

Genetic diversity of the invasive box tree moth, *Cydalima perspectalis*, in its native and invaded areas and preliminary phylogeographic approach.

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Introduction

The box tree moth *Cydalima perspectalis* (Lepidoptera: Crambidae) is native to East Asia (China, Korea, Japan) and is present in natural and urban areas. Larvae feed on the leaves of box trees, *Buxus sp.*, resulting in defoliation, which can cause death (Wan et al, 2014). This invasive pest was recently introduced into Europe causing widespread damage to ornamental *Buxus* species but it is also a serious threat for natural box trees. It was first observed in Germany in 2007. Since its arrival, it has spread quickly into Europe and on time today, 25 European countries are invaded (Fig 1). The ornamental plant trade between Europe and China could be the introduction pathway of the box tree moth in Europe while the trade between European countries could be the reason of its rapid spread.

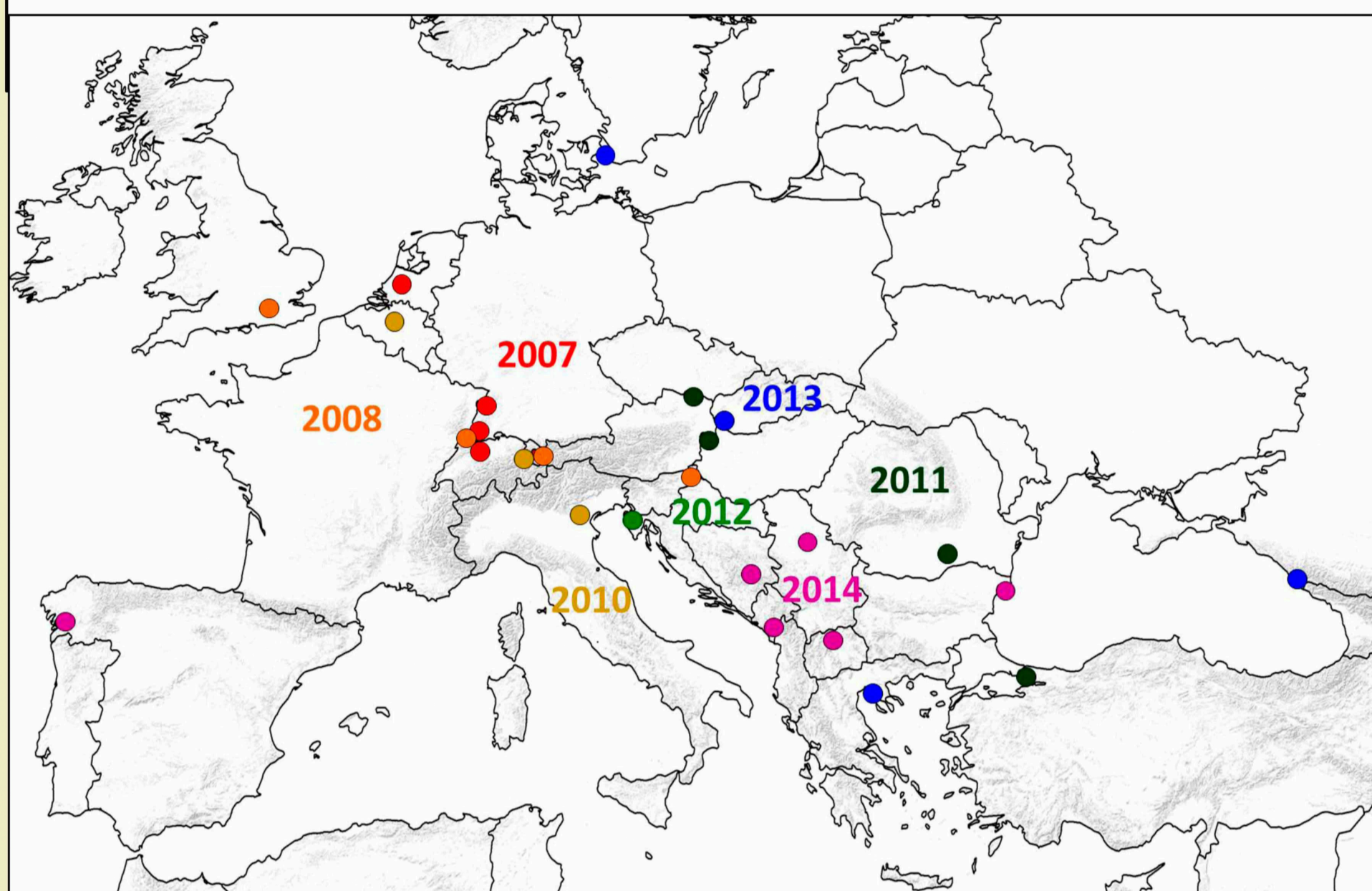
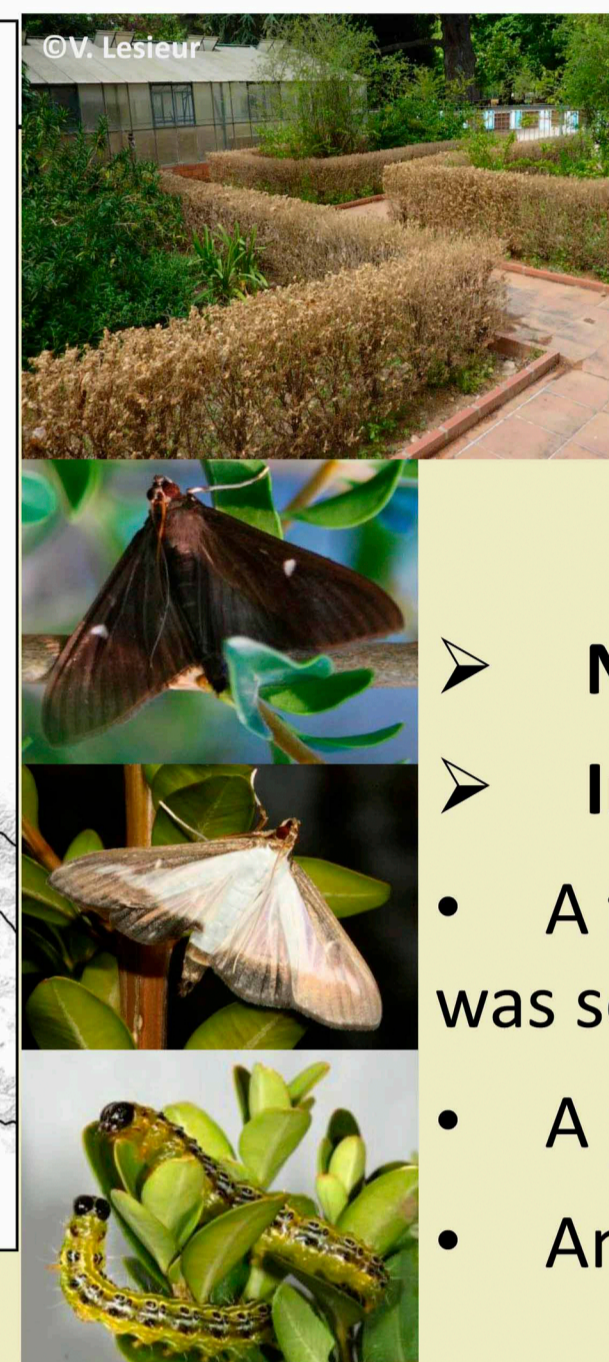


