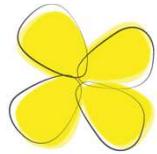




Development of molecular tools to identify the main weevil pests of oilseed rape and their natural enemies.

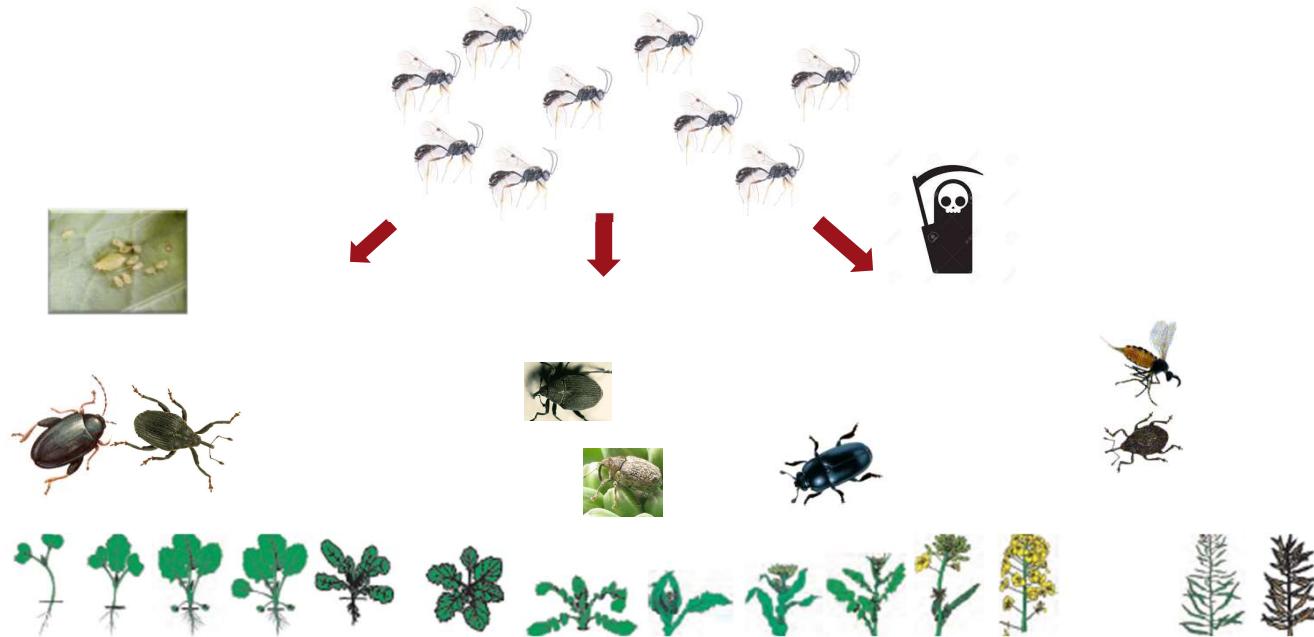
Robert C., Bothorel S., Luce S., Lauvernay A., Leflon M., Delvare G., Streito J.C., Pierre E., Cruaud P., Ollivier M., Genson G., Cruaud A., Rasplus J.Y.

Contact : c.robert@terresinovia.fr



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OSR pests regulated by many parasitoids

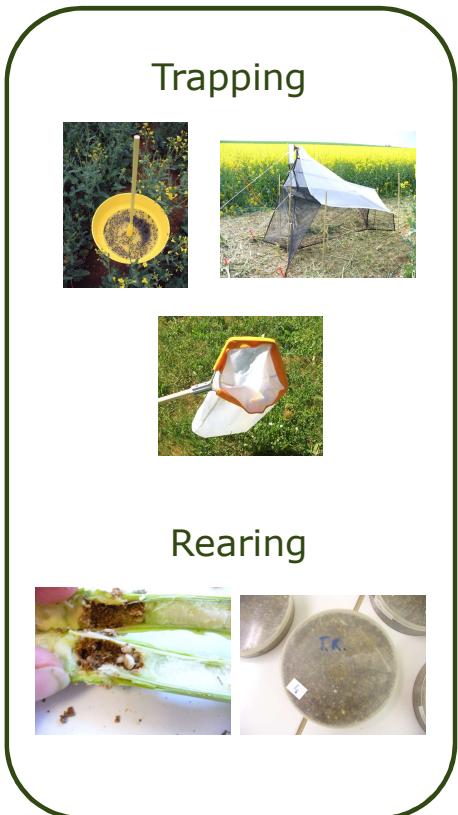


- Natural enemies can help farmers to regulate pests populations in their fields -> **conservation biological control**.
- To promote their action, a good knowledge of their biology is essential.

