



## EXOTIC

# EXperimentally Orientated genomics to Tackle Insects' adaptive Challenges during bioinvasions: the ladybird *Harmonia axyridis* as a model species

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### Main participants

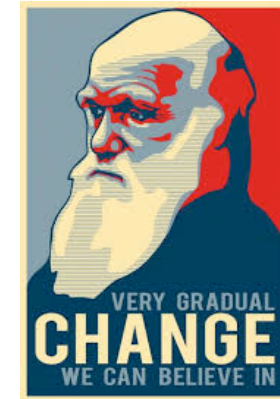
- A. Estoup (INRA, France)
- M. Gautier (INRA, France)
- F. Verheggen (Gembloux Agro-Bio Tech, Belgium)
- A. Vilcinskis (University of Giessen, Germany)
- H. Vogel (Max-Planck Institute, Germany)



An ecological vision of invasive populations



Genetically stable entities



However, a situation conducive to evolutionary changes

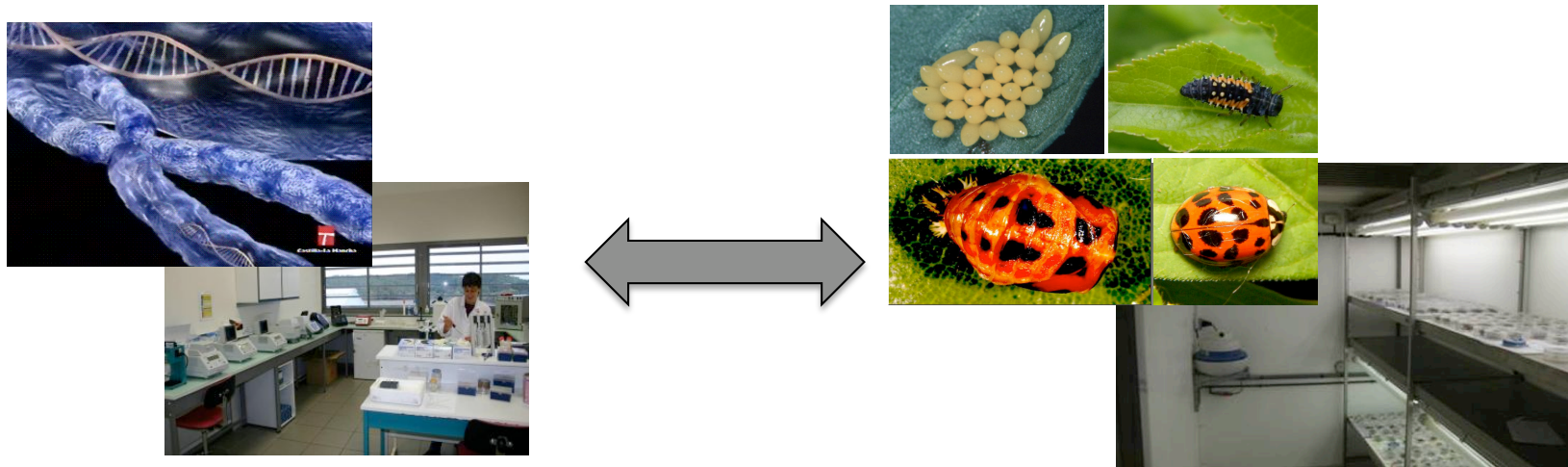
- New biotic and abiotic environments
  - **Shift in selective pressures**
- Introduction events associated with bottlenecks, multiple introductions and admixture
  - **Changes of the adaptive potential**





EXOTIC aims to decipher the adaptive pathways underlying the worldwide invasive success of the ladybird *Harmonia axyridis* and to assess its negative impacts on native communities.

Close integration of evolutionary genomics with experimental studies





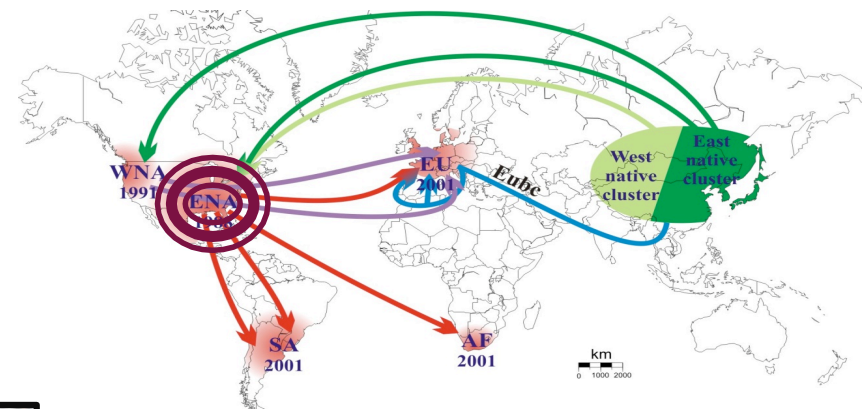
## *Harmonia axyridis* – an emblematic invasive species and a model to study contemporary adaptations

