Integrative biology: From ecology to molecules

October 19-20
2012

Université Libre de Bruxelles (ULB) & Vrije Universiteit Brussel (VUB)
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Acknowledgements

We thank the Fund for Scientific Research – FNRS for their financial support to the congress.

The Royal Belgian Zoological Society and the Royal Dutch Zoological Society provide the 4 prizes to best presentations for master and PhD students, which will be awarded at the end of the meeting.

Welcome to Brussels

In the heart of Europe, just 1h20 by train from Paris, 1h30 from Amsterdam, and 1h50 from London and Cologne, the city of Brussels offers all the advantages of a capital city and the quality of life of a large and lively town. Located in the city centre, the University campuses and surrounding areas are extremely attractive, providing just the right mix between study and leisure.

Welcome to the Congress

The boundaries between classical biological disciplines such as systematic, development, behavior, ecology, evolutionary biology, cellular biology, genetics and molecular biology are increasingly crossed through the development of trans-disciplinary research projects. This leads to the integration of all levels of biological organization, from the entire biosphere to molecules, which improves our ability to decipher biological complexity. Recent technological breakthroughs in DNA sequencing considerably facilitates our exploration of genomes, which has implications for virtually all areas of biology and contributes to the effort of integrating different biological disciplines. While it has first impacted mostly human genetics and molecular biology, new generation sequencing techniques are gradually reaching most other areas of biology and will probably considerably modify our way of studying natural systems in the future. Undoubtedly, this is an exciting time for biologists.
General conference Information

Conference venue

- from Midi/Zuid Station, 
  Metro 2 or 6 direction Simonis (Elisabeth) to “Louise”, and 
  Tram 94, 
  direction “Musée du Tram/TramMuseum” up to ULB stop.

- from Etterbeek Station, 
  Tram 25, direction “Boondael Gare/Boondaal Station” up to ULB stop.

- from Centrale/Centraal Station, 
  Bus 71, direction “Delta” up to ULB stop.

Registration desk

The congress information and registration desk will be located in the hall of the Sociology building, avenue Jeanne 44 (see map above), on the 1st floor, next to the staircase.

It will be open according to the following schedule:

- Friday, October 19, 2012: 8:30 AM - 10:30 AM and 3:00 PM - 3:30 PM
- Saturday, October 20, 2012: 8:30 AM - 9:30 AM and 10:55 AM - 11:30 AM

Registration fees

<table>
<thead>
<tr>
<th></th>
<th>Early bird</th>
<th>Normal</th>
<th>Late</th>
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<tbody>
<tr>
<td>Master and graduated students</td>
<td>0 eur</td>
<td>0 eur</td>
<td>10 eur</td>
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<tr>
<td>PhD student member</td>
<td>40 eur</td>
<td>50 eur</td>
<td>60 eur</td>
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<tr>
<td>PhD student non-member</td>
<td>60 eur</td>
<td>70 eur</td>
<td>80 eur</td>
</tr>
<tr>
<td>Member (RBZS(^1), RDZS(^2))</td>
<td>60 eur</td>
<td>70 eur</td>
<td>80 eur</td>
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<tr>
<td>Non-member</td>
<td>80 eur</td>
<td>90 eur</td>
<td>100 eur</td>
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</tbody>
</table>

Your registration includes the conference program, coffee breaks, your name tag, the reception of the poster session. Maps of Brussels (including public transport system) and of the ULB campus are available upon request.

Poster mounting

Participants will be able to start affixing their poster on Friday morning, from 8:30.

\(^1\) RBZS=Royal Belgian Zoological Society

\(^2\) RDZS=Royal Dutch Zoological Society
Oral Presentations
Presentations will be possible using a PowerPoint or PDF file. Speakers should load their presentation at least 15 minutes before the session starts (morning before the plenary lecture for those speaking during the first sessions, or during breaks afterwards), in the corresponding session room. Please come with a USB drive on which your presentation file is copied, and introduce yourself to the person in charge of the room computer. To avoid delays, it will not be possible to use your own computer for your presentation.

Coffee breaks – Evening reception
Coffee, tea and cold drinks will be offered during breaks on Friday between 8:30 and 10:00, between 15:00 and 15:30, and on Saturday between 10:55 and 11:30. The Poster Session Reception will start on Friday at 18:00, during which drinks and snacks will be provided.

Scientific & organizing committees
Scientific Committee
Patrick Mardulyn - Université Libre de Bruxelles
Denis Fournier - Université Libre de Bruxelles
Guy Josens - Université Libre de Bruxelles
Marc Kochzius - Vrije Universiteit Brussel
Franky Bossuyt - Vrije Universiteit Brussel
Dominique Adrians - Universiteit Gent
Nico Van Straalen - Vrije Universiteit Amsterdam
Johan Bolhuis - Universiteit Utrecht

Organizing Committee
Université Libre de Bruxelles: P. Mardulyn, D. Fournier, G. Josens, F. Detournay
Vrije Universiteit Brussel: M. Kochzius, F. Bossuyt
Université de Liège: P. Daubry, B. Frederich
Université Catholique de Louvain: E. Le Boulengé
Universiteit Hasselt: T. Artois
Universiteit Gent: D. Adriaens
Universiteit Antwerpen: R. Blust, F. De Vree, Ph. Helsen, H. Leirs, M. Switten, O. Vanderborgh
Katholieke Universiteit Leuven: L. Brendonck, R. Huybrechts
Royal Museum for Central Africa: M. Louette
Royal Belgian Institute of Natural Sciences: I. Schön
Royal Belgian Institute of Natural Sciences: E. Verheyen
Internet access
Internet access on the campus will be available through a Wi-Fi network. If you need internet access, please ask for an access code to the Information desk.

Emergency numbers
Campus phone: 7 (general security on the campus)
European number: 112

Website
http://www.beneluxcongress.com/

Best presentation awards
Prizes for best presentation will be awarded to students at the end of the congress. Four awards, worth 250 € each, are provided by the Royal Belgian Zoological Society and the Royal Dutch Zoological Society:

› Best oral presentation for master students
› Best poster presentation for master students
› Best oral presentation for PhD students
› Best poster presentation for PhD students

A panel of referees will evaluate all contributions competing for these prizes, based on scientific quality and relevance, and presentation skills. The winners will be made public during the closing ceremony on Saturday.
### Daily Event schedule

#### Friday 19 October

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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</thead>
<tbody>
<tr>
<td>8:30 - 10:00</td>
<td>Registration - Poster mounting - Coffee</td>
</tr>
<tr>
<td>10:00 - 10:10</td>
<td>Opening remarks and welcoming address</td>
</tr>
<tr>
<td>10:10 - 11:00</td>
<td>Plenary lecture I: “Next generation sequencing in non-model organisms: applications for conservation genomics” by Robert Ekblom (Dupréel Room)</td>
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<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>11:05 - 11:20</td>
<td>N. Konijnendijk**</td>
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<tr>
<td>11:20 - 11:35</td>
<td>J. Delroisse**</td>
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<tr>
<td>11:35 - 11:50</td>
<td>P. Klenren</td>
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<tr>
<td>11:50 - 12:05</td>
<td>D. Michez</td>
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<tr>
<td>12:05 - 12:20</td>
<td>S. Edwards**</td>
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<tr>
<td>12:20 - 13:30</td>
<td>Lunch</td>
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<tr>
<td>13:30 - 13:45</td>
<td>S. de Gelder**</td>
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<tr>
<td>13:45 - 14:00</td>
<td>S. Gombeer**</td>
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<tr>
<td>14:00 - 14:15</td>
<td>N. Tonne*</td>
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<tr>
<td>14:15 - 14:30</td>
<td>E. Langen*</td>
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<td>14:30 - 14:45</td>
<td>N. Wauters**</td>
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<td>14:45 - 15:00</td>
<td>J. Mergeay</td>
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<tr>
<th>Time</th>
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<tbody>
<tr>
<td>15:00 - 15:30</td>
<td>Coffee break</td>
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<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>15:30 - 15:45</td>
<td>F. Huyghe*</td>
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<tr>
<td>15:45 - 16:00</td>
<td>Q. Jossart**</td>
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<td>16:00 - 16:15</td>
<td>H.A. Ratsimbazafy*</td>
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<tr>
<td>16:15 - 16:30</td>
<td>I. Schöhn</td>
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<tr>
<td>16:30 - 16:45</td>
<td>F. Mayer**</td>
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<tr>
<td>16:45 - 17:00</td>
<td>S. Dellicour**</td>
</tr>
<tr>
<td>17:15 - 18:05</td>
<td>Plenary lecture II: “Evolution in Darwin's Dreamponds: The adaptive radiations of cichlid fishes in East Africa” by Walter Salzburger (Dupréel Room)</td>
</tr>
<tr>
<td>18:05 - 20:00</td>
<td>Poster session - Reception</td>
</tr>
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### Saturday 20 October

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>9:00 - 9:50</td>
<td>Plenary lecture III: “The DNA metabarcoding, a new insight into studies of animal diet” by Eric Coissac (Dupréel room)</td>
</tr>
<tr>
<td>9:55 - 10:10</td>
<td>Behavioural ecology (Dupréel)</td>
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<tr>
<td>10:10 - 10:25</td>
<td>Functional ecology and Morphology (Baugniet)</td>
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<tr>
<td>10:25 - 10:40</td>
<td>Behavioural ecology (Dupréel)</td>
</tr>
<tr>
<td>10:40 - 10:55</td>
<td>Functional ecology and Morphology (Baugniet)</td>
</tr>
<tr>
<td>10:55 - 11:30</td>
<td>Coffee Break</td>
</tr>
<tr>
<td>11:30 - 11:45</td>
<td>Behavioural ecology (Dupréel)</td>
</tr>
<tr>
<td>11:45 - 12:00</td>
<td>Functional ecology and Morphology (Baugniet)</td>
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<tr>
<td>12:00 - 12:15</td>
<td>Behavioural ecology (Dupréel)</td>
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<td>12:45 - 14:00</td>
<td>Functional ecology and Morphology (Baugniet)</td>
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<tr>
<td>14:00 - 14:15</td>
<td>Behavioural ecology (Dupréel)</td>
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<tr>
<td>14:15 - 14:30</td>
<td>Functional ecology and Morphology (Baugniet)</td>
</tr>
<tr>
<td>14:30 - 15:20</td>
<td>Systematics (Baugniet)</td>
</tr>
<tr>
<td>15:20 - 16:10</td>
<td>Plenary lecture IV: “Escaping the Mouse Trap: Comparative Genomics and Evo-Devo in New Model Amniotes” by Michel Milinkovitch (Dupréel room)</td>
</tr>
<tr>
<td>16:10 - 16:30</td>
<td>Awards and closing session</td>
</tr>
</tbody>
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* competing for a Msc student award
**competing for a PhD student award
### Scientific Program

#### Oral Presentations

**Friday 19 October**

#### Session 1: Evolution

(Dupréel room): Chair: N. Van Straalen

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
</table>

#### Session 2: Ecology

(Baugniet room): Chair: P. Mardulyn

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:05 - 11:20</td>
<td>Stable isotope analysis: from individual diet determination to complex food web disentanglement</td>
<td><em>Jacquemin J</em>**, Delsinne T, Roisin Y, Leponce M.*</td>
</tr>
</tbody>
</table>
*Kieffer D*, George I, Bosire JO, Cannicci S, Dahdouh-Guebas F.  
p. 23

11:50 - 12:05  Metal exposure and accumulation patterns in free-range cows (*Bos taurus*) in a contaminated natural area: influence of spatial and social behavior  
*Roggeman S**, van den Brink N, Van Praet N, Blust R, Bervoets L.  
p. 24

12:05 - 12:20  How annoying dirt can be - a coral immunity perspective.  
p. 25

Session 3: Conservation biology

(Dupréel room): Chair: P. Klaren

*de Gelder S**, Lock E-J, Klaren PHM, Olsvik P, Lundebye A-K, Berntssen MHG.  
p. 26

13:45 - 14:00  Using molecular barcodes in the development of a tool to screen environmental samples for the presence of biomonitoring taxa.  
*Gombeer S***, Bervoets L, Knapen D  
p. 27

14:00 - 14:15  Change detection as a basis to estimate loss or gain of suitability of landscape features of high biological value in Greece.  
*Tonné N*, Merken R, Teunen J, Koeda N.  
p. 28

14:15 - 14:30  Nesting sea turtle populations in Suriname: threats and conservation.  
*Langen E*, Stolwijk R.  
p. 29

14:30 – 14:45  Invasion of the tropical fire ant *Solenopsis geminata* in the Galápagos Archipelago: population genetic structure, dispersal strategies and range expansion.  
*Wauters N***, Martin M, Dekoninck W, Fournier D.  
p. 30

14:45 - 15:00  The importance of being first: persistent priority effects within and among species, across space and time.  
*Mergeay J*, Declerck S, De Meester L.  
p. 31
Session 4: Behaviour

(Baugniet room): Chair: M-J. Duchateau

*van Leeuwen K L, Koops K, Sterck EHM, Matsuzawa T.*  
p. 32

13:45 - 14:00  Spatio-temporal distribution and behaviour of three common seabird species in Laganas gulf and Argassi (SE Zakynthos, Ionian Sea, Western Greece).  
*Drechsel F*, *Karris G, Kokkali A, Voulgaris M-D, Poulicek M.*  
p. 33

14:00 - 14:15  Preference hierarchy in the Madagascar hissing cockroach *Gromphadorhina portentosa*: conflict between social and environmental choices.  
*Crabeels A*, *Deneubourg J-L, Sempo G.*  
p. 34

14:15 - 14:30  Collective fleeing of a gregarious insect.  
*Laurent M-O, Deneubourg J-L, Sempo G.*  
p. 35

14:30 - 14:45  Short-term evolution of *Viola odorata* seed harvesting by the red ant *Myrmica rubra*.  
*Bologna A*, *Detrain C.*  
p. 36

14:45 - 15:00  Dispersal, aggregation and Allee effects in the foraging behavior of *Ips typographus*  
*Louis M**, *Grégoire JC.*  
p. 37

Session 5: Population genetics and Phylogeography

(Dupréel room): Chair: T. Backeljau

15:30 - 15:45  Connectivity of *Amphiprion akallopisos* (Skunk Clown Fish) in the Indian Ocean.  
*Huyghe F*, *Kochzius M.*  
p. 38

15:45 - 16:00  Weak differentiation according to host species and small spatial scale in a parasite crab.  
*Jossart Q**, *David B, De Bruyn C, De Ridder C, Rigaud, Wattier R.*  
p. 39
16:00 - 16:15  Genetic population structure and connectivity of the mud creeper *Terebralia palustris* (Linnaeus, 1767) in Kenya, Tanzania and Madagascar.
*Ratsimbazafy HA*, Kochzius M.
p. 40

16:15 - 16:30  Integrative analyses of valve outlines and molecular DNA sequence in *Eucypris virens* (Crustacea, Ostracoda)
*Schön I*, Koenders A, Halse S, Martens K.
p. 41

16:30 - 16:45  Comparative phylogeography of two forest pests: do *Ips typographus* and *Dendroctonus micans* share same patterns?
*Mayer F***, Piel F, Cassel-Lundhagen A, Mardulyn P, Grégoire J-C.
p. 42

16:45 - 17:00  Study of a range expansion using a geographical model of coalescence.
*Dellicour S***, Vereecken NJ, Hardy, OJ, Mardulyn P.
p. 43

Saturday 20 October

Session 6: Behavioural ecology

(Dupréel room): Chair: M. Kochzius

9:55 - 10:10  Territory pattern of male Dickerson’s collared lizard, *Crotaphytus dickersonae*.
*Faber L*†, Plasman M., Duchateau MJHM.
p. 44

10:10 - 10:25  Male courtship pheromones control female mating responses in salamanders.
*Treer D***, Van Bocxlaer I, Matthijs S, Du Four D, Janssenswillen S, Willaert B, Bossuyt F.
p. 45

10:25 - 10:40  The ability to recognize diseased host by smell; Symbiotic harlequin crabs chemically detect and avoid their sea cucumber hosts when they suffer from skin ulceration disease
*Caulier G***, Flammang P, Gerbaux P, Eeckhaut I.
p. 46

*Chacón DA*†, Snijders L, van Roij E, Naguib N, van Oers K.
p. 47
<table>
<thead>
<tr>
<th>Time</th>
<th>Topic</th>
<th>Authors</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:45 - 12:00</td>
<td>Genetically mediated division of labor in the polyandrous desert ant <em>Cataglyphis cursor.</em></td>
<td><em>Eyer PA</em>*, Aron S.*</td>
<td>49</td>
</tr>
<tr>
<td>12:00 - 12:15</td>
<td>The honeybee queen egg marking pheromone- a peptide?</td>
<td><em>Ernst U</em>*, Cardoen D, Wenseleers T, Verleyen P, Schoof L.</td>
<td>50</td>
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</table>

**Session 7: Functional ecology and Morphology**

(Baugniet room): Chair: D. Adriaens

<table>
<thead>
<tr>
<th>Time</th>
<th>Topic</th>
<th>Authors</th>
<th>Pages</th>
</tr>
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<tbody>
<tr>
<td>10:25 - 10:40</td>
<td>The mechanics of steady bipedal running in lizards: how do they keep their front limbs off the ground?</td>
<td><em>van Wassenbergh S, Aerts P.</em></td>
<td>54</td>
</tr>
<tr>
<td>11:30 - 11:45</td>
<td>Structure and function of the median finfold in larval teleosts.</td>
<td><em>Osse JWM, van den Boogaart JGM, Muller M.</em></td>
<td>56</td>
</tr>
<tr>
<td>11:45 - 12:00</td>
<td>Influence of large stag beetle mandibles on cost of transport and stability.</td>
<td><em>Goyens J, Dirckx J, Aerts P.</em></td>
<td>57</td>
</tr>
<tr>
<td>12:00 - 12:15</td>
<td>Choose your weapon; defensive performance in scorpions.</td>
<td><em>van der Meiijen A, Coelho P, Herrel A, Sousa P.</em></td>
<td>58</td>
</tr>
</tbody>
</table>
12:15 - 12:30  Identification of potential epithelial stem cells responsible for continuous tooth replacement in the African Bichir (*Polypteryx senegalus*), a basal Osteichthyan.
*De Clercq A*, Vandenplas S, Huysseune A.