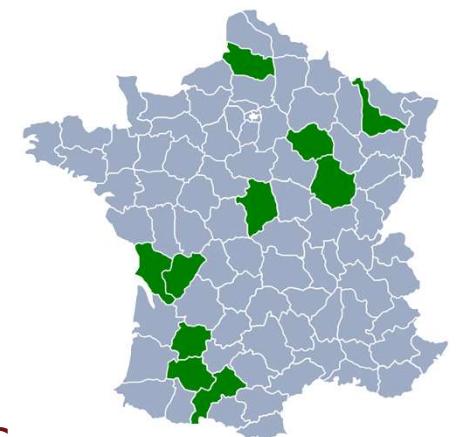
→ Tools to identify species and quantify parasitism rates are needed
-> Coleotool Project



A massive field collection for two years to create the database



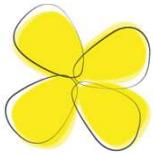
159 collected samples in spring and in autumn 2014, in most French regions



Sampling location

35 larval populations of weevils were reared in 2014 and 2015 in most French regions





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Updated references on endoparasitism rates (PR)

C. pictarsis

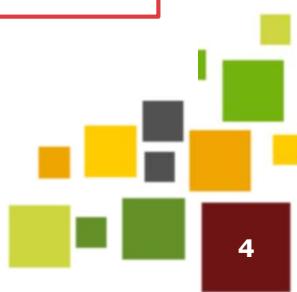
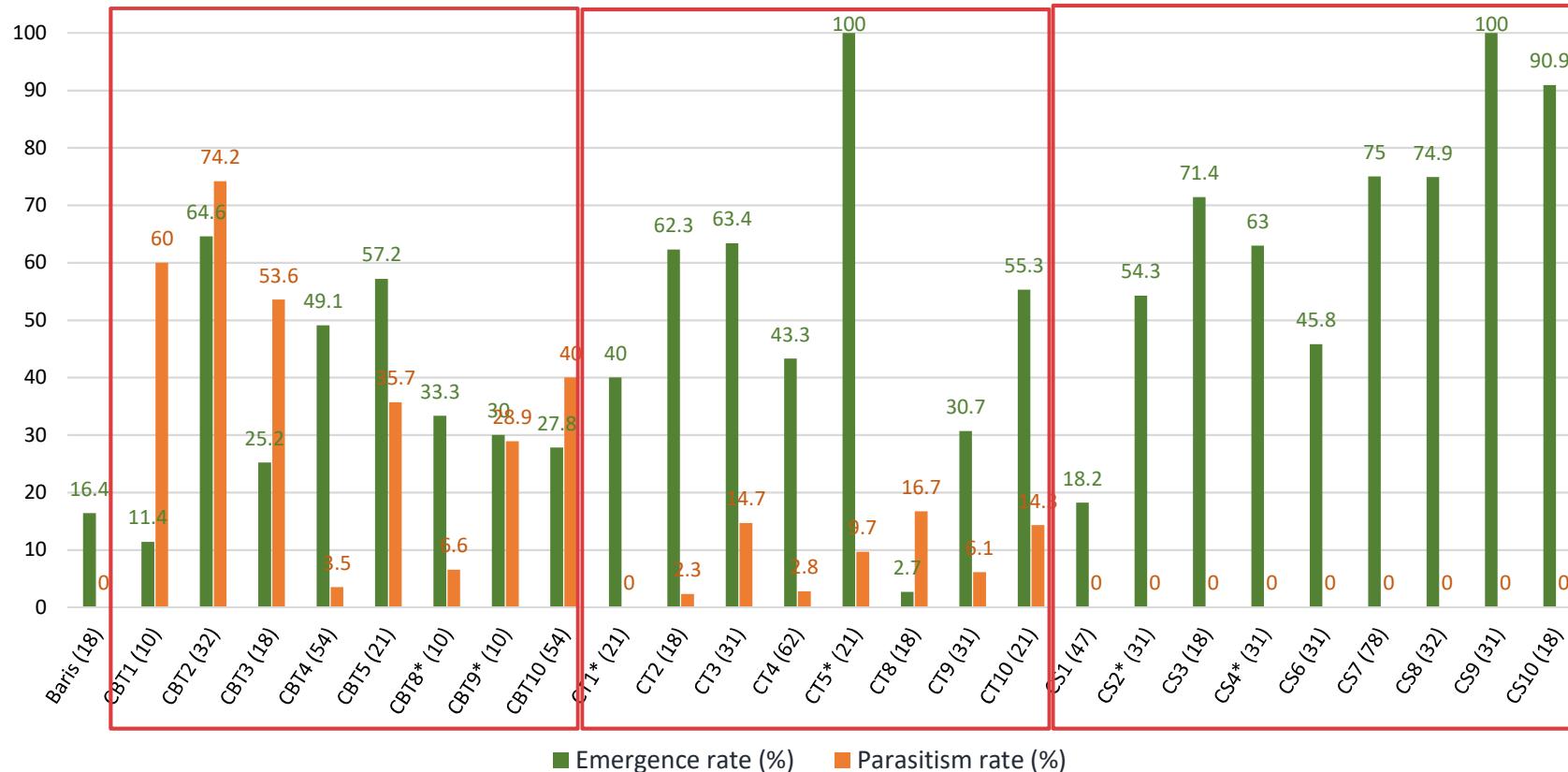
PR mean = 37.8 (sd=24.8)

