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Genotype x site interaction, climatic change and selection in *Pinus pinaster* : a new glance on old data

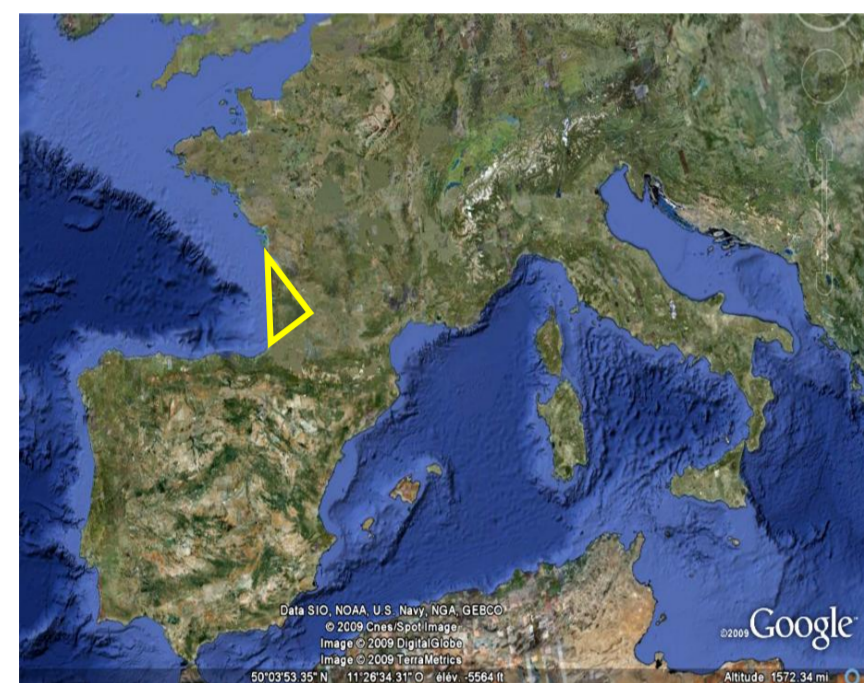
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Climatic change and *Pinus pinaster* breeding



Maritime pine in France: first planted species (900.000 ha).

