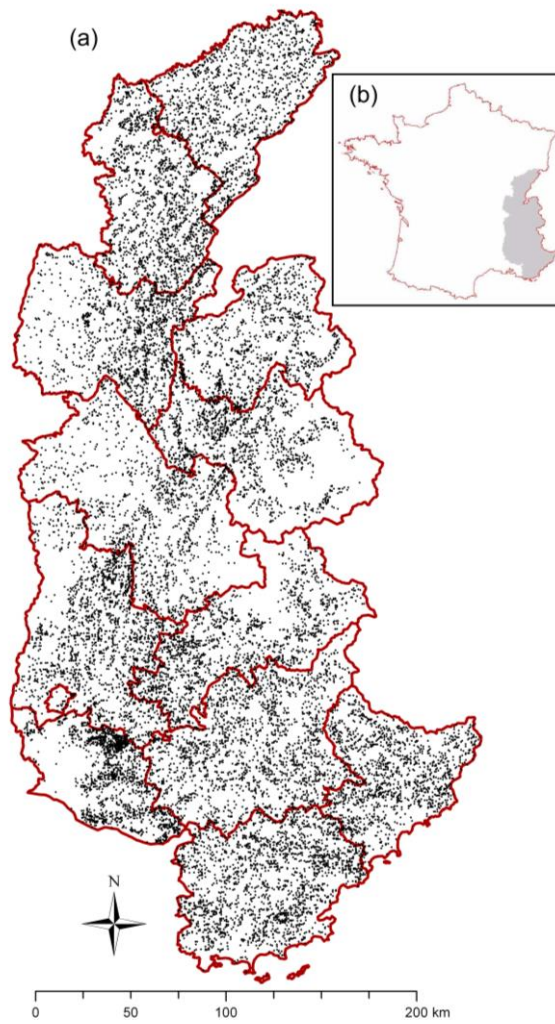


## Supporting Information

**Figure S1.** Map of the location of French National Forest Inventory plots over the study area, showing limits of the 12 administrative regions (a). The location of the study area within France (b).



# Supporting Information

## Appendix S1 Description of the water budget model.

The monthly potential evapotranspiration ( $PET_m$  in mm/month) was computed using the Turc equation (Turc, 1961) (see eqn S1.1).

$$PET_m = n \times 0.0133333 \times (Rg_m + 50) \times (t_m / (t_m + 15)) \quad \text{eqn S1.1}$$

with  $n$  = number of days of the month,  $t_m$  = the monthly temperature ( $^{\circ}C$ ) and  $Rg_m$  = the monthly potential radiation ( $cal/cm^2/day$ ).

The water budget computed monthly soil water content ( $SWC_m$ ) for each plot over the period 1980-2001, with initial condition for January 1980  $SWC_m$  set as  $SWC_{max}$  (the maximum soil water content). Then monthly soil water content was iteratively computed using eqn S1.2.

$$SWC_{m+1} = \min(SWC_m + Precip_{s\ m} - AET_m, SWC_{max}) \quad \text{eqn S1.2}$$

With  $Precip_{s\ m}$  = the infiltrating precipitation,  $AET_m$  = the monthly actual evapotranspiration computed by eqn S1.3.

$$AET_m = \min(D_m, S_m) \quad \text{eqn S1.3}$$

with  $D_m = PET_m - Precip_{i\ m}$  where  $Precip_{i\ m}$  is the intercepted precipitation (mm/month).

and  $S_m = c_w * SWC_m / SWC_{max}$  where  $c_w$  is a parameter denoting the maximum evapotranspiration from a saturated soil under conditions of high demand (as in Bugmann & Cramer 1998 we assume that  $c_w = 120$  mm/month).

$Precip_{i\ m}$  and  $Precip_{s\ m}$  are computed with eqns S1.4 and S1.5

$$Precip_{i\ m} = \min(f_i * P_m, PET_m) \quad \text{eqn S1.4}$$

with  $f_i$  = a parameter denoting the fraction of precipitation that is intercepted and is set at a value of 0.3 following Bugmann & Cramer (1998), and  $P_m$  = the monthly precipitation.

$$Precip_{s\ m} = P_m - Precip_{i\ m} \quad \text{eqn S1.5}$$

## References

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# Supporting Information

## Appendix S3 Methods used to develop a species-resolved phylogeny

We developed a species-resolved phylogeny for all model species by combining published phylogenetic trees and sequence data. As no gene sequence data were systematically available for all study species, we had to first build a genus-level phylogeny and then resolve each genus with published phylogenetic information. To do so, we downloaded sequence data from GenBank for each study genus for the genes *matK*, *rbcL* and *ndhf* (sequence matrix available upon request). Sequence data of each gene were aligned with the algorithm implemented in MUSCLE (Edgar 2004) and alignments were then depurated by removing poorly aligned blocks with the program trimAl (Capella-Gutierrez *et al.*, 2009). Then, a genus-level phylogeny was inferred by maximum likelihood using the program RAxML (Stamatakis 2006) by constraining heuristic searches with a family-level phylogeny derived from Davies *et al.* 2004). The resulting tree was then transformed into a chronogram (time-calibrated tree) by penalised likelihood (Sanderson 2002). As a final step, genera were resolved, using available species level phylogenies, by applying a time-uniform bifurcation process. The position of all species, except for in the genus *Ulmus*, were thus resolved, based on the following published trees: Suhl *et al.* 2000; Manos *et al.* 2001; Evans & Campbell 2002; Navarro *et al.* 2003; Grotkopp *et al.* 2004; Hamzeh & Dayanandan 2004; Gleiser & Verdü 2005; Grimm *et al.* 2006.

