Swiss Barcode of Life

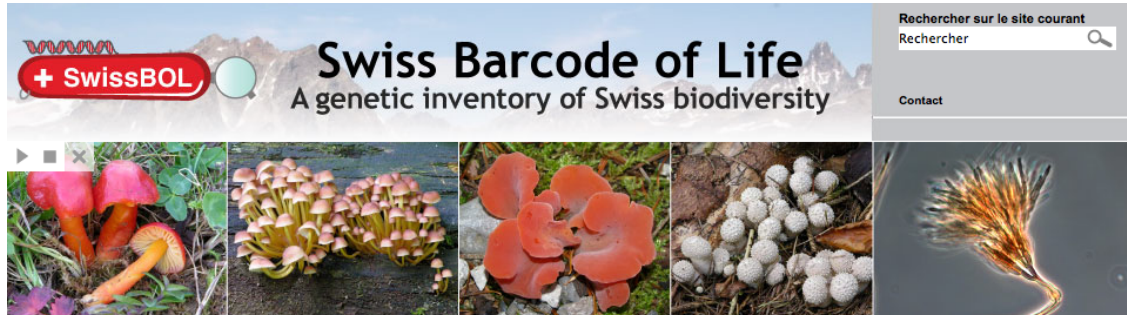## A genetic inventory of Swiss biodiversity

Final Report

2012-2014

SwissBOL Steering Committee: Jan Pawlowski (Chair), Sofia Wyler (Coordinator), Jessica Litman (Scientific collaborator), Alexandre Aebi, Alice Cibois, Jürg Frey, Yves Gonseth, Sebastian Kiewnick, Edward Mitchell, and Yamama Naciri

PRESENTATION

The Swiss Barcode of Life (SwissBOL) project was founded in June 2012 by the Swiss Federal Office for the Environment, with the goal of creating a network of Swiss institutions and researchers involved in the study of genetic diversity and willing to contribute to the national inventory of genetic biodiversity. The project effectively started in 2013, when the proposals from participating institutions and researchers were selected and subsequently funded. Despite being operational for just a short period of time, SwissBOL achievements are considerable. The network established in 2013 has been strengthened during the course of this year and SwissBOL has made significant progress toward the creation of the DNA reference database for Swiss specimens. This report outlines the activities in which we participated.

The SwissBOL website was created in 2013 (http://www.swissbol.ch) and remains an updated platform where our initiative is presented. The site is available in three languages (French, German, and English) and represents a window of our main activities. The goals of the project are presented, together with a list of the network members and a short summary of each project we are currently engaged in. The website also shows the barcoding progress made in Switzerland to date and includes general material on DNA barcoding and biodiversity.

THE PRESENT STRUCTURE

The initial structure of the SwissBOL suffered a slight change in the beginning of the year. Jessica Litman became the scientific collaborator working at 20% always at the CSCF in Neuchâtel. She continued to be in charge of the development of the protocols and platforms for the data management, as well as of the update of the web site. Sofia Wyler took the coordination of the project, in what it concerns the national and international relationships, exchanges with the network partners and management of the activities related to the Molecular Facility. Emanuela Reo was engaged at 10% to reinforce the laboratory activities of the Molecular Facility and she has mostly been engaged in the Butterflies and the Endemic Beetles projects.

The present schematic view of the SwissBOL represents the workflow of our bicephalous structure.
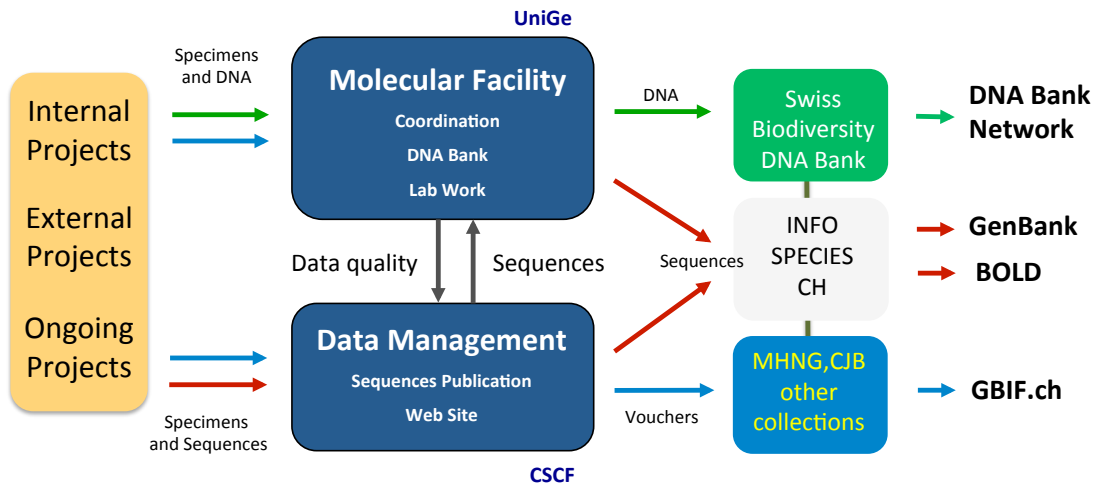
The SwissBOL network currently comprises 16 national partner institutions involved in the realization of 26 individual DNA-barcoding projects. These institutions include the University of Neuchâtel, the University of Geneva, the University of Zürich, the Natural History Museum of Geneva, the Natural History Museum of Lugano, the Natural History Museum of Lausanne, the Natural History Museum of Bern, the Naturmuseum Luzern, the Conservatory and Botanical Garden of Geneva, the CSCF, Agroscope, ETH Zürich, EAWAG, WSL, the Institute for Work and Health (affiliated with the Universities of Lausanne and Geneva), Biodiversity Monitoring Switzerland, and Ecogenics.

During the course of the project, two meetings were scheduled. The first one took place in the 5th of December 2012 at the Natural History Museum of Bern and was organised with the main goals of informing the community about the beginning of SwissBOL funding and opening a call for projects.

