

XVII INTERNATIONAL
SYMPOSIUM ON
TRICHOPTERA



5-9 SEPTEMBER 2022
LUNZ AM SEE – AUSTRIA

**Book of Abstracts and
other Information**



IHG⁺
Institute of
Hydrobiology and Aquatic
Ecosystem Management



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Logo design: Simon Vitecek & Astrid Schmidt-Kloiber; species: *Drusus alpinus*

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Welcome message

It is a pleasure for us that – 48 years after the first meeting – the International Symposium on Trichoptera (IST 2022) returns to Lunz am See, Austria. The conference takes place from 5th to 9th September 2022 in the “Haus der Wildnis” in the middle of Lunz. The meeting is organised as a joint effort by the Institute of Hydrobiology and Aquatic Ecosystem Management (University of Natural Resources and Life Sciences, BOKU Vienna) and the WasserCluster Lunz – Biologische Station GmbH.

After two years of planning and postponements due to the pandemic, we are looking forward to meeting old and new colleagues, having fruitful discussions and exciting new insights into the wonderful world of aquatic environments focusing on their dazzling inhabitants, the caddisflies. In that sense, we are grateful that all of you have made the long and tedious journey to Lunz to attend this event in person despite the interesting times we live in. We had planned the meeting to be a live event, but as the COVID situation still is not entirely under control, we decided to open up the meeting also for remote access. This also gives us the opportunity to welcome the contributions of scientists who cannot attend in person and share this conference with more caddisfly enthusiasts and specialists.

The IST 2022 now ensembles researchers from 21 different countries, the majority of them attending live. In total we have 55 registered scientific contributions (3 keynote talks, 26 live and 12 video talks as well as 14 posters) ranging from evolution, taxonomy and phylogeny to ecology, conservation and assessment.

The mid-conference excursion will bring most of the participants to the IUCN category Ia protected area “Wildnisgebiet Dürrenstein-Lassingtal” (wilderness area Dürrenstein-Lassingtal), a unique region in Austria with pristine and unaffected forest areas, which also was recognised as Austria's first and only UNESCO World Natural Heritage Site. This excursion will not only bring you into fascinating nature, but also will allow for loose but lively discussions among friends and colleagues.

We hope you will all enjoy the 17th International Symposium on Trichoptera in Lunz!

Wolfram Graf, Simon Vitecek, Hans Malicky, Astrid Schmidt-Kloiber





Introduction

compiled by Hans Malicky

The event

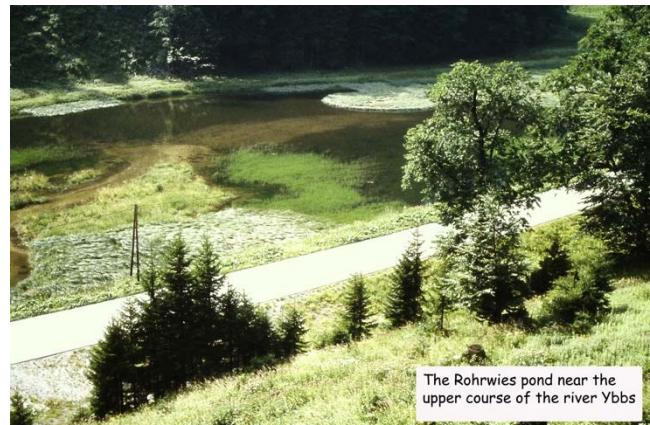
The 17th International Symposium on Trichoptera comes back to Lunz am See, where the first Symposium was held in 1974. Earlier attempts to organise an International Symposium exclusively for Trichoptera were not successful. In the former Soviet Union, Sofia Grigorievna Lepneva had planned such a meeting, but she died before she could realise it. In the former Czechoslovakia, Karel Novák made a similar attempt but could not get the permission from his authorities. In 1974, Hans Malicky intended to meet fellow caddisfly workers of those days but could not travel all over the world to visit them all because of the lack of funding. So he invited them to a meeting in Lunz, and they came.



The Teichbach in the immediate vicinity of the Biological Station, with members of the First International Symposium on Trichoptera, 1974.

The region

Lunz am See is situated in the mountains of southern Lower Austria and has a long history. The name Lunz is of Slavic origin which means that the settlement had already existed in the 6th Century. The original name may have been lomnica. The oldest name „liunze in montanis“ is found in a document by the bishop Wolfger of Passau in 1203. As a curiosity it may be mentioned that in the same document the existence of the famous Austrian medieval poet Walther von der Vogelweide was documented. His poems were well known, but this is the only document which says that he had really existed.



The Rohrwies pond near the upper course of the river Ybbs

Lunz am See is situated in the district of Scheibbs, which is unusually well researched in a faunistic respect. Except for the research activities at the Biological Station Lunz, it is mainly the result of the monumental work of Franz Ressl, which is documented in five book volumes up to now (Ressl 1980, 1983, 1995, Ressl & Kust 2010, Kust & Ressl 2015). Ressl was an amateur scientist who devoted himself in an admirable manner to research in the historical and natural sciences of his native land (Malicky 2015). He died in 2011, but his notebooks and records are not yet completely evaluated.



The Biological Station Lunz

The Biological Station Lunz was founded in that place because the site lies in a largely undisturbed landscape of mountains and lakes, and because the private owner of the area, Carl Kupelwieser, was fond of natural sciences. Later it turned out that this place is unique in the high diversity of its running waters. We know of no other site worldwide where a research institution has such a rich variation of streams of different types in a short distance. The photographs may give an impression. The Teichbach, which runs in the immediate vicinity of the building, shows extreme daily temperature fluctuations: in early spring it may have 2°C at 7 h in the morning, but 12°C at noon. The Schläglbergbach on the other hand has a minor daily variation of not more than 3°C, and in winter it has over 0°C. The outlet of the lake may have up to 24°C during fine summer weather, but may quickly drop to 15°C after heavy rainfall, and in winter it is always close to 0°C. On the other hand, the Schreierbach has a constant temperature of 6,5°C all over the year, with a rare fluctuation between 5,5°C to 8°C.



The Biological Station Lunz had a long tradition in biological field research¹. This institution was founded in 1906 and was first intended to facilitate any zoological, botanical or similar field work. In those years scientists did not have cars to go quickly out of towns for a short research on plants or animals. The way to Lunz was long: first by railway, changing the train several times, and then a five kilometres walk from the railway station to the Biological Station at the eastern edge of the lake, with all the necessary equipment in the rucksack. Therefore, the usual stay of researchers was for weeks or even months. The studies were performed within walking distance of the building, and usually one could meet fellow workers of related sciences from all over the scientific world. It was a unique opportunity to sit together during long coffee breaks and endless discussions and to start co-operation on joint field projects: geology, climate and weather research, study of insects, lichens, mosses, ornithology and the like. One remarkable result of this co-operation was the detection of a site

¹ <https://www.wcl.ac.at/index.php/en/about-us/history>



(*Grünloch*, a large *Doline*, which is a karstic depression) high in the mountains where in winter, temperatures lower than -50°C were recorded. Newspaper people with a need for sensation made Lunz itself to be the “European coldness pole”, an opinion which now is still widespread among people. In reality, Lunz has a rather cool climate with high rainfalls like many other sites at the northern slope of the Alps.

In 1924, *Franz Ruttner* was called from Prague to join the Biological Station. A short time later he became its director until his retirement. He died in 1961. He was a unique and dominant personality. He had originally studied aquatic organisms, so the main work of the Station was focussed on the newly established scientific branch called *Limnology* (of which he was one of its founders). In these days, limnology was understood as the study of lakes. Running waters were “detected” by limnologists much later. Franz Ruttner was one of the leaders of the famous Sunda Expedition to Indonesia in the years 1928 to 1929, which created the fundamentals of tropical limnology, and the results of which were published in many volumes of the *Archiv für Hydrobiologie*.

The Biological Station Lunz was closed in 2003. The freshwater studies are however continued by a newly founded institution called WasserCluster Lunz². The WasserCluster Lunz is an inter-university centre for freshwater ecosystem research with a broad focus: research targets include nutrient and carbon dynamics, plankton ecology, trophic ecology and freshwater biodiversity.

Caddisfly research in Lunz

Among the visitors of the Biological Station who worked over a longer time period, were amateur scientists who used the summer holidays for their studies. One of them was Hans Krawany, a teacher from St. Pölten. He started to study the caddisflies in 1925, mainly the larvae, in the streams in and around Lunz. He found important connections between the composition of the fauna and the water temperature. This pioneer work (Krawany 1928 – 1933) shows clearly the situation of the knowledge on Trichoptera in those years. In later years, Gertrud Pleskot and Ernst Pomeisl (Pleskot 1951) continued this study in Lunz. Elisabeth Danecker studied the hygropetric fauna including *Tinodes zelleri* and two *Stactobia* species (Danecker 1961).

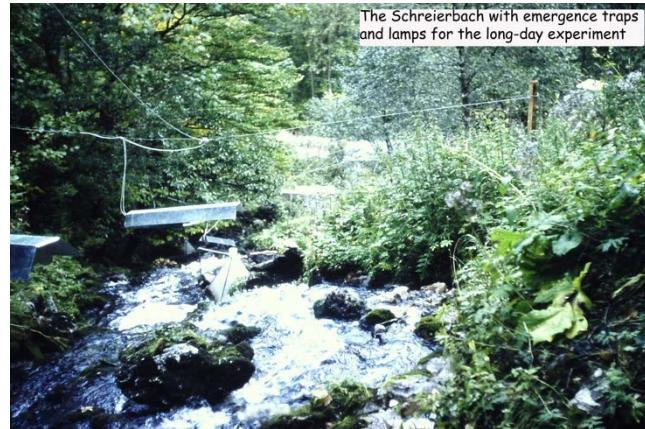
From 1969 onwards, Hans Malicky had the opportunity to continue these studies. He came as a zoologist to the Biological Station Lunz of the Austrian Academy of Sciences and started with the study of running water ecology and, in particular, with the taxonomy and biology of caddisflies. He studied the water temperatures of the streams over a whole year (Malicky 1978, 2014) and improved the identification of species by extending to the adult caddisflies. More tasks followed, and the result was a better taxonomic knowledge of the adult Trichoptera of the whole of Europe. The *Atlas of European Trichoptera* was published in 1983, and its second edition in 2004. More than 30 streams in the immediate surrounding of Lunz were studied with emergence traps, usually over one-year periods, but the Schreierbach, the Teichbach

² <https://www.wcl.ac.at/index.php/en/>



and the upper part of the Kothbergbach over eight years, with the assistance of Erich Lanzenberger. At several sites, light traps helped to complete the survey of caddisflies. The caddisflies in the samples were immediately identified, and other trapped insects were given to fellow workers in other institutions for further study. The resulting data may be found in the Zobodat database³.

As daylength plays an important role in the phenology of plants and animals, a field experiment was performed at the Schreierbach, a stream with a constant water temperature of 6,5°C over all the year. Lamps were placed over the stream to supply the bottom with daily 18 hours of light over two years (Malicky 1981). In the Kothbergbach, several types of construction of emergence traps were compared over a period of eight years (Malicky 2002, 2002a). More information on these streams, including the lists of species, may be found in the book "Lebensräume von Köcherfliegen" (Malicky 2014). More examples of streams with their caddisflies over the whole of Europe are found in this book, as well as examples of tropical streams.



The Schreierbach with emergence traps and lamps for the long-day experiment

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- Krawany, H., 1932, do., 4. Das Schlöglmoosbächlein. – l.c. 26:388-391.
- Krawany, H., 1932, do., 5. Zur Metamorphose von *Synagapetus ater* Klap. – l.c. 26:391-394.
- Krawany, H., 1932, do., 6. Eine neue Goerinenlarve. – l.c. 26:394-396.
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³ www.zobodat.at



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- Ressl, F., Kust, T., 2010, do. 4. Teil. – Wiss. Mitt. Niederösterr. Landesmuseum 20:11-436.



General information about the meeting

Lunz am See

The mountaineering village of Lunz am See is located in the heart of the Mostviertel region and offers numerous hiking routes as well as the only natural lake in Lower Austria, Lake Lunz with its unique lake stage. Every year the "Wellenklänge Festival" with international artists takes place here and attracts culture enthusiasts to the market town.

The small village of Lunz has around 1,800 inhabitants and is called the "cold hole" of Austria. The average annual temperature in Lunz is 12°C and it rains 537 mm a year. The highest average temperature in Lunz is 24°C in July.

More information can be found here: <https://www.ybbstaler-alpen.at/en/lunz>



Impressions of Lake Lunz

The venue

The "Haus der Wildnis" (House of Wilderness) – where our conference takes place – is located in the centre of Lunz. It opened in 2021 and is a gateway to the surrounding wilderness area. The House of Wilderness is intended to convey to all visitors that the wilderness area Dürrenstein-Lassingtal is unique in its kind in Austria, in the Alps and in Western Europe. Together with areas of the Kalkalpen National Park, large parts of the Wildnisgebiet Dürrenstein-Lassingtal have been awarded recognition as Austria's first and only UNESCO World Natural Heritage Site.

