



## **BINGO-ITN is hiring: 13 PhD positions available**

BINGO - Breeding Invertebrates for Next Generation BioControl, develops innovative research training to improve the production and performance of natural enemies in biological control by the use of genetic variation for rearing, monitoring and performance. BINGO is a Marie Skłodowska-Curie Innovative Training Network, and invites applications for 13 Early Stage Researcher positions (PhD student). BINGO is funded by the EU Horizon 2020 programme and involves 12 partners from academia, non-profit organizations and industry located in the Netherlands, Germany, France, Spain, Czech Republic, Austria, Switzerland, Greece and Portugal. BINGO's approach is multidisciplinary, encompassing a broad range of scientific disciplines, including the application of state-of-the-art population genomics. The programme combines integrated training workshops and internship opportunities across the network, with career opportunities in academia, public or the private sectors. For more information on the BINGO network, please see: [www.bingo-itn.eu](http://www.bingo-itn.eu)

### **Ideal candidates**

- Are highly motivated PhD candidates with a background in evolutionary ecology and/or genetics
- Have a keen interest in the application of this knowledge in biological control
- Are able to cooperate in a multidisciplinary team
- Should be keen on intra-European mobility
- Have good communication skills
- Are fluent in English

### **Benefits**

- Hired early stage researchers will be paid a salary plus mobility allowance;
- The opportunity to register for a PhD degree at excellent universities;
- Training in state-of-the-art scientific and complementary skills;
- The possibility to travel to other partners from academia, industry and international agricultural organizations for workshops and conferences;
- Secondment placements and internships with other network's partners.

### **Application information**

#### **Selection criteria**

A university degree in a relevant field. Candidates should have a background in evolutionary ecology, entomology, microbiology and/or genetics and a keen interest in the application of this knowledge in biological control. Candidates are expected to cooperate in a multidisciplinary team and should be keen on intra-European mobility. Good communication skills and fluency in English is expected from all candidates.

BINGO aims to ensure equal opportunities, i.e. no job applicant or employee will receive less favourable treatment on the grounds of race, colour, nationality, ethnic or national origins, gender or marital status. This policy will include disabled persons who have the necessary attributes for the research project they are interested in.

#### **Eligibility criteria**

Candidates must be, at the time of recruitment by the host organisation, in the first four years (full-time equivalent) of their research careers and have not yet been awarded a doctoral degree.

This is measured from the date when they obtained the degree which would formally entitle them to embark on a doctorate.

Eligible candidates may be of any nationality but must not, at the time of recruitment have resided or carried out their main activity (work, studies, etc) in the country of their host organisation for more than 12 months in the 3 last years immediately prior to the reference date.

For positions at international organisations CABI (RP6) and FAO (RP8): eligible candidates must not have spent with the host organisation for more than 12 months in the 3 years immediately prior to the recruitment date.

### **How to apply**

Please provide a letter of motivation and a detailed CV by e-mail to:

1. the contact address of the respective research project (provided in the detailed descriptions), and
2. CC to: [info@bingo-itn.eu](mailto:info@bingo-itn.eu)
3. Add subject: BINGO-Application RPnumber (providing the number of the RP you apply to)

We like to receive your application before 31 March 2015

Please note that it is possible to apply to more than one position. Candidates applying to several positions should indicate this in their application letter and motivate their choice, i.e. show an alignment of their research interests and expertise with the research projects. Please submit your application separately for each position you are interested in.

**RP1: Population genomics of natural enemies****Supervisor(s):** Bart Pannebakker & Bas Zwaan**Host Institution:** Wageningen University**Duration:** 48 months**Envisaged start date:** 1 May 2015**Planned secondment(s):** Bio-insekta (GR), University of Bremen (DE), IVIA (E) and BC (CZ)**Description:**

Intraspecific genetic variation in arthropods is often studied in the context of evolution and ecology. Such knowledge, can also be very usefully applied for selection of genotypes with optimal trait values to develop more effective biocontrol agents. Key for this approach is the presence of adequate genetic variation as it determines the potential of populations to adapt to breeding objectives. Therefore, fundamental knowledge on the genetic variation of natural enemies, both in the field and in commercial mass-cultures, is of prime importance to design sampling programs and mass-rearing protocols.