The second SwissBOL meeting occurred on Friday, 31st of October at the Natural History Museum in Neuchâtel, with nearly 50 participants. During the day, some of the accomplishments from both internal and external projects were presented and discussed (see the meeting's program in Annex). Moreover, the informal exchanges between the participants allowed demystifying the technical problems related to some projects and studying together possible solutions. We also opened the floor for feedback and discussion about the future of SwissBOL. There were two invited speakers from our international network, Nikola Szucsich from the Austrian Barcode of Life project (ABOL) and Peter Hollingsworth, chair of the Scientific Steering Committee of the International Barcode of Life Project (IBOL).

THE FINANCED PROJECTS

SwissBOL has undertaken five pilot projects designed to develop standardized laboratory protocols, including methods for the non-destructive extraction of DNA and the identification and quantification of organisms in environmental samples.

In December 2012, SwissBOL opened a call for projects that used DNA barcoding as a tool in taxonomic, systematic, conservation-based and/or evolutionary studies of species collected in Switzerland. Of the 31 total applications received, our Steering Committee accepted 22 projects for funding. Of the remaining nine projects, four projects were accepted but not financed (i.e. projects will be funded only in the event that additional funding is found).

The choice of these studies took into consideration the specific objectives outlined in both FOEN contracts 12.0011.KP/L233-1425 and 12.0002.KP/L173-0838 and tried to cover the widest possible range of taxonomic groups. SwissBOL-financed projects focus on priority species, including bioindicators, invasives, Red List species, organisms used in biocontrol, and microorganisms.


The focus on priority species

A project in collaboration with the CSCF and the Cantonal Museum of Zoology in Lausanne, is gathering genetic data on click beetles (Family: Elateridae), many of which are "Urwald relict species", as well as listed as endangered on European Red Lists and useful as bioindicators. Other projects include other Red List species, such as alpine fungi and fern allies.

Application on environmental surveys and biodiversity conservation

Several projects apply next-generation sequencing to environmental surveys and biodiversity conservation. A project in collaboration with the University of Zürich is currently developing a test kit to identify the fauna present in cow dung; their ultimate goal is to evaluate how livestock medications affect dung
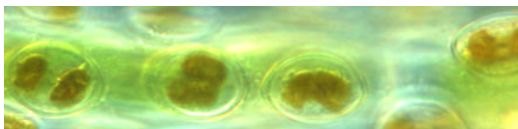
community biodiversity. Another project, in collaboration with the WSL, uses 454 sequencing techniques to quantify genetic diversity of lichen-forming fungus, a group particularly important as bioindicators of the ecological integrity of forest landscapes. A project in collaboration with the Agroscope is developing a protocol for the quantification of nematode diversity in mixed soil samples. Other projects also focus on bioindicators of soil and water quality, using classical barcoding methods (respectively, collembolan and aquatic oligochaetes).

All SwissBOL-financed projects gather valuable data which will contribute to improved understanding of intra- and inter-specific genetic diversity, as well as how that diversity is geographically distributed. This will thus ultimately serve as a tool in biodiversity conservation.

The focus on microorganisms

Several projects deal with the biodiversity of microorganisms, including oomycetes, amoebes and diatoms.

Relevance for ecosystem functioning and dealing with biosafety aspects

We are presently contributing to a number of projects related to both ecosystem functioning and biosafety. A project in collaboration with the University of Neuchatel is developing a protocol for the detection of an alien invasive oomycete in the Doubs River, *Saprolegnia parasitica*. Another project in collaboration with Andermatt Biocontrol is focused on obtaining genetic data for organisms that are currently used in Switzerland as biocontrol agents, including mites, nematodes, and insects.

Contribution to external projects that began before 2012

SwissBOL is currently contributing to a project to barcode the spiders of Europe, carried out in collaboration with the University of Bern and the Museum of Natural History in Bern. Our contribution will cover the costs associated with barcoding approximately one-third of the species living in Switzerland (~ 375 species). We are also contributing to a project to detect invasive river oomycetes, in collaboration with the University of Neuchatel. This is a project also funded by ISEFOR (Increasing Sustainability of European Forests).

CONTRIBUTION TO THE REFERENCE DATABASE

The molecular barcodes generated by SwissBOL-financed projects constitute a significant source of new genetic data to the international databases (GenBank, BOLD). DNA sequence data for the majority of insects included in some of our projects, such as Aquatic insects (EPT), Click Beetles (CB) and Endemic Beetles (SEB), have not yet been published in either of these databases. The same was found for the aquatic oligochaetes (OLG), for which more than half of the sequences obtained by the SwissBOL represent new genetic data.

The 27 individual SwissBOL projects include 12 internal projects performed entirely at the SwissBOL Molecular Facility at the University of Geneva and 15 external or semi-external projects developed either in conjunction with partner laboratories or for which sequencing is conducted at the SwissBOL Molecular Facility.

By March 2014 an interim progress report (see document in Annexe) was completed by the PI for each project. At that time the situation was the following:

a) all projects were underway but their progress was uneven;

b) two projects (Plants of Geneva and Hydrozoa) were already complete: the sequences are publically accessible on BOLD Systems (www.barcodinglife.com) and the specimen data have been incorporated into the GBIF-CH node

c) for the remaining 25 projects, sampling was about 60% complete and the generation of genetic data was still in a preliminary stage

d) more than 2300 DNA barcodes have been generated since the beginning of the project, of which 68% were produced at the SwissBOL Molecular Facility.

By October 2014 most internal and external projects have made considerable progress and results will be presented and discussed at the meeting organised on the 31st of October. For the 12 projects developed internally, progress thus far is as follows:

Plants of Geneva: Genomic DNA was extracted for 145 plant specimens collected in the canton of Geneva. 142 DNA rbcL and 128 matK barcodes are now publicly available on BOLD Systems.

Aquatic insects (Ephemeroptera-Plecoptera-Trichoptera): Genomic DNA was extracted for a total of 489 specimens, using non-destructive methods. A total of 337 COI barcodes are already available on the EPT database.