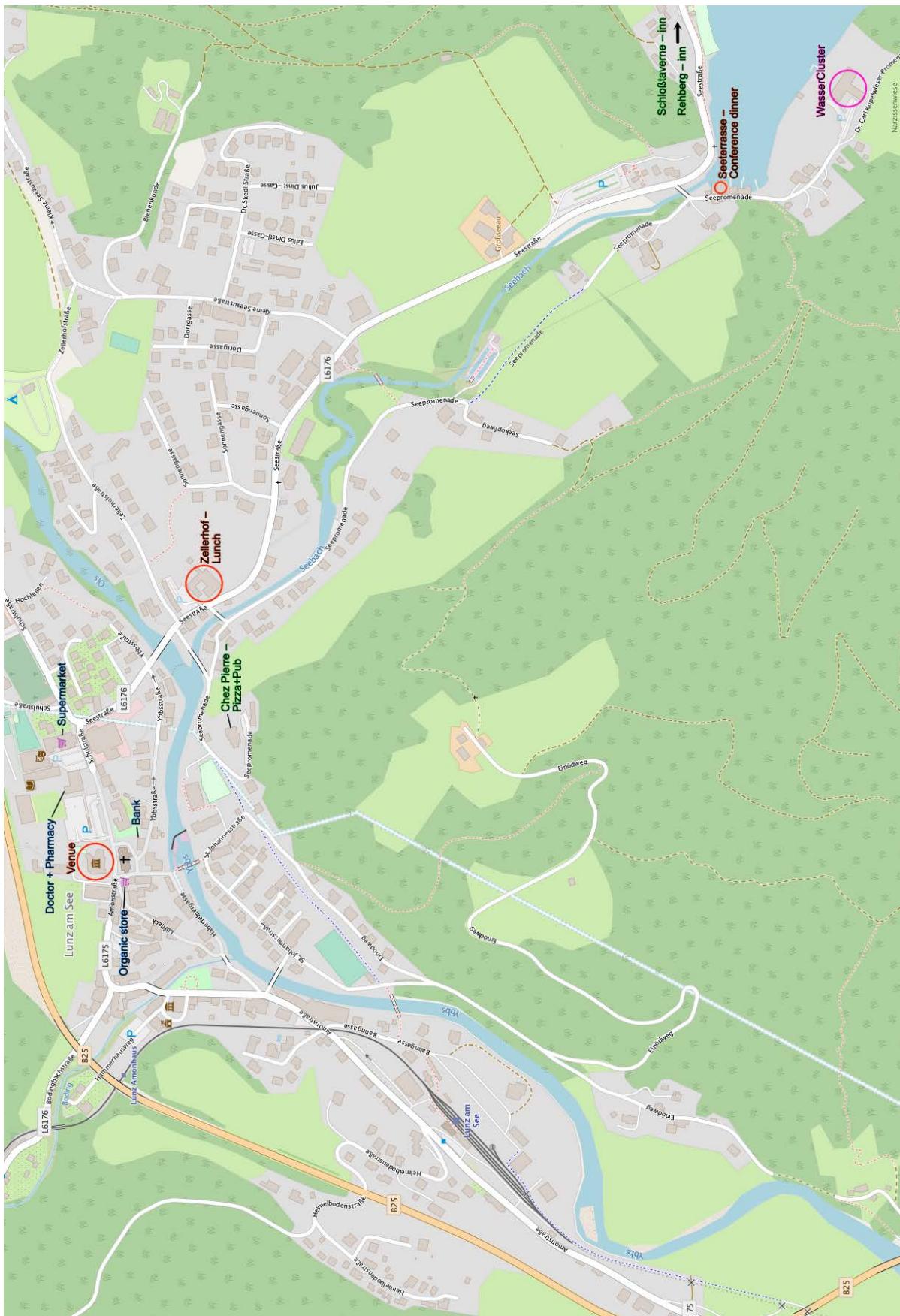


The "House of the Wilderness"



Map of Lunz

The following map illustrates the most important facilities in Lunz.





Venue

House of the Wilderness – Haus der Wildnis
Kirchenplatz 5
3293 Lunz am See
+43 7486 21122
info@haus-der-wildnis.at

Grocery

Supermarket Unimarkt
Schulstr. 7
+43 7486 8083
lunz.huber@unimarkt-partner.at

Organic grocery

Genuss Platz'l
Kirchenplatz 4
+ 43 680 205 11 92
kontakt@genussplatzl.at

Bank (including cash machine)

Raiffeisenbank Mittleres Mostviertel
Bankstelle Lunz Am See
Kirchenplatz 2
+43 7486 8254 2006
office@rbmm.at

office hours

Monday 08:00 - 12:00, 14:00 - 16:00
Tuesday 08:00 - 12:00
Wednesday 08:00 - 12:00
Thursday 08:00 - 12:00
Friday 08:00 - 12:00, 14:00 - 17:00
Closed on Saturdays and Sunday

Doctor (including pharmacy)

Dr. Wolfgang Dörfler
Schulstraße 1
+43 7486 88 00
www.dr-dorfler.at

Restaurants

Zellerhof (lunch location)
Seestraße 5
+43 664 44 20 237
+43 7486 8450
zellerhof@lunz.at
<https://www.zellerhof-lunz.at>

Joschi Schlosstaverne
Seehof 2
+43 7486 20276
<https://www.schlosstavernelunz.at>

Zur Paula
Bodingbachstrasse 28
+43 7486 8220

Seeterrasse (conference dinner)
Seepromenade 11
+43 7486 8303
lunz@seeterrasse.at
<https://www.seeterrasse.at>

Chez Pierre
Seepromenade 6
+43 7486 80417
<http://www.chezpierre.at>

also see here

https://www.tripadvisor.at/Restaurants-g2274952-Lunz_am_See_Lower_Austria.html



Registration

Registration is possible all Monday morning (9:40 – 12:00) as well as from 13:00 to 14:00 before the Welcoming notes. Additionally, you can register whenever the registration desk is open.

Oral presentations

Oral presentations should last 15 minutes maximum plus 5 minutes discussion time. Due to the tight schedule, speakers are requested to strictly respect the allowed time. Each session will have a chairperson to monitor timekeeping.

All live presenters are asked to upload their presentations to the conference laptop either in the morning before 9:00 or in the lunch break (12:00 – 14:00). The use of personal laptops for presenting is generally not allowed.

Video talks need to be delivered to the organisers as recorded sessions (preferably as mp4-files) prior to the conference starting date (September 5th). Recorded talks will then be played according to the schedule. Remote presenters are asked to be present during their talk and afterwards to answer questions of the live audience.

Poster presentations

Posters should be in a portrait orientation and not exceed the size of the A0 format (84,1 cm x 118,9 cm). Posters should be hung up at the foreseen and numbered display boards. Materials for pinning the posters can be found at the registration desk.

Posters will be displayed the entire conference time. On Thursday at 16:00 to 17:40 there will be a dedicated poster session. During that time authors are requested to be available at their stands to discuss their work. Please remove your poster at the end of the conference.

Breaks

Coffee and tea breaks will be directly on site in the little coffee shop. Please respect the break times.

Lunch will be served in restaurant “Zellerhof”. Zellerhof can be reached within an unhurried 10 minutes walk from the conference venue. If you need a lift to the restaurant, please inform the staff at the registration desk. Lunch also includes a vegetarian option according to your pre-selection. Vouchers are included in your conference bag.



Welcome reception and conference dinner

On Monday at 18:00 there will be welcome reception at the House of Wilderness. This reception will offer a range of local products and is organised in collaboration with regional farmers and manufacturers.

The conference dinner will take place on Thursday at 18:30 at restaurant “Seeterrasse” directly at Lake Lunz. The restaurant can be reached in a 20 to 30 minutes walk. If you need a lift to the restaurant, please inform the staff at the registration desk.

The conference dinner includes four courses and a soft drink and needs to be paid on site (42 €, cash only). Vouchers for alcoholic drinks are included in your conference bag.

Mid-conference excursions

The mid-symposium excursion takes place on September 7th, starting at around 9:00.

For the conference excursion we offer three different options:

- Excursion 1: Travel by bus to the “Wildnisgebiet Dürrenstein” (IUCN Strict Nature Reserve and Wilderness Area): this trip will take you to a stream headwater network in the Steinbachtal (around 47.7660 N, 15.0038 E) at the western flanks of the Dürrenstein Massive. Sturdy shoes and rainwear are recommended. Lunch will be offered as packed lunch.
- Excursion 2: Walk in the “Seetal” to visit the historical sites of the first Trichoptera Meeting. Lunch will be arranged in Zellerhof.
- Excursion 3: Boating on Lake Lunz. Lunch will be arranged in Zellerhof.

For further details see information at the registration desk.

Accompanying persons

Registered accompanying persons are welcome to all breaks (coffee/tea, lunch) as well as to the social events (welcome reception, conference dinner). The registration fee also covers a conference bag.

The following excursions are organised for accompanying persons:

- Tuesday: Lunz walk including the local museum. The excursion will last half a day. Lunch will be arranged in Zellerhof.
- Thursday: Excursion to the historical abbey Stift Melk⁴. The excursion will start at around 9:00 returning in the early afternoon. Lunch will be arranged in Melk.
- Wednesday: Accompanying persons are welcome to join the mid-conference excursions.

For further details see information at the registration desk.

Apart from that, Lunz offers a variety of nice walks including a walk around the lake.

⁴ <https://www.stiftmelk.at/en/stift-melk-stift-melk.html>



T-Shirts

Fair trade, organic cotton T-Shirts with the conference logo can be purchased for 22 € at the registration desk according to your pre-orders. We do have a few additional ones for latecomers.

Internet Access

WIFI is available at the conference venue. Check the board at the registration desk for details.

Photography and recording

Live sessions will be recorded via Zoom to make talks available after the conference and for remote participants of different time zones. All conference attendees acknowledge and consent that these recordings as well as pictures taken during the event by the organisers may be used on the internet and social media channels. If you take photographs of the presentations, please always make sure to respect authors' requirements in terms of distributing them via social media.

COVID regulations

Currently there are no COVID regulations in Austria. To make this conference a safe environment for everyone and to avoid a COVID cluster, we strongly recommend to have yourself tested before you start your journey. Please also feel free to wear a face mask if it makes you feel more comfortable. A number of rapid antigen self-tests will be available at the registration desk.

Insurance

There is no insurance included in the registration fee. All delegates are advised to make their own travel insurance arrangements for the duration of the symposium and the field trip. The general European emergency phone number is 112.

Further help

Please watch out for our organising staff in the yellow IST 2022 T-Shirts who will be happy to help you with any request. Also check the board at the registration desk for new information and changes.



Scientific programme

General information

The scientific contributions will be presented on

- Monday, 5th September, 14:00 – 17:40
- Tuesday, 6th September, 9:00 – 17:20
- Thursday, 8th September, 9:00 – 17:40
- Friday, 9th September, 9:00 – 15:00

For details please see the schedule below.

The contributions to the 17th International Symposium on Trichoptera were allocated to the following session:

- Session **Evolution & Phylogeny (EP)**
- Session **Taxonomy – Morphology (TM)**
- Session **Biogeography (BG)**
- Session **Biodiversity – Conservation (BC)**
- Session **Assessment (AS)**
- Session **eDNA – Genetics (EG)**
- Session **Ecology (EC)**

Please note that due to the time difference of the remote speakers we were not able to place all presentations into the respective sessions.

The following colour codes are used throughout the programme:

- yellow: live keynote talks
- light blue: live talks
- dark blue: video presentations
- orange: posters

Proceedings

The Proceedings of the 17th International Symposium on Trichoptera will be published as special issue in the journal *Denisia*. More details will be announced.