In this project, we aim to investigate the genetic variation in natural, as well as in mass-culture populations of three economically important natural enemies with contrasting biology, the predatory mite *Amblyseius swirskii*, the predatory bug *Nesidiocoris tenuis* and the parasitoid wasp *Trichogramma brassicae*. Particular focus will be on the comparison of the genomic diversity between field collected and commercially reared populations. Using next-generation sequencing data and analysis, we will generate whole-genome data for these three species. This will allow to detect the genomic regions that are under selection in both situations in order to adapt to environmental and laboratory conditions. The whole-genome data will also be used in by other projects (RP3, RP10 and RP12) to facilitate artificial breeding and monitoring of natural enemies.

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in evolutionary biology or genetics, with good background in population genetics, bioinformatics, genomics and computational biology. Candidates from other programs such as ecology or bioinformatics, with a strong interest in evolution and genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [bart.pannebakker@wur.nl](mailto:bart.pannebakker@wur.nl) & [bas.zwaan@wur.nl](mailto:bas.zwaan@wur.nl)**Link:** [www.gen.wur.nl/uk](http://www.gen.wur.nl/uk)

## **RP2: Mutation genetics in the flour moth, *Ephestia kuehniella***

**Supervisor(s):** František Marec

**Host Institution:** Biology Centre CAS

The student will be based at the Institute of Entomology, Biology Centre CAS in České Budějovice, Czech Republic, and registered at the University of South Bohemia in České Budějovice, Czech Republic.

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** Koppert Biological Systems (NL), FAO, Insect Pest Control Laboratory Seibersdorf (A), Wageningen University (NL)

### **Description:**

The Mediterranean flour moth, *Ephestia kuehniella*, had been an early model of developmental genetics in Lepidoptera. Currently, the eggs of this species are used for the production and performance of natural enemies in biological control, but the scales of the adults cause major allergy problems for biocontrol professionals. Considering the importance of mass production of *Ephestia* eggs for breeding parasitoids such as *Trichogramma* and considering possible health hazards for workers in rearing facility, the main objective of the project is to explore the potential of scale mutants of *Ephestia*.

We aim to characterize inheritance and performance of the only available *scaleless* (*Scf*) mutation of *Ephestia* with a unique female-limited expression, and to investigate the genetic and developmental mechanisms of the scaleless phenotype. This includes determining the mechanisms behind the sex-specific expression and the pleiotropic effects on female fecundity and other life history parameters. In addition, we intend to identify candidate genes of the sex determination pathway using bioinformatic tools and methods of molecular genetics and determine their role in the sex-specific expression of the scaleless phenotype. The PhD candidate will also conduct laboratory experiments to identify and isolate new scale mutations using classical genetic approaches, by screening of natural populations and by mutation experiments.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of an international team and independently. The ideal candidate shall have a master degree in molecular biology and genetics, preferably with a good background in bioinformatics and genomics. Candidates from other programs such as entomology, with a strong interest in genetics are also invited to apply. Good skills in statistical data analysis are required. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [marec@entu.cas.cz](mailto:marec@entu.cas.cz)

**Link:** <http://www.entu.cas.cz/en/departments/department-of-molecular-biology-and-genetics/laboratory-of-molecular-cytogenetics/>

**RP3: Promoting adaptability of *Amblyseius swirskii* predatory mites to tomato crop**

**Supervisor:** Alberto Urbaneja & Joel González Cabrera

**Host Institution:** Instituto Valenciano de Investigaciones Agrarias

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** Koppert BS (NL), Bioinsecta (GR), INRA (F) and Vetmeduni Viena (AT)