C. napi or pallidactylus

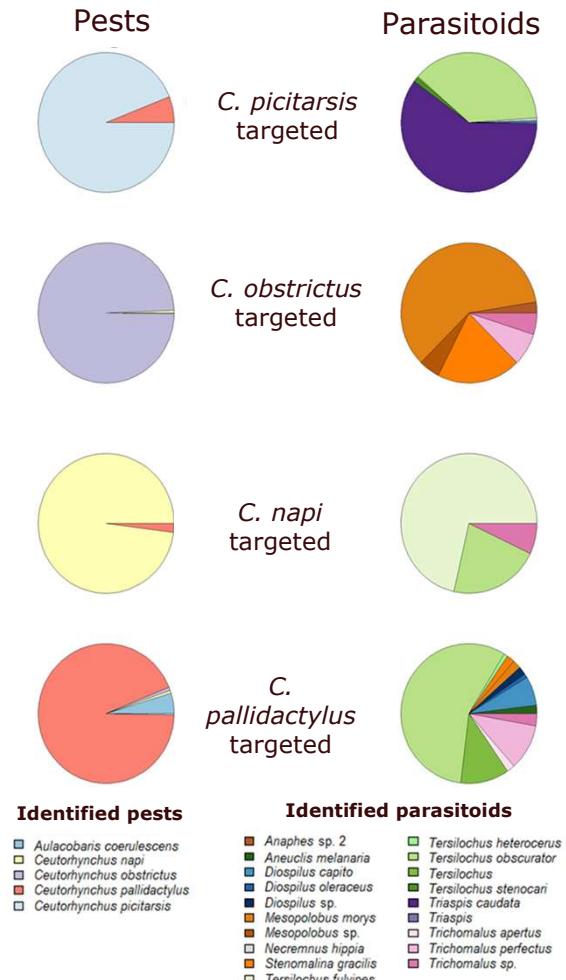
PR mean = 8.3 (sd=6.4)

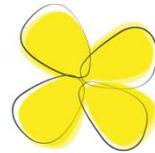
C. obstrictus

PR mean = 0 (sd=0)