Schedule overview

Monday 05.Sep.22	Tuesday 06.Sep.22	Wednesday 07.Sep.22	Thursday 08.Sep.22	Friday 09.Sep.22
9:00 - 9:20	Keynote Previšić		Keynote Frandsen	EC2
9:20 - 9:40				EC1
9:40 - 10:00	EP8		BG4	EC3
10:00 - 10:20	BG5		BC1	EC6
10:20 - 10:40	Coffee/tea break		Coffee/tea break	Coffee/tea break
10:40 - 11:00	Registration	DG2	BC2	EC7
11:00 - 11:20		DG3	BC3	AS1
11:20 - 11:40		TM2	BC5	AS3
11:40 - 12:00		TM4	BC7	AS5
12:00 - 12:20				
12:20 - 12:40				
12:40 - 13:00		Lunch break		
13:00 - 13:20				
13:20 - 13:40	Registration			
13:40 - 14:00				
14:00 - 14:20		TM5		
14:20 - 14:40	Welcoming notes	TM6		Farewell note Graf
14:40 - 15:00		TM7		
15:00 - 15:20	Keynote Malicky	TM8		
15:20 - 15:40		TM9		
15:40 - 16:00	Coffee/tea break	Coffee/tea break		
16:00 - 16:20	EP1	BG2		
16:20 - 16:40	EP2	BG3		
16:40 - 17:00	EP3	AS4		
17:00 - 17:20	EP4	TM3		
17:20 - 17:40	EP5			
17:40 - 18:00				
18:00 - 19:00	Welcome reception			
19:00 - 20:00				
20:00 onwards			18:30 Conference dinner	



Detailed schedule

	Monday	Tuesday	Wednesday	Thursday	Friday
	05 Sep. 22	06 Sep. 22	07 Sep. 22	08 Sep. 22	09 Sep. 22
9:00 - 9:20					
9:20 - 9:40					
9:40 - 10:00					
10:00 - 10:20					
10:20 - 10:40					
10:40 - 11:00					
Registration					
11:00 - 11:20					
11:20 - 11:40					
11:40 - 12:00					
12:00 - 12:20					
12:20 - 12:40					
12:40 - 13:00					
13:00 - 13:20					
13:20 - 13:40					
13:40 - 14:00					
14:00 - 14:20					
14:20 - 14:40	Welcoming notes				
14:40 - 15:00					
15:00 - 15:20	Keynote Malicky: Considerations about the "extinctions" of caddisflies and other insects				
15:20 - 15:40					
15:40 - 16:00	Coffee/tea break				
16:00 - 16:20	EP1 - Bishoff: Defensive phragmrosis and cathaptosis in Trichoptera larvae				
16:20 - 16:40	EP2 - DelMar: Nectopsynope Mueller—Lepidoptera: Lepidopteridae: Nectopsynope Mueller—as a Model Clade for the Study of Wing Patterning and Cellular Architecture				
16:40 - 17:00	EP3 - Ivanov: Sensory structures on mouthpart palps in Trichoptera: ground plan and basal evolution trends				
17:00 - 17:20	EP4 - Frandsen: Using genomics to uncover the evolution of caddisfly silk genes				
17:20 - 17:40	EP5 - Mey: Trichoptera: the extinct and enigmatic cousins of Trichoptera				
17:40 - 18:00					
18:00 - 19:00					
19:00 - 20:00	Welcome reception				
20:00 onwards					
09:30 Conference dinner					



Abstracts

List of talks

Keynote talks		
No	Presenter	Title
	Paul B. Frandsen	What has comparative genomics taught us about caddisfly biology?
	Hans Malicky	Considerations about the “extinctions” of caddisflies and other insects
	Ana Previšić	Advancing the understanding of aquatic-terrestrial contaminant transport using aquatic insects

(Video) talks		
No	Presenter	Title
EP1	Megan J. Bishoff	Defensive phragmisis and cathaptosis in Trichoptera larvae
		Nectopsyche Mueller – Leptoceridae: Leptocerinae: Nectopsychini – as a Model Clade for the Study of Wing Patternning and Cellular Architecture
EP2	Kyle A. DeMarr	Sensory structures on mouthpart palps in Trichoptera: ground plan and basal evolution trends
EP3	V. D. Ivanov	Using genomics to uncover the evolution of caddisfly silk genes
EP4	Paul B. Frandsen	Tarachoptera: the extinct and enigmatic cousins of Trichoptera
EP5	W. Mey	Fossil Trichoptera embedded in mid-Cretaceous Burmese amber
EP8	Wilfried Wichard	Taxonomic revision of <i>Cemotina</i> Ross and <i>Cymellus</i> Banks (Trichoptera, Polycentropodidae)
TM2	Lucas M. Camargos	A Proposal to Migrate Trichoptera World Checklist to Taxonworks
TM3	Ed DeWalt	Revision of <i>Pycnopsyche</i> (Trichoptera: Limnephilidae) Species Groups and Their Diagnosable Characters
TM4	Matthew W. Green	The Hydropsychidae of Israel – taxonomy and ecology of a little studied fauna
TM5	Almog Rivka Hershko Pnuel	Functional morphology on the genitalia of <i>Rhyacophila lezeyi</i>
TM6	Ryoichi B. Kuranishi	Progress in the taxonomy of Nearctic Polycentropus Curtis, 1835 (Trichoptera: Polycentropodidae)
TM7	Alexander B. Orfinger	Specialized characteristics of the larvae of <i>Rhyacophila</i> Pictet
TM8	John S. Weaver	What is in a head? Comparative morphology of larval head muscles in the three Drusinae clades
TM9	Carina Zittra	Generating DNA barcodes of Indian caddisflies (Hydropsychidae; Trichoptera): future prospects
DG2	Sajad Hussain Parey	DNA-barcode library of Finnish caddisflies
DG3	Juha Salokannel	Comparative phylogeography of alpine/subalpine <i>Himalopsyche</i> species revealed distinct genetic structures in the Himalayas and Hengduan Mountains
BG2	Xiling Deng	Phylogenomics of the Western Hemisphere caddisfly genus <i>Smicridea</i> (Trichoptera: Hydropsychidae)
BG3	Ernesto Rázuri-Gonzales	Investigation of Caddisflies, Insecta, Trichoptera Fauna in Kazakhstan
BG4	Dina Smirnova	Radiation of the microcaddisfly genus <i>Orthotrichia</i> , Trichoptera: Hydroptilidae, in Australia
BG5	Alice Wells	



(Video) talks		
No	Presenter	Title
BC1	Tabraq Ali	Modes of collection and constraints in the sampling of caddisflies
BC2	Aleksandar Božić	The Pešter plateau – a hidden jewel of caddisflies biodiversity
BC3	Alain Dohet	Changes in caddisflies community composition and distribution along 60 years timespan monitoring in Luxembourg
BC5	Pongsak Laudee	Biodiversity of Trichoptera in the Lower Mekong River Basin
BC7	Astrid Schmidt-Kloiber	The European Distribution Atlas of Trichoptera – Where to go from here?
BC8	Oskar Schröder	GloBios – Global Observatory Network for Freshwater Biodiversity in High Mountain Streams
BC9	Steffen U. Pauls	Diversity of Caddisflies in the Eastern Congo River Basin
EC1	Kokichi Aoya	Shrinking pupal cocoons of <i>Rhyacophila lezeyi</i> at a highly acidic stream in summertime
EC2	Gisli Mar Gislason	Dispersal rate of <i>Potamophylax cingulatus</i> and <i>Micropterna lateralis</i> , Trichoptera, in Iceland
EC3	Goro Kimura	Effect of Bt toxin on net-spinning caddisfly <i>Stenopsyche marmorata</i>
EC6	Akikazu Taira	Life cycles and larval and pupal habitats of eleven <i>Rhyacophila</i> species at a Japanese mountain-stream in central Honshu, Japan
EC7	Kazumi Tanida	Food habits of some net-spinning Trichoptera and food web characteristics of benthic invertebrates in a mountain stream in central Japan
EC8	Sara Schloemer	Species community of Trichoptera larvae in low mountain streams altered by the European beaver (<i>Castor fiber</i>) with special focus of beaver dams as habitat
EC10	Ian Wallace	Resting behaviour of newly-hatched caddis larvae from water bodies that dry up over summer
AS1	Isabella M. Errigo	Tracing the impact of mega-disturbances on Trichoptera and other organisms using environmental DNA
AS3	Kelly M. Murray-Stoker	Assessing effects of urbanization on Trichoptera assemblages within a regional context: A caddisfly community science project
AS4	V. H. Resh	Species versus generic identifications in water-quality monitoring and ecological studies of Trichoptera: Is this still unresolved after half a century?
AS5	Marina Veseli	Cross-ecosystem transfer of pharmaceuticals and endocrine disruptors through emerging caddisflies
AS6	Bindiya Rashni	Architects of the Fijian streams: a small island system Trichopteran tale



List of posters

Posters		
No	Presenter	Title
EP6	John C. Morse	Evolution of Functional Traits in Trichoptera Larvae
EP7	Johann Waringer	Hydraulic engineering of Drusinae larvae: head morphologies and their impact on surrounding flow fields
EP9	Steffen Pauls	Phylogeography of <i>Drusus bolivari</i> in the Iberian Peninsula
TM10	Patina Mendez	Team Caddis: undergraduate collaborative research during the COVID-19 pandemic in an online virtual lab space
DG1	Mladen Kučinić	DNA barcoding of caddisflies (Insecta, Trichoptera) in Croatia
BG1	Lucas M. Camargos	Filling the gaps: potential distribution of four Neotropical Polycentropodidae species (Trichoptera: Annulipalpia)
BC4	Ioannis Karaouzas	Towards the protection and conservation of Greek endemic caddisfly species: IUCN Red List assessment and inclusion in the updated Red Book of Endangered Species in Greece
BC6	David Tempelman, Maria Sanabria	Protection of nature needs data, especially about distribution of species, including Trichoptera
BC10	Marc Sonnleitner	Management of anthropogenically impacted springs in the Kalkalpen National Park
EC4	Jan Martini	Dynamic choriotope shifts in space and time of caddisfly larvae in a first-order calcareous mountain stream
EC9	Katarina Stojanović	Sympathy for the dark: new findings of cave-dwelling Trichoptera from Serbia
EC11	Mourine J. Yegon	Fauna and distribution of the Hydropsychidae family in Mt Kenya and Mt Elgon regions, Kenya
EC12	Pia Teufl	High on life: diversity patterns of caddisflies in Austrian high-mountain streams
AS2	Iva Kokotović	Effects of climate change and pollution on caddisflies: insights from a multiple stress experiment



Keynote talks

KEYNOTE TALK

Paul B. Frandsen
Brigham Young University, Provo, USA

What has comparative genomics taught us about caddisfly biology?

As DNA sequencing technology has continued to improve and become more affordable, it has become tractable to compile and analyze genomic data from biodiverse clades. In 2018, the first high-quality caddisfly genome was published by Luo and colleagues. Since that time, many more large genomic data sets have been compiled, which have collectively increased our understanding of the genomic diversity of caddisflies. These datasets have been applied in an increasing number of ways, including aiding in species delimitation, helping to resolve the caddisfly tree of life, and refining our understanding of the genomic basis of silk production. Here, I review recent progress in caddisfly genomics and share new and ongoing research focused on applying genomic data to improve our understanding of caddisfly biology.



KEYNOTE TALK

Hans Malicky
Lunz, Austria

Considerations about the “extinctions” of caddisflies and other insects

This talk is a contribution to the present discussion on “mass extinction of insects” (Insektensterben) and gives examples of Trichoptera species which were not found for a long time in particular areas. The only caddis species on earth for which there is reasonable evidence that is really extinct is *Hydropsyche tobiasi*, formerly known only from the River Rhine. *Platyphylax frauenfeldi* whose last population lives in the River Drava seems to be highly endangered. It is unlikely that cold stenothermous species will die out in a moderate increasing of temperature.



KEYNOTE TALK

Ana Previšić

Department of Biology, Faculty of Science, University of Zagreb, Croatia

Advancing the understanding of aquatic-terrestrial contaminant transport using aquatic insects

Emerging aquatic insects such as caddisflies, connect freshwater and terrestrial food webs. Moreover, they play a central role not only for energy and nutrient flow, but also for contaminant transfer to higher trophic levels in both aquatic and terrestrial environments. In our studies, we aim at advancing the knowledge on the role of aquatic insects in transport of emerging contaminants (ECs) such as pharmaceuticals, endocrine disruptors, metal ions and microplastics through food webs and ecosystems. In addition to disentangling effects of ECs on aquatic insects, we also focus on impact the type of insect metamorphosis and feeding behaviour determine the bioaccumulation patterns of ECs. While monitoring stress of caddisflies at the molecular level, we showed that combined effects of ECs and climate change on caddisflies cross the aquatic-terrestrial ecotone. Overall, our research helps of ECs in combination with increased water temperature, one of the stressors resulting from the climate change. We combine field-based research and laboratory experiments with simplified freshwater food webs consisting of moss and caddisflies in micro- and mesocosm settings. In one of such experiments, we have provided the first direct evidence of the transport of pharmaceuticals and endocrine disruptors through the aquatic–terrestrial ecotone by emerging caddisflies. We have also shown that to provide understanding of contaminant transport dependent on ecological processes linking aquatic and terrestrial ecosystems.



Session Evolution & Phylogeny

Talk EP1

Megan J. Bishoff, John C. Morse
Clemson University, USA

Defensive phragmrosis and cathaptosis in Trichoptera larvae

Phragmrosis, or the use of specially modified body parts and associated behaviors to block an opening as defense against predators, is a commonly observed phenomenon in ants and termites blocking entrances of their subterranean nests with large, flat heads. It has been reported in some beetles and other insects and even in some frogs. Common features of phragmrosis include a hard and usually flat body surface, with or without stout spines or camouflage materials, and the behavior of fitting that body surface tightly in an otherwise vulnerable opening when threatened. A different defensive strategy occurs in snails and case-making larvae of camptosomatid leaf beetles (Chrysomelidae: Cryptocephalinae and Lamprosomatinae) that protect themselves from predators by securing their shells or cases firmly against the substrate, a behavior we call “cathaptosis” (fastening down on, attaching oneself down on). Common features of cathaptosis include a case with its vulnerable opening oriented parallel with the substrate and behavior that grips the substrate, fixing the case opening firmly against it when threatened. We suggest that these defensive strategies have evolved multiple times in Trichoptera, especially in case-making larvae. We demonstrate some examples and provide a tentative list of caddisflies whose larvae appear to have evolved these defensive strategies.