**Description:**

The use of the predatory mite *Amblyseius swirskii* in horticultural crops is one of the most recent success in biological control. Nowadays, *A. swirskii* is a key player in IPM strategies due to its extremely efficacy for controlling whiteflies and thrips. However, better adapted strains to specific crops are needed. The main goal of this project is to obtain *A. swirskii* strains better adapted to tomato crop, by (1) laboratory selection of *A. swirskii* for better performance on tomato plants, (2) phenotypic characterization of selected strains/colonies assessing their performance as biological control agents, and (3) applying genetic, genomic and biochemical approaches to investigate the mechanisms regulating the adaptation.

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in entomology or ecology, with good background in biological control, molecular entomology, genomics and genetics. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [aurbaneja@ivia.es](mailto:aurbaneja@ivia.es)

**Link:** [www.ivia.es](http://www.ivia.es)

**RP4: Clutch size, sex ratio, and differential mortality in the *Bracon hebetor* / *B. brevicornis* species complex**

**Supervisor(s):** Andra Thiel & Thomas S. Hoffmeister

**Host Institution:** Bremen University

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** University of Wageningen (NL), University of Groningen (NL), AMW Nützlinge (DE)

**Description:**

Probably due to global warming, the European corn borer recently became able to produce two generations per year instead of just one, thereby drastically increasing its destructive potential in some areas. Wasps of the genus *Bracon* are very promising additional biocontrol agents against this important pest. By quantifying and mapping genetic variation for important traits, such as clutch size or sex ratio produced, we will be able to select for the most suitable *Bracon* populations. The main objectives of this project are thus (i) to analyse the natural variation and heritability in the above mentioned traits, (ii) to map the genomic variation for understanding phenotype/genotype links (SNP), to analyse differential developmental mortality using transmission ratio-distorting loci (TRDLs) and (iv) to analyse the trade-offs involved in phenotype expression.

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in natural science, preferably with a good background in entomology, ecology, genetics and/or biological control. Good skills in statistical data analysis (R) are a plus, but training will be provided. The language in the lab is English, and a high standard of spoken and written English is required. Basic knowledge of the German language and a valid driving license will be useful for the fieldwork.

**Contact:** [thiel@uni-bremen.de](mailto:thiel@uni-bremen.de)

**Links:** [www.popecol.uni-bremen.de](http://www.popecol.uni-bremen.de)

## **RP5: Genomic basis of life history traits and reproductive potential**

**Supervisor(s):** Leo Beukeboom & Louis van de Zande

**Host Institution:** University of Groningen

**Duration:** 48 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** FAO (Austria), Koppert Biological Systems (Netherlands)

### **Description:**

Knowledge about the genomic basis of life history traits is fundamental to understand how organisms adapt to their environment. Such knowledge can also be used in breeding programmes to artificially select for specific traits. Although this has been common practice for life stock, it has not been exploited for improving biocontrol agents. Key for this approach is the identification of life history genes and the allelic variation that is present at these loci. In this project, we will investigate the genetic basis of life history traits in the parasitoid wasp *Nasonia vitripennis*, which is a genetic model organism among the Hymenopteran insects.

With the availability of the complete *Nasonia* genome sequence and annotation, the identification of gene-networks underlying specific life history traits has become feasible in this model parasitoid. The focus will be on life history traits that are important for biocontrol, such as longevity, developmental time, fecundity, diapause and host specificity. We will perform genomic and transcriptomic analysis on artificially selected lines for these traits. In addition, we will investigate the effect of ploidy (number of chromosome sets) on life history traits. We have the genetic tools to manipulate the ploidy level of both sexes to study phenotype and gene expression alterations following polyploidization.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in evolutionary biology or genetics, with good background in population genetics, bioinformatics, genomics and computational biology. Candidates from other programs such as entomology, ecology or bioinformatics, with a strong interest in evolution and genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [l.w.beukeboom@rug.nl](mailto:l.w.beukeboom@rug.nl) & [louis.van.de.zande@rug.nl](mailto:louis.van.de.zande@rug.nl)

**Link:** <http://www.rug.nl/research/evolutionary-genetics/>

**RP6: Benefits and risks of using native parasitoids for augmentative biological control of the invasive pest *Halyomorpha halys* in Europe**

**Supervisor(s):** Tim Haye & Dirk Babendreier

**Host Institution:** CAB International ([www.cabi.org](http://www.cabi.org))

The student will be based at the CABI Centre in Delémont, Switzerland, and registered at the University of Bremen in Germany.

