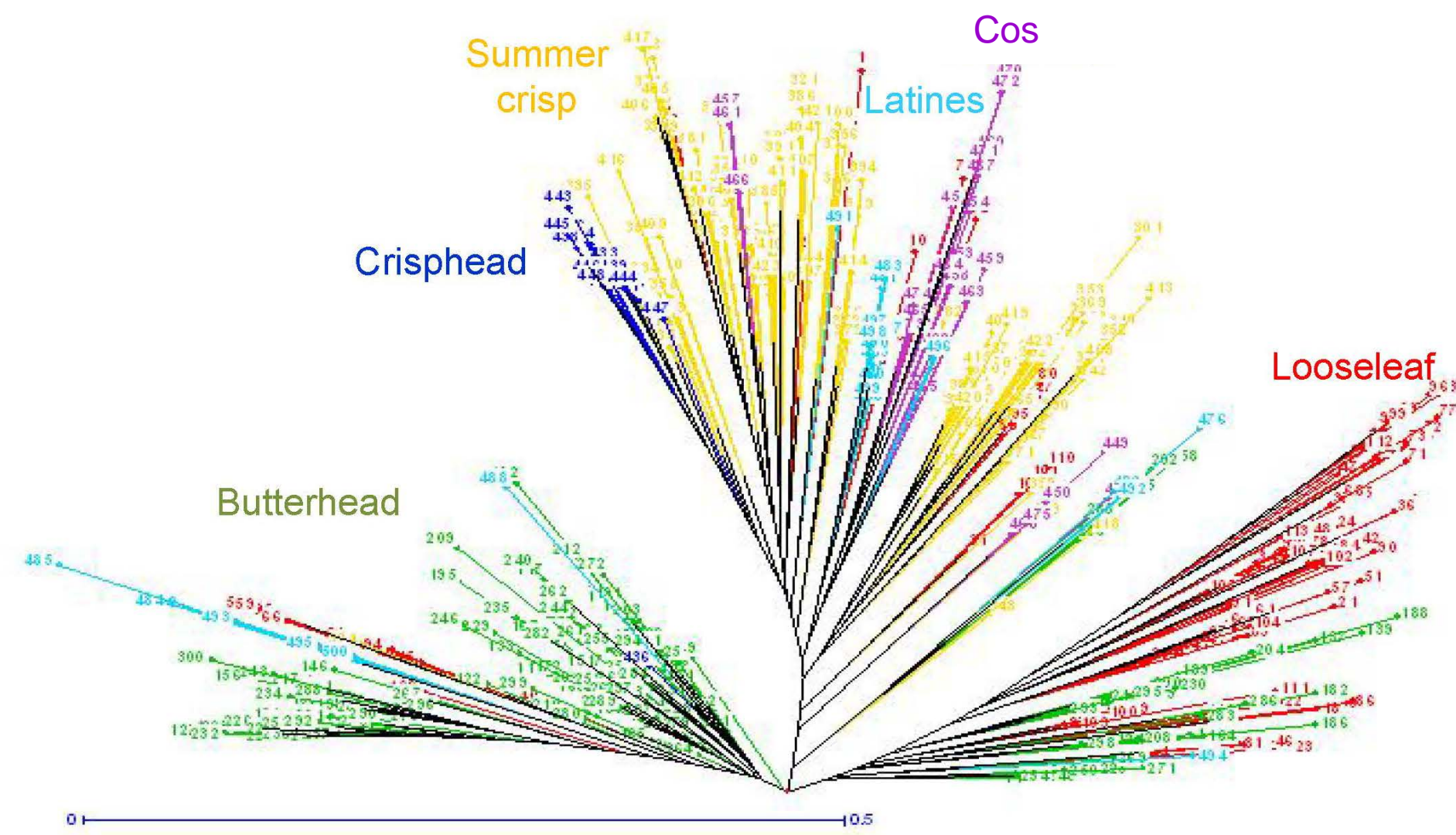
Allelic diversity introduced per period

	<1970	1970-1985	1985-2000	>2000
Number of new varieties	28	20	199	253
Number of alleles put in evidence in the period	117	94	152	155
Allelic richness	3.90	3.13	5.07	5.17
% of varieties couple with $Dr^* \leq 0.2$	0.20	8.95	3.61	1.82
% of varieties couple with $Dr^* > 0.6$	39.68	38.95	40.81	36.73