Session Evolution & Phylogeny

Talk EP2

Kyle A. DeMarr, Nipam H. Patel, Paul B. Frandsen
University of California, Berkeley, USA

Nectopsyche Mueller – Leptoceridae: Leptocerinae: Nectopsychini – as a Model Clade for the Study of Wing Patterning and Cellular Architecture

Researchers interested in trait evolution have started to deviate from traditional, singular model organisms and instead appoint clades as models for catalyzing evolutionary hypotheses. We take this approach in bolstering the long-horned caddisfly genus *Nectopsyche* Mueller as a model clade to understand how wing patterning evolves and how insect exoskeletal projections have converged upon similar morphological categories. *Nectopsyche* are New World endemics remarkable for their charismatic wing patterns which arise from the coordinated coloration of individual macrochaetes on the wing, much like as seen in Lepidoptera. These patterns employ motifs of stripes, bands, and bars upon fields of black, orange, and white, mirroring wing patterning elements seen among Lepidoptera. Furthermore, band motifs in several species are composed of flattened, ridged iridescent macrochaetes that morphologically resemble lepidopteran scales. We have constructed an anchored hybrid enrichment phylogeny to determine relationships among ~60% of the diversity in this genus and employed morphological inspection and scanning electron microscopy to determine the variation in scale and bristle attributes upon wings of these species. We determine that many previously recorded lepidopteran-specific macrochaetal traits actually arise in a pattern of “flicker” evolution, making them an ideal genus to dissect changes that lead to individual components of scale and bristle architecture. Furthermore, we document a phylogenetically disjoint occurrence of the ostensible “spider-mimic” pattern motif which may suggest convergent evolution. As a first step in facilitating a more mechanistic understanding of these trait variations, we have assembled and annotated a genome and transcriptome for a representative species, the exquisite miller *Nectopsyche exquisita* (Walker), and give notes on egg collection and its rearing. The findings from these explorations, combined with documented developmental and genomic resources for Lepidoptera, will provide the basis for answering whether the same genes are being commissioned to produce similar wing patterns and scale phenotypes across Amphiesmenoptera.



Session Evolution & Phylogeny

Talk EP3

K. T. Abu Diiak, M. Yu. Valuyskiy, S. I. Melnitsky, **V. D. Ivanov**

Department of Entomology, St. Petersburg State University, Saint Petersburg,
Russian Federation

Sensory structures on mouthpart palps in Trichoptera: ground plan and basal evolution trends

Comparative study of sensory structures on maxillary and labial palps in Philopotamidae, Rhyacophilidae, Glossosomatidae, Ptilocolepidae, and Hydroptilidae (12 genera, 30 species) obtained by the scanning electron microscopy and the light microscopy revealed significant diversity of the sensory structures. There are 7 principal types of sensilla: pointed trichoid, blunt chaetoid, campaniform, thin basiconic, thick basiconic, petaloid, and pseudoplacoid sensilla. The pointed trichoid and blunt chaetoid sensilla occur on every palp segment. The first and, especially, second segments of maxillary palps have bunches of very large blunt chaetoid sensilla on medial surfaces. Campaniform sensilla were found only on basal segments. Pseudoplacoid sensilla are common on the terminal segments of both labial and maxillary palps except for Ptilocolepidae and Hydroptilidae. The petaloid sensilla are specific for the mouthpart palps of Trichoptera, their structure varies in different genera and families. They are found in groups on the lateral/dorsolateral surfaces of apical segments either of both maxillary and labial palps (Philopotamidae, Rhyacophilidae) or only labial palps in other studied families. The pointed tips of both maxillary and labial palps usually have apical sensory complexes looking like small conical outgrowths without microtrichia, with one large thick basiconic sensilla on their tips and several shorter thick basiconic sensilla on lateral surfaces. We consider these seven types of sensilla along with the apical sensory complex and the assemblage of the petaloid sensilla as a part of Trichoptera ground plan. This primitive diversity might be decreased in evolution so the apical sensory complex, the fields of petaloid sensilla, the groups of very long blunt trichoid sensilla of basal segments, and the pseudoplacoid sensilla disappear in some advanced instances, more often on the maxillary palps. Interspecific variations of sensilla might be important for the species discrimination, while the distribution of certain sensory structures is important for higher taxonomy.

The study was financially supported by the Russian Science Foundation (project no. 22-24-00259).



Session Evolution & Phylogeny

Talk EP4

Paul B. Frandsen, Jacqueline Heckenauer, Ashlyn Powell, Steffen U. Pauls, Russell J. Stewart
Brigham Young University, Provo, USA

Using genomics to uncover the evolution of caddisfly silk genes

Caddisfly silk is a remarkable biomaterial. It adheres to wet surfaces, is viscoelastic, repeatedly regaining its original form, and is the mortar by which nature's underwater architects (caddisflies) build a myriad of structures as larvae. Caddisflies share an evolutionary origin of silk with their sister order, Lepidoptera, however, their silk varies in interesting ways. Here, we explore the evolution of the gene underlying the primary protein component of caddisfly silk, the heavy chain fibroin gene, or h-fibroin. We use new genome sequencing technologies to assemble full-length fully resolved gene sequences. We compare these sequences across the major clades within Trichoptera and with Lepidoptera. We find conserved patterns in highly divergent gene sequences, perhaps shedding light on the evolutionary processes responsible for their formation. We also find high allelic diversity within individual specimens suggesting potential balancing selective pressures on this diverse, highly repetitive protein.



Session Evolution & Phylogeny

Talk EP5

W. Mey, W. Wichard
Museum für Naturkunde, Berlin, Germany

Tarachoptera: the extinct and enigmatic cousins of Trichoptera

Tarachoptera is an extinct insect order assigned to the superorder Amphiesmenoptera, which contains the two extant orders Lepidoptera and Trichoptera. The order Tarachoptera was established by Mey et al. (2017a, 2017b). A current overview of the genera and species is presented in Wichard & Mey (2021). Species of Tarachoptera are known exclusively from mid-Cretaceous Burmese amber with an age of about 99 million years. The three orders occurred together at that time and individuals of Trichoptera and Tarachoptera are found occasionally in one and the same piece of amber. Concerning wing venation, Trichoptera and Lepidoptera are closely related and differ clearly from the venation in Tarachoptera. Characters of head, mouth parts and thorax provide further autapomorphies of Tarachoptera, which support the notion of an independent evolutionary line within Amphiesmenoptera. The presentation gives a synopsis on the contemporary knowledge of the order and the hitherto described taxa, including some new morphological details. We have attempted to identify amphiesmenopteran features in Tarachoptera which are relevant to further clarify the phylogenetic position of Trichoptera and Lepidoptera within Amphiesmenoptera.

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Session Evolution & Phylogeny

Poster EP6

Jessica A. Thomas, John C. Morse

Clemson University, USA

Evolution of Functional Traits in Trichoptera Larvae

Based on a recalibrated BEAST analysis and a parsimony analysis of ancestral character states, we are able to provide a revised timeline and interpretive scenario of the evolution of larval functional traits. Caddisflies evolved as early as the Carnian of Late Triassic (237–227 Ma) with gill-less campodeiform larvae clinging to substrate in fast-flowing, well-oxygenated streams. These larvae collected algae and fine particulate organic matter (FPOM) for nutrition and constructed pupation shelters with silk and substrate materials, pupated without cocoons, and emerged as adults reproducing in riparian habitats. The larva of the ancestor of Annulipalpia evolved also as early as the Carnian; it spun silk to build a stationary shelter for itself precociously in earlier instars and gleaned FPOM that became entrained in the silken margins of the shelter. Again, as early as the Carnian, the larva of the ancestor of Integripalpia was initially free-ranging and spun a semipermeable cocoon under the pupation shelter. As early as the Rhaetian of Late Triassic (208.5–201.3 Ma), the larva of the ancestor of Hydroptilidae-Ptilocolepidae evolved hypermetamorphosis with a precocious pupation shelter in the final instar that was portable and purse-shaped and that of Glossosomatidae evolved a precocious pupation shelter in all instars that was portable and tortoise-shell-shaped, with larvae of both ancestors feeding on attached algae and FPOM. Larvae of successive ancestors of Hydrobiosidae and Rhyacophilidae became predatory but otherwise retained their ancestral integripalpian larval and pupation traits. The larva of the ancestor of subterorder Phryganides lived as early as the Aalenian of Middle Jurassic (174.1–170.3 Ma); it was a suberuciform sprawler in slowly moving water or lentic habitats and evolved a precocious pupation shelter that was portable and generally tubular for all instars and pupated in it without a cocoon.



Session Evolution & Phylogeny

Poster EP7

Johann Waringer, Carina Zittra, Ariane Vieira, Simon Vitecek, Jan Martini, Stephan Handschuh, Hendrik C. Kuhlmann

Department of Functional and Evolutionary Ecology, Division Limnology, University of Vienna, Austria

Hydraulic engineering of Drusinae larvae: head morphologies and their impact on surrounding flow fields

Larvae from the Drusinae subfamily show a wide range of differently shaped head capsules. They live on the sediments of cold, well-oxygenated small mountain streams, where fluid flow is typically turbulent. In order to assess the impact of head capsule morphology on the surrounding flow field and the stresses acting on them, we use Large Eddy Simulations to compute the flow past different species of the subfamily. Three selected Drusinae species, *Drusus alpinus* Meyer-Dür 1875, *D. bosnicus* Klápálek 1899, and *D. discolor* (Rambur 1842), represent the three evolutionary lineages (shredders, grazers and carnivorous filter feeders) of the subfamily. Each evolutionary lineage uses a different hydraulic niche according to their foraging behavior. The three-dimensional body shapes from the selected species are reconstructed from X-ray microCT data. The flow parameters (Reynolds number) are selected based on spatio-temporally filtered velocity data measured during field excursions. The simulations with the tested range of Reynolds numbers did not show significant differences in the total forces acting on each morphotype. The dimensionless lift coefficients were in the 0.05-0.16 range and significantly smaller than the drag coefficients (0.32-0.48). Skin-friction coefficients calculated for the different species indicate repeated separation zones in the boundary layer where mean viscous streamwise surface stress is most pronounced near the edges of the bodies at head and pronotum. These are the regions from which vortices are shed into the flow. Highest streamwise normal stresses were observed upstream of the head of filter feeders where horseshoe-shaped vortices re-direct the flow directly to their filtering legs, thereby enhancing the encounter rates of particles with the filtering devices.



Session Evolution & Phylogeny

Talk EP8

Wilfried Wichard

Bonn, Germany

Fossil Trichoptera embedded in mid-Cretaceous Burmese amber

The presentation gives a current overview of the trichopterans found in Burmese amber and points out some aspects that help to draw a preliminary picture of the trichopteran fauna during the mid-Cretaceous period.



Session Evolution & Phylogeny

Poster EP9

Jesús Martínez, Sara Martínez, Felicitas Erzinger, Jürgen Otte, Luís Martín, Marcos A. González, Carola Gomez-Rodriguez, **Steffen U. Pauls**
Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany

Phylogeography of *Drusus bolivari* (McLachlan, 1880)

We studied the genetic population structure and phylogeography of the caddisfly *Drusus bolivari* across the Iberian Peninsula. This species is restricted to mountain regions and exhibits an insular distribution across the mountain ranges. DNA sequence data of the mitochondrial COI ($N=122$) and nuclear WG ($N=85$) regions from eight populations across most of the known species' range were assessed to study the species' population genetic structure. Phylogenetic analyses reveal the existence of old lineages unevenly distributed across the Iberian Peninsula. The high level of genetic differentiation between regional mountain lineages provides evidence for the existence of multiple refugia throughout the glacial and interglacial cycles. We also observe evidence for secondary contact in the Sierra de la Demanda. Combining this evidence with predictions of past climate, we suggest that past and current fragmentation is the prominent process structuring the populations, among the individual mountain ranges, and even within these in the case of the Sierra de la Demanda. This study shows that these aquatic organisms reacted differently to Pleistocene cooling than many terrestrial species. They persisted in numerous refugia over multiple glacial cycles, allowing many local endemic clades to form.



Session Taxonomy – Morphology

Talk TM2

Lucas M. Camargos, Ralph W. Holzenthal
Stuttgart State Museum of Natural History, Germany

Taxonomic revision of *Cernotina* Ross and *Cyrnellus* Banks (Trichoptera, Polycentropodidae)

The family Polycentropodidae occurs worldwide, and is represented in the Americas by *Cernotina* Ross 1938, *Cyrnellus* Banks 1913, *Nyctiophylax* Brauer 1865, *Polycentropus* Banks 1907 and *Polyplectropus* Ulmer 1905. *Cernotina* and *Cyrnellus* are exclusive to the New World, reaching their highest diversity in the Neotropics. We ran the first phylogenetic analyses on the diverse genus *Cernotina*, using morphological characters of the male adult, especially the genitalia. To analyze the character matrix, we used Maximum Parsimony and Bayesian inference. The results suggest the monophyly of *Cernotina*, adds phylogenetic evidence for synonymization of *Cernotina perpendicularis* with *C. lanceolata*, and *C. hastilis* with *C. nigridentata*, and group certain species with morphological and geographic congruence, such as *C. acalyptera* + *C. cystophora* + *C. encrypta*, and *C. lutea* + *C. cadeti*, respectively. We also revised the genus *Cernotina* at species-level. I discussed the complex homology of the morphological characters of the male genitalia. In addition, we described 16 new species. I also proposed 2 synonymies considering the phylogenetic data. We also revised the genus *Cyrnellus*, discussed the homology of the morphological characters and provided a key to species. We also synonymized 2 species based on morphological similarity and high variability among specimens.