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** University of Bremen (DE), University of Groningen (NL), AMW Nützlinge (DE)

**Description:**

The invasive heteropteran pest *Halyomorpha halys* is a rising threat to fruit crops in Europe but control measures are lacking. Native European egg parasitoids have started to adopt the new host *H. halys* and thus, show potential for augmentative biological control. The main objective of the project is to develop an innovative, environmentally safe control strategy such as biological control.

A thorough risk-assessment strategy and subsequent monitoring of the released organisms are key components of modern and environmentally safe biological control procedures. The PhD candidate will conduct laboratory and field experiments to quantify the risk of direct and indirect non-target effects of inundatively released egg parasitoids against *H. halys*. This may include studies on the effects of host preference, acceptance, suitability and parasitoid fitness, the impact of intraguild predation on parasitoid population dynamics and the persistence of biological control agents after release.

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of an international team and independently. The ideal candidate shall have a master degree in natural science, preferably with a good background in biological control, entomology or ecology. Good skills in statistical data analysis are required. Experience with molecular technologies is advantageous. The language in the lab is English. A high standard of spoken and written English is required. German or French language skills are a plus.

**Contact:** [t.haye@cabi.org](mailto:t.haye@cabi.org) and [d.babendreier@cabi.org](mailto:d.babendreier@cabi.org)

**Link:** <http://www.cabi.org/about-cabi/cabi-centres/switzerland/>



## **RP7: Improving pest control efficiency: a modelling approach**

**Supervisor:** Eric Wajnberg

**Host Institution:** INRA Sophia Antipolis, France

The student will be based at the INRA Sophia Antipolis, France, and registered at the University of Nice in France.

**Duration:** 36 months

**Envisaged start date:** August/September 2015

**Planned secondment(s):** FAO (AT), CABI (CH) and IVIA (E)

### **Description:**

Developing a sound biological control effort against noxious pests with beneficial insects requires an accurate identification of the most important biological traits that are involved in their crop protection efficacy, especially when the goal is to improve the efficacy of these beneficial insects through breeding selection programmes. Once these traits are identified, it is important to understand how their genetic variation is maintained in natural populations - or can be maintained in mass-reared artificial systems.

The PhD candidate will: (1) develop a theoretical framework trying to identify what the most important biological features of insect natural enemies are that determine their potential efficacy in biological control programmes, and (2) try to understand the environmental biotic and abiotic conditions under which genetic variation of these traits can be maintained in insect populations.

The theoretical models developed will remain as generic as possible, but – if needed – models will be parameterized for specific biological systems. The modelling framework will be essentially based on Monte Carlo simulations coupled to optimization numeric algorithms (e.g., Genetic Algorithms), and sensibility analyses.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of an international team and independently. The ideal candidate shall have a master degree in population ecology and evolution, with already a sound knowledge in computer sciences, language programming (C, etc.) and statistical data analysis. A high standard of spoken and written English is required. French language skills can be a plus.