Aquatic oligochaetes: Genomic DNA was extracted for around 400 individuals and standard COI sequences were obtained for 229 individuals. A scientific publication presenting the cryptic diversity of aquatic oligochaetes revealed by DNA barcoding was recently submitted to PLoS One. This project is carried out by Régis Vivien (UniGe).

Diatoms: Diatom samples were obtained, as part of routine sampling for watercourse quality assessment. Environmental DNA and RNA were extracted and amplified using diatom-specific 18S rDNA primers. Amplicon sequencing using Illumina high-throughput technology is underway. This project is carried out by Laure Apothéloz-Perret-Gentil and Joana Visco (UniGe).

Biocontrol: The project was momentarily interrupted due to the lack of interest and contact with the Swiss Andermatt Biocontrol company. Collaboration with French researchers, Nicolas Ris and Jean-Claude Streito, is being developed to overcome this problem and to share data and results.

Endemic Beetles: DNA was extracted, using non-destructive methods from the total 133 specimens available. DNA barcodes were obtained using COI for 119 specimens and using ITS2 for 67 specimens.

Butterflies (Rhopalocera and Zygaenidae): Of the total 900 projected specimens, genomic DNA has been extracted for 576 specimens and COI barcodes were generated for 348 of them.

Formicidae: A total of 140 specimens is available. DNA was extracted from 80 specimens, applying non-destructive protocols, and 36 COI barcodes were obtained. The phase of protocols' standardization was much more laborious and time consuming as initially thought.
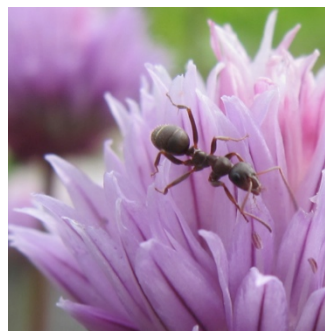
Click Beetles: 93 new specimens have been supplied in September 2014, and of the total 137 specimens, genomic DNA was extracted for 64 samples using non-destructive methods. Sequences were obtained for COI (46 specimens) and for ITS2 (40 specimens).

Long-legged Flies: We received 435 individuals for analysis in August 2014. Non-destructive DNA extractions, as well as COI amplification and sequencing are now underway.

Gastropods: A total of 150 specimens is available. DNA was extracted from 93 specimens and 43 COI barcodes were obtained. Protocols had to be adapted to each sample, as the size and the material among the different samples were highly variable (from one millimetre snails to eight centimetre slugs).

Collembola: The project was momentarily interrupted due to the lack of a new specialist that would do the sorting and identification of the samples. The person that was involved in the project from the beginning changed his professional direction in the meantime.

As a result of the internal projects alone, the DNA reference database currently contains over **1900 sequences** from **573 species** occurring on Switzerland.
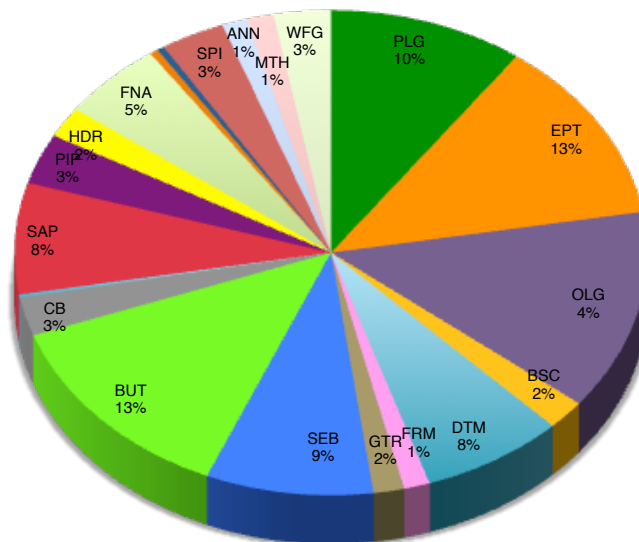
<u>**DATA UPDATED IN OCTOBER 2014**</u> **:** **PLG** Plants of Geneva (273 barcodes) ; **EPT** Ephemera-Plecoptera-Trichoptera (337) ; **OLG** Aquatic Oligochaetes (229) ; **BSC** Biosecurity Agents (54) ; **DTM** Diatoms (200) ; **FRM** Formicidae (36) ; **GTR** Gastropods (43) ; **SEB** Endemic Beetles (234) ; **BUT** Butterflies (357) ; **CB** Click Beetles (71)

<u>**DATA UPDATED IN APRIL 2014**</u> **:** **SAP** *Saprolegnia parasitica* (203) ; **PIP** Pipistrelle Bats (92) ; **HDR** Hydra (56) ; **FNA** Fern Allies (144) ; **DGI** Dung Insects (10) ; **SPI** Spiders (90) ; **ANN** Annelida (35) ; **MTH** Moths (38) ; **WFG** Wheat Fungus (90)

DATA MANAGEMENT & PUBLICATION

In order to satisfy the objectives defined in the contracts with the FOEN concerning the deposition of the specimens, all SwissBOL-financed projects are engaged in rendering the specimens publically accessible in a museum, herbarium or botanical garden.

Specimens used in internal projects are assigned a unique sample ID number (always directly attached to the specimen, thus ensuring the connection between a numbered specimen and the line in our database corresponding to that specimen). When specimens are finally deposited in a formal collection, they are typically assigned another number in accordance with the numbering system of that particular collection. For external projects, sample ID's are assigned to each specimen by the project's authors; collection ID numbers are assigned after deposition in a collection. For all projects, we work in close collaboration with GBIF.ch to ensure that each specimen receives a unique identification.