First used during decades as a biocontrol agent

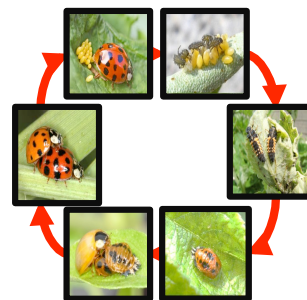
Now invasion at a worldwide scale with some harmful consequences



Good knowledge of the routes of invasion



Several evolutionary shifts during the course of invasion







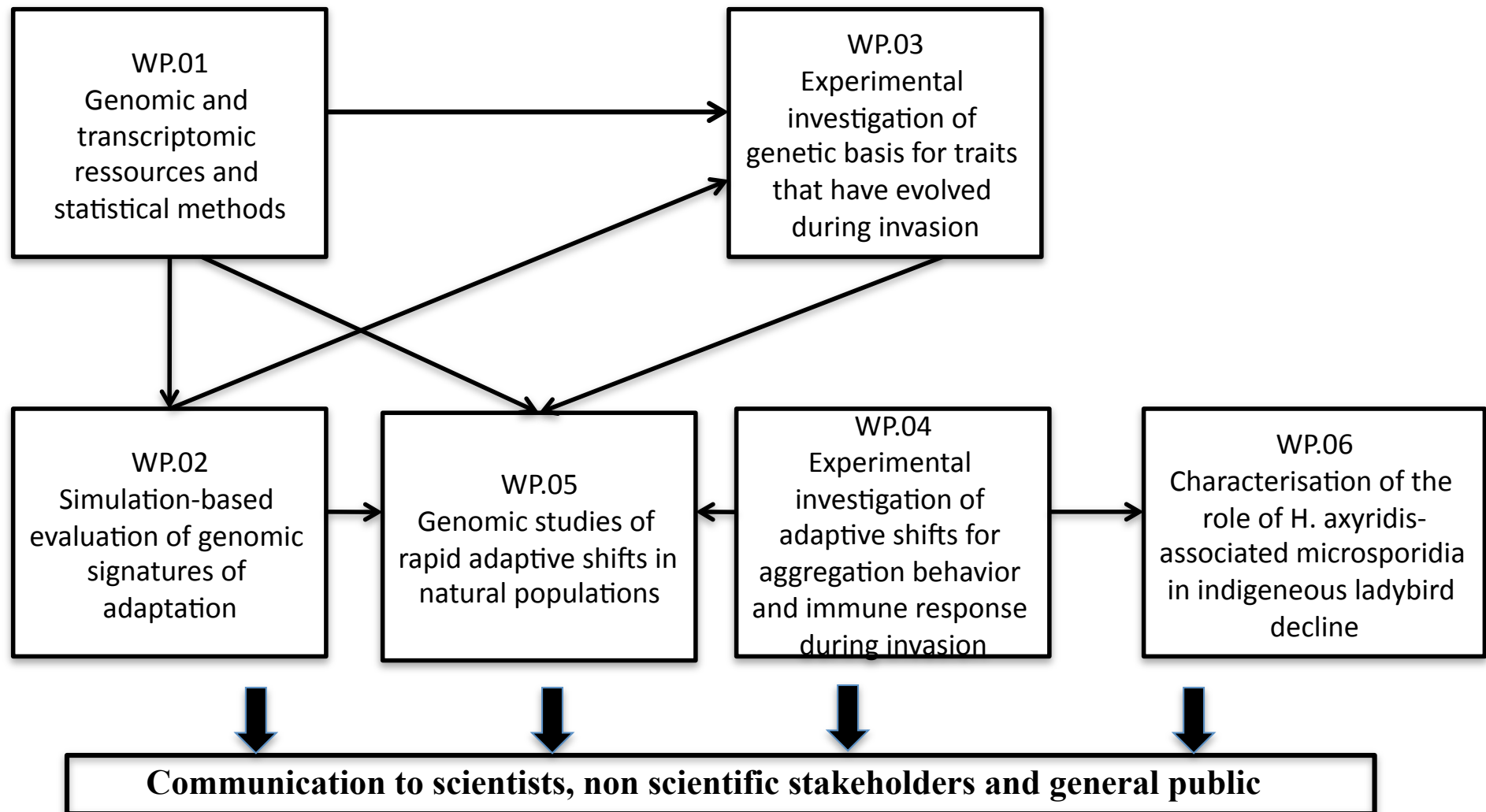
**EXOTIC aims at achieving the following outcomes:**