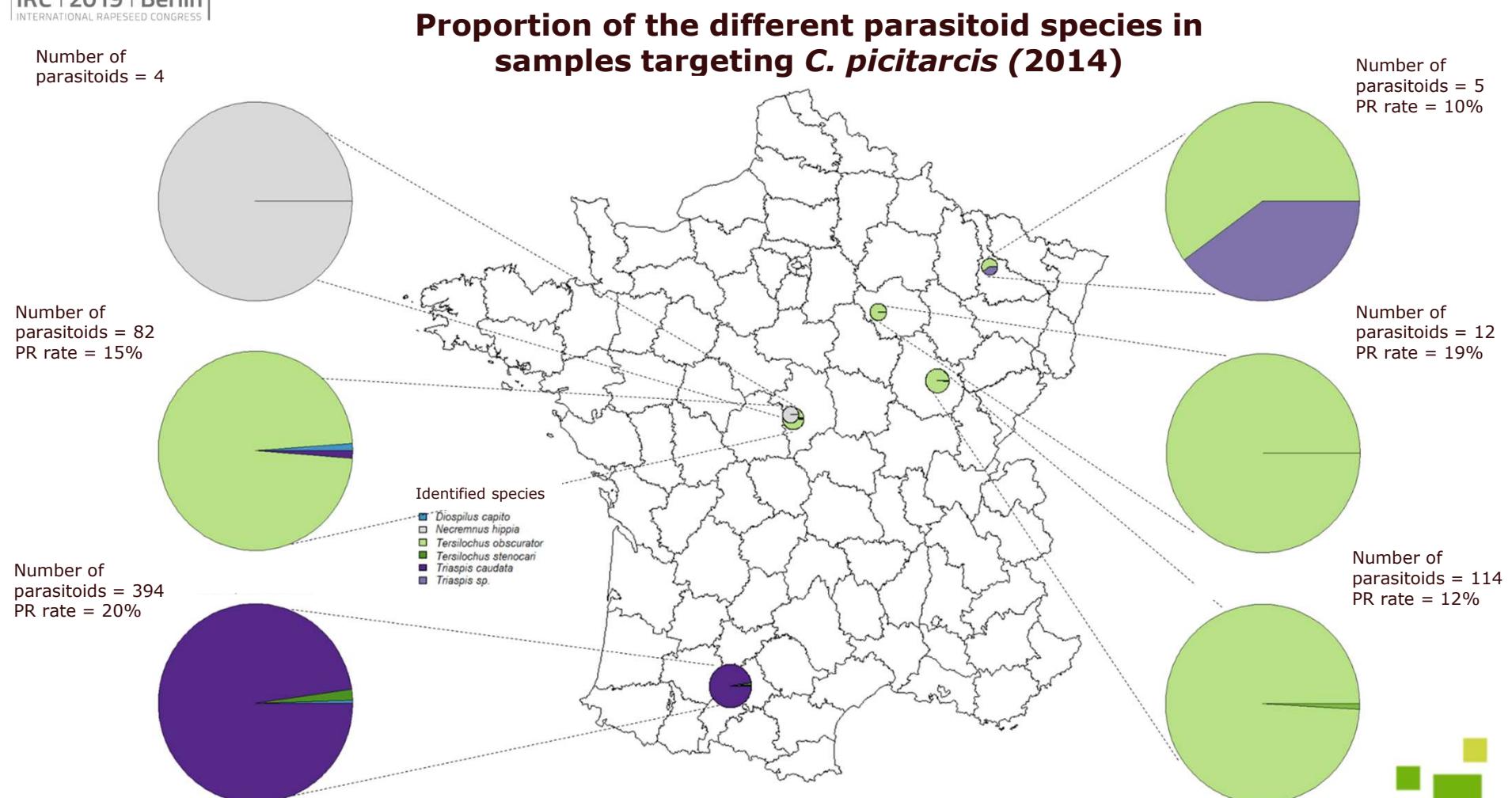
Updated references on the parasitoids species and their territorial distribution