The non-destructive DNA extraction protocol, successfully applied by SwissBOL to different taxonomic groups, was key for working with museum collections, as it does not affect the morphological characters of the specimens. This procedure is particularly useful when working with rare or type specimens, or any other specimens, which should remain intact. On the other hand, the generation of high-resolution multifocal images allows for the use of destructive methods of DNA extraction for organisms such as diatoms, nematodes or tiny gastropods from which tissue cannot be removed without destroying the specimen. In such cases, images are kept as vouchers, thus maintaining the link between the original specimen and the genetic data generated from it.
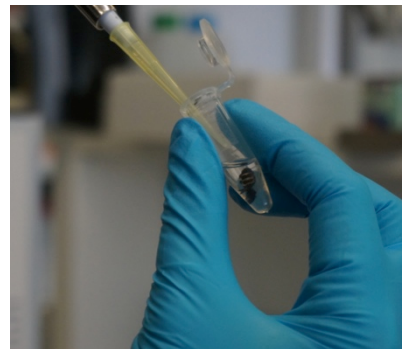
All DNA sequences are made available via BOLD Systems. This platform requires all sequence data to be linked to individual specimens that are also

registered on BOLD. Thus all those accessing sequence data posted by SwissBOL on the BOLD website also have immediate access to all of the data surrounding each specimen used to generate those sequences. SwissBOL would like to implement a protocol for data submission to BOLD Systems that would allow all the projects developed with our funding (and others that wish to do so) to be attached to the SwissBOL project. This protocol is being written and we will encourage our external partners to submit their sequences in accordance with it.

For the internal projects, sequences are generated and edited in Geneva and are then submitted to the BOLD, along with the information related to each specimen, which includes all requisite details (species name, date and place of collection, etc.) submitted by whoever has provided the specimens. Accordingly, the projects Plants of Geneva and Hydrozoa are already complete and the respective sequences are publically accessible.

According to informal exchanges with the PI's of SwissBOL-financed projects carried out externally, it will be difficult to incorporate the DNA sequences from the project until 2015.

By the end of the year, we intend to implement some changes in the GBIF.ch portal to allow for the presentation of genetic data, including DNA extractions and DNA sequences, that are associated with specimens registered on GBIF.

Our methods for specimen labelling and deposition, and sequence deposition are all considered international "best practices" by leading international institutions, including the DNA Bank Network, the BOLD Systems and the Global Bioinformation Facility (GBIF).

THE DNA BANK & PROTOCOLS

The creation of a Swiss Biodiversity DNA Bank was one of the specified objectives of the contracts with the FOEN. All DNA extractions generated during the course of the SwissBOL internal projects are currently stored at -80ºC in individual, barcoded microtubes with screw caps in the laboratory of Prof. Jan Pawlowski at the University of Geneva. DNA extractions generated from external projects will be incorporated into the SwissBOL DNA Bank by the end of 2014, after completion of these projects.

The SwissBOL DNA Bank has also been asked to store the genetic material from independent projects. We have now received DNA extractions from small mammals used in the Red List project; from beavers used in a study concerning the two subspecies *Castor fiber galliae* and *C. f. fiber*; and from the newly described paper wasp species, *Polistes helveticus*.

We intend to join the DNA Bank Network without depositing our DNA samples in their facility. This will allow us to retain autonomy over our DNA samples yet register the DNA via a public data portal that will allow members of the national and international community to formally request the use of our DNA samples during the course of their research. Accordingly, we have started to format the data related to the DNA extractions for some internal projects (Plants of Geneva, Biocontrol, Aquatic Insects, Click Beetles and Endemic Beetles). The incorporation of the total data related to the DNA samples deposited in the SwissBOL DNA Bank into the DNA Bank Network is set for 2015.

Another important objective stipulated on the contracts with the FOEN concerns the development of protocols for collection and storage of DNA samples following international standards. The different projects

developed in our Molecular Facility allowed us to design unique protocols for the collection of good quality DNA.

The laboratory protocols developed last year for the non-destructive extraction of DNA have been massively applied to different organisms and the success rate improves from day to day. This extraction method works particularly well with pinned specimens (90% success for the Click Beetles), but a high rate of success can also be obtained for specimens conserved in alcohol, if ideal conservation conditions have been maintained (90% success for Endemic Beetles). The protocol for the identification and quantification of organisms in environmental samples, using Illumina sequencing is now routinely applied to diatoms and its use in Aquatic Oligochaetes is being developed as well.

SwissBOL protocols follow international standards for the collection and utilization of DNA samples, as well as national and international regulations regarding access and benefit-sharing (ABS) as indicated in the Convention on Biological Diversity and in the Nagoya Protocol's section on access and benefit-sharing.

SPECIFIC RESULTS

Despite being operational for just a short period of time, SwissBOL success has been considerable. SwissBOL has significantly contributed to the inventory of genetic diversity in Europe and has also contributed to many spectacular scientific findings, including the recognition of cryptic diversity within different groups, the discovery of a new species of paper wasp and the detection of cases of misidentification in plants and aquatic insects.

Cryptic diversity

A number of SwissBOL-financed projects are geared toward the discernment of individual species in cryptic species complexes. These projects focus on diverse taxonomic groups, including protists, earthworms, collembola, wasps, ants, bats, hydrozoa and beetles.

Each of these projects will contribute to our understanding of the diversity that exists both within and among species, as well as to the geographical distribution of this diversity. High levels of cryptic diversity were discovered in aquatic oligochaetes, with 9 new lineages (diversity≥10%) commonly identified as belonging to two morphospecies (*Tubifex tubifex* and *Limnodrilus hoffmeisteri*).

The well-known earthworm, *Allolobophora chlorotica,* was also found to represent a species complex comprised of different cryptic species that appear to live in different soil types.

New species to science

A newly described paper wasp, *Polistes helveticus*, has been sequenced with the support of SwissBOL and its DNA has been deposited in the SwissBOL DNA Bank. The new species was previously misidentified and its distinction was only possible after using a combination of morphometric and molecular analyses.
http://www.pensoft.net/journals/zookeys/article/6611/

The sequencing of COI barcodes in nearly 40 Kuhl's pipistrelles (a bat) confirmed that two major lineages differing by up to 6% coexist in Switzerland. Such genetic differentiation is unusual among conspecifics and raises the question of whether the lineages together represent a single species or if each lineage represents a distinct, cryptic species.