Fig 1 : Map of the invasion of *Cydalima perspectalis* in Europe.



Objectives :

- First overview of genetic diversity of the box tree moth
- First phylogeographic approach to understand the invasion pathways

Materials & Methods

- **Native Area** : 4 sampling sites in China and 1 in Korea, 41 individuals
- **Invaded Area** : 13 countries, 33 sampling sites, 133 individuals
- A fragment of the cytochrome oxidase I (COI) and II (COII) mitochondrial genes was sequenced with specific primers
- A parsimony network was built to estimate the genetic variability
- Analysis of Molecular Variance (AMOVA) was used to determine the population structure

Results

Native Area :

- Observation of **7 haplotypes** (Fig. 2 & 3) :
 - Korea** : 2 haplotypes
 - **HT6** only in Korea, and **HT4**
 - China** : 6 haplotypes
 - **HT1** and **HT4** : the most frequently observed
 - **HT2, HT3, HT7** : private haplotypes (only found in one locality)
- 3 haplogroups (Fig. 2) separated by several mutation steps, and having diverged over thousands of years
- No evidence of phylogeographic pattern in Asia with AMOVA results
- The geographical co-occurrence of haplogroups A and C indicates a **complex story** including a possible past isolation following by a recent secondary contact in urban areas linked with human activities (ornamental trade).