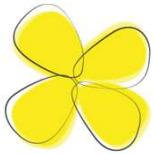




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Updated references on the parasitoids species and their territorial distribution





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Creation of a morphological identification key for weevils (9 sp) and their parasitoids (23 sp)

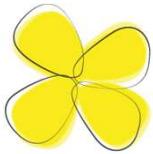


To identify parasitoids, the host must be known

The screenshot shows the COLEOTool software interface for creating a morphological identification key. The window title is "COLEOTool : Parasitoides". The left sidebar lists "Barre personnelle" with links to Leica IC80 HD, Citrix XenApp, Arthemis DB@se, Lonchaeidae Online, Wikis, Intranet, and COLEOTool Accueil. The main area has tabs for "Key", "Features", "Entities", and "View". The "Features Available" section contains 17 items: Corps à reflets métalliques, Taille du corps (du sommet de la tête à l'extrémité de l'abdomen), Antennes, Tête, Mésosoma, Aile antérieure, Pattes, Métaux, Ovipositeur, Hôte, and Stade parasite. The "Entities Remaining" section lists 24 entries with images: Aneulicus melanaria (Holmgren, 1860), Phradis mononellus (Holmgren, 1860), Tersilochus obscurator (Aubert 1959), Tersilochus microgaster (Szépligeti 1988), Tersilochus heterocerus (Thomson 1889), Tersilochus fulvipes (Gravenhorst 1829), Tersilochus stenocari (Gregor, 1841), and Triapsis caudata (Nees 1816). The "Entities Discarded" section is empty. At the bottom, there are tabs for "Trees", "Lists", and "Images", along with a toolbar with icons for file operations.

<http://www1.montpellier.inra.fr/CBGP/coleotool/index.html>





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Creation of a morphological identification key for weevils and their parasitoids

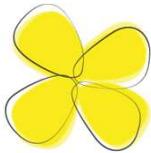


To identify parasitoids, the host must be known

The screenshot shows the COLEOTool software interface. On the left, there is a detailed image of a weevil larva labeled *Tersilochus obscurator* and *Tersilochus microgaster*. A scale bar indicates 150 µm. To the right of the image is a hierarchical morphological key. The key is organized into sections: Features Available: 31, Features Chosen: 21, and Entities Remaining: 5. The Features Available section includes categories like Cellule costale, Ptérostigma, Nervure 2m-cu, and Antennes. The Features Chosen section includes categories like Corps à reflets métalliques, Taille du corps, Antennes, and Tête. The Entities Remaining section lists five species with small images: *Tersilochus obscurator*, *Tersilochus microgaster*, *Tersilochus heterocerus*, *Tersilochus fulvipes*, and *Tersilochus stenoceri*.

<http://www1.montpellier.inra.fr/CBGP/coleotool/index.html>





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Creation of a morphological identification key for weevils and their parasitoids

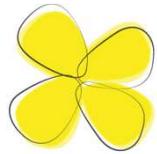


To identify parasitoids, the host must be known

The screenshot shows the COLETOOL software interface. On the left, there is a sidebar with various links and a search bar. The main window displays a morphological key for parasitoids. On the right, a detailed image of a parasitoid wasp, *Tersilochus obscurator*, is shown with a scale bar of 800 µm. Below the image, its scientific name and family (Ichneumonidae, Tersilochinae) are listed. To the left of the image, a smaller inset shows a comparison between *Tersilochus obscurator* and *Tersilochus microgaster*, with a 150 µm scale bar. The interface includes several dropdown menus and checkboxes for different morphological features.