Session Taxonomy – Morphology

Talk TM3

Ed DeWalt, Matt Yoder
Illinois Natural History Survey

A Proposal to Migrate Trichoptera World Checklist to Taxonworks

Trichoptera World Checklist (TWC) is a highly valued authority file for caddisfly hierarchy and species names. John Morse updates this resource, runs it from an older desktop version of Filemaker Pro, and receives local help to support the web version. John came to RED in May and expressed a desire to plan for eventual migration of the data to a new platform and turn over management of the database to others. We have no prior agreement. This talk is for informational purposes. TaxonWorks (<https://taxonworks.org/>), a taxonomic workbench developed by Species File Group (SFG) at the Illinois Natural History Survey, has a nomenclatural module designed especially for this kind of work. We wish to discuss with you a proposal that will help secure the data and give your community of caddisfly workers a web-based module that will allow one or multiple users to manage the data. SFG is endowment funded. Development is at no cost to you. Should you decide to use TaxonWorks, we will work together to plan the migration, data cleanup, testing, and discuss what is needed of a user interface and how to accomplish that. We have a training budget and would be willing to meet in person or virtually with potential editors of TWC. We may seek funding to recover some of our costs.



Session Taxonomy – Morphology

Talk TM4

Matthew W. Green, John C. Morse, Michael S. Caterino, Cathy M. B. Jackowski
Clemson University, Department of Forestry and Environmental Conservation

Revision of *Pycnopsyche* (Trichoptera: Limnephilidae) Species Groups and Their Diagnosable Characters

The North American endemic caddisfly genus *Pycnopsyche* Banks 1905 is the 2nd most species-rich genus of Nearctic Limnephilidae. Previous workers, including Schmid and Wojtowicz, attempted to group these species morphologically, yet some confusion has remained regarding species-group composition. Using morphological and molecular data, we revised *Pycnopsyche* species group composition by inferring Bayesian and maximum likelihood trees in MrBayes and IQ-Tree, respectively. Tree topologies were similar for both Bayesian and maximum likelihood phylogenies with the exception of the *Pycnopsyche limbata* Species Group, which was sister to the *P. scabripennis* Species Group in Bayesian analyses and sister to the *P. luculenta* Species Group in maximum likelihood analyses. We recognize seven species groups based on current phylogenetic evidence, which include the *P. scabripennis*, *P. limbata*, *P. guttifera*, *P. luculenta*, *P. lepida*, *P. virginica*, and *P. gentilis* Species Groups. These species groups can be distinguished morphologically using a combination of adult forewing color patterning, shape of the male inferior appendages, phallus, and endothecal parameres, shape of female abdominal segments IX and X, and larval case shape and material composition. Phylogenetic support for these Groups varied between Bayesian and maximum likelihood analyses, with the Bayesian tree providing the best phylogenetic support and the maximum likelihood tree providing relatively poor support. Inclusion of additional nuclear genes may help strengthen bootstrap support for these groups in maximum likelihood analyses, but current Bayesian phylogenetic support is good and should allow for adequate interpretation of evolutionary patterns in addition to predicting unknown character states for poorly known taxa.



Session Taxonomy – Morphology

Talk TM5

Almog Rivka Hershko Pnuel, Netta Dorchin, Armin Lorenz, Yaron Hershkovic

School of Zoology, Tel Aviv University, Israel

The Hydropsychidae of Israel – taxonomy and ecology of a little studied fauna

Hydropsychidae constitute important components in bioassessment and monitoring programs of streams and rivers due to their wide distribution and differing tolerance levels to water contamination or other disturbances. The family is represented in Israel by 11 species in two genera – *Hydropsyche* and *Cheumatopsyche* – but knowledge on the larval stages of these taxa is scarce, as most studies on Israeli Trichoptera focused only on the adult stage. In the present study we reviewed the taxonomic status of the hydropsychid taxa in Israel based on intensive sampling in diverse aquatic habitats throughout the country. We conducted a detailed study of the larval stages, their habitat requirements and distribution using morphological and molecular data, which enabled us to associate larvae and adults of the same species for the first time. Based on the molecular analysis, the family includes 5 species of *Hydropsyche* and 3 species of *Cheumatopsyche*, 5 of which are new to science. Two *Hydropsyche* species, and 2 *Cheumatopsyche* species previously reported from Israel were not found in the present study and their record from the country is probably erroneous. The morphological characters used in this research aided in separating some Hydropsychidae larvae into groups, but closely related species could be distinguished from each other only based on molecular data.



Session Taxonomy – Morphology

Talk TM6

Ryoichi B. Kuranishi, Ryo Sato, Masashi Murakami
Chiba University, Kanagawa Institute of Technology

Functional morphology on the genitalia of *Rhyacophila lezeyi*

In this study, we collected and fixed four pairs of *Rhyacophila lezeyi* (Navas, 1933) and examined their conditions; all four pairs were found to be in different states of copulation. How the morphology of each copulating device varies as a function of the state of copulation was described.

The male X segment has exhibited significant changes since the early stages of copulation. The female segment VIII approached to the male segment X which was pushed downwards by the female's VIII and IX segments, extending from it. As the mating stage progressed, the distended end of the female's VIII covered the male's X and pushed it further down. The male parameres were folded as bellows-like shapes under the aedeagus before copulation began; it extended to 2.5 times as long as its original length as the copulation stage progressed. The distended ends of both parameres were adhered to the position of the spiracles at the anterior margin of the lateral part of the VII abdominal sternite of the female. The attachment site was the external surface of the hair bulb. The movements involving the opening and closing of the male inferior appendices started at the middle stage of the copulation. The terminal segment of the inferior appendices made strong contact with the abdominal segment VIII of the female, and the contact pressure deformed the VIII of female. The female abdominal segment VIII and its extremity were well strongly extended and promoted the copulation. They significantly modified the condition of the male X-segment, particularly in its early stages. Although the important roles of the copulation vaginal apparatus were expected, only fragmentary observations have been made to date.



Session Taxonomy – Morphology

Talk TM7

Alexander B. Orfinger, John C. Morse, Raymond L. Hix, Andrew K. Rasmussen
Florida A&M University / University of Florida

Progress in the taxonomy of Nearctic *Polycentropus* Curtis, 1835 (Trichoptera: Polycentropodidae)

Trichoptera (caddisflies) are a diverse and ecologically important order of insects comprising over 16,250 nominal species worldwide. These holometabolous insects exhibit aquatic immature life stages that are important components of food webs and aquatic-terrestrial nutrient cycling. The larvae are of particular interest given their reputation as “underwater architects” and their use as sentinels in water quality monitoring programs. Despite the prominence of the larval life stage, alpha taxonomy of the order relies primarily on male genitalic characters, leaving larval taxonomy lagging far behind. The Nearctic members of the genus *Polycentropus* Curtis, 1835 (Polycentropodidae) are a prime example, with 29 of 30 larvae (97%) undescribed. To help remedy this taxonomic impediment, we use an integrative approach combining mtDNA and morphology to associate, describe, and diagnose larvae of Nearctic *Polycentropus*. Using > 400 barcoding fragments of cytochrome oxidase I (COI) from males of known identities and unknown larvae, we have now associated larvae of 15 Nearctic *Polycentropus* species, or 50% of the known fauna. Diagnostically informative larval characters have been identified, including muscle scar patterning, head color and pigment banding, and anal claw curvature. Ongoing efforts include generating identification tools such as discriminatory matrices for use by taxonomists, ecologists, and workers in water quality biomonitoring. Finally, current issues with the identification of Nearctic larval Polycentropodidae genera are discussed in light of new findings.



Session Taxonomy – Morphology

Talk TM8

John S. Weaver

United States Department of Agriculture, Jamaica, New York

Specialized characteristics of the larvae of *Rhyacophila* Pictet

While examining specimens of *Rhyacophila* larvae from North America, I observed morphological characteristics of the head, pronotum, forelegs, and anal prolegs that are unique. I hypothesize that these characteristics evolved to enhance the abilities of the free-living larvae of Rhyacophilidae to locate and capture prey.



Session Taxonomy – Morphology

Talk TM9

Carina Zittra, Simon Vitecek, Thomas Schwaha, Stephan Handschuh, Jan Martini,

Ariane Vieira, Hendrik C. Kuhlmann, Johann Waringer

Department of Functional and Evolutionary Ecology, University of Vienna, Unit Limnology, Austria

What is in a head? Comparative morphology of larval head muscles in the three Drusinae clades

The subfamily Drusinae (Limnephilidae, Trichoptera) comprises more than 150 currently recognized species. In their larval stages, a range of species show differently shaped head capsules. Intriguingly, head capsule shapes correspond to evolutionary lineages pursuing different larval feeding ecologies that moreover use different hydraulic niches: scraping grazers and omnivorous shredders share rounded head capsules and filtering carnivores have indented and corrugated head capsules. In this study, we assess whether changes in head capsule morphology are reflected by changes in internal anatomy of Drusinae heads. To this end, internal and external head morphology was visualized using μ CT methods and histological sections in four Drusinae species – *Drusus franzi*, *D. discolor*, *D. bosnicus* and *D. monticola* – representing the three evolutionary lineages. Our results indicate that Drusinae head musculature is highly conserved across the evolutionary lineages with only minute changes between taxa. Conversely, the tentorium is reduced in *D. discolor*, the species with the most aberrant head capsule investigated here. Integrating previous research on Drusinae head anatomy, we propose a fundamental Drusinae blueprint comprising 29 cephalic muscles and discuss significance of larval head capsule corrugation in Trichoptera.



Session Taxonomy – Morphology

Poster TM10

Patina Mendez, Minju Kim, Tammy Lee, Queenie Li, Stella Li, Ivy Lopez, Monika Mehta, Harsha Moyya, Vincent Resh, Lisa Saxton, Shahane Simonyan, Charlynn Teter

Department of Environmental Science, Policy & Management, University of California, Berkeley, USA

Team Caddis: undergraduate collaborative research during the COVID-19 pandemic in an online virtual lab space

Laboratory research can be a most memorable learning experience in college, but requires working in physical spaces with others. Disruptions such as the COVID-19 pandemic stopped access to campus buildings disrupting community in research spaces. We used gather.town to build a persistent, online, virtual lab space for collaborative research and meetings for Team Caddis, our undergraduate collaborative research group. In two connected spaces, the “library” and “lab,” members accessed google docs, data entry forms and files while meeting using video and audio. Although a persistent online space, we set regular lab schedules for student teams to work together. During COVID-19 we focused on two projects: (1) transcribing locality information from scans of Essig Museum of Entomology museum material, and (2) assembling “species pages” by harvesting species descriptions text and images from published papers for caddisfly species in California for our return to the laboratory. In sum, 10 students contributed as part of Team Caddis resulting in >330 species pages. By using a persistent space with more autonomy and character movement, we built community, had more natural and spontaneous interactions, helped each other, and kept research moving during uncertain times.



Session eDNA – Genetics

Poster DG1

Mladen Kučinić¹, Andela Cukušić²

¹ Department of Biology, Faculty of Science, University of Zagreb, Croatia

² Ministry of Economy and Sustainable Development, Zagreb, Croatia

DNA barcoding of caddisflies (Insecta, Trichoptera) in Croatia

One of the recent and most frequently used methods in analysis of biodiversity and determination of organisms within a particular area is the DNA barcoding method. This method is used to identify animal species and is based on sequencing of the standardized segment of the mitochondrial (mt) cytochrome c oxidase subunit 1 (COI) gene.

Caddisflies are used as biological indicators of water quality because they are highly sensitive to environmental stress and pollution. Therefore, they have an essential role in the standardized ecological assessment of aquatic ecosystems in most countries. However, reliable and rapid identification to the species level is proved challenging.

In this research, a DNA barcoding method was used as a fast and reliable tool that can classify an unknown sample into a known species or group of related species through phylogenetic analysis. Phylogenetic relations between 441 caddisfly individuals, sampled from 177 locations in Croatia are analyzed in this study.

A full-length DNA barcode was obtained from 85% of known caddisfly species (about 180 species), representing 89% of known genera and all 17 families of caddisflies known from Croatia.

DNA barcode sequences are stored in the BOLD public database. The DNA barcoding method confirmed findings of new and rare species in Croatian caddisfly fauna and identified specimens that were not possible using only morphology or for which no diagnostic features were described. Specimens with highly divergent DNA barcode with respect to known species are highlighted and some potentially new species for science.



Session eDNA – Genetics

Talk DG2

Aquib Majeed, Zahid Hussain, Tabraq Ali, **Sajad Hussain Parey**

Department of Zoology, Baba Ghulam Shah Badshah University Rajouri Jammu and Kashmir, India

Generating DNA barcodes of Indian caddisflies (Hydropsychidae; Trichoptera): future prospects

The order Trichoptera, which includes 49 extant families, is a group of holometabolous insects with terrestrial adults and larvae that inhabit a variety of freshwater environments (Jewel et al., 2018). With 16,266 extant species worldwide, Trichoptera are the seventh most speciose order of all insects with more species than the combined total of all the other primarily aquatic insect orders. In India the phylogenetic studies of Trichoptera at the species level is poorly known however they are important for studying of freshwater fauna and censorious use in biological indication. India records lowest number of insect DNA barcodes in BOLD. This investigation is concentrating on phylogenetic study of Trichoptera found in the India as only 03 Barcodes has been generated for Trichoptera from India so far. The Himalayas are representing the largest association of caddisflies. The DNA Barcoding approach, which relies on sequencing of the systemized portion of the mitochondrial (mt) COX subunit 1 (COI) gene to enable fast and precise identification of a wide range of biological samples, was used to infer evolutionary relationships within Trichoptera. The MT-CO1 gene encodes a component called cytochrome c oxidase I (COX1), also known as mitochondrial cytochrome c oxidase I (MT-CO1). The gene sequences of interest will be synthesized at designated barcoding centers, and the sequences will be submitted to the Barcode of Life Data System (BOLD) to infer evolutionary relationships within the Trichoptera. Using the BOLD identification method, the amplified DNA from the obtained sample will be compared to what is available in the BOLD data system.

