

# A method for molecular diet analysis of wild boar from their faeces

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## Introduction

In the current context of the dramatic increase of European wild boar (*Sus scrofa*) populations, the impact on biodiversity is often cited as an argument to urgently manage overabundant densities. But the impact of this omnivorous species is difficult to assess. The results based on the monitoring of vegetal and animal communities possibly affected by wild boar are difficult to interpret and the conclusions of the literature about this topic are quiet unclear or inaccurate. The present study focuses on the animal part of the wild boar diet.

## Material & Methods

We tested an original method based on a genetic diet analysis from faeces obtained by next generation sequencing methods (454 sequencing). A total of 500 fecal samples were collected on boar carcasses or directly on the ground during the hunting season 2012-2013 (November 2012 till February 2013). The DNA profiles from animal fragments present in the faeces were compared to a gene database in order to provide the list of animal species consumed by wild boar.

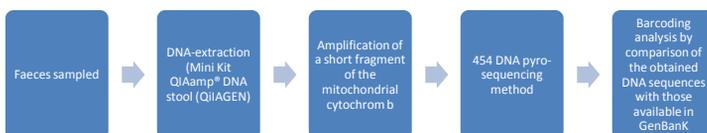
The sampling was designed to assume a contrasted spectrum of geographical, density and management situations. Collecting occurred in 4 study areas from 3 different regions in Belgium:

1. Hautes-Fagnes Eifel (low density, no artificial feeding),
2. Ardenne centrale (medium to high density, artificial feeding allowed locally),
3. Famenne (high density, no artificial feeding)

and 1 in France:

4. Loiret (high density, artificial feeding).

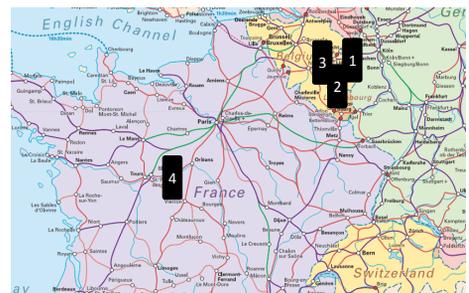
Each of these site is widely concerned by the Natura 2000 network and particularly sensitive to the impact of wild boar on biodiversity. The sampling year was characterized by a very low availability of forest fruit.



Process of identification of the consumed species

## Results

- The method tends to favor the DNA fragments from the host species (5.4%). Some cases of contamination (*Homo sapiens*, 2.2%) due to extreme sensitivity of the method are also highlighted. Moreover some DNA sequences could not be clearly assigned (5.4%).
- The overall result show a very low frequency of animal sequences in the wild boar faeces.
- *Anas platyrhynchos* is detected in 2 samples (Loiret and Ardenne centrale) and common chicken (*Gallus gallus domesticus*) in 1 of them (Hautes-Fagnes Eifel).
- Small rodents were detected in 7 samples (2 species were identified : *Apodemus sylvaticus* and *Mus musculus*).
- Cervids (*Cervus elaphus* and *Capreolus capreolus*) were detected in 6 samples, suggesting wild boar acting as a scavenger.



Location of the study sites

## Conclusions

- 454 pyrosequencing appears as a very powerful tool to study the wild boar diet based on DNA remains on their faeces
- Due to its high sensitivity the 454 pyrosequencing method may induce some contaminations
- The proportion of animal in the wild boar diet is low (max. 3% of occurrences in the sampled faeces).
- For example no snail nor slug, insect nor worm were detected during the study, probably because of the sampling period (Nov-Feb) reducing their availability
- The vegetal part of the wild boar diet has still to be analyzed.

## Acknowledgements

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