



**HAL**  
open science

## **A demo-genetic model to account for the impact of environmental and demographic changes on trees evolution**

Mariane Alleaume-Benharira, Sylvie Oddou-Muratorio, Francois Lefèvre

► **To cite this version:**

Mariane Alleaume-Benharira, Sylvie Oddou-Muratorio, Francois Lefèvre. A demo-genetic model to account for the impact of environmental and demographic changes on trees evolution. Forest ecosystem genomics and adaptation, Jun 2010, San Lorenzo de El Escorial, Spain. hal-02751267

**HAL Id: hal-02751267**

**<https://hal.inrae.fr/hal-02751267>**

Submitted on 3 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# A DEMO-GENETIC MODEL TO ACCOUNT FOR THE IMPACT OF ENVIRONMENTAL AND DEMOGRAPHIC CHANGES ON TREES EVOLUTION

Alleaume-Benharira Mariane \*, Oddou-Muratorio Sylvie, Lefevre Francois

*INRA, Unité d'Ecologie des Forêts Méditerranéennes, Avignon, France*

(\*) malleaume@avignon.inra.fr

Theoretical models dealing with local adaptation generally use individual fitness as a parameter driving the process of adaptation. This parameter is either directly controlled by the genotype, or indirectly derived from genetically controlled life history traits. Despite benefits of such assumptions and valuable theoretical concepts that emerged, partitioning evolutionary drivers into genotype-phenotype-demography maps is required to account for complex interactions among genes or traits regarding selection when environment or demography are unstable. In such demo-genetic models, individual fitness dynamically results from the demographic processes and environment quality that can vary in space or in time.

Trees can be considered as model organisms for testing such theoretical framework, because tree populations usually experiment a high spatial and temporal heterogeneity due to high longevity, size and dispersal abilities. In the context of increasing interest for short term evolution in non-equilibrium populations, we developed a demo-genetic model based on *Cedrus atlantica* colonisation in South East of France over three generations.

We studied the interactions between gene flow and environmental spatial heterogeneity during the colonisation process, by simulating evolutionary trajectories over three generations in two different landscapes (random or gradient variation of a site index) and under contrasted levels of seed/pollen dispersal. We show that few generations are enough for natural selection to handle genetic and phenotypic differentiations among micro-environments. As previously described, low gene flow allows genetic variability to be maintained, mostly in the random environmental pattern. We also show that gene flow interacts with spatial pattern of environmental heterogeneity. The divergence between differentiation patterns observed on neutral markers, QTL or adaptive traits increases when environmental conditions are spatially aggregated, and all the more when seeds and mostly pollen flow decreases. Thus, selection is more intense in a gradient than in a randomly arranged environment. Interestingly, heritability and evolvability decrease differently across generations. Heritability decreases continuously whatever the gene flow or the type of environment. On the other hand, evolvability decreases continuously when gene flow is low in both environment but declines strongly at first and stabilizes after the first generation when gene flow is high.