Misidentification

A plant taxonomically identified as *Cynodon dactylon* (L.) Pers. was identified as a species of *Digitaria* using DNA barcoding. This misidentification was subsequently confirmed and the specimen was finally recognized as *Digitaria ischaemum* (Schreb.) Muhl.

Some cases of taxonomic misidentification were also detected in Plecoptera larvae. According to specialists, the determination of Leuctridae larvae can be very difficult, sometimes impossible. In some cases, tentative identifications were proposed and were later revealed to be wrong. This kind of problem was only detected through the collaboration established between the specialist reponsible for the collection and the SwissBOL Molecular Facility.

VISIBILITY

Participation in national and international conferences

The SwissBOL chair (Jan Pawlowski), scientific collaborator (Jessica Litman), and coordinator (Sofia Wyler) participated in the following conferences:

- The Zurich Mycology Symposium at Agroscope Reckenholz-Tänikon Research Station ART (January 25, 2013).
- Insights into DNA Barcoding and Metabarcoding workshop at ETH Zürich (February 10-12, 2013).
- The BioSyst.EU 2013 Global Systematics Meeting in Vienna, Austria (February 18-22).
- Meeting of the International Scientific Collaboration Committee (ISCC) of the International Barcode of Life (IBOL) in Guelph, Canada (4-6 July 2013) http://ibol.org/about-us/project-governance/scientific-collaboration-committee/.
- Fifth Barcode of Life Conference in Kunming, China (27-31 October 2013).
- Swiss Systematics Society Day (November 15, 2013) at the Naturmuseum in Lucerne.
- Biodiversity Day at GEO-X "From observation to decision" (14th of January).
- The PACE 14 at the University of Geneva (12th of February).
- The Biology14 at the University of Geneva (February 13-14).
- Workshop on Fundamental and Applied Protistology, Université Neuchâtel (15-16 April 2014)
- Workshop on diatom monitoring, PhycoEco, La Chaux-de-Fonds (8 May, 2014)
- Joint Aquatic Science Meeting, Portland, USA (May 18-23, 2014)
- Workshop "Indices biotiques et génétiques", CSCF Neuchâtel (10 June 2014)
- Meeting of the International Scientific Collaboration Committee (ISCC) of the International Barcode of Life (IBOL) in Münich (25-27 October 2014)

Scientific Papers

Vivien R, Wyler S, Lafont M, Pawlowski J Molecular barcoding of aquatic oligochaetes: implications for biomonitoring. PLoS One (*submitted*).

Visco J, Apothéloz-Perret-Gentil L, Cordonnier A, Pawlowski J. Environmental monitoring using ultra-deep sequencing of diatom community. (*in prep*).

Neumeyer R, Baur H, Guex G-D, Praz C A new species of the paper wasp genus *Polistes* (Hymenoptera, Vespidae, Polistinae) in Europe revealed by morphometrics and molecular analyses. ZooKeys 400: 67-118.

Press Articles

"Species diversity in Switzerland – 50,000, 70,000 or 500,000? Hotspot 28, 2013

SwissBOL was recently featured in an article published in the Tierwelt journal. http://www.tierwelt.ch/?rub=4499&id=39663.

« La biodiversité genevoise sous la loupe du public » - Le Temps (19 September 2014).

Arten aufspüren – mit Augen, Ohren und DNA-Tests

Jede dritte Tier- und Pflanzenart der Schweiz ist bedroht. Um sie wirksam zu schützen, braucht es Artenkenner, die Pflanzen und Tiere im Feld erkennen. Gen-Analysen können klassische Artenkenntnis in Zukunft noch erweitern.

In der rechten Hand ein Fangnetz, in der linken Klemmbrett, Papier und Kugelschreiber, ums Handgelenk ein GPS-Gerät, geht André Rey über die Wiese. Plötzlich bleibt er stehen. Ein helles Zirpen hat seine Aufmerksamkeit erregt. Er sucht Gräser und Klee mit den Augen ab, um dann blitzschnell mit dem Fangnetz darüberzustreichen. «Das ist eine besondere Art», erklärt er, als er eine kleine Heuschrecke herausholt, ihre Sprungbeine vorsichtig zwischen Daumen und Mittelfinger geklemmt. Kaum länger als ein Daumennagel ist die Zweifarbige Beissschrecke. Der Grossteil ihres Körpers ist leuchtend grün, nur ihr Rücken, der untere Teil ihrer Beine, ihre Augen und ihre langen Fühler sind von einem zarten Heilbraun.

Eigentlich hätte Rey sie gar nicht fangen müssen. Häufigere Arten hat er direkt in seine Liste eingetragen und mit dem GPS erfasst, sobald er sie hörte. Denn was für ungeübte Ohren als ein einziger undefinierbarer Klangteppich über der Wiese liegt, setzt sich für Rey aus Einzelgesängen zusammen: Aus dem allgegenwärtigen ZedZedZedZed des Gemeinen Grashüpfers, dem Schrrrrrr – Schrrrrrr – Schrrrrrr des Nachtigall-Grashüpfers.

André Rey ist heute im Auftrag des Kantons Zürich unterwegs, um Heuschrecken, Schmetterlinge, Libellen, Wildbienen, Reptilien, Amphibien und Vögel zu kartieren in einem Gebiet, für welches eine kantonale Schutzverordnung erarbeitet werden soll. An anderen Tagen bestimmt er im Feld Insekten, Vögel, Amphibien oder Reptilien für Erfolgskontrollen – damit seine Auftraggeber tatsächlich etwas genützt haben.

