# Xylobios: Patterns, Roles and Determinants of Saproxylic Diversity in Belgian Deciduous Forests

*Philippe Fayt[1], Etienne Branquart[1], Marc Dufrene[1], Jean-Marc Henin[2], Christophe Pontegnie[3] and Veerle Versteirt[4]*

[1]Research Centre of Nature, Forests and Wood
[2]Gembloux Agricultural University
[3]Catholic University of Louvain
[4]Royal Belgian Institute of Natural Sciences

## Abstract

The XYLOBIOS project aims to study patterns, roles and determinants of saproxylic diversity (i.e., species richness and abundance of organisms which are dependent upon the dead or dying wood of moribund or dead trees, or upon the presence of other saproxylics) found in Belgian beech *Fagus sylvatica* and oak *Quercus spp.* forests. The project originates from recent international recommendations to retard loss of species and link biodiversity with ecosystem functioning. Main objectives, study sites and sampling methods are briefly described.

**Key words:** beech; biodiversity; ecosystem functioning; monitoring; oak; saproxylic organism; woody debris

## Introduction

Saproxylic organisms (1) account for a significant part of forest biodiversity (20-25% of all forest-dwelling species) (Siitonen 2001), (2) speed up wood decomposition and recycle large amount of nutrients through multitrophic interactions (Harmon et al. 1986, Edmonds and Eglitis 1989), (3) are threatened over much of their range, as a direct consequence of large-scale intensive forest management practices and the loss of primeval growth conditions (Speight 1989), and (4) suffer from a bad reputation world-wide in the northern hemisphere, based mainly on the tree damage and economic losses a few species may cause once their population increases above some abundance threshold (Vité 1989). Ultimately, one of the main arguments for maintaining dead wood habitats and preserving saproxylic assemblages is that losses of diversity may impair processes required for the long-term functioning of the ecosystems (Bengtsson et al. 2000), which, in turn, is expected to increase societal costs in a non-linear manner (Tilman 2000). This emphasises a need for a better understanding of interrelationships between biological diversity and forest management.

## Objectives

XYLOBIOS is a four-year research project started in Belgium in 2001 to address simultaneously and link both ecological and economical issues raised by forest management of beech *Fagus sylvatica* and oak *Quercus* spp. forests. Its goals are:

- clarify the national distribution of selected saproxylic families and species, indicators of microhabitats and processes found in natural and extensively managed deciduous forests
- identify the multi-scale determinants of their diversity
- relate saproxylic diversity and site factors with tree mortality and soil properties
- study co-variation in species richness among different saproxylic taxa

## Material and Methods

**Studied taxa:** insects (Coleoptera, Diptera), fungi (Polyporale, Corticiale) and cavity-nesting birds

**Monitoring:** enquiries sent to naturalists, biogeographical databases

**Field inventories:**

Study sites: 22 sites (10 beech/12 oak stands = 11 site pairs), distributed over 4 biogeographic areas (Fig. 1). A pair: sites with similar plant composition, soil properties and abiotic factors (altitude, climate) but with contrasting management histories and supply of woody debris

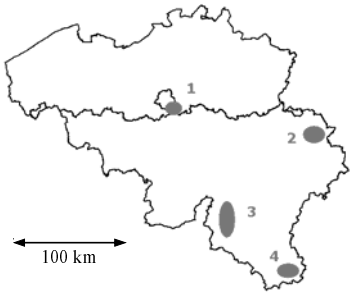

Figure 1.—Study sites

Insects: (i) a 0.8 ha circular study plot per site, in which 8 flight-window traps, 8 trunk-window traps[1], 1 Malaise trap, and 3 stump eclectors, and (ii) bark sampling and gallery eclectors on recently logged beech trees ([1] if standing dead trees available)

Fungi: hand-collected within the 0.8 ha study plots

Birds: point counts or transects within circular plots of 20 ha, centred on the 0.8 ha plots

Soil: 3 sample cores in the Ah layer (0-20 cm) per 0.8 ha study plot

Other habitat variables: (i) nested circular sample plots (0.006, 0.05 and 0.1 ha) located on a grid network of 50 x 50 m covering the study sites to gain information on small-scale structural heterogeneity, and (ii) regional circular sample plots (1,256 ha, centred on the 0.8 ha study plots), to measure modern landscape characteristics and its historical changes (Fig. 2)

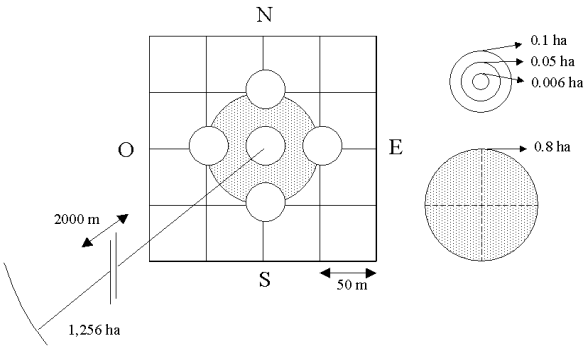

Figure 2.—Grid-based nested plots

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