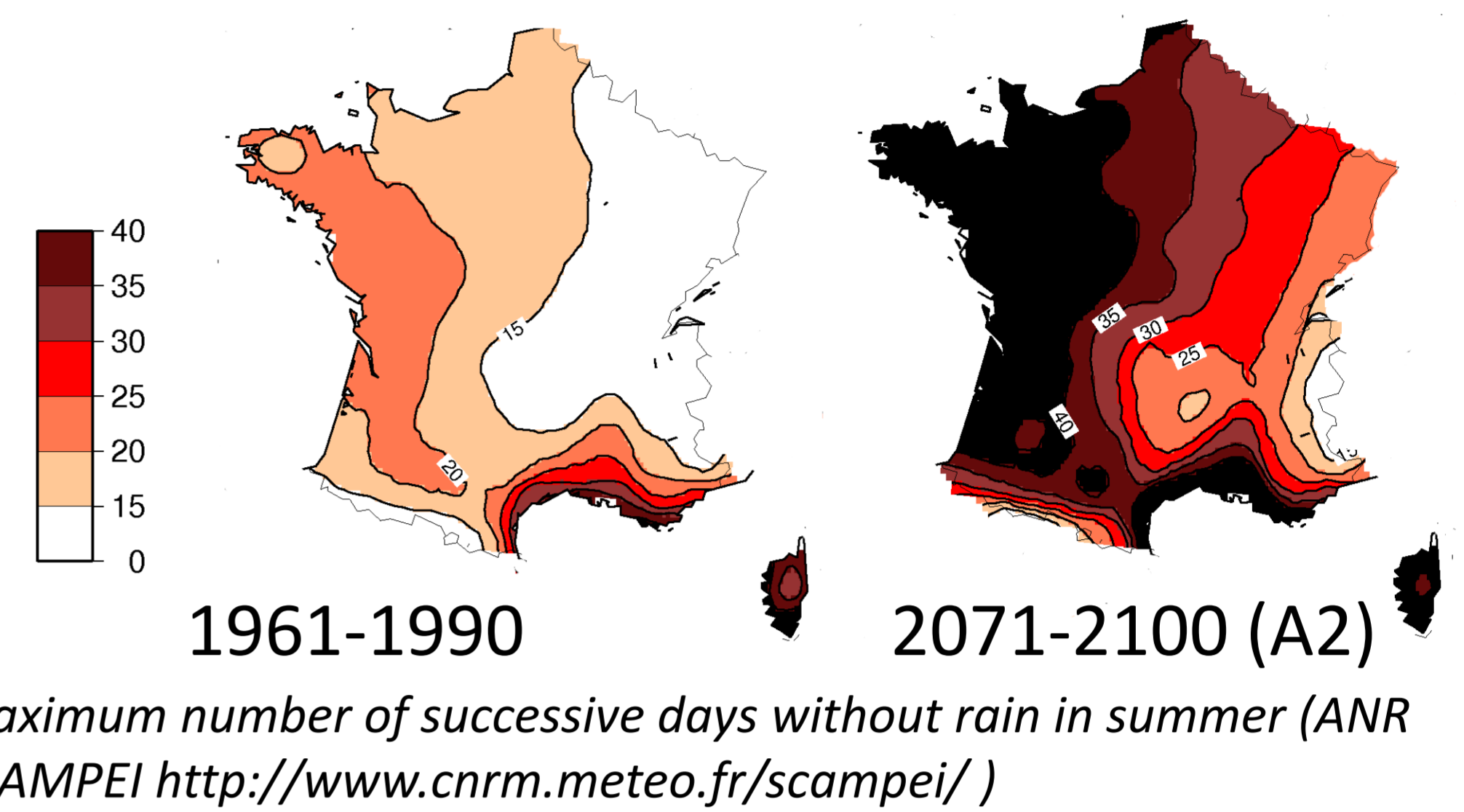


Humid site



Dry site

Current breeding program aims at improving volume and stem straightness over site types (different fertility levels, according to variations of water table level)



Climatic change scenarios based on CO₂ elevation predict drier summers in western France, with a negative impact on forest productivity around the second half of this century (Loustau et al., 2005). Breeding strategies are to be refocused towards maintaining productivity on drier sites e.g. :

- extension of breeding zones to drier sites,
- shortening selection cycle through forward instead of backward selection based on accurate bv estimates,
- accelerating seed orchard renewal to follow climate evolution,
- infusing new diversity with southern provenances,
- selecting for adaptive traits for drought tolerance (water use efficiency, dendroplasticity),
- integrating phenotypic and genomic data to improve selection efficiency.
- using multi-site data and re-analysing GxE interactions is also a possibility to give a new insight on genotypes adaptation to dry sites.

Multisite evaluation

Eight progeny trials with 100 to 200 families and 3 sites per trial are currently being re-analysed. Genetic gains on dry sites will be compared for classical selection based on over-site breeding values and for selection based on dry site breeding values.

An example is given for one trial with 3 sites : dry, semi-humid and humid types; 196 progenies (196 ♀ trees x polymix1 of 42 ♂ or polymix2 of 43 ♂) are tested with 35 reps of 1-tree-plots per site. Each tree was measured for circumference at 1.30m (cir08), total height (ht08) and stem straightness (ev08: deviation to verticality in cm at 1.50m) at age 8. Linear mixed models were used for statistical analysis, using ASReml v3.00 (VSNi) software.

Across site analysis was performed on spatially adjusted data using 2 different models :

- (1) overall mean and site as fixed, site.family as random, with additive and error variances modelled for each site
- (2) overall mean and site as fixed, family as random

Table 1: Mean (mm, cm, and cm respectively) and standard error per site, and between site genetic correlations for cir08 (1st line), ht08 (2nd) and ev08 (3rd).