12:30 - 12:45  Molecular markers in continuous tooth replacement in the zebrafish.
*Brunee B**, Vandenplas S, Huysseune A.

**Session 8: Systematics**

(Baugniet room): Chair: K. Jordaens

14:00 - 14:15  Assisted Identification Tool for Bumble Bee species based on Wing Shape.
*De Meulemeester T*, Michez D, Biesmeijer K.

14:15 - 14:30  Integrating DNA Barcoding in Taxonomic Practice: Experience from a Joint Initiative of Two Natural History Museums.
*Sonet G*, Jordaens K, Nagy ZT, Breman FC, Backeljau T, De Meyer M.
Poster Presentations

Friday 19 October

Poster session

18:00 - 20:00

1. Towards a molecular database for the identification of forensically important Diptera. 
   Jordaens K, Sonet G, Bourguignon L, Braet Y, Dupont E, Desmyter S. (p. 63)

2. Biological objects recognition: Artificial Neural Networks Identification: mayor step towards integrative taxonomy. 
   Vanhara J, Bocakova M, Fedor P, Janisova K, Peña Mendéz EM, Dvorakova-Murarikova N, Havel J.v (p. 64)

3. Two new species of the family Pterygosomatidae (Acari: Trombidiformes) 
   Moradi M.* (p. 65)

4. Effect of enrichment and cage size on growth in young rehabilitated hedgehogs (Erinaceus europaeus) 
   Vervaecke H, De Vriendt K, Laevens H. (p. 66)

5. Anthropogenic stressors on Moroccan temporary wetlands: how can we promote their sustainable use and conservation? 
   Van den Broeck M**, Waterkeyn A, Rhazi L, Brendonck L. (p. 67)

6. Chemical induction experiments in two crustacean-echinoderm model symbioses. 
   Caulier G**, Flammang P, Eeckhaut I. (p. 68)

   De Groot E, Briels N, Stevens JMG. (p. 69)

8. Study of Female’s Searching Behavior of Ectomyelois ceratoniae (Lep.:Pyralidae) to Volatiles of Pomegranate Fruits. 
   Najarpoor A*, Goldansaz SH, Ghajariyeh H, Zarabi M. (p. 70)

9. Experimental exposure to masking noise does not affect song structure and singing activity in grey-breasted wood-wrens. 
   Parson T*, Burbidge T, Slabbekoorn H. (p. 71)

10. Sleeping site selection of proboscis monkeys, Nasalis larvatus, along the Kinabatangan river, in Sabah, Malaysia. 
    Thiry V*, Vercauteren M, Stark D, Goossens B. (p. 72)

11. Study of Cuvierian tubule adhesion in the sea cucumber Holothuria forskali. 
    Demeulder M**, Wattiez R, Becker P, Hennebert E, Flammang P. (p. 73)

    Bil M, Nagaba Y, Huybrechts R. (p. 74)

    Rakotoarisoa P**, Tsiresy G, Eeckhaut I, Lavitra T. (p. 75)

14. Tissue- and species- specific accumulation of trace metals in two land snails (Gastropoda, Pulmonata). 
    Boshoff MC**, Bervoets L, Jordaens K. (p. 76)
15. Genome mining in the springtail *Folsomia candida* and its gut microbial community.  
**Agamennone V**, Suring W, Roling W, Brouwer B, van Straalen NM, Roelofs D. (p. 77)

16. Low Genetic Diversity in Tepui Summit Vertebrates.  

17. Characterization of innate immunogenes of the cichlid *Oreochromis niloticus*.  
**Deruyck B**, Hablützel PI, Volckaert FAM, Raeymaekers JAM. (p. 79)

18. Eco-evolutionary dynamics of antipredator defenses in temporally variable environments: An evolving metacommunity perspective.  
**Frey H***, Waterkeyn A, de Meester L, Brendonck L. (p. 80)

**Kastally C***, Dellicour S, Mardulyn P. (p. 81)

**Hui M***, Nuryanto A, Kochzius M. (p. 82)

21. Molecular and morphological evidence for several species within the cosmopolitan eurybathic deep-sea lysianassoid amphipod *Eurythenes gryllus sensu lato*.  

22. Evolution of softbodiedness and phylogeny of Cleroidea (Coleoptera).  
**Bocakova M**. (p. 84)

**Dohet L***, Fraser C, Grégoire J-C. (p. 85)

24. Identifying immune-linked cytokines in locust species Locusta migratoria and Schistocerca gregaria.  
**Duressa TF**, Huybrechts R. (p. 86)

25. Planktonic dispersal suggests a homogeneous genetic structure over large geographic scale. Is it mandatory?  
**Fourdrilis S****, Backeljau T. (p. 87)

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Co-adaptation versus immune competence and parasite virulence in the *Gasterosteus* – *Gyrodactylus* host-parasite system

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Local adaptation to parasites is one of the possible drivers of divergence among populations. If there is high host specificity, it is expected that parasites in their turn will adapt to their host, which can lead to local co-evolution. Examples of such reciprocal interactions are known, but whether this is a common phenomena in nature has yet to be determined. Several studies have shown that host populations often have differential infection rates when infected with the same strain of parasites, which is frequently interpreted as evidence for local co-adaptation among host and parasite. This is however not necessarily the case, alternatively local differences in infection rates might be an effect of differential immune competence among host populations or differential virulence among parasite populations. In the *Gasterosteus aculeatus* and its host specific parasite *Gyrodactylus gasterosteii* differential infection rates have been repeatedly found, but co-adaptation has not been tested yet. In this study we use a full factorial design of two populations of threespine sticklebacks and their respective co-occurring ecto-parasite *G. gasterosteii* to disentangle these three possible explanations for the differential immune resistance among host populations previously found. F1 lab bred fish originating from two populations were infected with parasites from sympatric and allopatric origin. In a 6 weeks period parasite numbers per individual were monitored. We found differences in infection rate between populations. Infections with parasites from allopatric and sympatric origin yielded the same results suggesting differential immune competence of the host rather than differential virulence among parasites or local co-adaptation.
Perceiving light without eyes - an echinoderm case

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Using new transcriptomic data, we targeted photoreception actors in Amphiura filiformis, a small burrowing brittlestar commonly found in muddy environments of the south coast of Sweden. Opsin-like sequences of Strongylocentrotus purpuratus (GPCR sequences closely related to opsins) were used for homology search in the transcriptomic database. We found 13 opsins-like sequences in A. filiformis. In silico analyses on these new sequences allowed us to pinpoint two putative visual opsins, one melanopsin-like protein and one rhodopsin-like protein. Moreover, in silico translation and sequence alignments permitted to localize the specific amino acids involved in retinal fixation in the rhodospin-like sequence. Additionally, the sequence of the eye morphogene Pax6 was also retrieved from the database. Specific primers were designed for all these sequences (opsins and pax 6) in order to study their mRNA expression in the tissues of A. filiformis by a qPCR method. Finally, immunodetection of the protein Pax6 was done on arm sections. Anti-Pax6 immunolabelling was observed in some cells from the spines and from the tube feet.
Ancient origin of thyroid hormone deiodinases

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Thyroid hormones are involved in development and metamorphosis of many animal groups. The vertebrate thyroid gland mainly secretes T4 that is metabolized by enzymatic outer ring deiodination (ORD) to yield the active hormone T3. Iodothyronine deiodinases are selenoenzymes that catalyse deiodination of thyroid hormones. Deiodinases regulate the intracellular availability of T3, and are therefore important determinants of thyroid hormone bioactivity. We were inspired by reports on the presence of deiodinase cDNA in a tunicate, and ORD activities in the crustacean brine shrimp genus Artemia [1]. Moreover, exogenous T4 accelerates metamorphosis in several different invertebrate phyla [2].

We have analysed deiodinase sequences in published genomes, and biochemically characterised ORD in Artemia. EST libraries were searched for conserved regions. Secondary structures of selenocysteine insertion sequence (SECIS) elements in the 3′-untranslated mRNA region (3′-UTR) that are crucial in the synthesis of deiodinases were predicted using the SECISearch software.

In addition to the known vertebrate and tunicate deiodinases we obtained 15 novel sequences from five invertebrate (sub)phyla/classes and even a choanoflagellate. Eight sequences contained a 3′-UTR SECIS element, and can thus qualify as a bona fide deiodinase. The thyrostatics propylthiouracil (PTU) and methimazole (MMI, both at 3 mM) inhibited hatching of dormant Artemia cysts and delayed larval development. Nauplius larvae displayed T4-ORD activity that was inhibited by 5 mM dithiothreitol and 10 µM PTU in vitro, and up-regulated by exposure to 10 nM T4 in vivo. T4 and T3 concentrations in cysts were higher than those in larvae. Surprisingly, neither PCR using an extensive set of primers nor gel electrophoresis/autoradiography using a specific BrAc-125I-T4 probe detected Artemia deiodinase mRNA or protein.

We conclude that deiodinases are primitive, early components of the thyroid system.

Do chemicals of pollen constrain the evolution of host-plant interactions in specialist bees?

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Although pollen foraging behavior of bees seems highly inherited in range and specificity, some rare “host-plant shifts” occurred during evolution inside clades of specialist species (i.e. oligolectic species). Selection of novel host plant seems mainly driven by morphological or phylogenetical similarities with ancestral host-plant but some host switches to unrelated plant families also occur. The origin and the constrain of these particular host-plant shifts remain misunderstood while the understanding of these mechanisms are essential to evaluate the capability of bees to colonize new host plants during evolution. Because the proportions of nutrients (e.g. proteins, lipids and amino acids) can vary widely among interspecific pollens, specialisation in a new host plant could be constrained by the chemical composition of its pollen, reducing the range of suitable alternative hosts. We studied herein protein content, total amino acids and sterols of host plant species of two groups of three sister species of solitary bees: the Colletes succinctus group (Colletes halophilus, C. hederae and C. succinctus) and the Melitta leporina group (Melitta leporina, M. nigricans and M. tricincta). The results show that chemical compositions of host plant pollen are quite similar in protein and sterol, corroborating the hypothesis that host plant specialisation and evolutionary shifts could partly be constrained by chemical composition of pollen.
Convergent evolution associated with substrate decouples phenotype from phylogeny in the southern African lacertid lizards (Eremiainae, Lacertidae)

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Convergent evolution can explain similarities in morphology between species, due to strong selection on a fitness-enhancing phenotype in response to local environmental conditions. Previous work has revealed how morphological convergence exists between ecotypes, with morphology being directly related to microhabitat usage, some well-known examples of which include cichlids, finches and anoline lizards. Southern Africa possesses a high diversity and endemism of reptile taxa. The southern African landscape is varied in terms of habitat, with many lizard species inhabiting a particular micro habitat (e.g. rock, compact sand, loose sand, grass, trees). Within the African radiation of lacertid lizards, species range from strictly rupicolous to strictly psammophillic, whilst others are generalists in terms of habitat choice. We hypothesised that in the African radiation of lacertid lizards (Eremiainae) overall body and limb morphology would be independent of phylogeny, but dependent on openness of habitat. To test this hypothesis Bayesian inference and maximum likelihood methods were used to examine evolutionary relationships for 17 species from all 5 Eremiainae genera using two mitochondrial (16S and ND4) and two nuclear (RAG1 and KIAA-2018) markers. Principal component analysis and clustering analysis on size-corrected linear measurements of body, head and limbs were conducted to examine congruence between evolutionary relationships and morphology. Our phylogenetic analysis reveals taxonomic mis-assignments of species within Australolacerta and Ichnotropis. However, morphological analyses indicate that the mis-assigned species are convergent in body features: species utilising cluttered habitats exhibited more slender bodies and shorter limbs compared to the stockier bodies and longer limbs of the species occupying more open habitat. We attribute this to convergence as a result of adaptation to substrate types, and we conclude that in the Eremiainae, similarity in body plan is not always congruent with shared ancestry, but in all cases it is coupled to habitat usage.
A fundamental goal in ecological studies is to understand the mechanisms that structure ecosystems, including trophic relationships. Ants play an essential role in terrestrial food webs but the variety of their diets and the difficulty of direct field observations complicates the study of their feeding habits.

Here, we illustrate the interest of stable isotope analyses at two distinct levels: first, at the individual level of a rare ant genus (*Tatuidris*) with previously unknown trophic habits, and second, at the global level of a leaf-litter food web.

Stable isotope analysis (i.e. the measurement of the heavy to light isotope ratio) is a powerful tool for determining the trophic position of an organism. Due to the concentration of heavier isotopes in consumer tissues during metabolic processes, the nitrogen isotopic signature ($^{15}\text{N}/^{14}\text{N}$) of a consumer is typically enriched by ~3.4‰ relative to its diet. Hence, the higher the position of an animal in the trophic chain, the higher its N isotopic signature. In contrast, carbon isotopes are little fractionated through trophic chains and their signature ($^{14}\text{C}/^{13}\text{C}$) can be used to determine the ultimate sources of carbon of an organism.

While feeding experiments on live *Tatuidris cf. tatusia* did not provide any information on their food preference, the N isotope analysis suggested that they are a top predator in the leaf-litter food web. The inclusion of other ants and various mesofauna taxa in a C and N isotope analysis revealed the existence of 4 trophic levels and the omnivory of several ant species (reflected by the intraspecific variability of their isotopic signatures).

Stable isotope analysis allows determining the trophic position of any organism, and is especially useful for small organisms with cryptic live habits. Other methods that will be discussed (e.g. gut content analysis) allow an even finer diet determination.
Mercury and stable carbon and nitrogen isotopes in the harbour seal (*Phoca vitulina*) from the Wadden Sea

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Due to its top position in the trophic network, its long life span and its low rate of pollutant elimination, the harbour seal (*Phoca vitulina*) can accumulate high levels of chemicals, as mercury. Total mercury concentrations ([THg]) were determined by atomic absorption spectrometry in whole blood of 79 wild harbour seals captured (and then released) between 2006 and 2012 in the German Wadden Sea of Schleswig-Holstein. In 2012, for the first time, [THg] were measured in 20 samples of hair. Stable carbon and nitrogen ratios (δ¹³C and δ¹⁵N) were also determined by mass spectrometry in 57 samples of red blood cells and in whole blood of 50 seals. δ¹³C and δ¹⁵N mean values were -16.8‰ and 18.5‰ respectively in whole blood and -17.2‰ and 18.4‰ respectively in red blood cells. δ¹⁵N mean value was significantly higher than that recorded in grey seals (*Halichoerus grypus*) from Scotland (14.1‰ in red blood cells; Habran, 2012). [THg] mean values in whole blood and hair of harbour seals were 0.27 µg.g⁻¹ wet weight and 14.8 µg.g⁻¹ dry weight respectively (between 2 and 3 times higher than the values recorded in hair and blood for grey seals from Scotland, Habran *et al.*, in press). Nevertheless, [THg] depended on several factors including δ¹⁵N values, age group and body mass. These results suggest that blood and hair are interesting substrates for mercury long-term monitoring of the harbour seal in the Wadden Sea.

Habran S., Pomeroy P., Debier C., Das, K. (in press) “Changes in trace elements during lactation in a marine top predator, the grey seal” Aquatic Toxicology.