Zuerst kennenlernen, dann schützen

Und wirksame Schutzmassnahmen sind dringend nötig. Laut der 2012 veröffentlichten Strategie Biodiversität des Bundesrates ist Umwelt sind von den rund 46 000 in der Schweiz bekannten Pflanzen-, Tier- und Pilzarten rund ein Drittel in ihrem Bestand bedroht. Auch viele einst häufige Arten sind betroffen von drastischen Arealverlusten und sinkenden Bestandesgrössen. Und noch immer wird jede Sekunde fast ein Quadratmeter Boden überbaut, Lebensräume werden durch Strassen zerschnitten oder so stark genutzt, dass viele Arten darin nicht mehr überleben können – eine Verbesserung der Situation ist derzeit nicht in Sicht.

«Um zu wissen, was verloren geht, wenn man irgendwo einen Wohnblock oder ein Einkaufzentrum auf eine Blumenwiese stellt, müssen wir wissen, welche Heuschrecken, Schmetterlinge, Mäuse oder Vögel da ihren Lebensraum haben. Wir können nur schützen, was wir kennen», sagt Roland Graf. Er leitet den Zertifikatslehrgang «CAS Säugetiere – Artenkenntnis, Ökologie & Management», der seit 2010 an der Zürcher Hochschule für Angewandte Wissenschaften (ZHAW) in Wädenswil angeboten wird, in Zusammenarbeit mit der Schweizerischen Gesellschaft für Wildtierbiologie und der Hochschule hepia in Genf.

Die ZHAW habe diesen und weitere Studiengänge zu Artenkenntnis eingeführt, weil Letztere an den Universitäten heute nur noch am Rande vermittelt werde. «Wer Biologie studiert, erfährt oft nur wenig über die einheimischen Tier- und Pflanzenarten. Viele Studienabgänger können nicht bestimmen, was sie draussen sehen – geschweige denn bei einer Gämse das Alter einschätzen oder bei einem Reh feststellen, ob es ein Männchen oder ein Weibchen ist. Ohne solches Wissen ist es schwierig, mit Jägern, Forstern oder Landwirten Lösungen zu Wildtierfragen zu diskutieren.»

Milbenspezialisten? Nirgendwo in Sicht

Schon die Grundkenntnisse, mit denen man heute ins Biologiestudium eintrete, seien viel tiefer als noch zu seiner Studienzeit, sagt Reto Nyffeler, Kurator des Herbariums und Dozent am Institut für systematische Botanik der Universität Zürich. «Ich habe am Gymnasium noch gelernt, wie man mit dem Bestimmungsbuch im Feld Pflanzen bestimmt. Das können wir heute selbst bei interessierten Studenten nicht mehr voraussetzen.» Zudem würden Artenspezialisten an Universitäten oft nicht ersetzt, wenn diese in Pension gingen. «Die Biologie ist heute sehr viel breiter als noch vor 100 Jahren», sagt er. Artenkenntnis sei neben Mikrobiologie, Immunologie, Genetik oder Neurobiologie nur eines von zahlreichen Teilgebieten.

«In gewissen Bereichen gibt es tatsächlich zu wenig Artenkenner», sagt Wolfgang Nentwig, Spinnen-Kenner und Professor für Ökologie an der Universität Bern. Dennoch: Im Lehrplan aufwerten müsse man Artenkenntnis nicht. «Verdonnert man einen Immunologen dazu, wird aus ihm ein grottenschlechter Artenkenner, weil ihm das nötige Herzblut fehlt.» Wer sich dafür interessiere, habe nach wie vor genügend Möglichkeiten, sich das Wissen anzueignen – an der Uni wie auch ausserhalb.

Dafür sieht Nentwig in den heutigen molekularbiologischen Methoden nie dagewesene Chancen, die Artenkenntnis zu erweitern. Denn klassische Artenkenner gebe es vor allem für Pflanzen und Wirbeltiere. «Die ma-chen aber nur einen Viertel der weltweiten Organismen aus. Drei Viertel sind Wirbellose wie Insekten, Spinnen, Krebstiere, Würmer. Und suchen Sie einmal einen Milben-Spezialisten. Sie werden keinen finden.» Dabei spielen diese laut Nentwig in Ökosystemen eine zentrale Rolle: Extrahiere man aus einer Bodenprobe Tiere, seien oft die Hälfte davon Milben, darunter viele Pflanzenschädlinge und Räuber, die Schädlinge befallen.

Er verfolgt mit Interesse das Projekt «Swiss Barcode of Life», kurz SwissBOL, 2010 gestartet, verfolgt es das Ziel, die Diversität des Lebens in der Schweiz zu erfassen: Für jede der schätzungsweise 50 000 bis 70 000 Arten soll ein DNA-Fragment oder eben «Barcode» gefunden werden, mit dessen Hilfe sich eine Art eindeutig bestimmen lässt. «Das ist natürlich ein ehrgeiziges Ziel», sagt Projektkoordinatorin Sofia Wyler von der Universität Genf, «wir sind erst am Anfang.»

Bisher sind «Barcodes» von etwas mehr als 200 Pflanzen und Tieren in der Datenbank erfasst. Doch dank genetischer Analysen habe man bereits eine neue Wespenart entdeckt. Mit der Methode liessen sich in Zukunft auch schwer bestimmbare Arten zweifelsfrei einordnen, und eine Bestimmung sollte auch dann möglich sein, wenn von einer Pflanze nur der Teil eines Blattes vorhanden oder von einem Insekt nur das Bein erhalten sei.

Keine Konkurrenz für den Artenkenner

Schliesslich könne man ein Tier auch unabhängig von seinem Stadium erkennen. Ein grosser Vorteil wäre dies etwa bei Insekten, wo bisher viele Larvenstadien nicht bestimmbar sind, oder bei sogenannten Wenigborstern – einer zahlreiche Arten umfassenden Gruppe von Würmern, die zur Beurteilung der Wasserqualität beigezogen werden. «Heute muss man sehr viele Tiere wegwerfen, weil man sie erst im ausgewachsenen Stadium bestimmen kann», sagt Wyler. Sie sieht SwissBOL nicht als Konkurrenz zu klassischer Artenkenntnis: «Barcoding kann Artenkennern in Zukunft zeitaufwendige Bestimm-Arbeit abnehmen – so können sie ihr Spezialwissen dort einsetzen, wo es unersetzbar bleibt.»