Developing a single unified genomic resource for scientists interested in *H. axyridis* genomics

Improving statistical methods to identify genomic regions under selection using population Next Generation Sequencing (NGS) data

Documenting the adaptive potential of invasive populations on key life-history traits

Deciphering the genetic basis of life-history, behavioral and immunity traits during an invasion process.

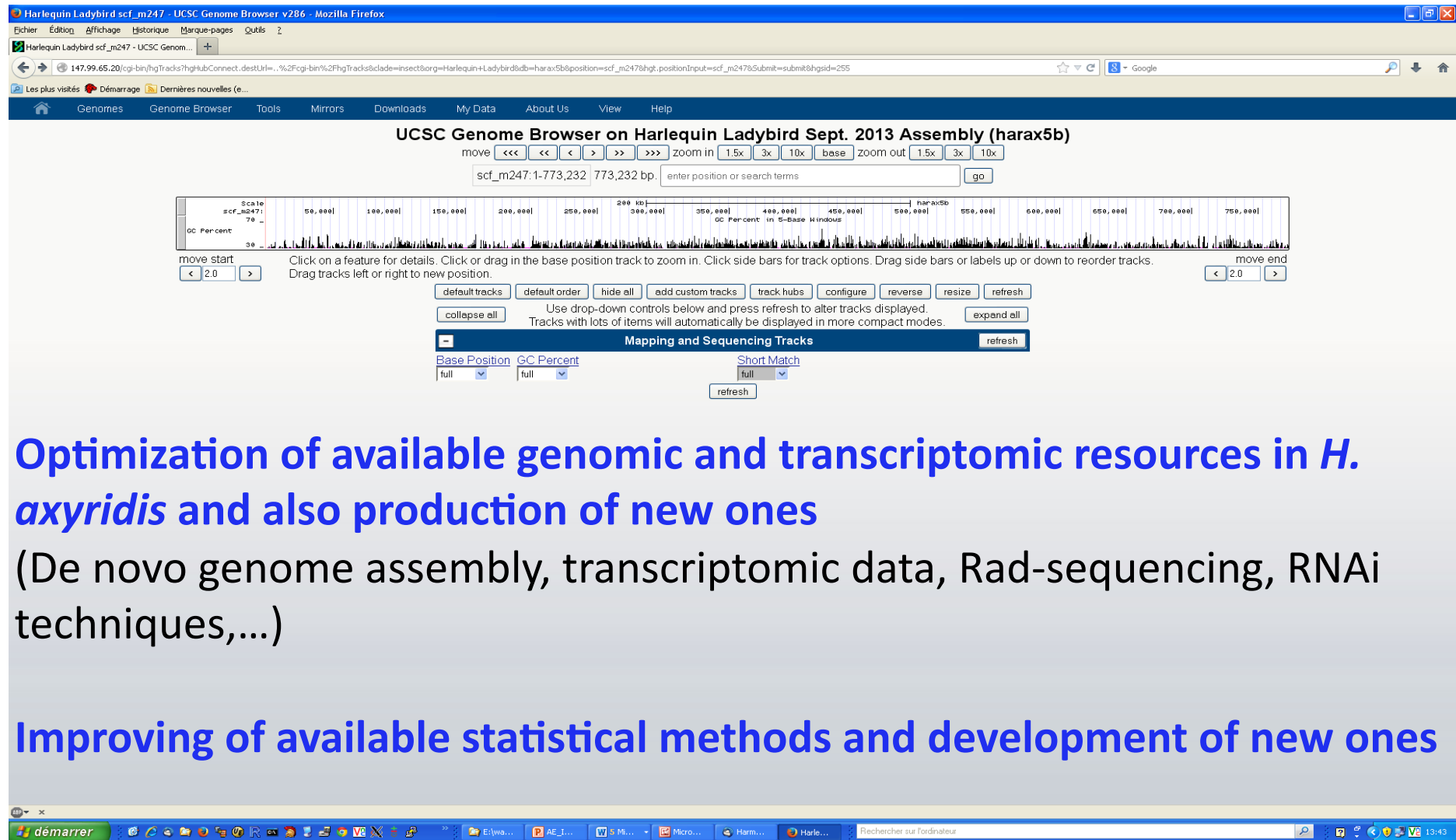




## WP.01: Development of genomic and transcriptomic resources and associated statistical methods



Task coordinators: A. Estoup (France) & H. Vogel (Germany)



Optimization of available genomic and transcriptomic resources in *H. axyridis* and also production of new ones

(De novo genome assembly, transcriptomic data, Rad-sequencing, RNAi techniques,...)