In the current investigation from year 2020 to 2022, we have covered almost 31 sites and conducted more than 50 survey programmes across Northwest Himalaya. Overall 1500 specimens were collected from all sites and out of which 253 specimens were identified as Hydropsychidae. Further identification of Hydropsychidae was done up to species level by both morphological and molecular method. DNA of all the 26 species has been extracted, amplified and have been sent for sequencing for molecular assessment and for the study of Phylogenetic relationships among them. Sanger sequences once received will be added to gene bank and it will be first contribution to gene bank from India. Sequences will be open in the BOLD and any person who wishes to work on Trichoptera can use them for phylogeography, phylogeny, genomics and other bioinformatics.

This study represents an important step towards a completion of a DNA barcode reference library for North West Himalayan species, and enables a variety of approaches of molecular data assessments. The barcode of 26 species from India shall be submitted to BOLD (Barcode of Life Data System). Our study shows that DNA taxonomy can facilitate and expedite the process of identifying and characterizing the diversity of caddisflies.



Session eDNA – Genetics

Video talk DG3

Juha Salokannel, Aki Rinne, Kyung Min Lee, Heidi Viljanen, Niklas Wahlberg, Marko Mutanen
Aquatic Insects Expert Group of Finland, Finland

DNA-barcode library of Finnish caddisflies

Finnish caddisfly fauna consists of 218 species of which 36 % (78 species) belong to the family Limnephilidae. This fauna is considered taxonomically well known, and only one subspecies has been proposed to be lifted to a species level in this millennium. The first modern DNA work, DNA-barcoding (COI) of the morphologically difficult genus *Apatania*, was published in 2010. Using the same approach, the following work on genus *Oxyethira* was published in 2012. Gradually the idea to create a COI library for the whole Finnish caddisfly fauna started to come true through the national DNA barcoding project FinBOL. Today the COI library includes 94% of all Finnish species and the percentage is still growing, partly because of improved sequencing techniques that allow analysis of the older specimens in museums. So far the COI library has enabled major progress with a larval identification key that was published already in 2017. In addition, the COI results have raised some new taxonomic questions, for example, since some species appeared to carry two distinctly separate COI haplotypes. A study of three such cases using high throughput sequencing technique (ddRAD-seq) was published in 2021. In conclusion, it seems that the taxonomy of Finnish caddisfly fauna still requires some further morphological and molecular studies.



Session Biogeography

Poster BG1

Lucas M. Camargos, Daniel P. Silva, Ralph W. Holzenthal
Stuttgart State Museum of Natural History, Germany

Filling the gaps: potential distribution of four Neotropical Polycentropodidae species (Trichoptera: Annulipalpia)

Reliable distributional data is of paramount importance for species conservation, although many groups, especially on the Neotropics, lack sufficient and unbiased occurrence data. In this work, we use occurrences of the polycentropodid species *Cernotina antonina* Almeida & Holzenthal, *Cernotina longispina* Barcelos-Silva, Camargos & Pes, *Cernotina perpendicularis* Flint, and *Cyrnellus mammillatus* Flint to model their potential distribution. Given their spread throughout the Atlantic Forest and the Amazon, in the case of *C. perpendicularis* and *C. mammillatus* specifically, we expected suitable conditions for their presence in areas historically undersampled, such as the Brazilian Cerrado and Pantanal biomes. We used components of 19 environmental variables from Wordclim database, and Maximum Entropy (MaxEnt) algorithm was used to predict species distribution in relation to the environment. The potential range of all four species is expanded to include areas in the Cerrado region. Except for *C. antonina*, there is also a potential distribution of the other species in vast undersampled regions in the Amazon, such as its northern portion around Guyana and Suriname. *C. longispina* has also a range expansion towards the Southern Cone of the continent. Directing collecting efforts to the predicted areas might improve our biogeographical understanding of the polycentropodid species, reducing the sampling bias.



Session Biogeography

Talk BG2

Xiling Deng, Sami Domisch, Sonja C. Jähnig, Steffen U. Pauls
Senckenberg Research Institute and Natural History Museum, Frankfurt am Main,
Germany

Comparative phylogeography of alpine/subalpine *Himalopsyche* species revealed distinct genetic structures in the Himalayas and Hengduan Mountains

As two adjacent mountain regions surrounding the Qinghai-Tibetan Plateau, the Himalayas and Hengduan Mountains are characterized by their unique topographical features and complex climates. Under the joint influence of topology and climate, these mountains are the most important freshwater sources in Asia: most of the major rivers originate or flow through these regions. These mountains and their rivers are also known to be hotspots of freshwater biodiversity and endemism. To exemplify the contributing roles of geology and historic climate on the evolution of present-day biodiversity, we conducted a comparative phylogeographic study on four endemic species of *Himalopsyche* in the Himalayas and Hengduan Mountains. Caddisflies of this genus are characterized by strong dependency on freshwater ecosystems and limited dispersal capability. These four species are preselected as two species pairs with alpine or subalpine lower altitude distributions in the Himalayas and Hengduan Mountains, respectively. We inferred the population structure and historical demography of the four species using genome-wide sequences, as well as a species distribution model at present and the last glacial maximum for each species. The results show that species inhabiting alpine and subalpine regions show distinct patterns: the alpine species are structured by the mountain range and independent of catchment, while the population of subalpine-distributed species is most likely structured by catchment system. Moreover, most of the four species went through a population expansion during the last glacial maximum based on the species distribution model and historical demographic inference. Our research not only reveals the different genetic diversity patterns of the four species occupying various elevational ranges in the Himalayas and Hengduan Mountains, but also illustrates how these different patterns are shaped by the local landscape and historical climate changes.



Session Biogeography

Talk BG3

Ernesto Rázuri-Gonzales, Paul B. Frandsen, Ralph W. Holzenthal
Senckenberg Research Institute and Natural History Museum, Frankfurt am Main,
Germany

Phylogenomics of the Western Hemisphere caddisfly genus *Smicridea* (Trichoptera: Hydropsychidae)

The genus *Smicridea* (Trichoptera: Hydropsychidae) is endemic to the Western Hemisphere and is one of the most abundant and species-rich genera in this geographic region. There are 255 species divided into two subgenera: *Smicridea* with 145 species and *Rhyacophylax* with 110. Flint informally established several species groups based on the morphology of the male genitalia. However, he did not perform any formal phylogenetic analysis of their relationships. To test the monophyly of these putative species groups and the subgenera of *Smicridea*, we performed a phylogenetic analysis using maximum likelihood and a multispecies coalescent-based method implemented in ASTRAL. We included ten outgroup taxa from all five Hydropsychidae subfamilies and 48 *Smicridea* species (25 *Smicridea* and 23 *Rhyacophylax*). We generated two datasets using hybrid target enrichment for our analysis: a complete dataset including 350 loci and a reduced one with 256 loci. The reduced dataset only included loci with >80% of our selected taxa. Our trees showed both subgenera as monophyletic. In the subgenus *Smicridea*, we only recovered four putative species groups with high support. The Chilean *annulicornis* and *frequens* species groups were always recovered (100% in the concatenated trees, 1.0 in the ASTRAL trees). However, their relationship to the remaining species in the subgenus was variable. We also recovered the *fasciatella* and *nigripennis* species groups with maximum support values in all trees. In the subgenus *Rhyacophylax*, the species *S. andicola*, *S. probolophora*, *S. talamanca*, and *S. ventridenticulata*, members of the *peruana* species group, were recovered as monophyletic with high support values. Additionally, other species previously unplaced in any species group formed interesting clades in both subgenera. The species in these clades were either morphologically similar or occurred in the same general area. Our work is the first attempt to assess the relationships of species groups in this large Neotropical genus of caddisflies using next-generation sequencing. Including additional species might improve the relationship between the species that did not cluster in expected groups or changed their position depending on the method and dataset used.



Session Biogeography

Talk BG4

Dina Smirnova, Olga Sklyarova, Juha Salokannel, Vladimir Ivanov, Stanislav Melnitsky
Kazakhstan Agency of applied Ecology, Almaty, Kazakhstan

Investigation of the Caddisfly Fauna in Kazakhstan

Unique geographical position of Kazakhstan in the center of the Eurasian continent, a wide variety of landscapes and water bodies creates conditions for the formation of a diverse fauna of caddisflies. At the same time, the geological history of this region with periods of glaciation and desiccation affected the formation of the caddis fauna. History of the study of caddisflies in Kazakhstan began with the work of A.V. Martynov at the beginning of the 20th century. In 2016, a faunistic summary of the fauna of caddisflies in Kazakhstan was made according to the literature data for almost a century. In 2015-17, in order to obtain the missing information about the fauna, distribution and place of caddisflies in biocenoses, and to preserve their diversity, the project "Assessment of the biodiversity of caddisflies (Trichoptera) in water bodies of Kazakhstan" was implemented. During this project, a Kazakh-Russian expedition to the north-east of the country took place. In 2019, trips took place with the participation of Finnish and Russian researchers to the south and southeast of Kazakhstan. Each trip brought new species for the fauna of Kazakhstan, so the 2017 study brought 6 new species, and 2019 - more than 10 species. Over the past five years, the list of caddisflies in Kazakhstan has been replenished by more than 2 dozen species. Clarifications were made to previously published data on the detection of some species in Kazakhstan. Thus, the presence of *Goera japonica* Bks, *Lepidostoma itoae* Kum. & Weav. was not confirmed in the middle reaches of the Ili River. It is obvious that the fauna of caddisflies in Kazakhstan has not been studied enough and further research will bring a significant replenishment of the faunistic list and will clarify the distribution of species across the territory of Kazakhstan.



Session Biogeography

Video talk BG5

Alice Wells

Australian National Insect Collection, CSIRO, Canberra, Australia

Radiation of the microcaddisfly genus *Orthotrichia*, Trichoptera: Hydroptilidae, in Australia

Orthotrichia is the most species rich of the hydroptilid genera found in Australia, and is postulated to be of relatively recent Oriental origin. The genus has an almost worldwide but patchy distribution, represented by close to 280 species among which the Australian fauna of 55 species represents around 20%. In an attempt to understand the radiation of the genus in Australia, this presentation explores the morphology and biology of Australian species and discusses a number of contrasts with reports on the biology of congeners in the Northern Hemisphere. The possible significance of these differences in Australian representatives of the genus is suggested to have played a role in the “success” of the genus in the region. The value of life history studies to our understanding of biodiversity and biogeography is emphasised.



Session Biodiversity – Conservation

Video talk BC1

Tabraq Ali, Aquib Majeed, Zahid Hussain and Sajad Hussain Parey

Department of Zoology, BGSB University Rajouri J&K India

Modes of collection and constraints in the sampling of caddisflies

Trichoptera are economically important insects as they are involved in bio-monitoring programs. Based on geography, their diversity varies from low altitudes to high altitudes, temperate to tropical regions and plains to mountains. There are mainly two collecting approaches to collect the caddisflies: active collecting, such as sweep netting, searching under the stones; and passive collecting, where traps are set to either attract or intercept insects including pitfall traps or baited pitfall traps, malaise and flight intercept traps, light traps and collecting at a light sheet, sticky traps, pheromone traps and yellow pans. For adults, the light traps are commonly used while as the larvae of caddisflies are collected by handpicking method.

As the collection of caddisflies from the tough terrains of mountains is a very hectic practice, we are sharing some field experiences so that the newcomers may get equipped while planning their survey trips to collect the caddisflies. The constraints in the field trips include the bad weather which is the major hamper while on the move. The other factors include full moon days, availability of freshwater and unpolluted streams, rich vegetation, familiarity with the area, the attack of wild animals and a strong and fit researcher. In this piece of work, we discuss all the factors encountering while sampling the caddisflies and various methods to collect the caddisflies effectively.



Session Biodiversity – Conservation

Talk BC2

Aleksandar Božić, Katarina Stojanovic, Melisa Curic, Ivana Živic

Faculty of Biology, University of Belgrade, Serbia

The Pešter plateau – a hidden jewelry of caddisflies biodiversity

The Pešter plateau is one of the largest karstic fields in Serbia and the Balkans. With remarkable geomorphological and hydrological characteristics, this area is unique and one of the biodiversity hot spots in Serbia. The Pešter region also represents the part of Serbia with the lowest measured temperature during the winter: -39,5°C.

The survey of caddisflies biodiversity in the area of the Pešter plateau was conducted in June 2021. Within 12 selected localities, we collected caddisflies species from springs, lakes, peat bogs, and rivers in the area of 50 km². As a part of field sampling, an important point was the canyon of river Uvac. The material was collected with an aquatic net and tweezers for larvae and pupae, and entomological nets and night light traps for adults.

We identified the following caddisflies families: Philopotamidae (*Philopotamus montanus* Donovan, 1813 was the most commonly found species), Glossosomatidae, Rhyacophilidae, Limnephilidae, Sericostomatidae, Brachycentridae, Beraeidae, Psychomyiidae, Hydropsychidae and Goeridae. Two species are recognized as new to Serbian fauna: *Limnephilus stigma* Curtis, 1834 and *Hydropsyche mostarensis* Klápálek, 1898. Some taxa (like a few specimens of *Rhyacophila* Pictet, 1834 genus) have unique morphological characteristics, suggesting potentially new species.