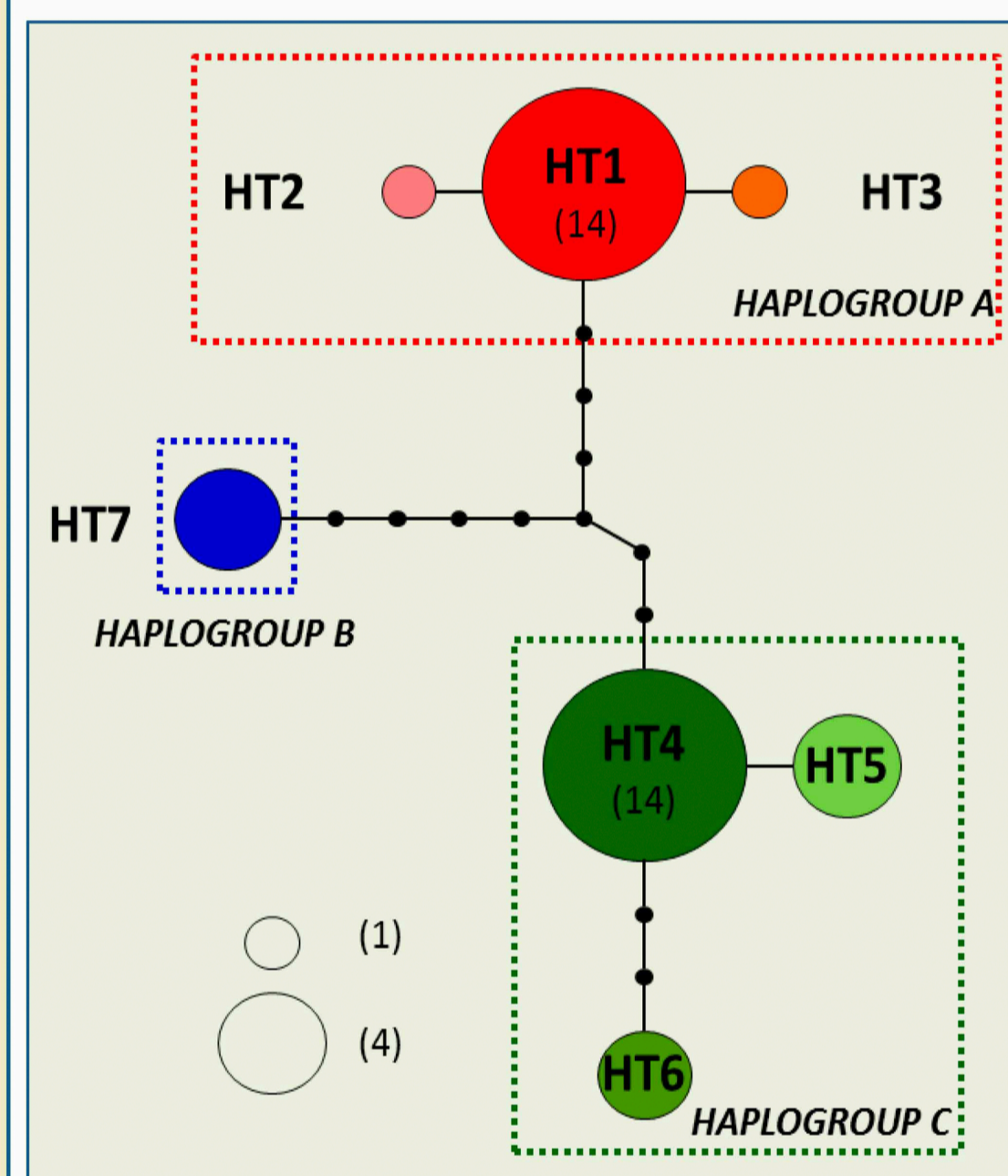


Fig 2 : Haplotypes COI-COII network. Size circle are proportional to the number of individuals.