Evaluating the impact on *Uca annulipes* (Milne Edwards, 1837) fiddler crabs on the structure of microbial communities in mangrove soils – a study in the mangrove swamp of Gazi, Kenya

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The fiddler crabs of the genus *Uca* are known to be an important component of the macrobenthos of mangrove forests. One central role already attributed to these crabs is the bioturbation activity by digging burrows, through which the crabs oxygenate the hypoxic or anoxic mangrove soil, positively affecting the vegetation. The aim of this study is to analyse mangrove sediment samples in order to focus on a second hypothetical role for these mangrove crabs: the stimulation of primary production (micro-algae, mostly diatoms and cyanobacteria) and of the activity of microbial communities through feeding behaviour and possibly a “gardening behaviour”. The latter is defined as a feeding behaviour that considers the amount and turnover of micro-algae. The crabs are producing so-called feeding pellets after filtration of the sediment and ingestion of organic matter. Comparison of these pellets and untreated sediment in terms of algal and bacterial abundance and diversity as well as chlorophyll a content should provide useful information. Sediment samples were collected on an open sandy space within the mangrove forest of Gazi, Kenya during low water of spring tide. Chlorophyll a content was measured in Kenya and this preliminary analysis revealed that crab activity and burrow density strongly influence it, but also that there is no significant difference between feeding pellets and untreated sediment. Further work will be realised in order to analyse the microbial and micro-algal taxonomic composition and their absolute abundance in the two types of sediment sampled under different conditions.
Metal exposure and accumulation patterns in free-range cows 
(Bos taurus) in a contaminated natural area: 
influence of spatial and social behavior

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Possible effects of spatial metal distribution, seasonal-, ecological- and ethological parameters, on the metal exposure of cows were investigated. Therefore the habitat use, vegetation selection and foraging behavior of two free ranging Galloway herds in a metal polluted nature reserve were observed. Metal concentrations in soil, vegetation, hair, blood and feces were measured. Although both herds lived in the same reserve, their metal exposure differed significantly. A high consumption of soft rush by herd 1 during winter for instance was responsible for a large increase in daily Cd intake. The results of this study suggest that the exposure and health risks of large grazers can probably not only be predicted by a general monitoring of soil and vegetation pollution. Also detailed information about the occurring vegetation types, spatial habitat use together with the social- and foraging behavior and diet selection of the species need to be studied.
How annoying dirt can be – a coral immunity perspective


Coral disease prevalence and diversity are increasingly affecting tropical corals worldwide, and these increases are in part due to the influence of various environmental and anthropogenic factors (e.g. temperature, seawater eutrophication). These factors have been shown to promote both coral disease prevalence and pathogen virulence. A recent study highlighted that land runoff and its associated effects (e.g. increased particulate organic matter (POC), lowered salinity) could also play a role as promoters of coral disease. Sediments associated with terrestrial runoff and seabed sediment resuspension can affect scleractinian corals through several mechanisms including increases in POC, dissolved inorganic nutrients, sedimentation and light reduction. Sediment deposits on corals have also been suggested to act as a reservoir of coral pathogens and can lead to coral tissue necrosis. Though sediments deposited on corals can generally be removed through mucus production and ciliary beating, such actions increase metabolic costs and could impact on the coral’s immune potential and health, making it more susceptible to infections. In order to explore the effects of sediment deposition on coral health and immunity, fragments of Montipora patula were inoculated with marine sediments under controlled conditions. The effects of this inoculation were assayed through the monitoring of several coral health and immunity proxies (e.g. phenoloxidase activity, presence of melanin deposits, lipid ratios).
Specific disruption of the thyroid axis in Atlantic salmon (Salmo salar) by Persistent Organic Pollutants

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Lipophilic persistent organic pollutants (POPs) can readily bioaccumulate in aquatic ecosystems and are often potent endocrine disruptors. We investigated the endocrine disrupting effects of the chlorinated insecticide toxaphene and the brominated flame retardant α-hexabromocyclododecane (HBCD) by measuring multiple parameters of an endocrine axis. We have fed toxaphene and HBCD to Atlantic salmon (Salmo salar) and measured different components of the thyroid system: TSH-β expression, the plasma concentrations of total and free T₄ and T₃, hepatic deiodinase (Dio1, Dio2) expression and hepatic T₄ outer-ring deiodination.

Salmon fed a low dose of toxaphene (0.005 mg/kg) had significant higher total T₄ plasma levels compared to controls. A correlation showed that total T₄ plasma levels were increased in fish fed intermediate (0.05 mg/kg) and high doses (0.5 mg/kg), probably to maintain similar free T₄ plasma levels. Fish fed intermediate and high doses had 25 percent lower total and free T₃ plasma levels that strongly correlated (R²=0.66, P<0.0001). Moreover, hepatic gene transcription of Dio1 decreased while the hepatic enzymatic T₄-ORD activity dose-dependently increased.

Exposure to HBCD for up to 2 months did not result in changes in plasma thyroid hormone levels and pituitary TSH- β expression. Depuration for three months with an unspiked diet decreased total T₄ by 50 percent while the ratios of the total and free fraction of plasma T₄ and T₃ had not altered between the exposed and control fish. Exposure to dietary HBCD resulted in a significantly increased transcription of both Dio2 and Dio3 genes in liver compared to control. Additionally, the hepatic T₄-ORD activity had significantly increased.

We conclude that both POPs mainly affect the peripheral thyroid system at different targets. Toxaphene affects thyroid hormone levels, probably by increasing conjugation pathways and deiodination activity. HBCD acts intracellularly by increasing deiodinase expression and activity.
Using molecular barcodes in the development of a tool to screen environmental samples for the presence of biomonitoring taxa

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Macro invertebrates are frequently used for the biomonitoring of freshwater quality. Identifications of the taxa used for index calculations are often limited to the genus or family level due to a lack of time, funding and/or taxonomic expertise. In the present study the potential offered by a molecular approach to develop a biomonitoring-tool for the automated detection of macroinvertebrate families in mixed samples is evaluated using the order of the caddisflies (Trichoptera; Insecta) as case-study organisms.

A database with accurate species level identifications linked to species specific sequences for three molecular markers (the mitochondrial cytochrome c oxidase I gene, the nuclear wingless gene and a fragment of 18S) was used to design family specific primer-sets for a real-time PCR (QPCR) assay. Single-target experiments were conducted to (1) test the specificity of the designed primers, (2) detect species that could possibly cause false positives and false negatives signals, and (3) identify reference species for each primer-set to be used as standard in mixed sample analyses. The results were used to develop a ΔCt-based method and to build decision trees which allowed to interpret the QPCR output of mixed samples. Next, the sensitivity of the assay was determined by detection limit experiments and a protocol for complex environmental samples was established. Finally, the developed QPCR assay was validated using fresh field samples containing a mixture of Trichoptera families and non-trichopteran freshwater invertebrates.
Change detection as a basis to estimate loss or gain of suitability of landscape features of high biological value in Greece

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Agricultural landscapes provide crucial biotopes for farmland-related wildlife, while wetlands sustain migrating waterbirds along their migration route. Current land use changes are driving biodiversity losses within Mediterranean ecosystems. Amongst those drivers agriculture land use changes also determine the future of biodiversity, even in areas considered well preserved by remoteness or legal status (LIFE, 2010).

By manual classification of old (1960) and recent (2003 or 2009) remotely sensed imagery, we quantified land cover changes in two different Greek landscapes: a Natura 2000 coastal lagoon and an unprotected heterogeneous agricultural landscape.

The agricultural landscape is still going through a series of profound modifications started since at least 1960. In this remote mountainous area extensive grazing land decreased at the cost of intensive cropland. Further, loss of hedgerows and scattered trees considerably changed the landscape structure. Populations of bird and herpetofaunal species (Birds and Habitats Directive species and non-listed species) may have been affected by these landscape changes in various ways depending on their relation to the structural elements, such as we established.

A thoroughly studied Mediterranean coastal lagoon in the Ionian flyway its present state was found more suitable as a stopover site for migratory waterbirds than during the 1960s after a drainage attempt. However, olive mill wastes, poaching and tourism currently form a threat to the quality of the water and the well-being of the wetland-associated wildlife. Other wetlands within the same flyway show signs of deterioration, and this is a reason for concern since the integrated migratory route must have a sufficient quality to sustain its role.

We have shown the importance of protected as well as unprotected areas in holding rich bird and herpetofaunal assemblages. The current economical crisis in Greece, has reduced nature conservation as a priority in spite of being more urgent than ever.

Nesting sea turtle populations in Suriname: threats and conservation

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Marine turtles have been inhabiting the world’s oceans for over 100 million years, playing an important role in marine and coastal ecosystems. They have survived multiple mass extinction events in the past, even the K-T extinction - the largest mass extinction in the late Cretaceous period. Nowadays however, all sea turtle species are threatened with extinction due to a number of ongoing threats, like hunting and poaching by humans, animal predators, bycatch in fisheries, pollution and climate change, which is now occurring at an unprecedented rate due to human activities. In order to prevent complete extinction, several global and regional agreements were enacted during the mid-20th century, backed-up by national legislation and regulations to protect them. Although a lot has been accomplished since these regulations, marine turtles remain vulnerable. The goal of this research was to investigate the influence of natural predation and the potential effects of future climate changes on marine turtle populations nesting in Suriname, in order to develop new conservation strategies. We monitored the sea turtle populations nesting in Suriname - mainly leatherback turtles and green sea turtles – on two major nesting beaches: Matapica and Galibi. We assessed the current situation at the two beaches by investigating the size of nesting turtle populations, and the nesting behaviour and reproductive success (through hatching success) of encountered females. Signs of predation were recorded and climate data were collected. The data were combined in order to determine present and future threats to the sea turtles of Suriname.
Invasion of the tropical fire ant *Solenopsis geminata* in the Galápagos Archipelago: population genetic structure, dispersal strategies and range expansion

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Majority of the flora and fauna of the Galápagos Archipelago (Ecuador) are highly endemic, meaning that they evolved and live only in these islands. Therefore, introduction of exotic species in these fragile and sensitive environments leads to major ecosystem alterations and to a decrease in biodiversity. In the Galápagos Archipelago, one of the most damaging invasive species is the tropical red fire ant, *Solenopsis geminata*. Our work showed that this species is completely dominant in disturbed areas and disrupts balance of local ant communities. To understand the life history traits, the population connectivity and the demographic history of these species, we characterised patterns of genetic variation in populations collected in Galápagos and South America using nuclear microsatellite loci (12 independent and polymorphic microsatellite markers). Genotypes from more than 800 individuals (103 nests collected on 7 islands and in Guayaquil, main Ecuadorian harbour) revealed that genetic diversity is very low and that the inbreeding coefficient is extremely high due to matings among relatives. Moreover, our results showed (i) that introduced populations of the Archipelago are constituted of two distinct genetic groups, resulting of two successive waves of introduction and expansion, and (ii) that these two groups might have originated from Venezuela and Costa Rica, two countries that have trade relations with Ecuador and the Galápagos. Our results are discussed in the light of the invasion risk of *S. geminata* in preserved areas of the Archipelago and across all continents, and in terms of potential threats to native fauna and economic impacts.
The importance of being first: persistent priority effects within and among species, across space and time

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The way we practice nature restoration is typically founded on restoration of environmental conditions, and the reliance on natural processes such as dispersal for this restoration to happen. There is a general consensus that also we need to restore processes of dispersal to be successful in the short term, or either be very patient. Nevertheless, other processes may interfere, as a result of which dispersal potential is not translated into realized dispersal and establishment, because the window of opportunity for successful colonization may be strongly narrowed due to biotic interactions.

Here we present such a very potent process, namely that of priority. Due to priority effects, genotypes or species with overlapping niches can pre-empt resources (space, light, nutrients, food, ...) at the detriment of competing genotypes or species. The first founders to colonize a habitat can grow and multiply and thereby reduce essential resources below a sustainable level for later colonists, thus exerting a potentially long-lasting priority effect.

Using a zooplankton model, we present a series of empirical, experimental and simulation studies to infer the role of priority effects in community assembly. We show 1) that priority effects can be important at both the genotypic and species level, 2) that even inferior competitors can outcompete superior species when exerting a priority effect, 3) that priority effects are not merely transient lags in responses to change but can be long-lasting, and 4) that local genetic adaptation of founders can strongly enhance priority effects and thereby affect community structure.

We discuss the implications of this phenomenon for practical nature conservation and restoration.
Chimpanzees live in fission-fusion societies in which members of a community form temporary parties that frequently change in size and composition. Numerous factors have been found to influence chimpanzee party-size and various methods have been used to measure party-size. Factors that are proposed to influence party-size are fruit availability and estrous females. Frequently used methods to estimate party-size include direct observations, day nest counts and night nest counts. However, a systematic comparison of these methods is lacking, in particular concerning their accuracy in semi-habituated chimpanzees. Hence, we set out to compare these methods of party-size. In addition, we used a novel method: motion-triggered cameras (MTC). We compared all four methods in the semi-habituated chimpanzees at the Seringbara study site, Nimba Mountains, Guinea (West Africa). When comparing the party-size estimates of the different methods on a monthly basis, we found no significant correlations between methods. However, we did observe the following differences: (1) direct observations gave larger party-size estimates than day nest counts and MTC observations; (2) night nest counts gave larger party-size estimates than day nest counts. Furthermore, our results showed that adult sex ratios differed significantly between direct observations and MTC observations. In addition, no significant relationship was found between any measure of party-size and fruit availability, but parties with estrous females tended to be larger. These preliminary results provide new insights into the different methods to estimate chimpanzee party-size. Especially when dealing with unhabituated or semi-habituated chimpanzees, these insights are important, as the different methods do not measure the same party-sizes and may thus overestimate or underestimate the actual party-sizes and the size of the community. Furthermore, with the assessment of the different factors that seem to influence party-size, this study stresses the importance of future research for the thorough understanding of the flexible fission-fusion societies of chimpanzees.
Spatio-temporal distribution and behaviour of three common seabird species in Laganas gulf and Argassi (SE Zakynthos, Ionian Sea, Western Greece)

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The distribution of seabirds in the Eastern Mediterranean is poorly known while species like Phalacrocorax aristotelis desmarestii, which is an endemic Mediterranean subspecies and of conservation priority for the European Union, and Larus michahellis, which is considered as a superabundant species and a possible threat for other seabirds, are known to live in this area. This work which was partly funded by the LIFE07 NAT/GR/000285 aimed to establish baseline information about the spatial and temporal distribution of the two pre-mentioned species as well as their associated behaviour in SE Zakynthos (Ionian Sea, Western Greece) which mostly belongs to the National Marine Park of Zakynthos. A third species, Calonectris diomedea diomedea, was included since it was abundant at one of the stations were the observations took place. The methodology was based on a combination of coastal counts sessions at 3 determined stations and onboard observations along the whole coastline of Zakynthos Island. Results showed that the location, the seasons and the daytime period had an effect on their distribution and behaviour to different extents. Behaviour was also a factor that influenced the species distribution. The total population of L.michahellis and P.a.desmarestii could be estimated as well as the average number of C.diomedea using Zakynthos’ eastern offshore. Conservation purposes include further monitoring of the three seabird species ideally thanks to telemetry, the further investigation of possible influences of anthropogenic food resources (e.g. fishery discards and landfills) as well as the maintenance or even reinforcement of the restricted access of the core area of the Marine Park.
Preference hierarchy in the Madagascar hissing cockroach *Gromphadorhina portentosa*: conflict between social and environmental choices

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Most lucifugous cockroaches collectively select shady resting sites where they form mixed aggregates. *Gromphadorhina portentosa* with their unique characteristics like aggressiveness and territoriality of males (shelter occupancy) is a good model to understand reproductive strategy of gregarious species with dominance hierarchy of males. In this context, the objective of our study was to determine whether environmental stress (luminosity) or social preferences (presence of conspecifics) may influence the aggregation behaviour of the Madagascar hissing cockroach.

Cockroaches placed under the light are confronted to “speed vs accuracy” conflict between a quick sheltering behavior or the aggregation in the shelter containing the more congeners. If some cockroach species promote “accuracy” (Halloy et al., 2007) and aggregate together under a dark shelter, we show here that *G. portentosa* favors “speed” and settle in the first shelter met. During the night, we observe a spatial reorganization of the population and “accuracy” prevails over “speed” as the presence of conspecifics drives the resting site selection.

When resource are limiting (only one resting site available), dominant male occupies the shelter and evicts actively dominated male. On the other hand, when two shelters are available, males tend to avoid each other and to segregate between shelters. In mixed groups, male tends to follow females and aggregate with them.