	Dry Site	Meso Site	Wet Site
Mean (se)	30.2 (0.1) 540.8 (1.1) 10.2 (0.2)	32.9 (0.1) 642.7 (1.3) 15.1 (0.3)	40.9 (0.1) 730.5 (1.3) 21.7 (0.4)
Dry Site		0.45 0.50 0.91	0.65 0.69 0.84
Meso Site			0.67 0.64 0.94

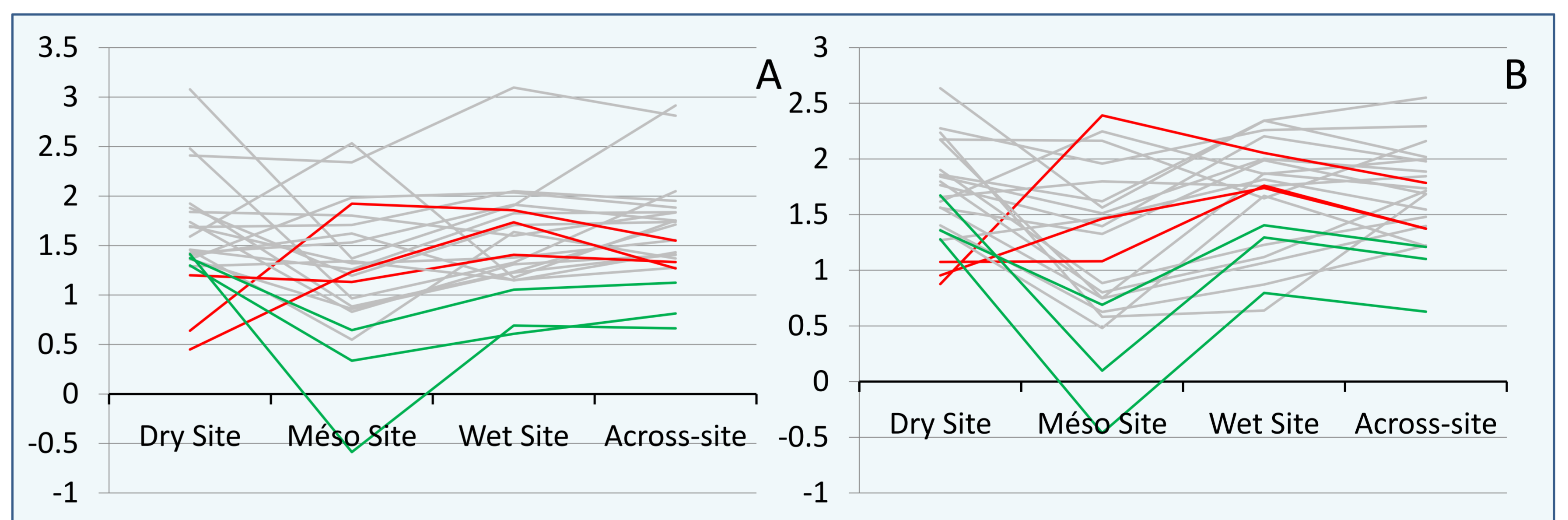


Figure 1: Standardized BV for A: cir08 and B: ht08 : across-site (model 2) and on each site (model 1), for the top 20 families selected on BV across-site (in grey and red lines) and for 3 additional families (in green lines) selected in top 20 on the dry site.

Overall, there are few changes of ranking over sites. But some good across-site families perform poorly on the dry site; whereas some of the top 20 families on the dry site will not be selected based on across-site performance.

For a growth index (equivalent weights on cir08 and ht08) the top 20 families classically selected on across-site performance will give 10% less genetic gain on the dry site, compared to the top 20 families specifically selected on dry-site performance.

Prospects for the breeding program

Analysis of GxE interactions can bring information on genotypes specifically adapted to dry sites, able to maintain an acceptable level of productivity with a low water availability in summer.

Such genotypes may carry a different set of alleles for traits involved in growth on dry sites, compared to those that perform best over all types of sites. Using assortative mating between those tolerant genotypes could improve genetic gain for future climatic conditions.

References

- Loustau, D. et al. Modeling climate change effects on the potential production of French plains forests at the sub-regional level. *Tree Physiology* 25, 313-323 (2005).