Based on collected material and predictable species richness diversity, we believe we'll discover even more species of trichopteran order at the Pešter plateau.



Session **Biodiversity – Conservation**

Talk **BC3**

Alain Dohet, Sarah Vray, Lionel L'Hoste
LIST Luxembourg Institute of Science and Technology, Luxembourg

Changes in caddisflies community composition and distribution along 60 years timespan monitoring in Luxembourg

In Luxembourg, caddisflies are systematically collected since the early sixties. Three periods of exhaustive sampling may be distinguished: the sixties; 1994 to 2002; and a long period from 2007 to nowadays in the frame of the Water Framework Directive.

Bearing in mind the uneven sampling procedure across periods, we aim to document changes in community composition and distribution through time including the nature of these changes (e.g., gains and losses of species) and their quantitative importance. We hypothesize different trends of species gains and losses for specialist species in comparison to generalist species. Therefore, we propose a method to identify specialist and generalist species in our dataset.

Rather than comparing caddisfly community assemblages across several series of sites repeatedly surveyed through time, we assess the changes that occur in these specific groups of species (i.e., specialist and generalist species) at subgroups of sites defined by their typologies. Six main stream types can be defined in Luxembourg: small high-altitude siliceous; small mid-altitude siliceous and calcareous; mid-sized mid-altitude siliceous and calcareous; large lowland streams.

The most obvious result is the almost complete disappearance of large lowland streams specialists caddisflies species already before the second period of investigations (the 1994 to 2002 period). For other stream types, results are more nuanced according to the sampling period and the specialist or generalist statuses of the species.

This complex picture of caddisflies species losses and gains in different ways through time, among river types and in response to different pressures, is discussed.



Session Biodiversity – Conservation

Poster BC4

Ioannis Karaouzas

Hellenic Centre for Marine Research, Institute of Marine Biological Resources and Inland Waters, Greece

Towards the protection and conservation of Greek endemic caddisfly species: IUCN Red List assessment and inclusion in the updated Red Book of Endangered Species in Greece

With today's update, the number of species at risk of extinction on the IUCN Red List has exceeded 40,000. The IUCN Red List now includes 142,577 species of which 40,084 are threatened with extinction. However, only 5 caddisfly species are listed in the Global Red List; four are extinct and one near threatened. The Mediterranean region is recognised as the second largest global Biodiversity Hotspot where at least 20% of all species are threatened with extinction. However, on a Mediterranean or European scale there is no Red List assessment due to lack of a complete dataset of occurrence records. Red Lists however, exist only on a national and regional scale (e.g. Austria, Germany, Poland, Slovenia, etc.). In the Red Book of the Threatened Animals of Greece (2009), aquatic macroinvertebrates, including caddisflies, are vastly neglected due to lack of comprehensive occurrence data. However, for the first time, Greek caddisfly species are to be included in the IUCN Red List assessed on both regional and global level. Forty-two Trichoptera species will be assessed under the IUCN Red List criteria. The vast majority of the species are Greek endemics, located mainly in the Aegean islands, where aquatic habitats are decreasing at alarming rates due to climate change, water deficiency and increased tourism development. Briefly, caddisflies that will undergo assessment for inclusion in the Greek Red List will be Psychomyiidae (10), Hydropsychidae (9), Limnephilidae (4), Apataniidae (3), Hydroptilidae (3), Glossosomatidae (3), Rhyacophilidae (2), Leptoceridae (2), and one species each from families Beraeidae, Helicopsychidae, Phryganeidae, Goeridae and Sericostomatidae. Although IUCN criteria are not compatible for invertebrates, this is the first major step towards the protection and conservation, or at least the recognition, of threatened caddisfly species.



Session **Biodiversity – Conservation**

Talk **BC5**

Pongsak Laudee, Hans Malicky, Kriengkrai Seetapan, Penkhae Thamsenanupap, Supawit Karnkasem, Chanda Vongsombath, Sai Sein Lin Oo, Pome Zalyan, Chamroeun Kong, John C. Morse

Faculty of Innovative Agriculture and Fishery Establishment Project, Prince of Songkla University, Surat Thani Campus, Thailand

Biodiversity of Trichoptera in the Lower Mekong River Basin

The Lower Mekong River Basin which is in five countries including Myanmar, Laos, Thailand, Cambodia and Vietnam. A survey of biodiversity of caddisflies in this area is limited but the biodiversity in this area is very high. In this study, more than 70 samples were collected along the Mekong River in the 5 countries. At the present, more than 25 species were described from the area as a new species and more than 200 species of caddisflies were identified such as *Arctopsyche mesogona*, *Rhyacophila malayana*, *Stenopsyche midian*, *Lepidostoma navasi*, *Ugandatrichia maliwan*, *Macrosternum dione*, *Cyrnopsis pingensis*, *Pseudoneureclipsis ramosa*, *Ceraclea idaia*, *Ecnomus plotin* and *Ecnomus volovicus*



Session Biodiversity – Conservation

Poster BC6

David Tempelman¹, Maria Sanabria²

¹ Stichting Semblis, The Netherlands

² Aquon, The Netherlands

Protection of nature needs data, especially about distribution of species, including Trichoptera

Since 2005, in the Netherlands, the Citizen Science platform "Waarneming.nl" and "Observation.org" started to gather records of birds. It quickly developed into a widely used platform for all species groups.

Thousands of Trichoptera records are now submitted every year, mostly by volunteers using apps on their smartphones. From 2018 on, automated identification tools are in development, aiding the identification process. It is estimated that 75% of these records are validated on species level, the rest being left at higher taxonomical levels.

The results are:

1. better knowledge on the distribution of species, including rare ones
2. much more data on phenology
3. open data on Trichoptera, including historical records

This development greatly enhances the knowledge of Trichoptera, which can be used for the protection of biodiversity.



Session **Biodiversity – Conservation**

Talk **BC7**

Astrid Schmidt-Kloiber, Peter Neu

University of Natural Resources and Life Sciences, Institute of Hydrobiology and Aquatic Ecosystem Management, BOKU Vienna, Austria

The European Distribution Atlas of Trichoptera – Where to go from here?

Knowledge about the distribution of species is an essential base for further investigating their ecology and an indispensable prerequisite for freshwater management and species conservation. However, occurrence data are often lacking or not generally accessible.

Initiated by the EU-funded research project BioFresh, caddisfly distribution data were collected from all over Europe. More than 80 caddisfly experts provided their (often private and unpublished) data to create the European Distribution Atlas of Trichoptera (DAET), which contains over 450,000 records of around 1,700 adult caddisfly species covering a time period from 1793 to 2017. The atlas allows a previously impossible insight into distribution patterns, range delineations, and ecology of individual species.

We present distribution examples of individual species, explain areas of application (e.g. climate change modelling) and discuss the value of such a dataset, especially in terms of establishing a IUCN Red List of European caddisflies.



Session Biodiversity – Conservation

Talk BC8

Oskar Schröder, Julio Schneider, Ernesto Rázuri-Gonzales, Steffen U. Pauls
Department of Terrestrial Zoology, Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany

GloBios – Global Observatory Network for freshwater Biodiversity in High Mountain Streams

While global climate change is affecting all limnic environments, its effects are especially pronounced in high-altitude mountain streams. The disappearance of alpine glaciers and the shifting of ecosystems to higher altitudes is projected to disturb and fragment benthic invertebrate communities in this vulnerable environment. GloBios is an international project aiming to assess taxonomy and functional biodiversity of trichopterans, plecopterans and chironomids of high-altitude streams in South America, Central America and Europe. Using barcoding, metabarcoding and species distribution modelling approaches, we aim to identify species that are especially vulnerable to climate change due to low genetic diversity, habitat specificity and small distribution ranges. Additionally, we intend to predict changes in distribution based on future climate scenarios, to identify areas of high conservation value to minimize loss of genetic and taxonomic diversity. Here we present first results of the benthic community data from 2020 and 2021 in the Alps.



Session **Biodiversity – Conservation**

Talk **BC9**

Steffen U. Pauls, Francois Ngera Mwangi, Ernesto Rázuri-Gonzales
Senckenberg Research Institute and Natural History Museum, Frankfurt am Main,
Germany

Diversity of Caddisflies in the Eastern Congo River Basin

In this project we assessed the diversity of highland and lowland caddisfly communities in the eastern Congo River basin in the D.R. Congo. Specimens were collected via light trapping campaigns at 5 lowland (elevation 580-860m asl) and 7 highland (2000-2300m asl) localities. We sorted 1,409 individuals to morphospecies, and subsequently successfully sequenced the mitochondrial cytochrome oxidase I locus (mtCOI) from 667 specimens. Our preliminary analysis resulted in ~140 molecular operational taxonomic units (MOTUs), i.e. initial surrogates for species-level diversity. We will present initial diversity patterns in the target region and compare these with results from other regions in sub-Saharan, tropical Africa. Also, we will outline the next steps to species description and species-level diversity assessment.



Session Biodiversity – Conservation

Poster BC10

Marc Sonnleitner, Erich Weigand, Wolfram Graf

University of Natural Resources and Life Sciences, Institute of Hydrobiology and Aquatic Ecosystem Management, BOKU Vienna, Austria

Management of anthropogenically impacted springs in the Kalkalpen National Park

Springs are ecotones, not only inhabited by typical spring-taxa (crenobionts), but also by groundwater (spring-)brook elements. Crenobionts are highly specialised organisms, which are adapted to the stable abiotic conditions like temperature and discharge. In general, springs are habitats of many small-scale endemic species of the Alps underlining their conservation value.

However, their small dimensions make springs vulnerable to disturbances by human cultivation. In the Austrian Kalkalpen National Park pasture farming has been exercised for several centuries and overgrazing by cattle has negative impacts on habitat quality altering the benthic community severely. In response a LIFE-project was set up, which aimed to identify altered spring biotopes and to start a monitoring campaign evaluating management actions. This study aims to identify the prevalent stressors and evaluate the effects of protection fences based on data from emergence traps over 20 years.



Session Ecology

Video talk EC1

Kokichi Aoya, Atsushi Hayakawa, Tomoya Iwata, Kazumi Tanida
Daisen City, Japan

Shrinking pupal cocoons of *Rhyacophila lezeyi* at a highly acidic stream in summertime

In a highly acidic mountain stream, the Shibukuro Stream, northern Honshu, the pupae in shrunken cocoons of *Rhyacophila lezeyi* increased in the summertime of 2018-2021, and ca. 90 % of the pupae died during the rearing in laboratory. Under normal condition, osmotic gradients were kept between the cocoon fluid and stream water by the semi-permeability of cocoon membrane. The osmolarity of inorganic components in cocoon fluids was higher than stream water (27 mOsmol L^{-1}). In normal condition the initial osmolarity of cocoon fluids (91 mOsmol L^{-1}) is reduced to 44 mOsmol L^{-1} and mean fluid volume per cocoon of prepupae, 12 mg, increased to 18 mg during the pupal phase, and most cocoons became turgid. However, mean fluid volume per shrunken cocoon of pupae had only 10 mg, which was lower than normal ones. The increase in the electrolyte content of stream water due to drought in summertime seemed to be the major factor resulting in shrinkage of pupal cocoons observed in *R. lezeyi*.



Session Ecology

Talk EC2

Gísli Már Gíslason, Erling Ólafsson and Matthías S. Alfredsson
University of Iceland, Institute of Life and Environmental Sciences, Iceland

Dispersal rate of *Potamophylax cingulatus* and *Micropterna lateralis*, Trichoptera, in Iceland

During the 20th and 21st century two species of caddisflies (Trichoptera) have colonized Iceland. One species is *Potamophylax cingulatus* and the other is *Micropterna lateralis*.

Potamophylax cingulatus is widely distributed in streams in Europe and is dominant at higher latitudes and elevations. The larvae feed on detritus in the streams and to some extent on invertebrates. In Iceland, it is a predator of the Holarctic caddisfly larvae *Apatania zonella*, which has become extinct in streams recently colonized by *P. cingulatus*, probably due to predation.

Potamophylax cingulatus was not found in several extensive surveys before WWII, conducted by several entomologists and published in 1942. During a survey in streams in 1974 – 1978 the species was found to be common in eastern and north-eastern part of Iceland, but the Trichoptera species *A. zonella* was absent from the same streams, where it was common before WWIII. Searching earlier collections of unidentified Trichoptera, a single specimen was found in East Iceland on 30 July 1959. The survey was repeated in 2004 – 2006, and the species had colonized most streams and rivers in Iceland, and *A. zonella* has disappeared from many of them.

Micropterna lateralis was found in a single light trap near Reykjavik in 2008. The annual catch has since grown from 2 specimens to 73, but the species has not been found elsewhere and the larvae have not been found, but they are supposed to occur in running waters.

It is possible to conclude from this that when species establish a population on a large island like Iceland, the population builds up and when it has established itself, it disperses fast. For *P. cingulatus*, the dispersal rate was about 7 km/year, but the dispersal rate for the more recent settler *M. lateralis* was 4 km/year.



