## GENETIC MAPPING AND F2 PROGENIES RAPD ANALYSIS OF QTL'S FOR HEIGHT GROWTH COMPONENTS OF MARITIME PINE (*Pinus pinaster* Ait).

## PLOMION C. <sup>1,2</sup>, DUREL CE.<sup>1</sup>, O'MALLEY D.<sup>2</sup>

1-Institut National de la Recherche Agronomique, 33610 Cestas, FRANCE ; 2-Department of Forestry, North Carolina State University, Raleigh, NC.

Early evaluation constitutes a challenge for forest tree breeding, but until now, only a few cases were successful (fungus or frost resistance). Early selection for height growth is much less conclusive.

One possible cause to the lack of juvenile-mature correlation could be a change in the genetic control of the traits with time. Results have been published showing differential expression of genes during maturation. Therefore a way to early predict growth performances might be to accelerate ontogenetical ageing, so as to assess adult characters on young seedlings.

## We plan •

- to construct a genetic map with RAPD and Protein markers based on segregation of markers in the haploid megagametophytes of seeds of one selected inter-racial hybrid (Landes x Corsican);

- and then to map quantitative trait loci (QTL) influencing height growth : this cross was selected because we expect it, to be segregating for loci which determine growth components.

About 400 F2 seedlings (resulting of self-pollination of the hybrid) are growing in southwest of France under two conditions (200 each) : nursery (NC = normal condition) and accelerated condition (AC = high nutrient and continuous light) giving accelerated ageing. Around 20 traits will be measured during the first and the second growth period.

The main purposes is to compare which chromosomal segments can account for a large proportion of the genetic variation of expression of the height growth components in the two environmental conditions (NC and AC).