**Contact:** [wajnberg@sophia.inra.fr](mailto:wajnberg@sophia.inra.fr)

**Link:** <http://www2.sophia.inra.fr/perso/wajnberg/> and [https://www6.paca.inra.fr/institut-sophia-agrobiotech\\_eng/](https://www6.paca.inra.fr/institut-sophia-agrobiotech_eng/)

## **RP8: Optimization of mass rearing of *Bactrocera oleae* and its parasitoids**

**PhD Supervisor(s):** Kostas Bourtzis<sup>1</sup>, Carlos Caceres<sup>1</sup> & Leo Beukeboom<sup>2</sup>

**Host Institution:** The Food and Agriculture Organization of the United Nations FAO

The PhD student will be based at the Joint FAO/IAEA Insect Pest Control Laboratory, Vienna / Seibersdorf, Austria<sup>1</sup>, and registered for a PhD degree at the University of Groningen in the Netherlands<sup>2</sup>.

**Duration:** 36 months.

This position is initially funded for 3 years, but a fourth year may be available based on the availability of funds.

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** University of Groningen (NL), Koppert Biological Systems (NL), and Instituto Valenciano de Investigaciones Agrarias - IVIA (ES).

### **Description:**

The olive fly *B. oleae* is the primary insect pest for the olive fruit worldwide. Its control is currently based mainly on chemical pesticides raising concerns on resistance, environment, fruit quality, and human health. This project will test the hypothesis that symbiotic bacteria play an important role in the nutrition and the fitness of both the olive fly *Bactrocera oleae* and its parasitoid *Psytalia lounsburyi*. The objective is to determine, characterize and exploit the symbiotic flora in both the olive fly and the parasitoid for optimizing their mass rearing towards large scale AW-IPM applications with a sterile insect technique (SIT) component. Such large scale applications require efficient, high-quality and cost-effective mass rearing of both olive fly and its parasitoid.

### **Qualifications:**

The ideal candidate shall have a master degree (or equivalent) in biology, entomology, microbiology or related experience in molecular biology, rearing insects, microbiological techniques and statistical analysis / bioinformatics methods. The candidate must be academically competitive, self-motivated, and rigorous, with a high standard of spoken and written English and an ability to collaborate in an interdisciplinary team and multi-cultural environment.

**Contact:** Marc Vreysen (M.Vreysen@iaea.org), Kostas Bourtzis (K.Bourtzis@iaea.org) or Carlos Caceres (C.Caceres@iaea.org)

**Link:** <http://www-naweb.iaea.org/nafa/ipc/index.html>

**RP9: Identification and characterization of naturally occurring variation affecting reproductive diapause**

**Supervisor(s):** Christian Schlotterer

**Host Institution:** Institut für Populationsgenetik, Vetmeduni Vienna

**Duration:** 36 months

**Envisaged start date:** 1 July 2015

**Planned secondment(s):** University of Groningen (NL), Wageningen University (NL)

**Description:**

The overwintering strategy differs among species. *D. melanogaster* enters an ovarian reproductive diapause where females have immature ovaries. The parasitoid wasp *Nasonia vitripennis*, on the other hand, enters a larval diapause. The genetic basis of these ecologically extremely important traits is not yet understood. In this project we will use a population genetic approach, which takes advantage of the latest sequencing technology [1, 2] to map the genetic variants contributing to diapause in natural *D. melanogaster* and *Nasonia vitripennis* populations. The position is perfectly suited for candidates, who like to combine state of the art bioinformatic approaches with ecology and functional genetics.

1 Schlotterer, C., *et al.* (2014) Sequencing pools of individuals - mining genome-wide polymorphism data without big funding. *Nature reviews. Genetics* 15, 749-763

2 Bastide, H., *et al.* (2013) A genome-wide, fine-scale map of natural pigmentation variation in *Drosophila melanogaster*. *PLoS genetics* 9, e1003534

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in evolutionary biology or genetics, with good background in population genetics, bioinformatics, genomics and computational biology. Candidates from other programs such as ecology or bioinformatics, with a strong interest in evolution and genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** christian.schlotterer@vetmeduni.ac.at

**Link:** <http://www.vetmeduni.ac.at/en/population-genetics/>

**RP10: Minimizing plant damage through selected *Nesidiocoris tenuis***

**Supervisor:** Alberto Urbaneja & Meritxell Pérez-Hedo

**Host Institution:** Instituto Valenciano de Investigaciones Agrarias

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** Koppert BS (NL), INRA (F) and Vetmeduni Viena (AT)