André Rey hat keine Angst, dass DNA-Analysen seine Arbeit eines Tages überflüssig machen. «Um eine DNA-Probe von einem seltenen Tier zu bekommen, muss man es erst einmal finden und fangen. Das geht nicht ohne Artenkenntnis.» So findet er seltene Heuschrecken oft nur, weil er ihre Stimmen kennt. An diesem Feldtag wird er Vögel bestimmen, die er nur hört oder vorbeifliegen sieht, sowie einen kleinen Schillerfalter, der wegflattert, ohne dass er ihn erwischt. Und das kaum einen Millimeter kleine Ei eines grossen Schillerfalters, das auf dem Blatt einer Salweide klebt, entdeckt er nur, weil er genau weiss, wo er danach suchen muss. *Martina Huber*

Feldarbeit: Eine Ökologin bestimmt eine Pflanze auf einer Kuhweide.

- A grant of 5'000CHF from the Société Académique de Genève was obtained to purchase a -80°C freezer. The department of Genetics and Evolution of the University of Geneva also contributed 4'180CHF to the purchase of this freezer.
- Further funding has been requested from the Direction Générale de la Nature et du Paysage (DGNP) through the Conservatoire et Jardin botaniques de la Ville de Genève to continue sequencing plant specimens from Geneva. The response was negative because an emphasis is being placed on intraspecific diversity but a collaboration in the near-future is still possible.
- The Aquatic Oligochaetes project was awarded an INNOGAP grant of 30'000CHF from the University of Geneva Technology Transfer Office (UNITEC; September2013-April2014).
- In the spring a grant of 10'000CHF was also obtained for the Aquatic Oligochaetes project from the Foundation Ernst et Lucie Schmidheiny.
- Due to the losses that correspond to the overheads and VAT charged by the University of Geneva, the department of Genetics and Evolution, through the budget of the Jan Pawlowski's lab, participated with 21'200CHF for the lab activities.
- A recent request for funding has been submitted by the Bioscope to the Foundation Hans Wilsdorf. If the request is accepted, a sum of 115'840CHF (over three years) is budgeted for the activities related to the barcoding part of this new project that focuses on the biodiversity of Geneva.

Funding Agency	Allocated Grant (CHF)	Project
Société Académique de Genève	5'000	SwissBOL DNA Bank
Department of Genetics and Evolution UniGE	4'180	SwissBOL DNA Bank
UNITEC INNOGAP Grant	30'000	Aquatic Oligochaetes as bioindicators
Fondation Ernst et Lucie Schmidheiny	10'000	Aquatic Oligochaetes as bioindicators
Department of Genetics and Evolution UniGE	21'200	SwissBOL Molecular Facility
TOTAL	**70'380**	

GOALS FOR 2015

Status & Fundraising

- To establish the SwissBOL as an Association
- To raise funds close to private foundations to ensure the development of well circumscribed projects (defined taxonomic groups, specific questions raised by previous SwissBOL projects, etc)

National & Local Level

- To sustain the national network through the organization of specific workshops for the definition of the SwissBOL future (needs, goals, measures, contributions, etc)
- To compile the outcomes of the individual SwissBOL financed projects in a single document, where hands-on methods and difficulties would be described and commented
- To participate at the application of the Action Plan for the Swiss Biodiversity Strategy in what it concerns the comprehension of the national genetic diversity and the implementation of Biomonitoring studies
- To define a field of mutual interest between the SwissBOL and the Direction Générale de la Nature et du Paysage (DGNP) and to develop cooperating projects

International Relationships

- To develop and reinforce collaborations with similar European and international barcoding programs
- To participate in national and international conferences to promote the SwissBOL project (Workshop for European National Barcode Campaigns, 27-28 January in Bonn; Seventh International Barcode of Life Conference)

Biodiversity DNA Bank

- To define the role of the Museum of Natural History of Geneva and the Botanical Garden of Geneva in the secure, long-term DNA storage
- To work toward the integration of the SwissBOL DNA bank with that of the DNA Bank Network

Data Publication

- To finalize the work toward the presentation of genetic data via GBIF.ch
- To contribute data from all internal and external projects to the national database, as well as to BOLD Systems and GenBank

I. Program of the SwissBOL meeting (31st of October)

9:30-9:45   **Pre-conference coffee**

9:45-10:10   Welcome, SwissBOL achievements
Sofia Wyler (University of Geneva, sofia.wyler@unige.ch), Jessica Litman (Museum of Natural History Neuchatel, jessica.litman@unine.ch)

10:10-10:35   ABOL, the Austrian Barcode of Life Initiative: examples preceding the conquest of air
Nikolaus U. Szucsich (Natural History Museum Vienna, Nikolaus.Szucsich@NHM-WIEN.AC.AT), Daniela Bartel, Thomas Dejaco, Oliver Macek, Monika Carol Resch, Julia Shrubovych, Manfred Walzl, Loris Galli,and Günther Pass

10:35-11:00   DNA barcoding plants
Peter Hollingsworth (Royal Botanic Garden Edinburgh, P.Hollingsworth@rbge.ac.uk)

11:00-11:15   **Coffee break**

11:15-11:30   Barcoding of (selected) Swiss endemic beetles
Marco Bernasconi (Natural History Museum Luzern, Marco.Bernasconi@lu.ch),
Christoph Germann (Natural History Museum Bern and Natural History Museum Luzern, germann.christoph@gmail.com)

11:30-11:45   Morphology or molecules? Species delimitation in Western Palearctic leaf-cutting bees
Christophe Praz (University of Neuchâtel, christophe.praz@unine.ch)

11:45-12:00   A cryptic species of paper wasp (*Polistes*) detected due to barcoding
Rainer Neumeyer (Oekoservice Neumeyer and Funk, neumeyer.funk@bluewin.ch), Hannes Baur, Gaston-Denis Guex and Christophe Praz