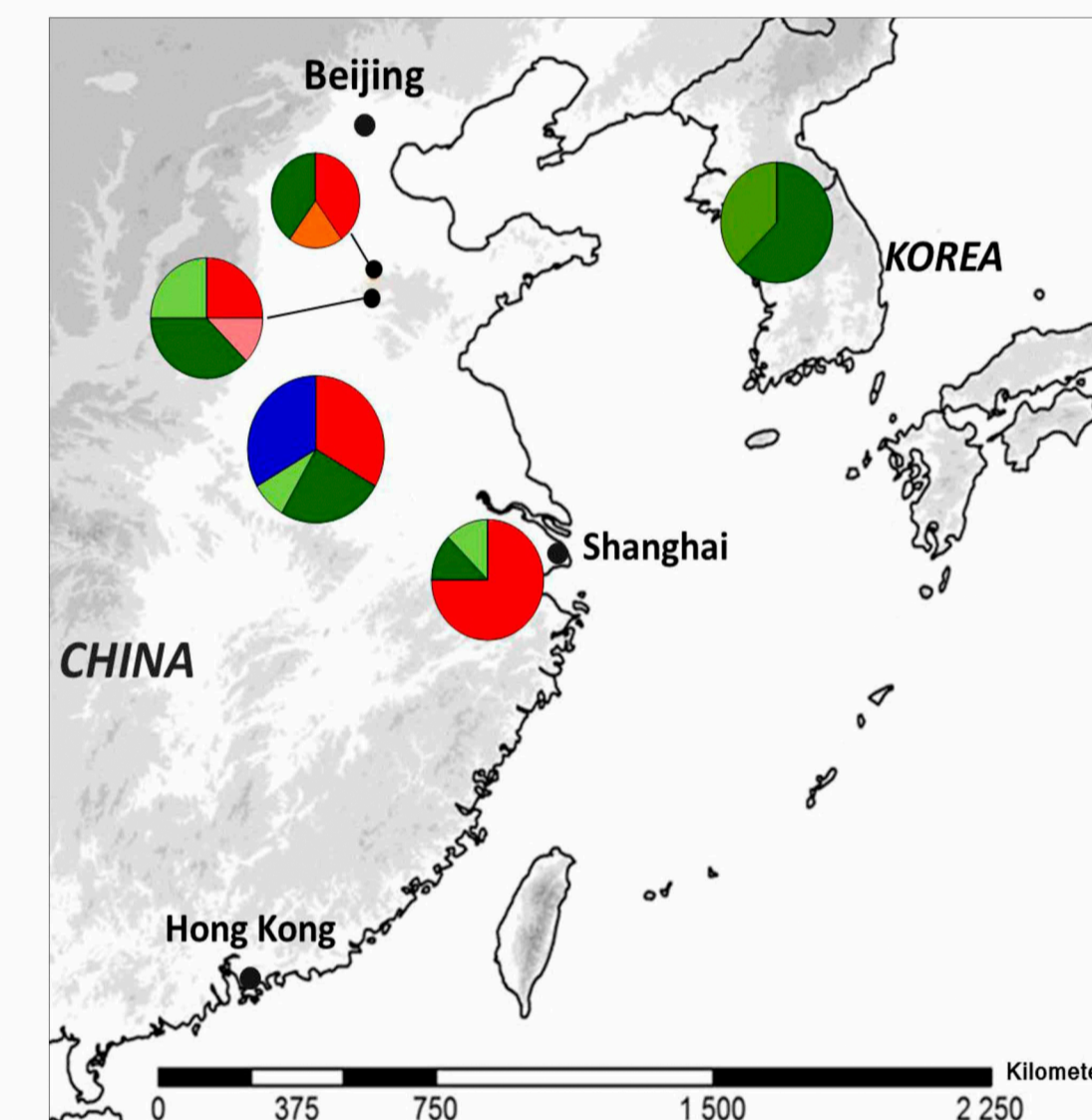


Fig 3 : Map of Haplotypes distribution of *C. perspectalis* in China and Korea.

Invaded Area : (Fig. 4)

- Observation of 4 asian haplotypes
 - **HT1** and **HT4** are the most abundant such as in Asia
 - **HT2** was observed in 10 sampling localities (1/3 of sites)
 - **HT5** was found for 1 individual in 1 locality in Europe (unique & private)
- Evidence of a spatial genetic structure (3 geographic regions) demonstrated by AMOVA results :
 - **West Europe** : France, Belgium, Switzerland, Germany, Italy
 - **Central Europe** : Austria, Slovenia, Hungary, Croatia, Serbia
 - **East Europe** : Turkey, Bulgaria, Russia
- Genetic diversity and population structure are **in favor of multiple introductions** of *C. perspectalis* in Europe.