Thus, criteria involved in decision-making differ between females and males and the reproductive strategy of males is based on the monopolization of the resource (the shelter) while females tend to aggregate with the more congeners possible.
Collective fleeing is the complex result of the interactions of stimuli coming from the environment and from fellow group members which modify the behaviour of the individuals. In this context of collective behaviour, we link the individuals’ responses to the collective fleeing dynamics in a group where all individuals were simultaneously stimulated by a light stimulus.

Using a gregarious species, the American cockroach (*Periplaneta americana*), we show that group size has an impact on the global fleeing pattern expressed by cockroaches stimulated to flee a shelter. Firstly, due to the inhibitory roles of the immobile individuals and the amplification by moving individuals, the individual response probability to the stimulus decreases with group size, without alteration of the group reaction capability. This suggests that individuals in large groups are in a deeper sleep-like state, while the collective mean reaction time decreases. Once individuals had reacted, the average time a group takes to find the exits of the shelter is not influenced by group size or mobility level of group members. Finally, having reached the exit, the insects mark a stop and the time the individuals take to leave the shelter after finding the exits decreases with the number of moving individuals within it.

This fleeing dynamics based on the highlighted behavioural cascade is validated through a stochastic model.
Phenomena like pollination or seed dispersal are key processes occurring in the life cycle of a plant allowing it persist and colonize new habitats. Abiotic vectors are involved in the seed dispersal process but also biotic vectors such as seed dispersal by ants (myrmecochory) on which our study will be focused. In this insect-plant interaction, usually considered as a mutualism, ants, among many other services, disperse the seeds. In return seed bear a lipid-rich appendage: the elaiosome upon which ants may feed. However the effective benefits received by the ants are variable and poorly-known.

The main objective of our study is to see if a repeated exposure to a same seed species (Viola odorata) could induce a change in seed harvesting and seed rejection by the red ant, Myrmica rubra. After 5 weeks, we clearly saw an extinction of the seed harvesting process. While all the seeds were harvested at the first exposure, already after two weeks, almost no seeds were brought back and not any elaiosome consumed by the ants. Furthermore, this is a long term process that still persisted after almost 2 months. This temporal change in foraging activity was species-specific since a reactivation of the seed harvesting appeared when a new seed species (Chelidonium majus) was offered. Seeking for a possible generalization of the extinction phenomenon to other food types, we proposed to new Myrmica rubra colonies, seeds of C. majus during 5 successive weeks. In this case, the extinction process is more variable: it doesn’t occur and when it is, a reactivation is observed the 5th week. Preliminary studies focused on the mechanisms involved in the extinction process showed that a case of associative learning about the poor nutritive benefit- or even possible toxicity- of the elaiosome consumed by the ants.
Dispersal, aggregation and Allee effects in the foraging behavior of *Ips typographus*

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*Ips typographus*, the major pest of spruce forests in Europe, reproduces generally (endemic conditions) on weak or wind felled trees. Those resources are scarce and unpredictable and the spruce bark beetle should have acquired an efficient foraging behavior during the course of its evolution. We hypothesize that this behavior emerges from a set of simple individual rules which are: a long-range dispersal (Weslien & Lindelöw 1990); the emission of pheromones by pioneers to attract both females and males; and an aggregation of individuals on the resources. We predict that this dynamic is dependent on the population density at different levels (discovery, aggregation, etc.) which is a definition of the Allee effects (Stephens et al. 1999).

The aim of my PhD thesis is to confirm those hypotheses by modeling the foraging behavior, based on estimated key parameters and search for the by-products of the dynamic (density-dependence) in natural populations.

Like many coral reef associated organisms, *Amphiprion akallopisos*, which lives in mutualistic symbiosis with two species of giant sea anemones, is unable to migrate from one coral reef to another during its adult life stage. Dispersal between reefs in the patchy coral reef environment is assured during the pelagic larval stage. Because small pelagic larvae are extremely difficult to track in the open ocean, population genetics is a useful technique to evaluate gene flow and connectivity between populations of coral reef associated organisms. *Amphiprion akallopisos* has a disjunct distribution, occurring in the Western Indian Ocean (WIO) and the Eastern Indian Ocean (EIO) but not in the Central Indian Ocean (CIO). In this study, a 337 base pair long sequence of the Control Region of the mitochondrial DNA is used as a genetic marker to study the genetic population structure. A total of 263 samples from 17 different sites in the WIO and the EIO have been analysed. Strong population structure (ΦST=0.28), strong differentiation (ΦCT=0.61), and low gene flow between the EIO and the WIO populations was observed. Within both the WIO and EIO populations, low population structure and high gene flow was revealed. Selective neutrality tests indicate that the WIO population underwent a population expansion. The EIO population was identified as the source population. Two hypotheses are offered as an explanation for the disjunct distribution. In the first hypothesis, the WIO was directly colonised from the EIO. In the second hypothesis, *A. akallopisos* first colonised the CIO from the EIO and then the WIO from the CIO, but disappeared from the CIO either as a result of competition with other anemone fish or due to isolation of the CIO population from the WIO and EIO populations which might have led to speciation.
Weak differentiation according to host species and small spatial scale in a parasite crab

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The pinnotherid crab *Dissodactylus primitivus* lives parasitically on two burrowing echinoids (*Meoma ventricosa* and *Plagiobrissus grandis*). The fecundity of female crabs varies between hosts: being higher on *P. grandis* than on *M. ventricosa*. Furthermore, crabs living on *M. ventricosa* are more chemically attracted by this host than by *P. grandis*. Finally, the hosts present great variations in morphology and behavior. Altogether, these characteristics are leading toward a potential differentiation of crabs according to host species.

We investigated the genetic (microsatellites) and morphometric (outline analysis) differentiation of this parasite crab between two host species at one Jamaican site (Western Lagoon, Discovery Bay), and compared it with geographic differentiation among four sites along the north coast of Jamaica where one host (*M. ventricosa*) is present. A higher genetic structure between the two sympatric hosts than between different geographic locations for a given host would be a good marker of host differentiation.

Results from genetic analyzes (*F*ST, AMOVA, Fisher tests of differentiation, Bayesian approaches) showed an absence of spatial differentiation, probably related to the local hydrography. Moreover, no genetic differentiation according to host species was evident. This lack of host-differentiation could be notably explained by mobility of adult crabs between hosts. However, a small morphological differentiation (MANOVA, Discriminant Analysis) was observed between crabs issued from the two hosts, but only for females. The morphological difference may result from several mechanisms including plasticity related to host morphology.
Genetic population structure and connectivity of the mud creeper *Terebralia palustris* (Linnaeus, 1767) in Kenya, Tanzania and Madagascar.

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*Terebralia palustris* (Potamididae: Gastropoda), the largest prosobranch of the muddy substrates in mangrove forests is widespread in the Indian Ocean as well as the Indo-Pacific region. The duration of the larval phase remains unknown but the estimate from other prosobranch suggests a possible larval stage of two months which could enhance a high potential of dispersal. Mitochondrial cytochrome c oxidase subunit I (COI) gene was used to investigate 177 individuals from 10 sites over Kenya, Tanzania and Madagascar by means of DNA sequencing. 624 base pairs were examined and 26 haplotypes were identified. Two haplotypes were shared among all the populations and only three mutational steps were found as a maximum genetic distance from the estimated ancestral haplotype. Moderate haplotype diversity and extremely low nucleotide diversity were found. Genetic diversity as well as historical demography analysis indicates population expansion. Isolation-by-distance analysis revealed no significant increase in genetic distance with increasing geographic distance. Analysis of molecular variance (AMOVA) revealed no significant genetic differentiation among populations. These results indicate high gene flow as well as high level of connectivity between the Kenyan and Tanzanian part of the Eastern African coast and Western Malagasy coast for *Terebralia palustris* even within large geographic distances reaching more than one thousand kilometres. Geological history is more likely the origin of this population expansion. And the oceanography acting more likely as drift factor for the larvae combined with the occurrence of Islands which could act as stepping stones as well as the possibility of a long duration of larval stage that *Terebralia palustris* could have are potential factors driving to this population panmixing in that area.
Integrative analyses of valve outlines and molecular DNA sequence in *Eucypris virens* (Crustacea, Ostracoda)

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Ostracods are small, bivalved crustaceans with the most extensive fossil record of extant arthropods and a variety of reproductive modes making them ideal model organisms for evolutionary research. Bode et al. (2010) found that *Eucypris virens*, an ostracod with mixed reproduction, geographic parthenogenesis and Holarctic distribution, forms a species complex with more than 35 cryptic species in Europe. Koenders et al. (2012) could meanwhile report that three of these cryptic species have also invaded Western Australia. We have analyzed valve outlines of about 100 European and 30 Australian specimens for which also mitochondrial COI sequences are available. Comparisons between molecular and morphological trees reveal very little similarity for the European *E. virens*. Also, grouping according to valve outline or geographic origin does not match. In *E. virens* from Australia, there is more congruence between geographic populations and their valve outlines but this could be due to reduced variability because of the relatively recent invasion. Our results indicate that the shape of ostracod valves is probably mostly environmentally determined.


Comparative phylogeography of two forest pests: do *Ips typographus* and *Dendroctonus micans* share same patterns?

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The last 700,000 years are well known to have had a drastic effect on European organisms by periodic alternations between glacial periods and short warm and wet intervals. So far, very few studies have focused on histories of well-adapted-to-harsh-climate species, like the boreo-montane ones. The European spruce bark beetle (*Ips typographus*, Curculionidae: Scolitinae) and the great European spruce bark beetle (*Dendroctonus micans*, Curculionidae: Scolitinae) are both Palaearctic boreo-montane species sharing a same host, the Norway spruce. However, they exhibit obvious differences in their life-history traits reflecting contrasted ecological strategies: *I. typographus* is exogamous, secondary in endemic conditions, known to disperse far away and attacks trees in mass by producing aggregation pheromones. Its strategy can be categorized as well adapted to scarce resources, variable in space and time. On the other side, *D. micans* mates among siblings, is always primary, rarely observed in flight and a solitary colonizer. Living like a parasite of trees, it evolved toward a cryptic and well adapted to stable condition strategy. This presentation highlights the impact of such differences on haplotype networks of these species. Samples from the whole Europe were sequenced for a fragment of the mitochondrial marker COI. To confirm the mitochondrial results, a subset of the samples was also sequenced for 4 nuclear markers (coding genes: EF1a, G6PD, Wingless and Arginine kinase, sized between 600 and 900 bp). As expected, our results show contrasted haplotype networks. *I. typographus* networks (mitochondrial and nuclear) reveal to be poorly structured but expose a high number of polymorphisms. On the other hand, *D. micans* COI network is extremely structured and nuclear networks show an extreme low level of polymorphism. Unexpected similarities suggest a same differentiation history between Asian and European populations.
Study of a range expansion using a geographical model of coalescence

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Among the very few pollen-specialist bee species that have resisted a population decline is \textit{Colletes hederae} (Hym. Colletidae), a species that was described as new to science in 1993. At the time of its description, \textit{C. hederae} was considered to be of very sporadic occurrence in southern and western Europe, yet over the past decade the number of available records has increased dramatically outside of this species’ initial distribution range. We conducted a genetic analysis based on three nuclear DNA sequences markers, using our newly developed computer program PHYLOGEOSIM, (that simulates the evolution of DNA sequences under a geographic model of coalescence, based on a two dimensional grid). Despite the recent geographic expansion experienced by this species, we did not detect a drastic decrease in genetic diversity inside the recently colonized area. Simulations of DNA sequence evolution were performed and compared to our observed data to evaluate the likelihood of different scenarios of geographic expansion.
Territory pattern of male Dickerson’s collared lizard, Crotaphytus dickersonae

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It is assumed that good males can obtain better territories, resulting in enhanced survival and reproduction. In our study we investigated how male lizards of the highly territorial and sexually dimorphic species Crotaphytus dickersonae are distributed in a defined area in the coastal hills close to Bahía de Kino, Mexico. We examined whether phenotypic traits related to male lizard quality play a role in obtaining the best territories. While most studies on lizard territories focus on territory size and overlap, we also assessed territory quality.

Of each lizard that we caught, we measured snout-vent length, weight, head width, hind limb length and tail length as phenotypic traits that might promote success in competitions over territories. We estimated territory size based on minimum convex polygons. Territory quality was assessed by determining the number of shelters (bushes) and the amount of basking sites (rocks). We used the number of overlapping female home ranges as an estimate for mating success.

We found that males with larger territories had more overlapping female home ranges and tended to have fewer overlapping male territories. However, territory size was not related to any of the phenotypic traits. Larger territories had less shelters per m², the amount of basking sites per m² did not change. Males with larger head widths and males with longer tails had more overlapping female home ranges in their territory. Males with longer tails had less overlap with territories of other males. There was no relationship between the measured phenotypic traits and the number of shelters or basking sites.

Our results suggest that head width and tail length are phenotypic traits in male C. dickersonae that lead to a higher mating success by obtaining the territories that overlap more female home ranges and less overlapping male territories.
Male courtship pheromones control female mating responses in salamanders

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Internal fertilization without copulation or another form of prolonged physical contact is a rare reproductive mode among vertebrates. In newts (Salamandridae), the male deposits a spermatophore on the substrate in the water, which the female subsequently takes up with her cloaca. Such an insemination without amplexus requires intense coordination of both sexes. Male newts have evolved a courtship display, essentially consisting of tail-waving towards their partner under water. The female reacts by following the male, and the latter leads the female over the spermatophore, which adheres to her cloaca. Although this courtship has been first described nearly two centuries ago, and the involvement of both visual and olfactory stimuli has been proposed, the exact effect of male tail-waving on females remains obscure. Pheromone experiments until now focused on attraction and therefore don’t provide a function for courtship at close distance. Here we developed a series of experiments comparing behavior in courtship water and control water in newts. We show that species-specific male pheromones emitted during tail-waving can induce all typical features of natural female mating behavior and therefore are the key to successful reproduction without physical contact.
The ability to recognize diseased host by smell; Symbiotic harlequin crabs chemically detect and avoid their sea cucumber hosts when they suffer from skin ulceration disease

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Skin Ulceration Disease (SUD) is a bacterial infection that induces serious lesions on the body wall of sea cucumbers. It is highly contagious and can cause the death of 95\% of sea cucumbers when they are reared in aquaculture ponds. The harlequin crab \textit{Lissocarcinus orbicularis} is a common ectocommensal of the sea cucumber \textit{Bohadschia vitiensis}. Using host choices experiments in a Davenport olfactometer, we recently demonstrated that these crabs are attracted by kairomones that enable them to specifically recognize their hosts by means of chemical sensing. In this study, we observed that individuals of \textit{B. vitiensis} presenting skin ulcerations are no longer attractive to the crabs. Moreover, when given the choice between two sea cucumbers, harlequin crabs are able to distinguish healthy individuals from diseased ones, with a significant preference for sea cucumbers that are not infected by skin ulceration disease. Three hypotheses were tested in order to discover the reason of this avoidance behavior: the effect of the bacteria responsible of SUD, a possible change in the quantity of saponins produced by reared sea cucumbers, and the release of other secondary metabolites that could be emitted in surrounding water of skin ulcerated holothurians. This study is the first to highlight that a symbiont would be able to discriminate if its host is ill or not by sniffing its surrounding water. This ability certainly confers a selective advantage to these crustaceans which are obligatory symbionts of sea cucumbers.
Behavioural cues for promiscuity: Individual variation in a female's nest-behaviour during egg-laying is not associated with personality in great tits

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Extra pair paternity is a widespread phenomenon in songbirds and the debate of why it occurs is centred into four main hypotheses: direct benefit, good genes, genetic diversity and genetic compatibility. Apart from differences in quality, individuals might also differ consistently in the propensity of having extra pair copulations. A study in Great tits (Parus major) showed that depending on the interaction between the personality of a female and her mate, it is possible to predict the occurrence of promiscuity. Therefore, we expect that depending of both individuals personality, females from couples that are likely to cheat are behaving differently during the fertile period. To test this, we recorded departure times in the morning, arrival times in the evening and nest box visits from wild, personality-tested female great tits during egg laying. We found that the variation in the behaviours was influenced by the length of the day and the onset of incubation, but not by the personality of the pair members.
Social hybridogenesis in clonal ants of the *Cataglyphis altisquamis* group

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With a few rare exceptions, the vast majority of animals reproduce sexually. Some species have, however, evolved alternative modes of reproduction by shifting from classical bisexuality to unorthodox reproductive systems, like parthenogenesis, gynogenesis, or hybridogenesis. Under hybridogenesis, females of hybrid origin discard their paternal genome prior to meiosis and produce gametes carrying no paternally derived genes. Therefore, both the maternal and paternal genomes are expressed in their somatic tissues, while their germ line is purely maternal. Here, we report a unique case of hybridogenesis at a social level in desert ants of the *Cataglyphis altisquamis* group (Eyer et al., in review; Leniaud et al., 2012). Each species comprises a pair of distinct genetic lineages, with queens mating exclusively with males of the alternate lineage. All workers are inter-lineage hybrids, whereas male and female sexuals are produced by asexual reproduction through parthenogenesis. As a consequence, only maternal genes are perpetuated across generations. The characteristics and evolutionary stability of "social hybridogenesis", as well as its distribution within the genus *Cataglyphis* are presented.