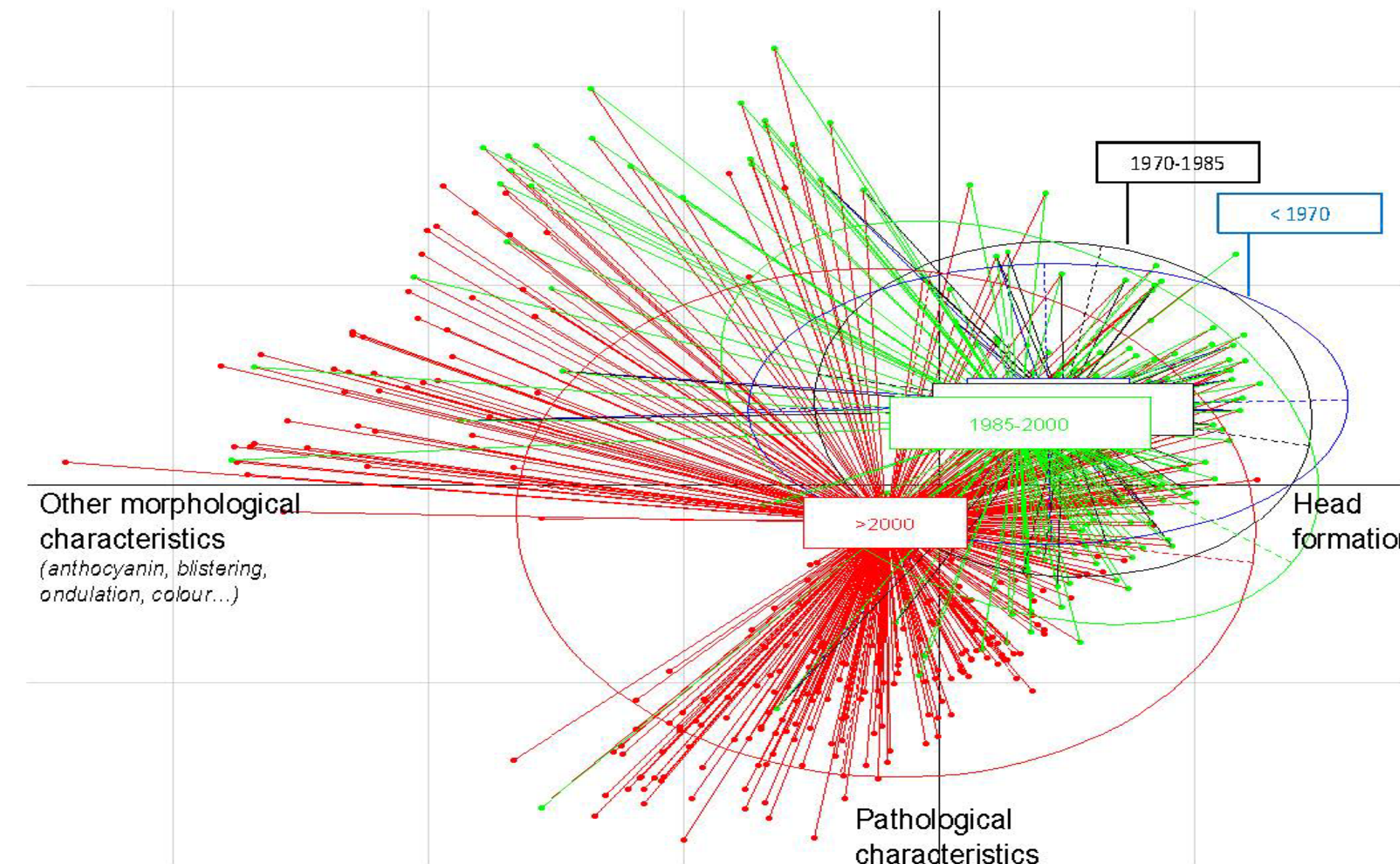
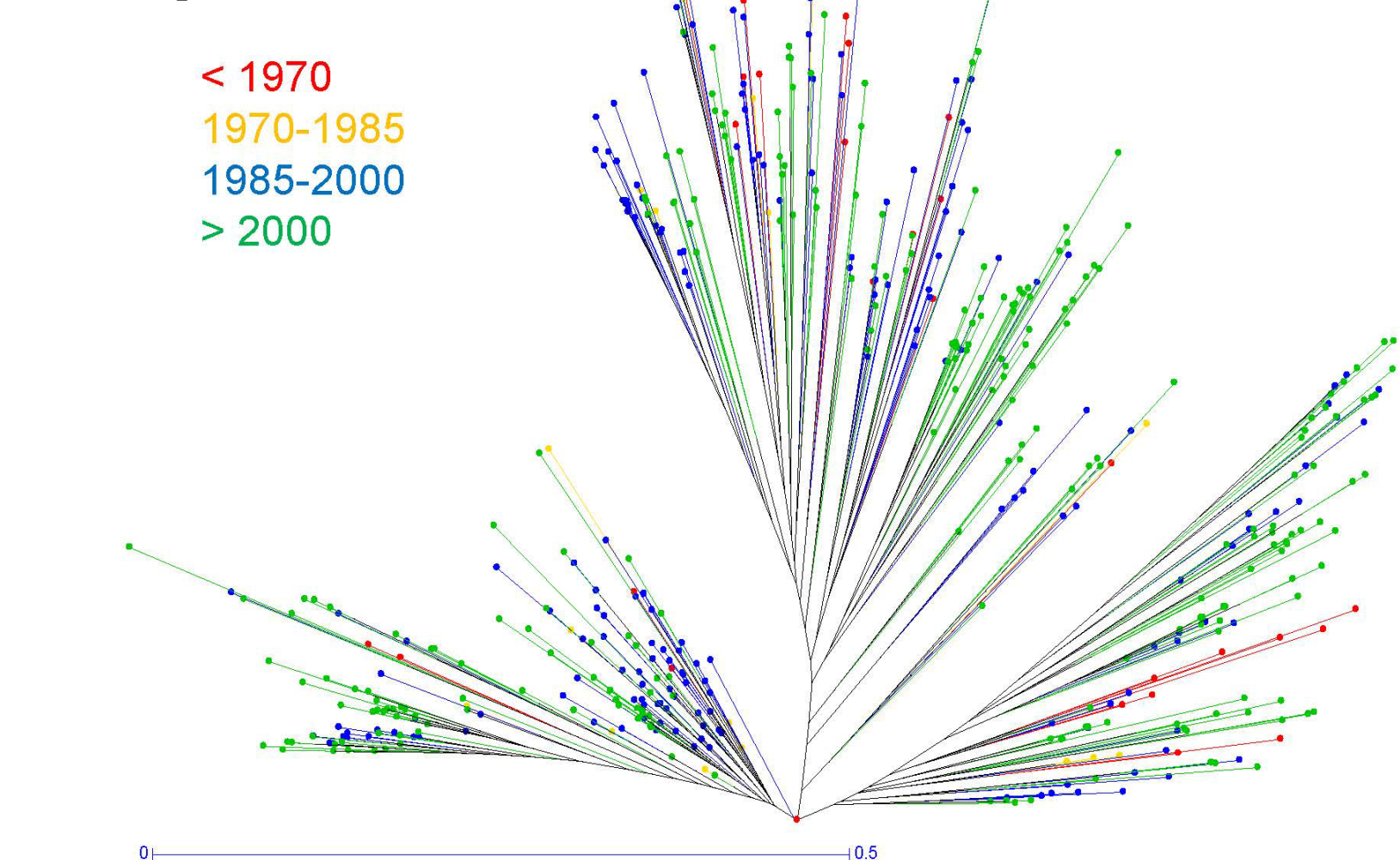
*Dr = Rogers distance

PCA & Trees of representation of the 500 lettuce varieties

Per growth type



Per period



The genetic structure of the *Lactuca sativa* species is principally based on morphotype linked to the growth types.

Nevertheless, some varieties issued from one growth type and lost among varieties of another growth type, are the result of more original selection schemes.

New allele introduction is principally linked to the introgression of diseases resistances often realized by interspecific crossing: *Bremia lactucae* races, in constant emergence, still force breeders to find new sources from resistances in old varieties or wild species (e.g. *L. serriola* or *L. saligna*...); resistance to aphids (*Nasonovia ribisnigri*) is introgressed from *L. virosa* with *L. serriola* as bridge-species.

During last 25 years, progress has been made with introduction of novel traits including disease and insect resistances, novel leaf colors and shapes, open head, slow bolting or broad environmental adaptation.



Conclusion

Nearly all enhancements have targeted traits from the primary gene pool especially for morphological traits in old varieties or populations. The secondary and tertiary pools have been recently used for diseases resistances traits.

In a context of sustainable intensification of global

agriculture, the creation of varieties having more stable resistances seems to go through the genetics resources.

Crossing with landraces are a current trend by breeders which will allow to obtain some new morphotypes and perhaps by the way a new typology.

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