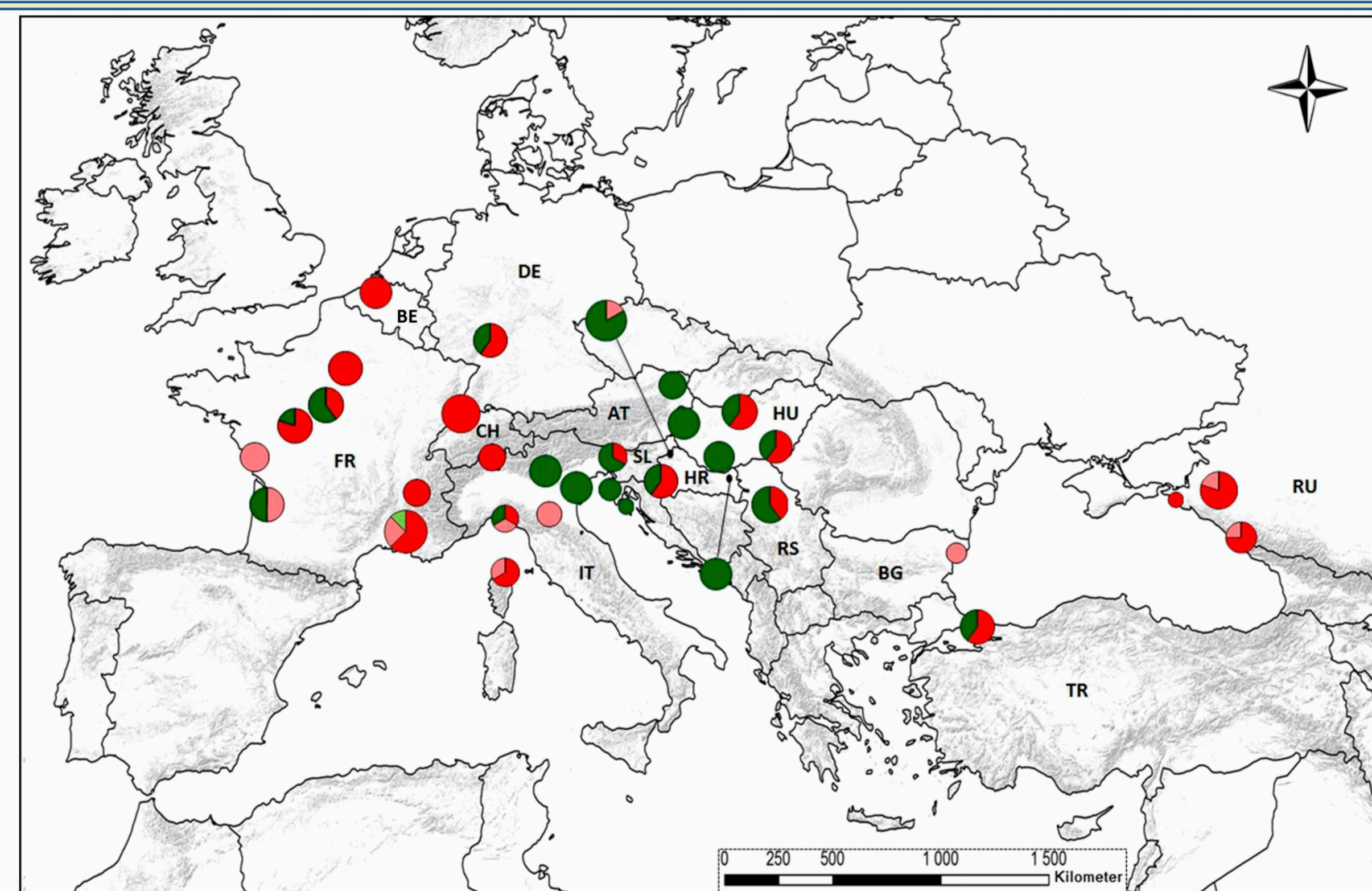


Fig 4 : Map of HT distribution of *C. perspectalis* in Europe. AT: Austria, BE: Belgium, BG: Bulgaria, CH: Switzerland, DE: Germany, FR: France, HR: Croatia, HU: Hungary, IT: Italy, RS: Serbia, RU: Russia, SL: Slovenia, TR: Turkey.

Conclusions – Perspectives

- Our results are in favor of : - a Chinese origin of the box tree moth (all haplotypes observed in Europe are present in China).
 - multiple introductions in Europe and a very fast expansion linked with human activities.
- A larger sampling in Asia and Europe, and the use of polymorphic markers (i.e. microsatellites) are needed to better understand invasion pathways of the box tree moth in Europe. It could help to define how those multiple introductions took place over time: (i) direct and successive introductions from Asia in different European places, or (ii) secondary human-mediated dispersal between European countries, after first introduction(s) from Asia into one or few European localities.