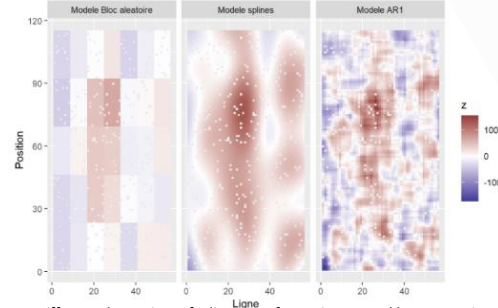


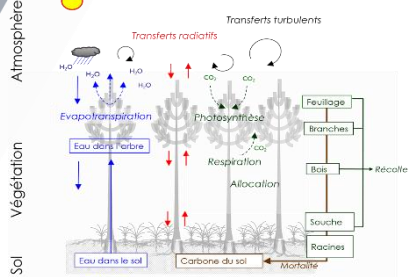
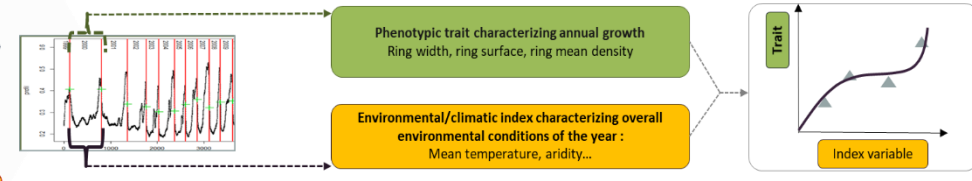


Progeny trial used in the study

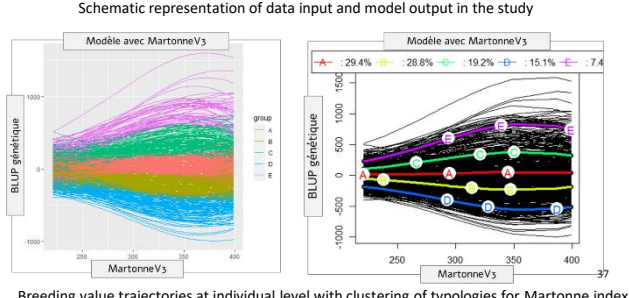


Different alternatives of adjustment for environmental heterogeneity in the trial, using spatial statistics and breedR software

Relating annual growth to the overall climate of the year



Schematic representation of the phases modelled in growth model GO+



Breeding value trajectories at individual level with clustering of typologies for Martonne index

GENOMIC SELECTION FOR REACTION NORMS ON CLIMATIC INDEXES IN MARITIME PINE

Léopoldo Sanchez-Rodriguez
INRAE, BioForA, France
Moderator :
Eduardo Pablo Cappa, INTA, Argentina

November 18
15H
CET/Paris time
On line

LIA FORESTIA
web seminars round
2022 #8

ABSTRACT :

A new proof-of-concept study for genomic selection (GS) in maritime pine is presented here with two major steps forward compared to previous case studies of GS in the species: a greater number of informative markers and the focus on wood related phenotypic plasticity traits. The main objective of this study was to combine genomic, phenotypic and environmental data in order to build GS models for norms of reaction (NoR) to climatic indexes.

The GS population is composed of 650 trees from 25 half-sib families established on two contrasted sites (dry vs. humid site) in 1996. These progenies are representative of the second generation of the breeding program of the species in France. The 650 trees were genotyped with the 4TREES Axiom array developed within the B4EST project. Wood related phenotypic records were obtained from X-rayed increment cores collected on all trees, and phenotypes related to each ring (from 1999 to 2019) were extracted, namely: ring width, ring surface, ring density and several other variables describing the within-ring variability.

Two kinds of climatic indexes were used, a classic and simple Martonne aridity index combining temperature and rainfall, and a complex ecophysiological growth model (GO+) able to predict water availability at a very fine scale. The outputs of both models were summarized at annual levels to be used as alternative climatic covariables for ring traits. GS was modelled following different cross-validation scenarios representing operational schemes in the breeding program, and compared to current evaluation system using exclusively pedigree information. Modelling with the climatic indexes as covariables was obtained by a random regression approach, which offered the possibility to predict genetic and genomic breeding value trajectories at individual level over the environmental gradients represented by the sample of years of growth.

Results showed the advantages of GS over the pedigree counterparts in prediction quality over the ranges in the two climatic indexes. The more complex GO+ model provided the best performance overall. Individual trajectories made of breeding values were easily clustered by their shapes over the climatic indexes, with typologies of trajectories showing systematic advantage in growth over the whole range of environments compared to the other less performing NoR typologies. The driest extremes produced less variation among individual trajectories than that observed for the wettest extremes. The wettest range of the cline resulted in large discrimination among individual trajectories. A similar modeling work was done using outputs from a resistograph, with faster a cheaper operational setting.

Results are discussed in the context of breeding of maritime pine facing global changes, with propositions in terms of GS implementation, the strategic use of NoR on climatic indexes, and the choices of partial or cheap phenotyping among candidates to selection.



Short Curriculum Vitae :

Leopoldo Sanchez is INRAE research director at the BioForA forest genetics research unit. His research focuses on optimising the genetic improvement process in wood-producing forest tree species, to make it more relevant to the environmental challenges that threaten the adaptation of varieties, more efficient by considering the different constraints that affect their performance, and by integrating the potential offered by genomic tools. He uses the tools of quantitative genetics, population dynamics modelling, statistics and genomics, and these tools have led him to explore various key aspects of genetic improvement, such as optimising genetic diversity management, incorporating plasticity traits into genetic evaluation, and adapting genomic and multi-omic selection to the forest tree model. He has made substantial contributions to the implementation of genomic selection in key species such as poplar and maritime pine in France, and in other forest species in the framework of several European initiatives on innovative selection. Prior to INRAE, he worked on different theoretical aspects of genetic diversity management, starting as a geneticist in Drosophila melanogaster. Today, he considers himself lucky to work with large trees, which are challenging models for experimental biologists.

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