Genetically mediated division of labor in the polyandrous desert ant *Cataglyphis cursor*

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Several genetic and non-genetic hypotheses have been formulated to account for the evolution and maintenance of multiple mating by females (polyandry) in social Hymenoptera. A major hypothesis argues that polyandry allows production of a genetically diverse worker force, enhancing division of labor and colony task efficiency. We tested the relationship between patriline, worker size and task specialization in the desert ant *Cataglyphis cursor*, a species showing natural variation in queen mating frequency. Our results show a significant association between patriline and task preference: workers belonging to different patrilines differ in their propensity to perform a given task (foraging, nest construction, waste management or food-storage). Furthermore, we found that worker size is closely associated with task specialization, but not with paternal origin. Overall, these results indicate that division of labor is at least partly genetically influenced in the ant *Cataglyphis cursor*, lending support to the ‘polyandry for a more efficient polyethism’ hypothesis.
The honeybee queen egg marking pheromone- a peptide?

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The eusocial Western Honeybee (Apis mellifera L.) lives in colonies with some 10'000 female workers and one fertile queen. Reproduction is highly skewed towards the queen who sires virtually all offspring. However, there is potential conflict about male parentage. Occasionally, a few workers lay viable male eggs despite the presence of the queen. These worker laid eggs however are recognized and quickly destroyed by other workers in a process called ‘worker policing’. Queen laid eggs are usually not removed, thus worker bees are able to discriminate between eggs laid by queens or workers. It was hypothesised that honeybee queens mark their eggs with an egg marking pheromone to protect them from removal. Worker bees should not be able to produce a similar signal. Physical and chemical analysis hitherto didn’t reveal which cues or signals are used by the policing workers to discern worker and queen laid eggs. We suggest that peptides might have been overlooked in previous analysis. Here we present evidence for the presence of several peptides on the egg surface, including venom components and antimicrobial compounds. We discuss the significance of this finding for the recognition of eggs by honeybee workers, as well as the potential function of peptides in the protection of eggs.
Pollen content: what does it matter for polylectic bees?

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Larvae and imago of bees rely exclusively on floral rewards as food source. However host-plant range can vary deeply among bee species. While oligolectic species forage on a few host-plants (e.g. particular host-plant family or genus), polylectic bees collect pollen and nectar from many plant families. This is the case for most of social species like bumble bees and honey bees because the colony lives longer than the blooming of some restricted plant hosts. If all pollens contain lipids, carbohydrates, proteins, amino acids, vitamins, carotenoids and flavonoids, previous studies clearly showed that they do not represent an universally exploitable resource showing species-dependent chemical composition. Interspecific variability in essential nutrients like proteins could be a constrain for population conservation of polylectic species when females have to face to poorly diverse environment. We tested what does it matter in pollen content of unifloral diet for development of colonies of the polylectic bumble bee, Bombus terrestris (Apidae). We investigated five different pollen sources: (i) Calluna vulgaris, (ii) Cistus sp., (iii) Cytisus scoparius, (iv) Salix caprea and (v) Sorbus aucuparia. We analyzed proteins, sterols, amino acids and sugars of these five diets. Diet quality was evaluated by three parameters: (i) pollen consumption by workers, (ii) weight of larvae and (iii) pollen efficacy (ii/i). Results show that diets influence bumblebee’s colonies development. Best diets are S. aucuparia and C. scoparius (i.e. highest pollen efficacy). They both show highest percentage of proteins and high concentration of 24-methylenecolesterol. We discuss how quantitative value of proteins and quality of sterols can impact on conservation of generalist bees.
Immunity on colour morphs of the lizard *Podarcis sicula*

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Island populations often differ notably from conspecifics populations on the mainland in aspects of their morphology, physiology, behaviour and life history. For instance, in ectothermic vertebrates island populations tend to be more darkly coloured. Which of the many hypotheses explaining the evolution of melanism is responsible for this phenomenon remains unclear. A recent idea is that increased pigmentation is a mere by-product of selection for other traits that enhance fitness on islands. This effect may arise through pleiotropic effects of the proopiomelanocortin gene.

In this study we investigate the relationship between colour variation and immunocompetence in the Italian wall lizard *Podarcis sicula*. This species exhibits great variability in (dorsal) colour patterns, both between and within populations. I compare a melanistic population to a 'normal' coloured mainland population. A high immunocompetence should come with a low parasitic load and a high cell mediated immune response (induced by a phytohaemagglutinin injection). To examine seasonal effects, analyses were performed at an early and late stage in the reproductive season. The results show that melanistic island individuals differ quantitatively from the mainland population in colour and aspects of the immune function. Melanistic variants have a less pure red skin colour and less bright, but pure blue throat, lower ectoparasitic load and higher immune response. This result confirms the idea that individuals of the melanistic island population are more immunocompetent and corroborates the hypothesis that a darker colouring may arise as a by-product of selection for other adaptive traits (here: immunity). In addition, I found that aspects of both colour and immunity may differ considerably between seasons and sexes, and often in a complex way. In general, the mainland population has a higher seasonal colour difference, probably because of the higher predation pressure and inter- & intrasexual competition on the mainland than on the island.
Physiological Colour Change in the Moorish gecko (*Tarentola mauritanica*): Effects of Background, Light and Temperature

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Body coloration can influence the fitness of animals through its effects on thermoregulation, predation avoidance or social status. Changes in any ecological factor affecting these functions will likely elicit concordant changes in coloration. Many taxa have independently evolved the ability to modify body colour over a period of seconds or minutes. The environmental context and functional significance of rapid colour changes have been studied extensively in cephalopods, crustaceans, fish, and amphibians, but have received comparatively little attention in reptiles. The Moorish gecko, *Tarentola mauritanica*, is capable of actively changing its body coloration. In the present study, we investigated colour change in this gecko as a function of background, temperature, and light. Our study demonstrates that this gecko indeed changes its dorsal colour in response to changes in environmental conditions. This rapid colour change however does not appear to be associated with thermoregulation in contrary to several other reptilian species. The major function of the physiological colour change in the Moorish gecko seems to be background matching, although illumination appears to be an essential trigger¹. Future research should concentrate on its effectiveness with respect to antipredatory mechanisms.

The mechanics of steady bipedal running in lizards: how do they keep their front limbs off the ground?

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The front limbs of lizards are often lifted from the ground when they start sprinting. Mathematical modelling and experiments have pointed out that this is a mechanical consequence of the propulsive forces from the hind feet. However, despite that forward acceleration is hypothesised to be necessary to lift the trunk, front limbs and head, some species of agamids, teiids and basilisks have been observed to sustain running in a bipedal posture at a constant speed for a relatively long time. Here, we investigate the effects of three potential mechanisms to generate the angular impulse that is necessary to cancel or oppose the effect of gravity during steady bipedal running in the agamid *Ctenophorus cristatus* by biomechanical modelling. Firstly, inclination of the trunk displaces the centre of mass towards the hip joint, but this does not entirely cancel out the nose down effect of gravity. Secondly, a nose up pitching moment by the aerodynamic forces exerted at the lizard’s surface running at 3 m s⁻¹ is present, but the contribution thereof is also not sufficient to explain how posture can be maintained. Our model reached the stable condition only when the latter two mechanisms are combined with a third one: vertical ground-reaction forces at the hind feet showing temporal asymmetry towards the initial instant of foot contact. Although such a pattern remains to be demonstrated *in-vivo*, previous measurements on quadrupedal running in lizards as well as bipedal water running in basilisks do suggest that an asymmetrical vertical ground-reaction force profile is inherent to the wind-milling, splayed-legged running style of lizards.
The feeding apparatus of first feeding European eel (Anguilla anguilla) larvae: a functional morphological approach.

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The European eel (Anguilla anguilla Linnaeus 1758; Actinopterygii, Anguillidae) is faced with a severe decline (up to 99%) in its natural populations over the last 40 years. Due to the absence of knowledge regarding the exact cause for this decline, a lot of effort is recently put in obtaining a complete artificial breeding program for this endangered, but still globally traded species. Unfortunately, the artificially reared eel larvae are, at present, unable to stay alive for more than three weeks after hatching. Since the larval mortality rate peaks at the onset of active food uptake, and literature regarding the larval feeding capacities, strategies and natural prey preferences is rather scarce, a functional morphological analysis of the feeding apparatus of first feeding larvae is performed. This analysis includes modeling the theoretical bite force by using a graphical 3D-reconstruction of the musculoskeletal system of these extremely small organisms (< 1cm). Based on the acquired 3D data of joints, levers and muscle insertions, as well as muscle data, very small bite forces (10⁻⁵ N) are obtained for these European eel larvae. Additionally, preliminary data on kinematics (from video recordings) of jaw and hyoid movements in pre-feeding larvae demonstrates a rather limited ability of jaw movement by both ligaments and muscles. Combining both results, rather small and soft food items are suggested to be preferable in both natural and artificial environments, which appears to be in line with the existing hypothesis that these larvae feed on either small and/or gelatinous prey items in nature (Hydrozoa, Thaliacea, Ctenophora, Polycystenia) and, additionally, may be useful information to optimize the artificial breeding program.
Structure and function of the median finfold in larval teleosts

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Nearly all fish larvae have a median finfold. Proposed functions of this finfold are mixing perivitelline fluid in embryos, increasing area for respiration, providing space for the finrays to develop, and/or contributing to the effectiveness of undulatory larval swimming. These functions may change during ontogeny. As the fold is generally resorbed at TL (total length) < 10 mm we addressed the question about its adaptive significance, taking into account that larval resources in most cases are quite limited.

The present paper offers a structural and mechanical analysis of this median finfold. It is strengthened by bundles of collagen fibres, actinotrichia. Amount, dimensions, orientation and growth of actinotrichia were measured at various locations along the finfold in several developmental stages of common carp (Cyprinus carpio) and zebrafish (Danio rerio). Actinotrichia morphology (e.g. diameter, orientation) correlated with expected lateral forces exerted on the water during swimming. The ultrastructure of the finfold was studied by electron microscopy, which revealed the anchoring of the actinotrichia at their proximal and distal ends. The construction of the finfold causes it to camber during undulatory larval swimming, measured from high speed video and artificial bending of the larval body. Actinotrichia support and restrict camber, thus increasing stiffness of the finfold so that the mass of the accelerated water is increased. A mechanical model predicting the extent of camber from the arrangement of the actinotrichia and curvature of the body was confirmed from these high-speed video recordings. The model also predicts optimal orientations of actinotrichia. We conclude that the finfold contributes to larval swimming, especially in fast escape motions.
Influence of large stag beetle mandibles on cost of transport and stability

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Sexual selection has caused a wide variety of mandible shapes and sizes in stag beetles. Males try to obtain mating opportunities by fighting other males with these large mandibles. Morphological measurements and ct-scans of the stag beetle species \textit{Cyclommatus metallifer} show that the mandibles as well as the entire heads form a larger part of the total body mass in males (resp. 4,3\% and 30,5\%) than in females (resp. 0,6\% and 12,3\%). These extensive intersexual morphological differences make us expect influences on locomotion. Since locomotion is an important ecological function, it seems reasonable to expect that the effects of the enlarged male mandibles on the cost of transport and motor control are optimized. We tested these hypotheses and observed spatio-temporal differences (duty factor, step and stride frequency) between running male and female individuals. These adjustments apparently suffice to prevent a larger cost of transport for male stag beetles, since the mass specific energy does not significantly differ between sexes (males: $2,12 \pm 0,56$ J.kg\textsuperscript{-1}m\textsuperscript{-1} and females $1,72 \pm 0,51$ J.kg\textsuperscript{-1}m\textsuperscript{-1}; $p=0,18$). Concerning the motor control, we calculated the static stability as the smallest distance of the center of mass to the edge of the support triangle. Both in male as in female strides we observe periods of static instability, but these are more frequent and more severe in males. However, this does not need to imply an instable situation, if the static instability is compensated by dynamic stabilization. The moment caused by the ground reaction force about the BCOM, has to be equal to instantaneous change of the total angular momentum. Based on the direction (sign) of the angular momentum in relation to the position of the BCOM with respect to the support triangle, we evaluated whether male stage beetles actively stabilize their body dynamics.
Choose your weapon; defensive performance in scorpions

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Scorpions are a highly diverse group, with nearly 2000 species distributed on all major landmasses except Antarctica. They occur in nearly all habitat types, from desert through rainforest, temperate zones and even the littoral zone. Despite their ecological breadth, their morphology is relatively conserved. Most morphological variation can be found in the relative size and shape of the chelae (pincers) and metasoma (“tail”). These structures are used in defense and prey incapacitation, while the chelae also serve a sensory function. In defensive, scorpions therefore can either respond with the chelae, the metasoma carrying the venomous stinger, or both. We find that the performance and functional morphology of the chelae are correlated. Finite element analyses show robust chelae having lower mean stresses during maximum performance. We also study the correlations between the morphology of these defensive structures, their performance, and the defensive behavior. We found that morphology and defensive performance are correlated, as are morphology and defensive behavior, even when phylogenetic relationships are taken into account.
Identification of potential epithelial stem cells responsible for continuous tooth replacement in the African Bichir (*Polypterus senegalus*), a basal Osteichthyan.

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In this thesis we wished to test the hypothesis that stem cells are involved in the process of continuous tooth replacement in the basal actinopterygian, *Polypterus senegalus* (African bichir).

First, we studied the morphology of the dentition and the tooth replacement pattern on the premaxillary, maxillary and dentary, using cleared and alizarin red stained heads of juvenile *Polypterus*. Each of these bones bears one row of functional teeth. In addition, a replacement tooth develops at the lingual and posterior side of each single functional tooth. Functional teeth of a similar stage of maturation tended to be in alternate tooth positions. Two mechanisms are proposed to explain this alternate pattern.

Using serially sectioned heads of juvenile fish, we could next reveal the cellular details of the replacement process. The anlage of the replacement tooth is first seen as a local differentiation of the outer dental epithelium of the predecessor, at its postero-lingual side. Throughout the development of the replacement tooth, an epithelial cell population, termed here the ‘middle dental epithelium’, connects the predecessor to the replacement tooth. The bulk of the cells of the ‘middle dental epithelium’ are irregular and separated by small intercellular spaces. In contrast, the cells closely opposed to the inner dental epithelium of the replacement tooth have a stellate reticulum phenotype. The mode of tooth replacement in *Polypterus senegalus* displays several characters highly similar to those observed in Atlantic salmon (*Salmo salar*).

In the second part of this study we concentrated on the proliferation pattern and the identification of label retaining cells using PCNA (proliferating cell nuclear antigen) and BrdU (bromodeoxyuridine) immunostaining, resp. Proliferation was found in the predontoblasts and dental organ of the replacement tooth. Strikingly, we found a focus of proliferating cells in the outer dental epithelium of the replacement tooth. This is the presumptive site of initiation of a third tooth family member. In addition, these proliferating cells could represent a transient amplifying cell population, suggesting the possible presence of putative stem cells in the outer dental epithelium of the replacement tooth.

To identify label retaining cells we adapted a BrdU pulse-chase experiment for use on *Polypterus senegalus*. After two weeks of chase time we still observed a number of BrdU positive cells in the outer dental epithelium of the replacement tooth. In addition there were a few labeled cells in the ‘middle dental epithelium’ postero-lingual of the replacement tooth. After four weeks of chase time labeled cells were found in the basal layer of the oral epithelium only.

In conclusion, we are tempted to speculate that putative dental stem cells could be localized in the outer dental epithelium of the replacement tooth, in the ‘middle dental epithelium’ or in the oral epithelium. The presence and exact location of dental stem cells in the process of continuous tooth replacement of *Polypterus senegalus* needs to be further explored.
Molecular markers in continuous tooth replacement in the zebrafish

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The study set out to investigate the involvement of putative epithelial stem cells in the processes of continuous tooth replacement in the zebrafish (Danio rerio).

A first approach encompassed the localization of these cells by the use of epithelial stem cell markers in in situ hybridizations (ISH). Probes for the zebrafish orthologues of the stem cell markers bmi1 and lgr6 were used in whole mount ISH on zebrafish. The observed signal resembled only in a small part the expression patterns found for lgr4 and lgr6 by Hirose et al. (2011).