12:00-12:15   Morphometric analysis and taxonomic revision of *Anisopteromalus* Ruschka (Hymenoptera: Chalcidoidea: Pteromalidae) – an integrative approach
Hannes Baur (Natural History Museum Bern, baur.hannes@gmail.com), Yvonne Kranz-Baltensperger, Astrid Cruaud, Jean-Yves Rasplus, Alexander V. Timokhov, Vladimir E. Gokhman

12:15-12:30   Barcoding of the Swiss aquatic insects: Stoneflies as a study case
Jean-Luc Gattolliat (Cantonal Museum of Zoology Lausanne, jean-luc.gattolliat@vd.ch), Sofia Alexandra Caetano Wyler, Michel Sartori, Jan Wojciech Pawlowski

12:30-12:45   Quantitative mass barcoding of dung organisms
Wolf U. Blanckenhorn (University of Zürich-Irchel, wolf.blanckenhorn@uzh.ch), Patrick Rohner, Andres Buser, Johannes Haugstetter

12:45-13:45   **Lunch** (served at the MHNN)

13:45-14:00	DNA barcoding applied to bioindication: case studies of diatoms and oligochaetes **Jan Pawlowski** *(University of Geneva, jan.pawlowski@unige.ch); Laure Apothéloz-Perret-Gentil, Joana Visco (diatomées); Régis Vivien, Sofia Wyler (oligochaetes)*
14:00-14:15	Swiss NEMA-BOL: Barcoding of Swiss soil nematodes - a proof of concept **Sebastian Kiewnick** *(Agroscope - Wädenswil, sebastian.kiewnick@agroscope.admin.ch), Jürg Frey*
14:15-14:30	Earthworm diversity in Switzerland: focus on potential cryptic species **David Singer** *(University of Neuchâtel, david.singer@unine.ch), Claire LeBayon*
14:30-14:45	Barcoding the shelled terrestrial Gastropoda of Switzerland – preliminary results *Bertrand Fournier, Jan Mysak, Sofia Wyler, Enrique Lara,* **Edward Mitchell** *(University of Neuchâtel, edward.mitchell@unine.ch)*
14:45-15:00	DNA barcoding of Swiss spiders **Tamara Spasojevic** *(University of Bern, tamara.spasojevic@students.unibe.ch), Christian Kropf, Wofgang Nentwig, Liana Lasut*
15:00-15:15	All hiding behind a morphospecies: the problem of cryptic species in protists exemplified by *Quadrulella symmetrica* **Enrique Lara** *(University of Neuchâtel, enrique.lara@unine.ch), Anush Kosakyan*
15:15-15:30	**Coffee break**
15:30-15:45	Bar-coded amplicon 454 pyrosequencing for barcoding the mycobiont in Swiss lichens **Kristiina Mark** *(Swiss Federal Research Institute WSL, krismark@ut.ee), Carolina Cornejo, Christoph Scheidegger*
15:45-16:00	How alpine are alpine fungi? First results from barcoding alpine taxa of macrofungi **Beatrice Senn-Irlet** *(Swiss Federal Research Institute WSL, beatrice.senn@wsl.ch), Michèle Lerch, Carolina Cornejo*
16:00-16:15	Variation in the composition of above ground fungal communities of wheat and consequences for human health **Hélène Hirzel** *(Institute for Work and Health, University of Lausanne and Geneva, Helene.Hirzel@hospvd.ch)*
16:15-16:30	Barcoding approach for strain identification of pathogenic oomycete *Saprolegnia parasitica* in the diseased fish population on the Doubs **Lenka Luptakova** *(University of Neuchâtel, lenka.luptakova@unine.ch), Lassaâd Belbahri, Christophe Paul and Marion Quartier*
16:30-16:45	Barcoding Kids: A Citizen Science Biodiversity Project *Candice Yvon, Céline Brockmann,* **Bruno J. Strasser** *(University of Geneva, Bruno.Strasser@unige.ch)*
16:45-17:00	DNA-based identification of rosewood from Madagascar **Sonja Hassold** *(ETH Zürich, sonja.hassold@env.ethz.ch), Alex Widmer*
17:00-17:30	Future of SwissBOL and discussion **Jan Pawlowski** *(University of Geneva, jan.pawlowski@unige.ch)*
Poster:	DNA barcoding of horsetails in Switzerland (*Equisetum*: Equisetaceae) *Alessio Maccagni, Frédéric Sandoz, Jason Grant (University of Neuchâtel)*

II. Interim Report (31st of March)

Swiss Barcode of Life
A genetic inventory of Swiss biodiversity

SwissBOL interim progress report   31 March 2014

Please answer the following questions by either filling in the blank or by highlighting one of the responses.

1. Project author (just first author is fine): _____

2. Project target organism: _____

3. Project target genes: _____

4. Approximately how many species/specimens do you expect to sequence during the course of your project? _____ species; _____ specimens

5. The sampling (of specimens) for our project
        1. has not yet begun.
        2. is in progress.
        3. has been completed.
    (If you answered 2., approximately what percentage of your total expected sampling has been finished? _____%)

6. The DNA extractions for our project
        1. have not yet begun.
        2. are in progress.
        3. have been completed.
    (If you answered 2., approximately what percentage of your total expected DNA extractions has been finished? _____%)

7. The DNA sequencing for our project
        1. has not yet begun.
        2. is in progress.
        3. has been completed.

8. For those who answered 2. or 3. to the previous question (if you answered 1. to the

previous question, leave the present question blank)

        1. Approximately how many species have you sequenced so far? _____

        2. Approximately how many specimens have you sequenced so far? _____

        3. Approximately how many sequences have you generated so far? _____

        4. Have any of your sequences been submitted to GenBank, BOLD Systems, or any other repository for DNA sequence data? If so, where? _____

        5. Have any of your results been published? If so, please give the citation here:

9. What is the tentative deadline for finishing your project (month/year)? _____

10. Please use this space to make any further comments. We'd like to hear about any obstacles that may have arisen during the course of your project, any changes made to your original project, your preliminary results, or about anything else that may be relevant to your project.