<http://www1.montpellier.inra.fr/CBGP/coleotool/index.html>

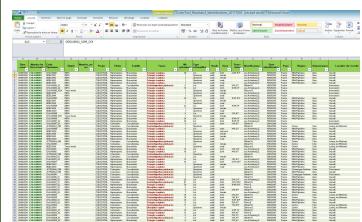
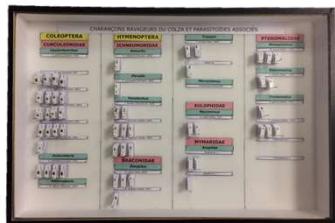




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Identification by entomologists

Specimen collection



Creation of a database containing 149 validated sequences of weevils and 177 of their parasitoids

Sequencing and validation CO1 gene

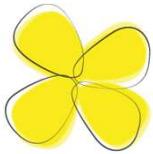


Latin names	Number of validated sequences (number of identified specimens)
WEEVILS	
<i>Ceutorhynchus pallidactylus</i>	35 (996)
<i>Ceutorhynchus napi</i>	32 (511)
<i>Ceutorhynchus picitarsis</i>	19 (633)
<i>Ceutorhynchus obstrictus</i>	39 (1199)
<i>Ceutorhynchus assimilis</i>	7 (17)
<i>Ceutorhynchus typhae</i>	5
<i>Aulacobaris coerulescens</i>	12 (381)
PARASITOIDS	
Braconidae	
<i>Diospilus</i> sp.	0 (2)
<i>Diospilus capito</i>	9 (14)
<i>Diospilus oleraceus</i>	1 (1)
<i>Triaspis</i> sp.	7 (10)
<i>Triaspis caudata</i>	19 (435)
Eulophidae	
<i>Necremmus hippia</i>	3 (4)
Ichneumonidae	
<i>Aneulcus melanaria</i>	2 (3)
<i>Phradis</i> spp.	2 (4)
<i>Phradis morionellus</i>	1 (2)
<i>Tersilochus</i> sp.	0 (19)
<i>Tersilochus fulvipes</i>	6 (10)
<i>Tersilochus heterocerus</i>	0 (2)
<i>Tersilochus obscurator</i>	76 (311)
<i>Tersilochus stenocari</i>	7 (7)
Mymaridae	
<i>Anaphes</i> sp. 1	3 (3)
<i>Anaphes</i> sp. 2	1 (1)
Pteromalidae	
<i>Mesopolobus morys</i>	16 (26)
<i>Mesopolobus</i> sp.	1 (2)
<i>Stenomalina gracilis</i>	5 (10)
<i>Trichomalus</i> sp.	2 (6)
<i>Trichomalus apertus</i>	2 (3)
<i>Trichomalus lucidus</i>	5 (5)
<i>Trichomalus perfectus</i>	9 (16)

Database creation (available online -> Arthemis database)

The screenshot shows the Arthemis software interface for pairwise sequence alignment. It includes a header with navigation links like 'Arthemis Home', 'Search on Taxa', 'Search on specimen(s)', 'Identification tools', 'Database Information', 'Contributors', 'Sponsors', 'Contact us', and 'Unknown user'. Below the header, a title 'Pairwise sequence alignment' is displayed next to an image of a green insect. A disclaimer checkbox is present. The main area contains alignment parameters and a table for selecting reference files. At the bottom, there's a sequence input field, a 'Start alignment' button, and a large preview window showing the aligned DNA sequences.

<http://arthemisdb.supagro.inra.fr/>

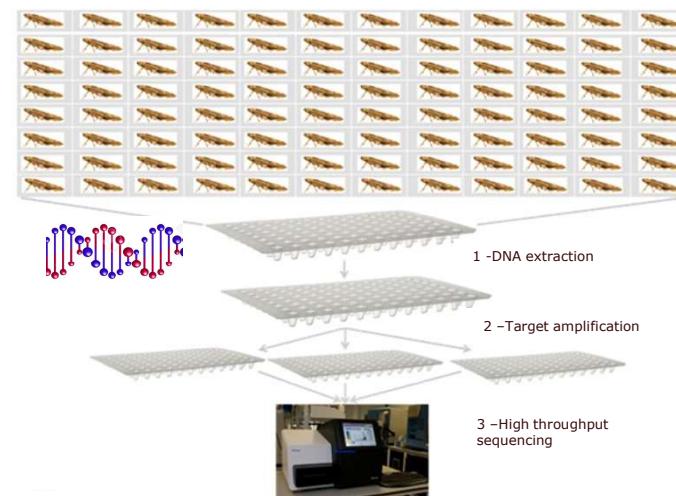


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Development of molecular identification tools