In a second approach, the employment of the BrdU pulse-chase technique and PCNA-immunostaining on zebrafish material revealed proliferation patterns in replacement teeth in the stage of cytodifferentiation. A proliferating successional lamina gave rise to a replacement tooth that in the stage of cytodifferentiation shows a decreasing gradient of proliferation from the base to the tip of the tooth. Dilution of the BrdU label throughout the chase times enabled the identification of label retaining cells in the enamel organ near the base of the tooth.

These observations, together with the hypothesis of Huysseune and Thesleff (2004) regarding a putative epithelial stem cell niche in the base of the epithelial crypt surrounding the tooth, led to the proposition of a model in which cells residing near the tip of the enamel organ proliferate in an upwards direction. Near the pharyngeal epithelium they give rise to cells of this epithelial layer and to the successional lamina forming the successor tooth.


Assisted Identification Tool for Bumble Bee species based on Wing Shape

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Bees are among the most important group of pollinating insects and responsible for seed and fruit production in wild and managed plants, making up 1/3 of human diet, i.e. fruits, vegetables, and nuts. There is evidence of recent declines in bees, which can result in loss of pollination services and ecosystem stability. Species identification is the first key step to allow a continual monitoring of bee biodiversity. However, this task is still difficult to assess because of difficulties in taxonomy and the worldwide lack of experts (there are probably fewer than 50 taxonomic experts worldwide able to identify bee species). To overcome this taxonomic impediment, we develop a computer Assisted Identification Tool (AIT) for bumble bee species from images of their forewings. Species discrimination and identification are developed on 29 Bombus species from 10 subgenera. Shapes are captured from 2D-Cartesian coordinates of 18 landmarks digitized on the wing photographs. Using geometric morphometric procedures, our analyses validate the wing venations as diagnostic tool. We show that a characteristic shape can be defined for each studied subgenera and species. Using predictive discriminant analysis based on the reference dataset, unidentified specimen can be assigned to species. Making the AIT open source and publicly available should allow non-specialists to rapidly and reliably identify bumble bee species from images of the bees’ wings. Such tool based on morphology does not require highly specialized equipment, and can be easily adapted to all bees and to all taxa for which shape of a morphological structure is diagnostic.
Integrating DNA Barcoding in Taxonomic Practice: Experience from a Joint Initiative of Two Natural History Museums


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DNA barcoding is a system for species identification based on one or a few standard DNA fragments. It has been designed to complement taxonomy and assist in for example inventorying biodiversity and detecting invasive species, agricultural pests and food contaminants. Reviews on DNA barcoding unanimously emphasize 1) the importance of a close co-operation with taxonomists and 2) the necessity of using barcodes in concert with other types of data (e.g. morphological, ecological or nuclear DNA characters). Since 2007, the Joint Experimental Molecular Unit (JEMU) – a joint initiative of the Royal Belgian Institute of Natural Sciences and the Royal Museum for Central Africa, and funded by the Belgian Science Policy – has been involved in several scientific projects where DNA barcoding has been used in collaboration with taxonomists. Based on these experiences focusing on a variety of animal taxa, we will illustrate the strengths and weaknesses of DNA barcoding in integrative taxonomy. Some of the aspects that will be highlighted include: the selection of DNA barcoding markers (e.g. discriminative power, occurrence of pseudogenes, effects of endosymbionts), the use of museum collections (e.g. degraded DNA and mini-barcodes), the use of incomplete DNA reference libraries (e.g. identification success and database errors) and the lack of a sound or stable taxonomy (e.g. dearth of diagnostic morphological characters). In all cases, confronting data from different origins appeared to be necessary to evaluate the limitations of the DNA barcodes in discriminating species and to improve the utility of the DNA barcoding tool.
Towards a molecular database for the identification of forensically important Diptera in Belgium

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Forensic Entomology (FE) is the use of the insects, and their arthropod relatives, that inhabit decomposing remains to aid legal investigations. The medicolegal section of FE focuses on the criminal component of the legal system and deals with the necrophagous (or carrion) feeding insects that typically infest human remains. Dipteran species of some families (e.g. Calliphoridae, Sarcophagidae, Muscidae,...) are among the first insects to colonize corpses and may help to estimate the post-mortem interval (PMI), i.e. the time that has elapsed since a person has died. Yet, to do so a correct identification of larvae and pupae is essential since closely related species may differ in their developmental times and a misidentification may therefore result in a wrong PMI estimate. Unfortunately, the larvae and pupae of these fly species are difficult, if not impossible, to identify to the species level. The mitochondrial cytochrome c oxidase subunit I gene (COI) may show enough interspecific differentiation and discriminatory power to be a candidate gene to compile such molecular reference databases. Here, we present, and evaluate, a preliminary COI-database for dipteran insects of forensic interest for Belgium and show how such a database constitutes a significant part in FE. Our results show that many, but not all, dipteran species of forensic interest, can be identified correctly using the COI reference database and that the database is best complemented with DNA sequences from additional markers.
Identification based on several independent methodological approaches is seldom in entomology. Artificial Neural Networks (ANN) are used here, as a part of an integrative taxonomic approach, together with morphological or molecular evaluation. The advantages of ANN include an ability to learn from examples and to generalize observed characters. ANN are able to help us not only with species identification but also with resolution of some taxonomic problems. The use of supervised feed-forward ANN with back-propagation of errors was applied on morphometric and qualitative characters and chemometric data (Patella) in a training database with species correctly identified by experts. Precise and accurate training set is a basis for obtaining reliable identification.

ANN were applied on limpets (Patella, Molusca), thrips (Thysanoptera), insect pests (Fedor et al., 2009), and flies (Diptera) (Murarikova et al. 2011). Libnetis (Coleoptera: Lycidae) Scatella (Diptera: Ephydriidae) are studied now by the authors.

ANN represent an efficient tool for fast identification of zoological objects. ANN methodology can be applied for classification of any objects for which suitable characters can be found and specified. ANN are able to determine even hardly distinguishable species or to distinguish new species. Higher number of objects for the training of ANN improve the accuracy of the identification. The high success and efficacy of ANN use as demonstrated in this work show the possibility of a wide applicability of this approach in zoological practice.
Two new species of the family Pterygosomatidae
(Acari: Trombidiformes) from Iran

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Mites of the family Pterygosomatidae are permanent parasites of lizards and various arthropods that typically live in concealed habitats. This family represents the only example of mites belonging to one exclusively parasitic eleutherengone group occurring on both invertebrate and vertebrate hosts. The most probable explanation of the occurrence of this family on such varied host groups is host switching. Some species of this family may be associated with disease and debilitation of captive reptiles, including anaemia, skin lesions and the transmission of parasitic blood diseases. In a survey which was conducted in order to find some parasitic mites on the body of lizards in south and center parts of Iran in 2010-2012, two new species of family Pterygosomatidae were collected from Trapelus agilis (Olivier, 1807) (Squamata: Agamidae) and identified as Geckobia sp. nov and Pimeliaphilus sp. nov. These two new species were found on dorsal side and near eyes of lizard.
Effect of enrichment and cage size on growth in young rehabilitated hedgehogs (*Erinaceus europaeus*)

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Hedgehogs are difficult to raise successfully in some rehabilitation centers, with high sudden mortality and bad growth, even when the animals feed well. This may relate to multiple factors, one of which may be the stressful captive environment. Enrichment and larger cage size are generally expected to enhance welfare if it allows the animals to perform strongly motivated behavioral needs such as locomotion and exploration. It can be assumed that animals whose basic biological needs are fulfilled, will show lower stress and will grow better than animals in restrictive environments. We examined the growth of 8 young hedgehogs, 4 males, 4 females, weighing between 500 and 800 grams, in an experiment with a Latin square study design, in order to examine the effect of size (small i.e. 60x60x60 cm versus large i.e.120x60x60 cm) and enrichment (enriched versus poor). The hedgehogs were kept in the VOC Brasschaat. They had been hand-raised coming in from the wild in a weakened state or were captive-born to rehabilitated mothers. During four periods of 13 days each, the hedgehogs were kept in different experimental conditions. All the animals changed four times to another cage: to a large cage with or without enrichment or a small cage with and without enrichment. Prior to the start of each “experimental period” the hedgehogs stayed in the experimental cage for 6 days to habituate to the novel environment. The entire period covered 52 days (from August till October 2011). In the experimental period, the hedgehogs were weighed every three days. Analyses were performed with a SAS 9.2 Proc MIXED model, taking into account the starting weight. The effect of cage size and cage enrichment (four classes), period (1 to 4), and of individual (1 to 4) on average weight gain was analyzed for males and females separately. For the males, we found no significant effects. They grew roughly equally well in all cages and periods for all individuals. For the females, we found a significant effect of treatment ($P<0.05$), period ($P=0.03$) and individual ($P=0.03$) on weight gain. The comparison showed that on average they gained more weight in larger cages and in enriched cages. Best results for the females were seen in the large enriched cages. We hypothesize that males may have a lower sensitivity to environmental stressors than females, given their larger home range and risk-taking behavior in the wild.
Anthropogenic stressors on Moroccan temporary wetlands: how can we promote their sustainable use and conservation?

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In the subtropics, temporary wetlands are valuable ecosystems. They house unique species and contribute to regional biodiversity. Moreover, temporary wetlands are vital for the local people that make use of these systems by farming, irrigation and grazing and drinking of cattle. Unfortunately, due to population growth and urbanization, these systems are degrading rapidly. Studying communities in relation to the use of wetlands and the land use intensity around them, will lead to a better understanding of the ecological processes and will help assessing the impact of anthropogenic stress. In addition, the ecology of harmful mosquito larvae will be studied, in terms of their relation with anthropogenic influence on the wetlands and their possible control. A cluster of 40 Moroccan temporary wetlands, situated along a land use intensity gradient, will be used as a model system. We focus on three main objectives: studying biodiversity patterns and presence of harmful species; developing indicators (e.g. hatching patterns of zooplankton resting egg banks) to assess quality of temporary wetlands; and determining sustainable management practices using manipulative experiments. In this last part, we study the effects of cattle manure and biological control of mosquitoes by the tadpole shrimp *Triops granarius*. We expect that the intensive use of temporary wetlands results in the loss of biodiversity and reduced water quality. We also expect that pest species will favor impacted wetlands more than pristine ones. Since these temporary wetlands are intensively used by the local people, access to good water quality in a healthy environment will increase in importance. By developing easy and accurate biomonitoring tools, we will get a reliable picture of the quality of the temporary wetlands. Combined with the results of our manipulative experiments, we will contribute to research-based suggestions for the sustainable management of the resources offered by these vulnerable ecosystems.
Chemical induction experiments in two crustacean-echinoderm model symbioses

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Symbiosis is defined as a sustainable interspecific relationship between two organisms from different species. Communication is needed to insure symbionts recognition and the longevity of the association. Most of the time, interaction between host and symbionts is allowed through the production and the detection of natural secondary metabolites, corresponding to chemical communication. Two different crustacean-echinoderm symbiosis models were investigated in this study: the harlequin crabs *Lissocarcinus orbicularis* and the snapping shrimp *Synalpheus stimpsoni*, two ectocommensals found, respectively, on the body wall of different species of holothuroids and crinoids. Behavioral experiments using a Davenport olfactometer were realized in order to discover if (1) symbionts are preferentially attracted by the chemical stimulus produced by their original host species (*i.e.*, host on which they were collected) or randomly chose between different host species; and if (2) the odor of a non-host species, originally non-attractive, can attracts the symbionts when cohabitation occurs for a long time. Results suggest that chemical impregnation plays an important role in host selection, but also that chemical sensing can be modified by learning.
What’s new? Novel object testing in captive Psittacine birds

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Members of the order Psittaciformes are known for their relative large forebrain and they may be considered as one of the most innovative taxa. However, little is known about variation between species in innovativeness. Innovation can correlate with processes such as exploration, social and individual learning and neophobia. The neophobia level in birds can influence their response towards new feeding situations and so influence their ability to assess and learn about new environments. A well-established test to assess neophobia is the response to novel objects. In the current study we investigate the level of neophobia in two novel object tests in five pairs of Psittacine birds of five species at Antwerp Zoo (Salmon-crested cockatoo; Kea; Yellow-headed amazon; Blue-headed macaw; Hyacinth macaw). After studying the birds’ baseline response to a food dish placed in their enclosure, we presented to each pair two separate experimental novelty tests. First, we placed an orange cone next to the feeding tray. One week later we used a blue plastic box as novel object. We measured 1) the latency to approach a familiar food dish next to a novel object, 2) the frequency of approaches, 3) the duration of the time spent close to the object. All subjects were video-recorded for analysis. Preliminary results indicate that the presence of novel objects increased the latency to approach. The orange cone elicited more neophobic response in all species, compared to the blue box. Despite the fact that all species tested are considered to be innovative, the species differed in their latency and frequency of approaches and time spent in proximity. While Kea and Hyacinth macaw showed the least neophobic response, Salmon-crested cockatoos never approached the novel objects. More research and an increase of the sample size are needed to draw firm conclusions about innovation and its correlated processes.
Study of Female’s Searching Behavior of *Ectomyelois ceratoniae* (Lep.:Pyralidae) to Volatiles of Pomegranate Fruits

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Many insects use airborne volatiles emitted from plants to find and locate their host plants. Information on volatile chemicals that attract insects to their hosts and that stimulate oviposition upon arrival could be benefit to pest control programs. In order to determine if the females of carob moth prefer intact pomegranate or infested ones as oviposition site, four treatments were used: 1) intact fruits, 2) infested fruits by larvae, 3) infested fruits by fungi (*Aspergillus* sp. and *Penicillium* sp.) and 4) infested fruits by larvae and fungi simultaneously. The first experiment carried out in a wind tunnel, using 2-3 days old mated females (n=80). The results showed that the first and forth treatments were significantly more attractive for the females of carob moth than the others (P=0.002). After that for studying the female’s oviposition behavior, a choice test carried out in a large cage in laboratory condition with mentioned four treatments, using one day old mated females (n=60). The results showed that females of carob moth prefer to oviposite on infested pomegranate by larvae and fungi simultaneously to other treatments (P=0.01). Our data showed that oviposition behavior of *E. ceratoniae* is significantly modified by the presence of both larvae and fungi on pomegranate fruits. We suggest that activity of the fungi in presence of the larvae occur a synergistic effect on volatiles of fruits. So, Herbivore Induced Plant Volatiles (HIPVs) that emitted from these contaminated fruits attract more females to oviposit.


Experimental exposure to masking noise does not affect song structure and singing activity in grey-breasted wood-wrens

T. Parson, T. Burbidge, H. Slabbekoorn

Song divergence has the potential to lead to reproductive isolation and speciation. Environmental factors such as ambient noise have been shown to shape songs, although experimental studies have only focused on urban populations. Two genetically and acoustically distinct subspecies of grey-breasted wood-wren (*Henicorhina leucophrys*) have been found to replace each other along an elevational gradient in a tropical mountain region in Colombia, with one subspecies living at high elevations in a relatively quiet habitat. We tested whether experimental exposure to masking high-frequency noise bands typical for low-elevation habitat affected spectral and temporal characteristics of the high-elevation subspecies' song. Both spectral and temporal characteristics did not differ before, during and after exposure treatment, suggesting that the differences in song between the two subspecies do not reflect short-term adaptation to habitat-dependent differences in ambient noise patterns. These findings stand in contrast to the phenotypically plastic response of urban birds.
Sleeping site selection of proboscis monkeys, *Nasalis larvatus*, along the Kinabatangan river, in Sabah, Malaysia

**V. Thiry**, M. Vercauteren, D. Stark, B. Goossens

We studied characteristics influencing the sleeping sites selection by proboscis monkeys, *Nasalis larvatus*, along the north riverbank of the Kinabatangan river, in Sabah, Malaysia. Primates spend about half of their lives at sleeping sites, and their choice of sleeping sites may affect individual survival. We identified 81 sleeping trees of one-male and multi-male groups from November 2011 to January 2012. 17 variables were recorded for each tree and more general data was collected for the entire site. To determine if habitat has an impact on sleeping tree selection by proboscis monkeys, different sites were studied: sleeping plots and control plots. First, we compared sleeping trees to other trees present in the sleeping plots. Secondly, trees of sleeping plots were compared to control trees, characterising non-sleeping areas.

All sleeping trees were close to the river (<35m). They were taller (27,402±9,922 m), larger (159,324±101,504 cm), with larger and higher first branches (11,732±5,056 m) and had less vines. One-male group sleeping sites also presented a good connectivity with surrounding trees and a higher crown density. The selection of sleeping tree (and site) characteristics was likely to be related on the one hand to risks of predation and injuries of falling, and on the other to social interactions and efficiency to locomotion. Sleeping tree is not the only determinant factor in sleeping site selection: global area also plays an important role.