**Description:**

In the last decade, biological control programs for greenhouse tomatoes and other crops have been successfully implemented using zoophytophagous plant bugs (Miridae), which can feed on both plant tissues and insect prey. Among the different mirid bugs that can be found naturally feeding on tomato plants, the cosmopolitan *Nesidiocoris tenuis* has been extremely effective in controlling the invasive South American tomato pinworm *Tuta absoluta* and the whitefly worldwide, *Bemisia tabaci*. However, *N. tenuis* can damage the plant due to its phytophagy behaviour when prey is scarce. Because plant damage is currently limiting the widespread use of these bugs (Miridae) our aim will be to determine the metabolite cause of this plant damage and through artificial selection produce natural enemy strains that reduce plant damage.

**Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in entomology or ecology, with good background in biological control, molecular entomology, genomics and genetics. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [aurbaneja@ivia.es](mailto:aurbaneja@ivia.es)

**Link:** [www.ivia.es](http://www.ivia.es)

## **RP11: Expanding the range of uses of *Phytoseiulus persimilis***

**Supervisor(s):** Dr. Tom Groot (Koppert Biological Systems), Dr. Markus Knapp (Koppert Biological Systems) & Prof. dr. Marcel Dicke (Wageningen University)

**Host Institution:** Koppert Biological Systems

The PhD student will be based at the Koppert head-office in Berkel en Rodenrijs, the Netherlands, and registered at Wageningen University to enrol in a graduate school with the aim to obtain the PhD degree. The training component will be executed in Wageningen.

**Duration:** 48 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** Wageningen University (NL), Instituto Valenciano de Investigaciones Agrarias (SP), University of Lisbon (PT)

### **Description:**

The predatory mite *Phytoseiulus persimilis* is perhaps the best known example of a predatory mite species used for augmentative biological control. It was the first species to be reared and utilized at a mass-scale, and still is successfully applied to control spider mites around the world. Although *P. persimilis* is a very effective control agent for some species of spider mites on many host plants species, it is ineffective against some other damaging species and/or on some crop species. In addition, the use of *P. persimilis* is limited by its sensitivity to adverse climatic conditions. The main objective of this project is to exploit natural variation to expand the range of uses of *P. persimilis*.

We will use naturally existing genetic variation to select for desirable traits such as tolerance to adverse climatic conditions and unsuitable host plant species, acceptance of certain pest species as prey, and the foraging behaviour. Further improvements will be made by selective breeding. The PhD candidate will collect and maintain genetically variable strains of *P. persimilis* and design bioassays to quantify the relevant phenotypic variation. The candidate will develop a breeding and selection program for certain desirable traits. The performance of the new phenotypes will be compared to the existing commercial strains in (semi-) field tests. Finally, the stability of the new phenotypes in the mass-rearing will be studied.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of an international team and independently. The ideal candidate shall have an MSc degree in Biology or Plant Sciences, with a proven track record in biological control, entomology, ecology and/or population genetics. Excellent practical skills in working with small arthropods and an accurate working mentality are required in addition to an interest in the underlying ecological theory. Experience with working with mites or molecular techniques is advantageous. The language in the lab is English and/or Dutch. Furthermore, the candidate is fluent in English and has excellent communication, scientific writing and presentation skills.

**Contact:** [tgroot@koppert.nl](mailto:tgroot@koppert.nl) and [mknapp@koppert.nl](mailto:mknapp@koppert.nl)

**Link:** <http://www.koppert.com>

## **RP12: Monitoring pre- and post-release diversity in local parasitoid populations**

**Supervisor(s):** Andra Thiel, Thomas S. Hoffmeister & Bernd Wührer

**Host Institution:** Bremen University

**Duration:** 36 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** University of Wageningen (NL), CAB international (CH), AMW Nützlinge (DE) and University of Lisbon (PT)

### **Description:**

The inundative release of large numbers of beneficial insects could possibly not only effect populations of the targeted pest insect, but might also effect populations of other insects in that area (non-target effects). While effects on non-target hosts (e.g. local butterfly populations) are usually considered, effects on local parasitic wasp populations (intraguild-competition) have rarely been studied.