Improving of available statistical methods and development of new ones



## WP.02: Simulation-based tests of methods to determine genomic signatures of adaptation



Task coordinators: M. Gautier & A. Estoup (France)

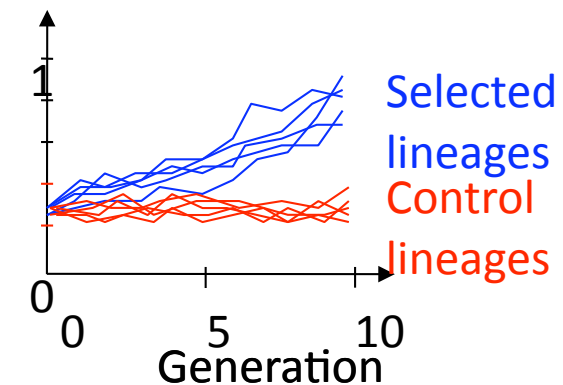


**Using simulated data to evaluate our ability to detect genomic regions under selection assuming different historical/demographic situations, genomic architecture, sampling and SNP designs**

Situations of interest = those studied in WPs 03 and 05

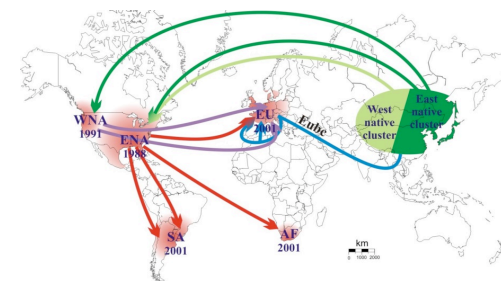
1/ **Experimental-selection** assays (WP 03)

- How many replicates?
- What level of drift (i.e.  $N_e$ )?
- What selective pressure?
- Genomic architecture?



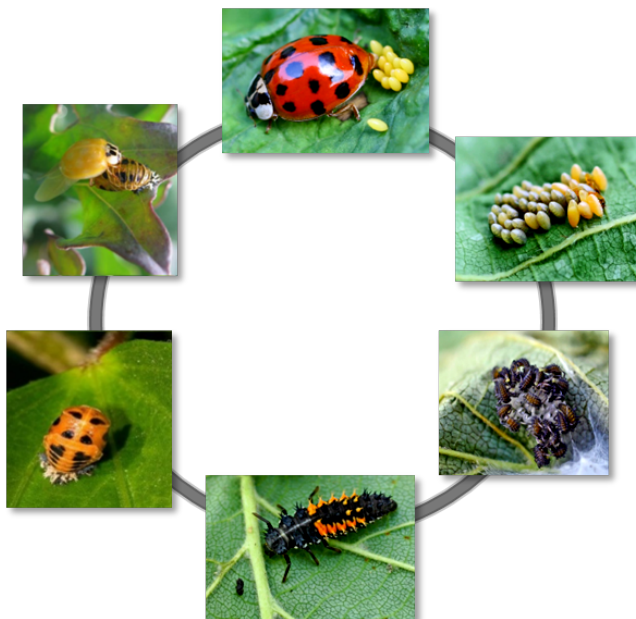
2/ **Natural populations** (native + invasive = WP 05)

- Intensity/type of selection?
- Genomic architecture?
- How many individuals in DNA pools?