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# Supporting Information

## Appendix S5

### Likelihood of the model and prior description

The likelihood of the observed five years radial growth ( $y_{pi}$ ) based on a log-normal distribution of mean  $G_{pi}$  (see eqn 1) and variance  $\sigma^2$  is given by:

$$L(Y / X, \sigma^2) = \prod_{p=1}^P \prod_{i=1}^{N_p} \text{LN}(y_{pi} / G_{pi}, \sigma^2) \quad \text{eqn S5.1}$$

We used a flat conjugate prior with inverse-gamma distribution for variance  $\sigma^2$ , a conjugate log-normal prior for  $\alpha_p$ ,  $\beta_1$ ,  $\beta_2$  and  $\beta_3$ , and a flat unconjugate prior for  $\lambda_{ks}$ . The first-level priors were a log-normal prior for  $\beta$   $p(\log(\beta_k)) = N(\text{mean} = 0, \text{precision} = 0.000001)$  (based on the results of models with no species specific competitive effect), an inverse-gamma prior for  $\sigma^2$   $p(\sigma^2) = IG(1, 0.1)$ , and a normal prior for  $\lambda_{ks}$   $p(\lambda_{ks}) = N(\text{mean} = 5.7, \text{precision} = 0.0125)$ .  $\alpha_p$  was modelled as a random log-normal variable accounting for plot effect, with mean  $\alpha$  and variance  $V_p$  ( $p(\alpha_p) = \text{LN}(\alpha, V_p)$ ). The second-level priors were a flat inverse-gamma prior  $p(V_p) = IG(1, 0.1)$  and a non-informative log-normal prior  $p(\log(\alpha)) = N(\text{mean} = 0, \text{precision} = 0.000001)$ .

To keep the parameters within a biologically meaningful range and to help MCMC convergence we bounded prior within a plausible range of values. Studies have generally concluded that there is a positive effect of degree-day sum ( $DD$ ), and a negative effect of drought, on tree growth (see Rickebusch *et al.* 2007). We therefore decided to constrain our estimation to have a positive effect of both  $DD$  and  $WB$  by setting a positive boundary to the prior.

### MCMC simulation and diagnostic

All statistical analyses were performed in R.2.13 Software (R Development Core Team 2008) for data manipulation and JAGS 2.1.0 (Plummer 2003) for hierarchical Bayesian modelling.

We checked for convergence with two Monte Carlo Markov Chains (MCMC) using the potential scale reduction factor Rhat, setting our convergence threshold at Rhat < 1.1 as

recommended by Gelman *et al.* (2004). We ran MCMC for 30 000 iterations with a 5000-iteration burn-in period and selecting every 25<sup>th</sup> iteration to estimate the posterior distribution.

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# Supporting Information

## Appendix S6

Model selection statistics for the relationship between the interaction coefficients and predictors for an analysis restricted to the angiosperm

In order to explore whether the stronger support found for a relationship between interaction coefficients and hierarchical trait distance than between relationship with functional trait absolute distance or phylogenetic distances, we repeated the analysis while restricting the data to interaction coefficients between angiosperm species. We focused only on the two functional traits (LMA and WD) found best predictor in the global analysis because we believe our data set is too small explore whether functional traits effect differ between angiosperm and conifer. The Table S6 clearly show that an analysis restricted only to competitive interaction between angiosperm lead to similar results than the global analysis with a strong support for a link between competitions coefficients and their hierarchical distance.

**Table S6.** Model selection statistics (Deviance Information Criteria, DIC) for the five candidate models of the relationship between the interaction coefficients between pairs of species and their phylogenetic distance, functional trait absolute distance or functional trait hierarchical distance (LMA or wood density). This analysis is based on a data set restricted to the angiosperm. The best-fitting model is highlighted in bold black and the second best fitting model in bold grey.

<b>Model</b>	<b>DIC</b>
<b>Phylogenetic distance</b>	<b>404,1</b>
<b>Wood density (WD)</b>	<b>405,7</b>
Absolute distance	<b>391,7</b>
Hierarchical distance	<b>404,9</b>
<b>Leaf mass per unit area (LMA)</b>	<b>397,8</b>
Absolute distance	<b>404,9</b>
Hierarchical distance	<b>397,8</b>