



Simulating the Holocene re-colonization of Europe by tree species using dynamic vegetation models

Marie Dury (1), Dörte Lehsten (2), Stefan Dullinger (3), Anneli Polska (2), Karl Hülber (3), Rachid Cheddadi (4), Henri Laborde (4), Martin T. Sykes (2), Thomas Hickler (5), Joy Syngarayer (6), and the Unité de Modélisation du Climat et des Cycles Biogéochimiques (Louis François and Pierre Warnant) Team

(1) Unité de Modélisation du Climat et des Cycles Biogéochimiques, University of Liège, Liège, Belgium (marie.dury@ulg.ac.be), (2) Department of Earth and Ecosystem Sciences, Lund University, Lund, Sweden, (3) Vienna Institute for Nature Conservation and Analyses, Vienna, Austria, (4) Institut des Sciences de l'Évolution de Montpellier, Université de Montpellier II, Montpellier, France, (5) Biodiversity and Climate Research Centre, Goethe-University Frankfurt, Frankfurt am Main, Germany, (6) Department of Geography, University of Bristol, Bristol, United Kingdom

At the beginning of the Holocene (10.000 BP) started a progressive re-colonization of Europe by temperate tree species from a limited number of glacial refugia. To reconstruct the speed, seemingly species-specific, and the routes of the postglacial spread of European tree species, fossil records collected from various localities in Europe are invaluable. However, the relative roles of climatic fluctuations, dispersal capacities of individual species, and inter-specific competition in controlling the re-colonization rates remain controversial. We investigate these different aspects with two dynamic vegetation models (DVM), LPJ-GUESS and CARAIB. Transient runs of both models were performed over the Holocene, using HadCM3 GCM-reconstructed climate. Large-scale species migration at $0.5^{\circ} \times 0.5^{\circ}$ is represented in these models using migration rates derived from a small-scale cellular automaton, CATS. Individual tree species migration rates were pre-calculated with CATS every 1000 years over each grid cell used by the DVMs in the climatic conditions reconstructed by the GCM. In the DVMs, these migration speeds were influenced by the response to competition from other species, expressed as a function of net primary production ratios. The DVMs were used to study the migration of one species, from its 10.000 BP refugia, within a landscape defined by a set of other species for which no dispersal limitations are assumed. Here, we illustrate the results obtained for wind-dispersed tree species and compare them to their past distributions reconstructed from pollen and macrofossil data.