# Monitoring population dynamics of a cryptic biological indicator of managed forest using non-invasive genetics.

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## Abstract

Current forest managers must deal with an increasing societal demand to set up management rules that are compatible with high wood production and ecosystem conservation. While wood production can be easily measured, ecosystem conservation remains difficult to evaluate. The lesser horseshoe bat (*Rhinolophus hipposideros*) is a sensitive woodland specialist and hence could represent a perfect biological indicator of forest conservation. Nevertheless, we lack sufficient knowledge to link *R. hipposideros* population dynamics to forests management practices. To address this knowledge gap, non-invasive genetic sampling was performed twice a year in 18 maternity colonies of this species in Picardie, Northern France, during three consecutive years. The DNA of more than 10,000 bat droppings was extracted and genotyped with one sexual marker and eight microsatellite loci. The genetic data allowed us to obtain individual life histories for capture-mark-recapture models, to estimate population size with a Bayesian estimator, and to assign individuals to cohorts using parentage inference. All those information were combined in an integrated population model to estimate survival, fecundity, and dispersal rates. These rates were then related to the landscape matrix and forest features around sampled colonies by multi-model inference, to better understand the impact of the environment and forests management practices on population dynamics of the bat. We thus provide here crucial information about vital rates in an indicator species and also show that integrated population models are useful tools to take into account the diversity of information provided by genetic data.

**Keywords:** Conservation genetics, Non invasive sampling, Population dynamics, Chiroptera

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