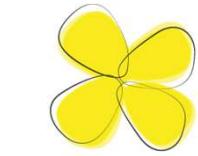


High throughput sequencing methods



- Allow the sequencing of several hundred insects in parallel
 - Cost reduction
- Allow to study trophic relationship





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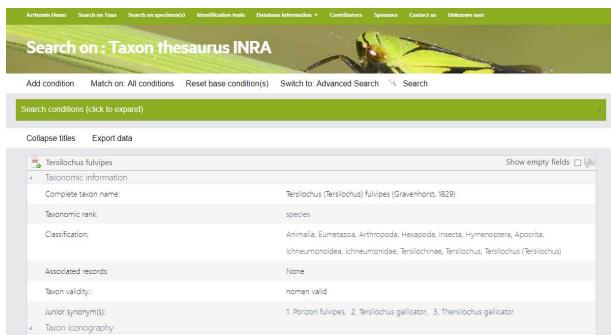
Outlooks

- Development of simplified molecular methods to identify specimens at any stage and quantify parasitism rates on a regular basis (quick results, easy to use...)
- Development of tools for *Psylliodes chrysocephala* and their parasitoids.
- Practical application of the developed methods in the R2D2 project (poster)

Tools available online on the Coleotool website

<http://www1.montpellier.inra.fr/CBGP/coleotool/index.html>

Sheets on species

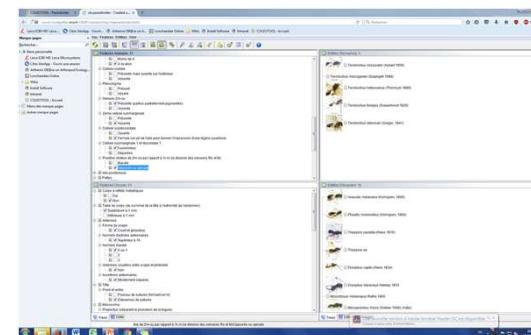


The screenshot shows a search results page for the taxon 'Terelochus fulvipes'. The results include the complete taxon name (Terelochus (Terelochus) fulvipes (Gravenhorst, 1829)), taxonomic rank (species), classification (Animalia, Eumetazoa, Arthropoda, Hexapoda, Insecta, Hymenoptera, Apocrita, Ichneumonoidea, Ichneumonidae, Terolochinae, Terelochus, Terelochus (Terelochus)), associated records (None), taxon validity (nomen valid), and junior synonym(s) (1. Ponzon fulvipes, 2. Terelochus gallicator, 3. Thersilochus gallicator).

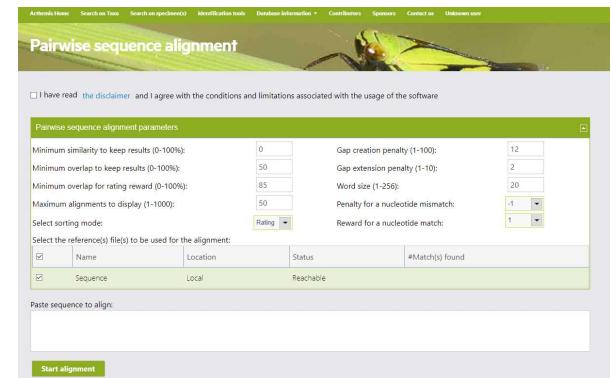
Link to:

<http://arthemisdb.supagro.inra.fr/>

Morphological identification key



Sequence database



The screenshot shows a pairwise sequence alignment interface. It includes parameters for minimum similarity (0-100%), minimum overlap (0-100%), maximum overlap for rating reward (0-100%), maximum alignments to display (1-1000), gap creation penalty (1-100), gap extension penalty (1-10), word size (1-256), and penalty for a nucleotide mismatch (-1 to 1). Below these are tables for selecting reference sequences and a search table for sequences, locations, and status. A 'Start alignment' button is at the bottom.

Link to:

<http://arthemisdb.supagro.inra.fr/>

Thank you for your attention !