A thorough risk-assessment strategy and subsequent monitoring of the released organisms are key components of modern and environmentally safe biological control procedures. Therefore, in this project, we will monitor genetic variation in natural populations of *Trichogramma* species, tiny parasitoids of butterfly eggs, in cabbage fields across Germany. Monitoring will take place before and after *Trichogramma brassicae* has been released for biocontrol purpose. Laboratory studies on fitness effects of non-target hosts are included. In addition, genetic markers for this wasp will be developed together with ESR1 at Wageningen University. These will allow us to study wasp persistence at the release site and thus, to optimise commercially used *Trichogramma* lines.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in natural science, preferably with a good background in entomology, ecology, genetics and/or biological control. Good skills in statistical data analysis (R) are a plus, but training will be provided. While the language in the lab is English, and a high standard of spoken and written English is required, the field work will bring the candidate in close contact with local farmers, which makes a good knowledge of the German language essential. A valid driving license is required.

**Contact:** [thiel@uni-bremen.de](mailto:thiel@uni-bremen.de)

**Links:** [www.popecol.uni-bremen.de](http://www.popecol.uni-bremen.de) and [www.amwnuetzlinge.de](http://www.amwnuetzlinge.de)

## **RP13: Genome-based selection for the improvement of natural enemies in biocontrol**

**Supervisor(s):** Piter Bijma, Martien Groenen, Bart Pannebakker & Bas Zwaan

**Host Institution:** Wageningen University, Animal Breeding and Genomics Centre and Laboratory of Genetics

**Duration:** 48 months

**Envisaged start date:** 1 May 2015

**Planned secondment(s):** University of Groningen (NL), The Food and Agriculture Organization of the United Nations FAO (AT) and Vetmeduni Vienna (AT).

### **Description:**

Intraspecific genetic variation in arthropods is often studied in the context of evolution and ecology. Such knowledge, can also be very usefully applied for selection of genotypes with optimal trait values to develop more effective biocontrol agents. For complex life-history or behavioural traits that lack easily recordable morphological phenotypes (i.e. longevity, development time, fecundity), the selection process can be laborious. Knowledge of the genomic regions underlying the traits can facilitate the screening and selection process. Genome-based selection (GS) methods use information from genome-wide DNA-markers to efficiently select for such complex traits. While they have been shown to hold great potential for plant and animal breeding, GS methods have not yet been applied for the improvement of natural enemies.

In this project, we will seek proof-of-principle for the use of genome-based selection for key life history and natural enemy traits in the model parasitoid *Nasonia vitripennis*. Genome-based selection techniques will be built that accommodate the haplodiploid nature of parasitoids and other natural enemies. We will generate protocols for insect natural enemies and apply these protocols for the genome-based selection of *Nasonia* lines for complex life-history traits.

### **Qualifications:**

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in evolutionary biology, quantitative genetics or animal breeding, with a good background in population genetics, bioinformatics, genomics or computational biology. Candidates from other programs, with a strong interest in quantitative genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. Insect experimental work will be part of the project. The language in the lab is English. A high standard of spoken and written English is required.

**Contact:** [bart.pannebakker@wur.nl](mailto:bart.pannebakker@wur.nl) or [piter.bijma@wur.nl](mailto:piter.bijma@wur.nl)

### **Link:**

[www.gen.wur.nl/uk](http://www.gen.wur.nl/uk) and <http://www.wageningenur.nl/en/Expertise-Services/Chair-groups/Animal-Sciences/Animal-Breeding-and-Genetics-Group.htm>