## WP.03: Laboratory selection experiments and the genetic basis of traits that evolve during invasion

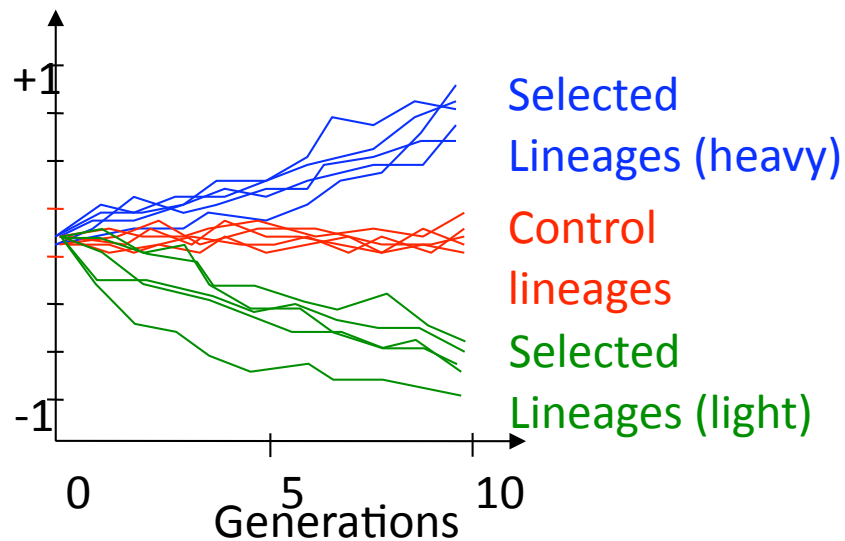


Task coordinator: B. Facon (France)



**Carry out laboratory experiments to mimic adaptive shifts that may occur during invasion for several traits known to be associated with invasiveness in *H. axyridis***

Ex: experimental selection of body mass



Measure the phenotypic response (amplitude, speed and associated traits shifts)

Analyze the genomic basis of the phenotypic changes in evolved populations with the genomic tools developed in WP.01

Other potential traits to be investigated: generation time, cannibalism, cold resistance, inbreeding depression, ...





## WP.04: Quantitative genetic analysis of phenotypic differences in aggregation behavior, immunity and stress responses between the three types of *H. axyridis* populations



Task coordinators: F. Verheggen (Belgium) & A. Vilcinskas (Germany)

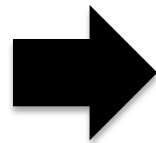


Working hypothesis:

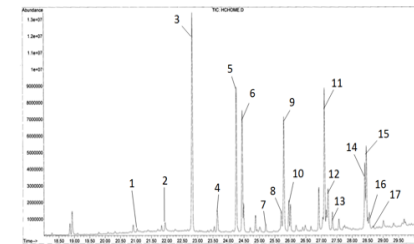
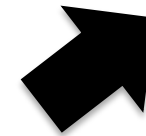
The aggregation behavior has evolved during the invasion process



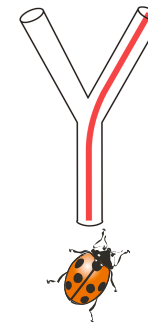
Through modifications in semiochemical production



hexane



Chemical characterization

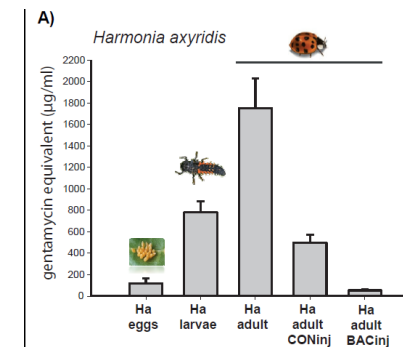


Behavioral assays

**Comparisons between native, biocontrol and invasive populations**



The innate immunity and stress responses (e.g. heat shock response) will also be studied by the comparative analysis of immune competence and stress-related traits in the three different populations of *H. axyridis*.



Candidate genes will then be identified by comparing RNA-seq-based gene expression dynamics :

- between non-challenged and immune-challenged beetles,
- between non-challenged beetles and those subjected to abiotic stress conditions such as heat shock or water deprivation.

Finally we will functionally characterize selected immunity and stress related genes using RNAi.