Seeds eaten by proboscis monkeys were studied by fecal analysis. Their abundance and specific diversity were inversely correlated. This analysis provided more information about fruit consumption of proboscis monkey. Two major seed species were identified: *Nauclea sp.* and *Ficus spp.*

Finally, proboscis monkey behaviours were recorded by scan sampling method at sleeping sites, where the resting accounted for the major part (53.6%) of the activity budget. We also observed several variables for each individual: its height in the tree, its position in the canopy and its distance from its closest neighbour. Members of different age-sex classes did not use sleeping sites in a similar way. Differences primarily occurred between adult males and other more vulnerable individuals: adult females with infant and juveniles. The observed patterns seem to be explained by anti-predation strategies.
Study of Cuvierian tubule adhesion in the sea cucumber *Holothuria forskali*

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Marine bioadhesive research has been gaining increasing interest because of its high potential for the development of novel adhesives for technological applications like in surgery for the replacement of stitches or in dentistry. In the search for new bioadhesion models, we investigated Cuvierian tubules, a specialized defense system occurring in some species of sea cucumbers, all belonging to the family Holothuriidae. When an animal is stressed, it expels a few tubules, which lengthen considerably and become sticky upon contact with any object. Their biomechanical properties make Cuvierian tubules very efficient at immobilizing potential predators. In terms of composition, their adhesive consists of an inorganic fraction accounting for 10% of the dry weight and an organic fraction made up of 36% neutral carbohydrates and 54% proteins. Different methods were used to characterize further the adhesive produced by Cuvierian tubules. First, proteins were extracted from glue prints following a protocol developed in our laboratory. Glue prints, which consist of patches of adhesive material left on the substratum after mechanical detachment of the tubule, are indeed extremely enriched in adhesive secretions. After separation by electrophoresis and enzymatic digestion, the extracted proteins were analysed by tandem mass spectrometry with the goal of finding some new adhesives proteins. The automatic analyses of the results revealed the presence of several intracellular proteins and thanks to the manual analysis, a recurrent *de novo* generated peptide rich in glycine was detected. The sequence of this peptide was used to design degenerate primers that could be used for cloning and sequencing Cuvierian tubule cDNA. Secondly, based on the detection of proteins post-translational modifications on tubule sections, Western blots were performed to identify the presence of phosphorylated residues and oligosaccharidic structures in proteins. These two types of modifications are very common in marine adhesives and play a key role in adhesion. Finally, a random screening was performed on a Cuvierian tubules cDNA library. Fifty clones were sequenced highlighting two interesting results: (*i*) a sequence rich in proline and glutamine and (*ii*) a second sequence related to fibrinogen, a molecule responsible for coagulation.
The influence of the neurotoxic 6-hydroxydopamine on physiological processes: focus on digestion of the anautogenous fleshfly, Sarcophaga Crassipalpis.

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6-Hydroxydopamine (6-OHDA) also known as Oxidopamine, is a neurotoxin used in vertebrates to induce Parkinson’s disease or schizophrenia in laboratory conditions. As an analogue of naturally occurring dopamine, 6-OHDA is entering dopaminergic neurons through the plasma membrane dopamine transporters. Once inside 6OHDA causes the occurrence of the reactive oxygen species which result in destruction of the dopaminergic neurons [1].

Our test animal, Sarcophaga crassipalpis is an anautogenous fleshfly that, like female of mosquito, needs a protein meal to produce its first batch of eggs. As a result of digestion, free amino acids are released into the hemolymph. Besides the nutritional function, they also trigger a signal cascade between the brain and the ovaries to start production of the ovarian ecdysiotropic hormone (OEH). As a result ecdysteroids are transported to the fat body to stimulate large-scale synthesis and secretion of the yolk proteins (vitellogenesis) that are subsequently accumulated in the developing oocytes [2]. Decapitation shortly after the liver meal interrupts this entire signaling cascade as do by simple injection of 6-OHDA. Seemingly injection of 6OHDA mimics the effect of decapitation. In this way the brain should not be able to receive or send any endocrine signal. Since the exact mode of action of 6OHDA in insects is not known it is not excluded that, there are also some dopamine receptors present in other tissues. One of the organs predicted to be innervated by dopaminergic neurons is the midgut. Flies injected with this neurotoxin indeed show much lower enzymatic activity of the midgut. As a consequence of these disabilities, liver fed 6OHD injected flies die within 3 days. These findings suggest a role of dopamine in the midgut.


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Development of a promising polyculture involving the sea cucumber *Holothuria scabra* and the red algae *Kappaphycus alvarezii* in the South West of Madagascar

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In the Indian Ocean, coastal villagers often collect sea cucumbers as a source of income. However, with the depletion of natural sea cucumber stocks, the introduction of hatcheries to farm sandfish (*Holothuria scabra*) as a community livelihood is being promoted in a few African countries, especially in Madagascar. There, the farming of *H. scabra* is experienced since 2007 in the South West of the country with a growing success. Since 2010, we experienced in Sarodrano, a village located 30 km South of Toliara, a polyculture involving *H. scabra* and the red algae *Kappaphycus alvarezii*. *K. alvarezii* also named cottonii is reared, collected and dried by villagers. The dried algae are exported later to industrial countries for the extraction of carrhagenans that are principally used in the food industry. Today, 50 villagers are polyaquaculturists: they daily work with sandfishes and cottonii. We here presented the first results concerning the monthly growth rates of *H. scabra* and *K. alvarezii*. The highest growth rate is obtained in the hot season for *H. scabra* and in the cold season for *K. alvarezii* which are thus very promising candidates for the development of an economically viable farming in developing countries.
Tissue- and species-specific accumulation of trace metals in two land snails (Gastropoda, Pulmonata)

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The main aim of this study was to elucidate accumulation patterns in two land snail species in order to better understand their potential to transfer metals within the terrestrial food web. To do so, the tissue distribution of Ag, Cr, Cu, Ni and Zn was examined in Cepaea nemoralis and Succinea putris. Snails were sampled at four polluted dredged sedimentation zones and three control plots situated along the waterways of Flanders, Belgium. The polluted sites had elevated levels of Cd, Cr, Cu and Zn in the soil. Similarly snails from polluted plots had elevated levels of Cd and Zn in their tissues. The metal concentrations in the tissues of both species were: (1) site-specific (differed among polluted sites and within sites), (2) tissue-specific (higher levels of Ag, Cr, Cu and Ni were found in the digestive gland), and (3) species-specific (differences in accumulation patterns between species). This study highlights the importance of including dietary, behavioral and species-specific parameters to facilitate correct interpretation of bioaccumulation patterns.


Genome mining in the springtail *Folsomia candida* and its gut microbial community

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The soil-dwelling invertebrate *Folsomia candida* is a model organism in ecotoxicology and ecogenomics. Recent work has shown that antibiotic biosynthesis genes are present in the genome of this springtail, probably as result of Lateral Gene Transfer events. This PhD project aims at mining the genome of *F. candida* for additional genes in antimicrobial activity that may have been subjected to lateral gene transfer. As a first step in this direction, we are characterizing *F. candida* interacting gut microbiota, a potential source of LGT and target for the production of antibiotics.

In order to characterize *F. candida*’s gut microbial community structure we apply PCR amplification of 16S rRNA gene fragments, DGGE fingerprinting and next-generation sequence analysis. We will also analyze the metagenome of the gut microbiota in order to explore its functional potential (Engel et al., 2012).

We hypothesize that *F. candida* is able to manipulate the microbial community in its gut and environment. Therefore we expect uniformity of bacterial composition across strains and low inter-individual diversity, with a predominance of the intracellular parasite Wolbachia *pipiens* (Czarnetzki & Tebbe, 2004).

This project will provide further insights into the genetics and ecological interaction between *F. candida* and its microbial community.

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Low Genetic Diversity in Tepui Summit Vertebrates

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The Pantepui region of South America, located in southern Venezuela, northern Brazil, and western Guyana, is characterized by table mountains (tepuis) made of Proterozoic (> 1.5 billion years old) sandstone - the highest reaching nearly 3 km - that are isolated from their surroundings by up to 1000 m high vertical cliffs. Tepuis are among the most inaccessible places on earth, and the majority of their summits have been visited less than the moon. Due to its age and topography, this region has been assumed to be an ideal nursery of speciation and a potential inland counterpart to oceanic islands. High endemism has been reported for the flora (25% in vascular plants) and fauna (68.5% in amphibians and reptiles) of single tepuis, and an ancient origin has been postulated for some of these organisms. But, it has also been suggested that a few taxa living in habitats extending from lowlands to summits (e.g., savannah) invaded some of the more accessible tepuis only recently. Taken at face value, the overall timing and extent of biotic interchange between tepui summits has remained unstudied. Here, we show that recent faunal interchange among currently isolated tepui summits has been extensive, and affected even taxa living in some of the most tepui-specific habitats and on the most inaccessible summits.
Characterization of innate immunogenes of the cichlid

*Oreochromis niloticus*

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The genetics behind adaptive evolution and speciation processes remain a central question in evolutionary biology. Because of their recent explosive radiation, the cichlids of the East African Lakes became a well suited vertebrate model system to investigate this question. During the past few years focus was mainly set on ecological adaptations. There is increasing evidence that adaptation to contrasting environmental conditions plays a key role in driving species divergence. An important selective pressure may be contrasting parasite communities among allopatric cichlid host populations. The molecular genetic characterization of immunogenes is a first critical corner stone in studying immunogenetic adaptation. In this study we characterized four genes of the cichlids innate immune system: Toll-like receptors 2,3 and 9 and the interferon regulatory factor 7. Because of their role in pathogen recognition, Toll-like receptors have, like MHC molecules, been recognized to be primary targets of parasite-mediated selection.
Eco-evolutionary dynamics of antipredator defenses in temporally variable environments: An evolving metacommunity perspective

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There is growing awareness that ecological and evolutionary processes can occur at the same time scale and can strongly interact. Ignoring these interactions may distort our view on population, community and ecosystem responses to environmental change. The evolving metacommunity framework integrates both ecological and evolutionary processes. It focuses on more diverse communities and includes responses to all kinds of environmental gradients. Thus, it can help e.g. to improve our understanding of the impact that keystone species exhibit on aquatic ecosystems on the (meta-)community level.

In the course of this PhD, we will study the impact of a key invertebrate predator, the tadpole shrimp *Triops*, inhabiting isolated pond habitats along a connectivity gradient as a model of a selection pressure that impacts an evolving metacommunity of zooplankton prey. Our aim is to integrate data concerning different endpoints (regional variation in neutral genetic markers, antipredator traits, species composition and community trait values) to generate new insights in the structure and dynamics of evolving metacommunities. First, we will investigate the genetic metapopulation structure of both *Triops* and its focal prey species *Daphnia* in relation to environmental and connectivity gradients. Then, we will analyze patterns of genetic variation in *Daphnia* antipredator traits, prey communities structure and associated community trait values in relation to predation and connectivity gradients, both experimentally and in the field. Integrating these data will allow us to analyze the degree to which genetic variation in traits of a key species may impact species sorting or community trait responses to environmental gradients.
Efficiency of Various Summary Statistics for the Comparison of Phylogeographic Scenarios and Case Study of a Leaf Beetle (Chrysomelidea).

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Numerous methods using a coalescent approach have been developed in the field of phylogeography, among which the recent approximate Bayesian computation (ABC) that uses simulations and summary statistics to infer demographic scenarios. The summary statistics are used to reduce the data sets and should capture the relevant features of the data in order to allow computation efficiency. However, there is still no general rule as to which and how many statistics should be used [1]. PhyloGeoSim is a coalescent-based simulator recently developed by Simon Dellicour using both demographic and spatial characteristics to simulate evolution of DNA sequences [2]. Using this software, several summary statistics commonly used in phylogeography have been analyzed under three different demographic scenarios in order to provide insights on the relevancy of each one of them to infer demographic and historical scenarios. Moreover, a phylogeographical study currently in progress about *Chrysomela aeneicollis* aims to test the connectivity of the populations located in West North America. A preliminary and exploratory study of this case is given.

The results show for each statistic tested if the distinction between scenarios is possible and, when it is, for which range of parameters values (population size, migration rate, time of expansion,...). In the study case, the exploration doesn’t allow yet any assumption about the connectivity of the natural populations, and need to be prolonged. However, the results show the necessity to better define the geographical and demographical scenarios tested and, more specifically, the ancestral state of the populations simulated.


Concordance of microsatellite and mitochondrial DNA markers in detecting genetic population structure and connectivity in the boring giant clam, *Tridacna crocea*, across the Indo-Malay Archipelago

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Many studies using mitochondrial DNA (mtDNA) have been conducted to investigate connectivity among populations. Mitochondrial DNA is a single, non-recombining locus and therefore its ability to reveal recent gene flow among populations in order to estimate connectivity is questioned. By using 10 microsatellite markers, the genetic population structure of 366 individuals of the Boring Giant Clam *Tridacna crocea* was examined in 16 populations from the Indo-Malay Archipelago (IMA) in order to compare these results with previous studies using mtDNA. Genetic population structure patterns were mostly congruent, with only minor difference. The studied populations could be divided by both marker systems as following: (1) Eastern Indian Ocean, (2) central Indo-Malay Archipelago, and (3) Western Pacific. Similarly, the microsatellite data showed that the divergence in *T. crocea* likely dates back to the global fluctuation of sea level during the Plicocene and Pleistocene. Populations in the central IMA showed panmixing, being well connected by surface currents, as shown by pairwise comparison among populations in this area. However, the structure patterns through the IMA revealed by microsatellites are not as strong as pronounced by the mtDNA analysis, with a \( F_{st} \) value of 0.023 (\( P < 0.001 \)). The highly divergent mtDNA clades suggested there might be cryptic species, which cannot be revealed by microsatellite data. Additionally, the genetic divergence of populations in the Java Sea revealed by mtDNA was not detected by microsatellites. mtDNA might reveal historic rather than recent population connectivity due to its much lower mutation rate than microsatellite DNA. Also, the differences might be induced by the smaller effective population size of mtDNA comparing with nuclear DNA (nDNA), which might show stronger signals of genetic drift. However, the general concordant structures revealed by the two marker systems supported that the mitochondrial cytochrome oxidase subunit I (COI) gene is applicable for population genetic analysis and precise recovery of connectivity patterns of giant clams. The combination of mtDNA and nDNA markers in population genetics can supply more information and might facilitate the understanding of population structure at different time scales.
Molecular and morphological evidence for several species within the cosmopolitan eurybathic deep-sea lysianassoid amphipod *Eurythenes gryllus sensu lato*

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*Eurythenes gryllus* (Lichtenstein, 1822) is a presumed cosmopolitan eurybathic bentho-pelagic giant deep-sea amphipod. However, previous studies already highlighted genetically divergent lineages in the Atlantic and Pacific Oceans, which appeared to be vertically stratified, and minor morphological differences between populations were also recorded. With an aim to quantify the geographic and bathymetric patterns of genetic variations, the genetic diversity in *Eurythenes gryllus* was investigated at the global scale (Arctic, Atlantic, Pacific and Southern Oceans) using three different genes (COI, 16S rRNA, 28S rRNA). This genetic analysis was accompanied by a thorough morphological study. Phylogenetic and phylogeographic analyses revealed the existence of at least eight well-supported clades, two bathyal and six abyssal, which were separated by genetic distances at the level of usual interspecific divergences. A subsequent morphological analysis confirmed the genetic findings and revealed small but consistent differences between the different clades, which will be described as separate species. Furthermore, a clear genetic break was observed between specimens sampled above and below 3000 m. This bathymetric break below 3000 m has already been reported for several organisms and regions, suggesting its role as a ubiquitous phylogeographic barrier for barophysical tolerance. The *Eurythenes* clade, comprising specimens sampled at bathyal sites in the Arctic and Southern Oceans, is presumably the true *E. gryllus*. This represents, to our knowledge, the first molecular evidence for a bipolar distribution in a macro-benthic deep-sea organism. The present results clearly highlight the difficult nature of research on the systematics of deep-sea crustaceans and shows that the abyss is a more complex environment than previously assumed, likely to harbour an important hidden diversity.
Evolution of softbodiedness and phylogeny of Cleroidea (Coleoptera)

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The checkered beetles and allies associated in the superfamily Cleroidea form a lineage of the diverse Cucujiformia series. The current concept of Cleroidea proposed inclusion of both predominantly hard-bodied (Trogossitidae) as well as soft-bodied (Cleridae, Melyridae) lineages, while dermestids, passandrids, bothriderids, and ciids were excluded. Currently, the Cleroidea consist of 14 families, Phloiophilidae, Trogossitidae, Chaetosomatidae, Cleridae, Metaxinidae, Thanerocleridae, and 8 families of the melyrid lineage. Representatives of individual Cleroidea lineages show heterogeneous feeding habits. Whereas Phloiophilidae larvae and Peltinae are fungivorous, other groups are predaceous or polyphagous, and most of the melyrid lineage feed preferentially on pollen. Several cleroid taxa are protected by conspicuous coloration (Trichodes) or eversible vesicles (Malachiidae) that are used as aposematic signals. Latest DNA sequence analyses challenged the monophyly of Cleroidea. Partial sequences of 18S, 28S, 16S, and cox1 genes of 115 Cleroidea and 38 outgroup taxa were amplified and sequenced. Maximum parsimony analyses of concatenated data matrix supported monophyly of Cleroidea only if two former cucujoid families, Byturidae and Biphyllidae were included. Byturidae + Biphyllidae were shown to be the most basal split within Cleroidea, followed by separation of Phloiophilidae. The monophyly of Trogossitidae was rejected showing them to be a paraphyletic assemblage, although the monophyly of individual subfamilies Peltinae, Trogossitinae, Lophocaterinae, and Decamerinae were supported. The monophyly of checkered beetles was usually strongly supported, although sometimes only together with Chaetosomatidae. The monophyly of individual subfamilies Clerinae and Hydnocerinae was rejected while the clade Clerinae+ Hydnocerinae was strongly supported. Surprisingly, the subfamilies Enopliinae and Korynetinae were mostly paraphyletic, while the clade Enopliinae + Korynetinae showed high support. Results of the analyses suggested multiple origins of softbodiedness in Cleroidea clade.
Predators of bark beetles and alien species: a story of coevolution and odors

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The great European spruce bark beetle (*Dendroctonus micans*, Curculionidae: Scolytinae) and the boreal spruce beetle (*D. punctatus*) are two phylogenetically and ecologically close bark beetles. They bore galleries into the bark of spruce in Europe and Asia (*D. micans*) and North America (*D. punctatus*). We analyze the mechanisms of coevolution between these species and their specific predators: *D. micans*-Rhizophagus *grandis* (Coleoptera: Monotomidae) and *D. punctatus*-Hapalaraea *longula* (Coleoptera: Staphylinidae).

