

## Fine-scale genetic structure of *Nothofagus pumilio* (lenga) at contrasting elevations of the altitudinal gradient

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Received: 3 September 2012 / Accepted: 21 February 2013  
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**Abstract** Montane forests provide the natural framework to test for various ecological settings at distinct elevations as they may affect population demography, which in turn will affect the spatial genetic structure (SGS). We analyzed the fine-scale SGS of *Nothofagus pumilio*, which dominates mountain areas of Patagonia, in three pairs of sites at contrasting elevations (low- vs. high-elevation). Within a total area of 1 ha fresh leaf tissue from 90 individuals was collected at each of the six studied stands following a spatially explicit sampling design. Population genetic diversity parameters were analyzed for all sampled individuals using five polymorphic isozyme loci, and a subset of 50 individuals per stand were also screened for five microsatellite loci. The SGS was assessed on 50 individuals/stand, using the combined datasets of isozymes and microsatellites. Most low-elevation stands consisted of older individuals with complex age structures and genetically diverse plots. In contrast, high-elevation stands and one post-fire low-elevation population yielded even-aged structures with evidence of growth suppression, and were genetically homogeneous. All stands yielded significant SGS. Similarly to mature stands of the non-sprouter congener *Nothofagus dombeyi*, multi-age low-altitude *N. pumilio* yielded significant SGS weakened by competing species of the understory and the formation of seedling banks. Alike the sprouter *Nothofagus antartica*, high-altitude stands produced significant SGS as a consequence

of occasional seedling establishment reinforced by vegetative spread.

**Keywords** Clonality · Isozymes · Microsatellites · *Nothofagus* · SGS · South American beech

### Introduction

The combination of different ecological and evolutionary processes determines genetic structure. Selection for microsites and/or restricted gene movement by means of local mating and dispersal may result in a significant spatial genetic structure (SGS) within plant populations that is, the nonrandom spatial distribution of genotypes (Epperson 2000; Vekemans and Hardy 2004). Both forces have the potential to accelerate or reinforce the degree of spatial aggregation of relatives (Kalisz et al. 2001; Yamagishi et al. 2007). Also, combined demographic and ecological (i.e., intrinsic and extrinsic, respectively) processes affect spatial and temporal patterns of establishment and thus population dynamics, leading rates of population growth and changes in gene frequencies. Because trees are long-lived, they are more likely to suffer from disturbances (natural or human-induced), which will significantly impact stand composition, structure, and functional processes at distinct spatial and temporal scales (Dale et al. 2001). While some coarse-scale disturbances are mostly stand-devastating, others may affect stand structure and organization without causing massive mortality (e.g. opening of tree-fall gaps, ground fires) leaving few remnant trees from which forest will regenerate (Premoli and Kitzberger 2005). Even predominantly outcrossing species may have patterns of correlated mating (i.e. a restricted number of male trees contributing effective pollen) that may increase genetic relatedness

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