## WP.05: In natura genomic studies of rapid adaptive shifts associated with invasion

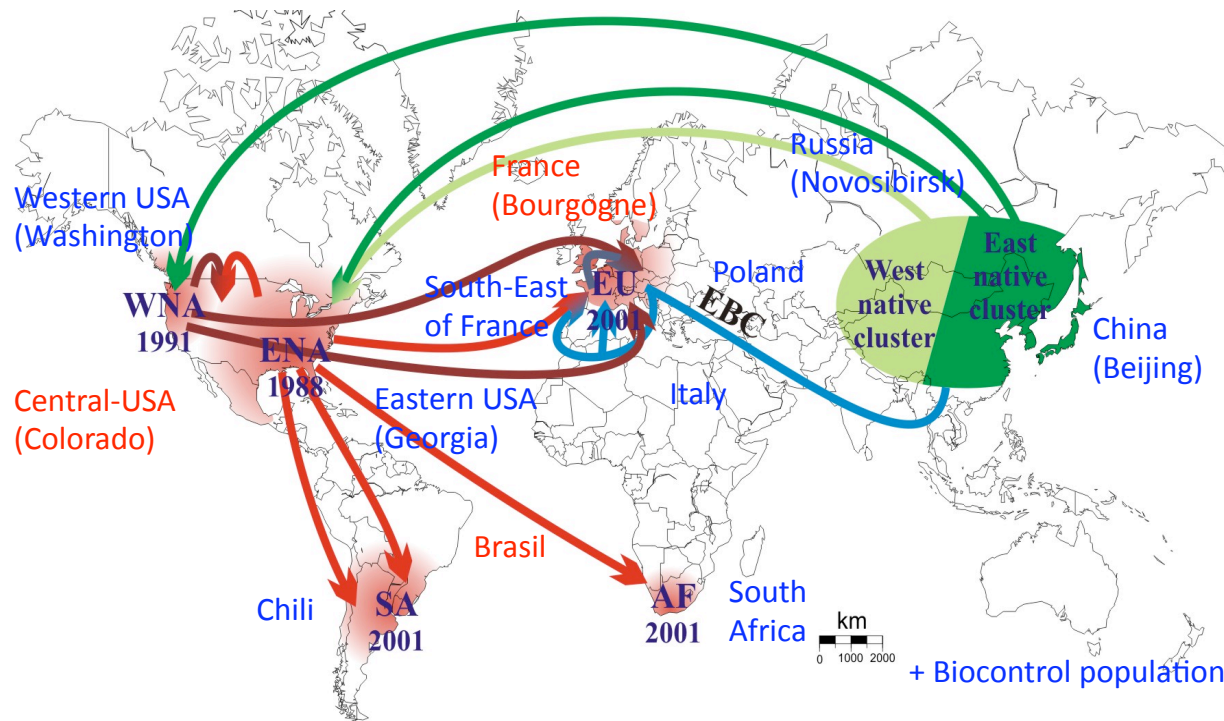


Task coordinator: B. Facon (France)





**A candidate-trait genomic study using natural populations, focusing on the candidate genomic regions and transcripts identified in WPs 03 and 04**



13 « key » populations to be SNP genotyped (shotgun; pool of 45 ind / pop)

- Congruence between experimentally-selected populations and natural invasive ones
- Action of few genes with major effects or a large number of genes with weak effects
- Type of selection involved (positive, disruptive, background selection, ...)



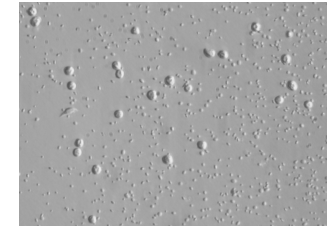
## WP.06: Characterization of the role of *H. axyridis*-associated microsporidia in indigenous ladybird decline



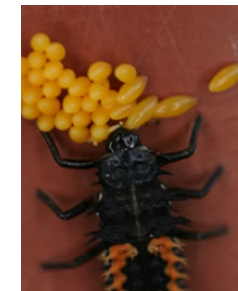
Task coordinator: A. Vilcinskas (Germany)



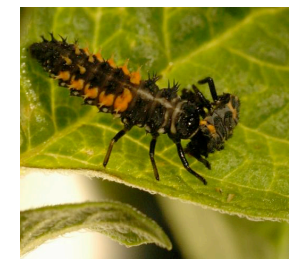
*H. axyridis* carries a high load of obligate parasitic microsporidia in its hemolymph, which can function like bioweapons against native ladybird species and contribute to its invasive success.



Testing for their presence in natural populations of indigenous ladybird species collected in areas where *H. axyridis* is present or absent.



Determining (under laboratory conditions) the transferability of *H. axyridis* microsporidia to indigenous ladybird species





## Communication plan

The information generated in this project will be disseminated in the following ways:

- Via a dedicated EXOTIC project website, with open-access and restricted areas.
- Through publications in prestigious peer-reviewed journals, with priority to open access publications.
- Through participation at events such as international congresses and workshops
- Through the dissemination of the key project results to the media, using the communication departments of each partner

At the end of the project, we will organize an international workshop to focus on the role of contemporary evolution in biological invasions





**Thanks for your attention**