David Pimentel² suggested that a prey could evolve resistance against a longstanding associated predator. To test this hypothesis we compare the reproductive success of each predator on both prey and on the red turpentine beetle (*D. valens*) which is an ecologically close bark beetle outside the geographical range of the predators.

*R. grandis* females fit their oviposition to prey availability probably relying on kairomones. It is likely (but not established) that *H. longula* developed a similar process. I proceed to chemical analyses (GC-MS using headspace extraction) to identify oviposition stimuli and inhibitors of each predator. Possible differences between prey may be linked to coevolution with the predator. Bioassays will be able to confirm the role of these molecules.

Microorganisms could influence the survival and success of bark beetles, and perhaps also the chemical cues involved in oviposition of the predators. To emphasize their role I consider characterizing the microflora of each bark beetle and using antibiotics.

*D. micans* adults have a reproductive diapause which has never been removed in laboratory. To get full life cycle rearing we use thermoperiods in conditioned rooms to simulate winter.

Identifying immune-linked cytokines in locust species *Locusta migratoria* and *Schistocerca gregaria*

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The locust species *Locusta migratoria* and *Schistocerca gregaria* are major tropical crop pests which can cause huge devastation of agricultural crops when they form adult swarms. Current locust control methods depend on post-outbreak chemical pesticide treatments which have drawbacks such as high pesticide expenditure, pesticide resistance and pollution (van der Valk and Everts 2003). We believe that by using entomopathogen-based locust biocontrol methods we can make the prevailing challenges in chemical methods obsolete. Developing optimal entomopathogen-based locust biocontrol requires comprehensive knowledge of the locust immune system since each time when resistant locusts evolve, the knowledge may allow us to use appropriate entomopathogens at the right developmental stage of the locust population. Locusts rely on innate immunity to defend themselves against invading pathogens. However, unlike many insect species for locusts no reports on production of antimicrobial peptides are documented (Li et al. 2012) and the locust immunity seems mainly cell based. Apart from demonstrating efficient bacterial clearance we are now screening cytokines which drive immune pathways such as pathogen recognition, signaling and hemocyte recruitment in the locust cellular immune system. Hence, we report *in vivo* and *in vitro* methods we developed for the cytokine screening. In parallel, we tell about our persistent attempts to develop cell-line from locust embryo and hematopoietic cells, which surely will facilitate the screening process of immune-linked cytokines in the locust species.

Planktonic dispersal suggests a homogeneous genetic structure over large geographic scale. Is it mandatory?

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Marine invertebrates with planktonic-dispersing larvae are assumed to be good dispersers over long distances. This high dispersal capacity implies a high gene flow between populations and a homogeneous population genetic structuring over wide geographic scales. The marine gastropod *Melarhaphe neritoides* has a long-lived planktonic larval dispersal stage and allozyme data suggest that it is genetically homogeneous over its whole European distribution area¹. In contrast, preliminary mtDNA sequence data uncovered a remarkable degree of genetic diversity and genetic structuring on smaller geographic scales².

In order to explore this mtDNA diversity and structuring in *M. neritoides* we started to survey sequence variation at COI and 16S rDNA all over the Azores archipelago. These data reveal that the Azorean populations share very few haplotypes, both between and within islands.

Hence, it seems that *M. neritoides* with its long-lived planktonic larval stage nevertheless shows a strong local population genetic structuring and thus challenges the current paradigm that correlates modes of larval development with levels of genetic structuring. It also stresses the importance of the sampling intensity (both in terms of numbers of specimens and genetic markers) to avoid experimental biases when assessing genetic diversity.


Development of efficient genetic markers to trace fish fraud and IUU fishing aimed at securing food safety and sustainable exploitation

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Due to the increasing demand for fish in combination with chronic overfishing and IUU (illegal, unreported and unregulated) fishing, fish stocks are declining worldwide and food security is likely to be hampered in the future. It is estimated that globally a quarter of the catches are through IUU fishing. This leads to major economic loses, undermines sustainable fisheries and causes unfair competition. Nowadays the deficiencies in wild fish are largely compensated through aquaculture production. However, the aquaculture industry has issues with sustainability and one of these are the escapes of cultured fish and subsequent mixing with wild populations. Escapes not only impose large economic costs, they also form a threat to local biodiversity through competition and genetic pollution. In addition, despite the strict national and European regulations there are increasing problems with mislabeling of fish (products). A major obstacle in all aspects of fish related fraud is that hard evidence is all too often lacking.

In this project we will develop informative SNP markers to unravel the fine scale population structure of European sea bass (Dicentrarchus labrax) across its full range - but with special attention for the North East Atlantic Ocean - and to distinguish wild fish from (escaped) aquaculture fish. We will focus on SNP markers linked to genes for local adaptation (natural population structure) and domestication and artificial selection (aquaculture escapees). After intensive validation and standardization procedures, a diagnostic tool based on a selected set of highly discriminatory SNP makers will be developed. This tool will be precise enough for forensic applications but at the same time cheap and efficient to be used as a routine control by fisheries authorities and in the food industry. The generic methods developed here for sea bass will facilitate similar future researches on other economical important marine fish.
Laelapidae (Acari: Mesostigmata) mites associated with insects in Iran

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Mites of the family Laelapidae are abundant in agricultural ecosystems, especially in association with Coleoptera and Hymenoptera. This project is based on a survey of Laelapidae that was carried out during 2010-2012 in Iran. During this study, 17 species from six genera and two subfamilies were collected and identified. Six of these species are new to science, and one genus and seven species are considered as new records for the mite fauna of Iran. The genera and species marked with one and two asterisks are new to science and the Iranian fauna, respectively. The name of the host is written in square brackets after the stage of the mite that is found associated with its host:

*Coleolaelaps ferdowski* Joharchi 2012*♀♂ [larvae of *Polyphylla* sp.]
*Hypoaspis campestris* (Berlese, 1887)**♀ [Pentodon sp.]
*Gymnolaelaps kabitae* Bhattacharyya, 1968 **♀ [Pheidole pallidula]
*Gymnolaelaps laevis* (Michael, 1891)**♀ [Tetramorium caespitum]
*Gymnolaelaps myrmecophilus* (Berlese, 1892) ♀ [Tetramorium caespitum]
*Gymnolaelaps myrmophila* (Michael, 1891) ♀ [Formica sp.]
*Gymnolaelaps canestrini* (Berlese, 1903) **♀ [Tetramorium caespitum]
*Laelaspis astronomicus* (Koch, 1839) ♀ [Tapinoma sp.]
*Laelaspis calidus* Berlese, 1924**♀ [Pheidole pallidula]
*Laelaspis dariusi* Joharchi & Jalaeian 2012*♀ [Tetramorium caespitum]
*Laelaspis equitans* (Michael, 1891) **♀ [Messor sp., Camponotus sp.]
*Laelaspis humeratus* (Berlese, 1904)**♀ [Tetramorium caespitum]
*Laelaspis kamalii* Joharchi & Halliday*♀ [Tapinoma sp., Pheidole pallidula]
*Laelaspis pennatus* Joharchi & Halliday*♀ [Tetramorium caespitum]
*Laelaspis persicus* Joharchi & Halliday*♀ [Pheidole pallidula]
*Pneumolaelaps hyatti* (Evans and Till, 1966) ♀ [Bombus sp.]
*Promacrolaelaps** sp. nov* ♀ [Propomacrus bimucronatus]

The ecological role of the mites discussed here is unknown but it is possible that these mites are not parasites, maybe harmless feeders on exudates from its host's body or predators that feed on other small invertebrates in the microhabitats created by its hosts.
Genetic diversity and connectivity of the corals *Acropora tenuis* and *Seriatopora hystrix* along the East African coast.

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The reefs along East Africa are declining and the ability of coral reefs to adapt to, and recover from, environmental stressors highly depends on genetic diversity and connectivity of the reefs. Connectivity of coral populations is suggested to depend on location, species and oceanographic barriers. Studies on the genetic diversity of *Platygyra daedalea* along the East African coast reveal higher diversity at reef slopes and islands, in comparison to the lagoon sites (1). Although the gene flow between the lagoon sites is found to be moderate, there was low dispersal among the islands and reef slope sites. Other studies show that the genetic subdivision was higher between the populations of brooding corals than mass spawning corals.

This study will utilise DNA microsatellite markers to analyse and compare the population structure of the mass spawning coral *Acropora tenuis* and the brooding coral *Seriatopora hystrix*, sampled at ten locations along the East African coast. Data will be analysed with the software Alequin (AMOVA, F-statistics) and the programme Structure (cluster analysis) to answer the following question: Is the genetic diversity and connectivity of *A. tenuis* and *S. hystrix* similar to *P. daedalea*, and is there a difference between mass spawning and brooding corals?

Non-sagittal movements of shank and foot in some marsupials

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Considerable doubt exists concerning foot movements in Thylacinæ, as well as in extant small marsupials, and their relevance to human bipedal gait. Historical footage freely accessible via the internet shows images in which thylacine feet are kept horizontally in sway. For a clearer image, we analyzed an archived live videotape of a walking wombat, frame-by-frame. From take-off, the lateral side of the wombat foot stays continuously lifted, causing throughout everted foot positions during sway. Non-sagittal movements in another marsupial, the common opossum, appear to be biomechanically “guided” by the cardan-like ankle joint transmitting shank axial rotation to foot-eversion or foot-inversion (1). Tracings of an in vivo opossum X-ray, displaying shank and foot, confirm that collum fibulae and spatium interosseum cruris are reliable landmarks to describe these non-sagittal hind-limb movements (1). Only since recently, quantitative measurements in higher primates e.g. man, allow extrapolating these data to bipedal gait. In man, after take-off, just a short distinct foot eversion helps to clear the foot from the surface, mainly during the onset of sway (2).

Creating a transcriptomic biomarker for water quality, using a vertebrate model organism.

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Human populations have a great (negative) impact on aquatic ecosystems. Pollution of aquatic systems is a big problem and can only be assessed by monitoring the water. Ex situ toxicity tests are based on individual organisms and pollutants, while in situ bio monitoring of aquatic systems, is usually done by looking at the whole living community of macro-invertebrates and/or fish. But in the environment pollutants are seldom found alone and the pollutants could have a different effect when present in mixtures appose to on their own. And since the community says little about the health of the individuals or of the health of the ecosystem, it is our thought that to assess sub lethal and chronic effects of mixtures of pollutants, another method is required. In this project (which is a PHD proposal) we will develop a new method for the monitoring of water quality in a whole (nl a mixture of different pollutants). This by using a vertebrate (three spined stickleback: *Gasterosteus aculeatus*) and by looking at transcriptomic markers. We will create an operational, reliable and general method in which fish (nl. Three-spined stickleback) can be used to assess water quality and health of the system. We will therefore link the found transcription profiles of three-spined stickleback to the known (by Vlaamse Milieumaatschappij or VMM) pollutants in water and create a database. Using this database, transcriptomic profiles obtained from specific microarrays can be back linked to the pollutants present in the water. It will be a relatively cheap, fast and easy way to assess the health of a whole aquatic system.
Predation modality of Sesarmid crabs on mangrove tree propagules.

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Some authors refer to ‘crabs’ as keystone species. To better understand the reciprocated relation between crabs and vegetation in mangrove forest, we did some experiments in Gazi Bay, Kenya.

We focus on the confirmation, consolidation or rejection of four hypotheses: (a) The dominance-predation hypothesis predicts that the propogule predation rate is lower where canopy is dominated by conspecific plants. We measured the consumption time of 200 Avicennia marina and Ceriops tagal propagules under different covers; (b) Crab density influences propagule predation rates. (c) Crab size influences food competition: the bigger crab, the more competitive it is. We observed which crab (the bigger or the smaller) in a pair, took the A.marina propogule first; (d) Vegetation densities influence crab densities.

We found that (a) C. tagal and A. marina propagules are consumed faster under adult conspecifics (p<0.001). Those results do not confirm the dominance-predation hypothesis, (b) there is a high correlation between crab density and predation rate (for C. tagal propagules: p<6.4$\times$10$^{-7}$; A.marina propagules: p<1.1$\times$10$^{-8}$). This is within the logical expectations and previous observations, (c) within 11 crab couples 8 presented a more competitive crab (p<0.05) but there are no competition differences with size (4 times the large one and 4 times the small one “won”). The more competitive crab seems to be the “fearless”, not the bigger one and (d) crab density is highly negatively correlated (p<2.2$\times$10$^{-16}$) to A. marina trees and pneumatophores densities. The structure of A.marina stands generates different pneumatophore densities that seem to determine crab density through space competition.

We therefore conclude that there is a mutual relationship between stand characteristics and crab fauna, where stand composition and density influence predation and crab density, crab density impacts predation rates and crab size does not influence competition for mangrove propagules.
Eating & entertaining

Some suggestions for lunch (walking distance from the campus)

1 : ULB cafeteria (Self Solbosch "Chez Théo", “Le Campouce”) – Building F1.
2 : « Picwick la Braisiere », avenue Adolphe Buyl laan 79
3 : « La Bastoche », chaussée de Boondael / Boondaelsesteenweg 473
4 : « Le pain quotidien », chaussée de Boondael / Boondaelsesteenweg 479
5 : « La Bécasse », chaussée de Boondael / Boondaelsesteenweg 476
6 : « Exki » (organic), avenue de l’Université / Hogeschoollaan 22
7 : « ô pâtes » (Italian), avenue Adolphe Buyl laan 62
8 : « La Grande Escale » (Vietnamese), avenue de la Couronne / Kroonlaan 445
9 : « Shanti » (vegetarian), avenue Adolphe Buyl laan 68
10 : « Tom Yam » (Thai), chaussée de Boondael / Boondaelsesteenweg 341

Nightlife in Brussels

Comic Strip Museum: (the Waucquez warehouse built by Victor Horta in 1906) devotes much of its space to the history of the comic strip in Belgium. Rue des Sables 20, 1000 Brussels,
http://www.comicscenter.net/en/home

City Hall of Brussels: Brussels Town Hall is one of Belgium’s finest civic buildings. Not only because of the numerous sculptures adorning its walls, but also because of its perfect proportions and the incomparable beauty of its tower, the spire of which is topped by the archangel Saint-Michael,
Grand-Place /Grote Markt, 1000 Brussels,
http://www.brussels.be/artdet.cfm?id=5757&highlight=grand%2Cplace

Spending your evening in a museum certainly makes a change from working up a sweat on a dance floor or going to a concert… Cauchie House, Grand Serment Royal et de St-Georges des Arbalétriers LIBRARUM (Royal Library of Belgium), Museum of Letters and Manuscripts in Brussels, Royal Museum of Central Africa, Royal Museum of the Armed Forces and of Military History.
http://www.brusselsmuseumsnocturnes.be
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