Session Ecology

Video talk EC3

Goro Kimura, Yoshitsugu Isumi, Hideo Shirai
Ikari Shodoku Co., Ltd., Japan

Effect of Bt toxin on net-spinning caddisfly *Stenopsyche marmorata*

Bacillus thuringiensis (Bt) toxin targets lepidopteran, dipteran, and coleopteran pests. Despite their close taxonomic relationship to Lepidoptera, only few studies examined the hazard of Bt toxins on Trichoptera. We used laboratory exposure tests to examine the effects of Bt var. aizawai on net spinning caddisflies, especially *Stenopsyche marmorata*. The mortalities ranged from 0 % for 1 ppm to 100 % at 100 ppm for a 48 hours exposure period. Trichopterans have diverse feeding strategies. Our results suggest that net spinning caddisfly larvae may indeed be sensitive to the Bt toxin when exposed higher the concentration.



Session Ecology

Poster EC4

Jan Martini, Johann Waringer
Department of Ecology, University of Innsbruck, Austria

Dynamic choriotope shifts in space and time of caddisfly larvae in a first-order calcareous mountain stream

The Schreierbach, a summer-cold calcareous first order stream, with a constant water temperature of about 6°C, has been a focus for Trichoptera research since the emergence studies of H. Malicky. These, inspiring results triggered caddisfly studies for decades. Trichoptera are highly diverse and can virtually colonize all types of freshwater habitats, thereby, triggering the specific evolution of various feeding strategies, such as shredders, grazers, predators and filter feeders. However, we only recently started to assess the microhabitat preferences and in situ hydraulic niche utilization for caddisfly larvae. Taken together, the Schreierbach allowed us to study the choriotope preferences of 25 caddisfly taxa and we could (i) assess its community and compare it with previous inventories; (ii) we aimed at detecting their microhabitat preferences in space and time. Therefore, we took six sets of bi-monthly adapted multi-habitat samples at three stream sections (360 samples). Resulting densities were highest in Drusinae juveniles (53.60%), *Micrasema morosum* (McLachlan, 1868; 15.14%), *Drusus discolor* (Rambur, 1842; 13.31%) and *D. monticola* (McLachlan, 1876; 4.46%), and were significantly higher in the upper stream section (1900 ± 1039 larvae m⁻²) than in the central (205 ± 23) and lower (141 ± 22). Ivlev electivity indices revealed preferences for Macrolithal in *Rhyacophila* spp. and *Tinodes dives* (Pictet, 1834), for Microlithal in Drusinae juveniles, for Megalithal and Phytal in filtering Drusinae and *Micrasema*, and for Xylal and Akal in Limnephilinae. Moreover, we were able to relate this information with ontogenetic choriotope shifts, and to explore relationships between feeding guilds and choriotopes chosen. Therefore, a cluster analysis of choriotope electivity yielded five clusters, corresponding with functional feeding types. At the instar level, the chosen grain size increased with increasing instar in some species. Observed habitat shifts in space and time reflected the interaction of instar-specific choriotope choice and longitudinal translocations.

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Session Ecology

Video talk EC6

Akikazu Taira

Osaka Metropolitan University, Osaka Museum of Natural History, Japan

Life cycles and larval and pupal habitats of eleven *Rhyacophila* species at a Japanese mountain-stream in central Honshu, Japan

I investigated life cycles and habitats of eleven *Rhyacophila* species living in a Japanese mountain stream, Nara Prefekture, central Honshu. Eight species had univoltine life cycles and seven of them had spring to early summer emergence seasons. Other one species, *Rhyacophila shikotsuensis*, had an autumn emergence season. Some univoltine *Rhyacophila* species had the period without any larvae, pupae nor adults, which appeared to be in egg stages. Other three species, *R. nipponica*, *R. brevecephala*, and *R. yamanakensis*, had bivoltine life cycles with wintering and non-wintering generations. Three species of the *nigrocephala* species group, *R. nipponica*, *R. kawamurae*, and *R. shikotsuensis*, were hyporheos in most larval stages, the first and final instar larvae changed microhabitat on stone faces. The first instar larvae seemed to live on stone surfaces immediately after hatching, and moved to interstices of sand after that. The final instar larvae firstly lived in the interstices of sandy bottom and moved to stone surfaces for pupation.



Session Ecology

Video talk EC7

Fuminori Shinmyo, Kazumi Tanida

Osaka Metropolitan University, Osaka Museum of Natural History, Japan

Food habits of some net-spinning Trichoptera and food web characteristics of benthic invertebrates in a mountain stream in central Japan

We conducted quantitative samplings of benthic invertebrates at the fast and slow riffles at the Takami Stream, the third order stream in Nara Prefecture, central Japan, in April and May 1994. Additional samples for gut content analyses of benthic invertebrates were also collected at the same riffles. Eight taxa of Trichoptera, 21 of Ephemeroptera, five of Plecoptera, more than nine of Diptera and more than five of other invertebrates were collected by quantitative samplings. The gut contents of nineteen major taxa were analyzed quantitatively and the food web of benthic invertebrates was constructed. Concerning prey items, however, we could distinguish only eight groups (units or guilds) of animals and other three groups, diatoms, other algae and detritus. Considering this asymmetrical taxonomical resolution between predators and prey, we will propose two indices of food web connectivity, one of the major characteristics of food webs. We will also show the changes of food habits accompanying the development and growth of some net-spinning caddis larvae, *Stenopsyche* and *Hydropsyche* species.



Session Ecology

Video talk EC8

Sara Schloemer, Daniel Hering

University Duisburg-Essen, Faculty of Biology – Aquatic Ecology, Essen, Germany

Species community of Trichoptera larvae in low mountain streams altered by the European beaver (*Castor fiber*) with special focus of beaver dams as habitat

Beavers and their dams, once common in small streams throughout the palearctic zone, are returning to their original range. The resulting beaver ponds, secondary streams, beaver meadows and a large amount of deadwood change and diversify the appearance and biocenosis of the stream ecosystems.

We studied how beaver activity affects the macro-invertebrate community 2018 and 2019 in low mountain streams in the northern Eifel (NRW/Germany), where beavers were reintroduced in 1981.

We investigated lotic and lentic habitats in water stretches with and without beaver influence.

One focus of the study was the beaver dams themselves, which were sampled with a specially designed device and taking into account the maintenance status as well as the different areas of a dam (upper, middle and lower areas).

The results show that beaver dams, turned out to be a very diverse Trichoptera habitat which provide multiple living conditions to a wide variety of caddisfly species.

For example, caddisfly community composition reflects higher flow velocities in the middle and lower areas of a dam. Passive filter feeders like representatives of Hydropsychidae and Philopotamidae dominate these areas, but prefer different maintenance states of the dams. Within the top of a dam, on the other hand, shredders e.g., representatives of the Limnephilidae, are particularly common.



Session Ecology

Poster EC9

Katarina Stojanović, Mladen Kučinić, Aleksandar Božić, Ivana Živic

Faculty of Biology, University of Belgrade, Serbia

Sympathy for the dark: new findings of cave-dwelling Trichoptera from Serbia

The majority of the caves and pits in Serbia are located within the two main limestone massifs, the most eastern parts of the Dinaric mountain system on the west of the country, and the most western areas of the Carpatho-Balkan Arc on the east. Only a few available subterranean habitats in Serbia are outside these two famous mountain ranges, with their independent genesis. The presence of Trichoptera species in caves is connected with the period of aestivation, indicating adaptation of their larval stages to live in intermittent streams. These species, so-called subtroglophile, leaving the caves to oviposit mostly in autumn. During the period 2008 – 2021, caddisflies were sporadically collected from 16 caves in Serbia, as a part of a subterranean fauna survey. The five common species were registered: *Micropterna sequax* McLachlan, 1875, *M. nycterobia* McLachlan, 1875, *Stenophylax mitis* McLachlan, 1875, *S. permistus* McLachlan, 1895, with *S. meridiorientalis* Malicky, 1982 being the most dominant one. Also, one female of the genus *Limnephilus* Leach, 1815 was registered. Adult specimens were noted from April to late October, except September. Besides adults, for the first time polycentropodid larvae were found in the total dark in a small pond in one of the caves suggesting, based on the habitat and its morphology, it could be a real troglobiont. Further studies will focus on genetic differences between the populations and the taxonomy of potentially unrevealed species.



Session Ecology

Video talk EC10

Ian Wallace

British Cadis Recording Scheme, United Kingdom

Resting behaviour of newly-hatched caddis larvae from water bodies that dry up over summer

Limnephilid larvae are very familiar inhabitants of ponds and streams that dry up over summer. The adults emerge before the waters dry up. Freshly emerged females have undeveloped eggs. Classic studies show that shortening day length induces egg development and females then lay in late summer and autumn in damp places that will hold water over winter for larval development. Eggs are within a sphere of firm jelly and develop and hatch within that. Most larvae do not escape from the jelly sphere until it is totally submerged in autumn or winter.

However, there are variations on this theme. In particular, that several species may lay, hatch and escape from the jelly as early as mid-summer, long before free water appears in the water-body.

The presentation summarises what is generally known about egg-laying and hatching seasons for British and Irish Limnephilid caddis, focussing on temporary water body species. Phryganeid and polycentropodid caddis of such sites are also discussed.

Physiology and behaviour of these newly hatched larvae does not seem to have been studied but would seem to be key to their survival.



Session Ecology

Poster EC11

**Mourine J. Yegon, Joshua M. Benjamin, Frank O. Masese, Charles M. Merimba,
Augustine Sitati, Wolfram Graf
WasserCluster Lunz – Biologische Station, Lunz, Austria**

Fauna and distribution of the family Hydropsychidae family in Mt Kenya and Mt Elgon regions, Kenya

The Hydropsychidae family is one of the most diverse, abundant and widely distributed group of Trichoptera in Afrotropical regions. Their abundance, diversity and distribution may however be limited by environmental quality from anthropogenic influences on streams and rivers due to deforestation, urbanisation and the expansion of agricultural lands which have been reported to be prevalent within East Africa, and especially in Kenya. Furthermore, there exists a gap in the taxonomic work, particularly for caddisflies (Hydropsychidae) in Kenya. This work therefore aims at forming key baseline information to guide on the future Trichoptera studies in the region. Our study presents larval morphotypes and their distribution along a land use gradient from 10 sites in the Gura-Sagana drainage system in the Mt Kenya catchment in the central region of Kenya and 21 sites in the Nzoia river system in the Mount Elgon catchment in the western region of Kenya. The sites sampled were all within the elevations of 1179 and 2977 m asl. Our work further examined the relationships between Hydropsychidae faunal structure and instream environmental variables to ascertain whether these variables play a role in their structuring. Land use change was a major driver of changes in physico-chemical water parameters and habitat quality in the streams as observed in the water temperature, dissolved oxygen, electrical conductivity and total suspended solids, which were significantly different across the land use types. There was also a clear and distinct clustering of the Hydropsychidae morphotypes along a land use gradient indicating the presence of both sensitive and more resistant types within the family. Knowledge of the occurrence and ecology of these taxa groups is crucial for biomonitoring and conservation planning of freshwater ecosystems in the face of anthropogenic influences in these regions.



Session Ecology

Poster EC12

Pia Teufl, Patrick Leitner, Wolfram Graf

University of Natural Resources and Life Sciences, Institute of Hydrobiology and Aquatic Ecosystem Management, BOKU Vienna, Austria

High on life: diversity patterns of caddisflies in Austrian high-mountain streams

High mountain streams are shaped by unique landscape characteristics and heterogenous framework conditions. Specialised faunal assemblages are natural consequences of the tough surroundings and vary in dependence of dominating water sources. However, alpine streams are facing dramatic changes. Not only are they increasingly affected by climate change, but also direct interferences like water abstraction, hydropower generation or land use practices show their imprints. Pristine streams are becoming increasingly rare, which turns them into valuable fields of research. Thus, this study contributes to the understanding of alpine streams and their biotic communities by assessing diversity and structural patterns of macroinvertebrates in eight near-natural high mountain streams. A comprehensive analysis of streams with and without glacial influence and the assessment of an altitudinal gradient via three sampling sites per stream should provide insights into the benthic communities of streams within the Austrian Alps. As EPT taxa (Ephemeroptera, Plecoptera, Trichoptera) can be designated as essential components of these fluvial systems, analyses were based on the mentioned groups, with a special focus on diversity patterns of caddisflies.

Firstly, abundance and dominance ratios of Trichoptera were analyzed to illustrate community structures of caddisflies under reference conditions and provide a taxonomic inventory of this insect group in undisturbed high mountain streams.

Secondly, effects of a glacial signature on caddisfly communities were assessed. In general, abundances were decreasing with increasing glacial influence. Even at low degrees of glaciation within the catchment (< 30 %), Trichoptera were strongly limited in their occurrence. Furthermore, the presence or absence of a glacial coverage in the catchment had clear implications on the taxonomic composition of caddisfly communities.

Lastly, the impact of altitude on Trichoptera abundance and composition was investigated. Abundances were generally decreasing with increasing elevation, whilst lower taxonomic resolution (genus or species level) revealed clearly shifting caddisfly compositions between various altitude classes.



Session Assessment

Talk AS1

Isabella M. Errigo, Ethan Tolman, Andrew Sheffield, John Chaston, Benjamin W. Abbott, Paul B. Frandsen
Brigham Young University, Provo, USA

Tracing the impact of mega-disturbances on Trichoptera and other organisms using environmental DNA

Anthropogenic climate change is causing shifting weather patterns and increasingly extreme natural disturbances world-wide. In the western United States, these changes result in larger, more frequent wildfires and extreme precipitation events. In the fall of 2018, the Pole Creek Megafire burned 610 km² in central Utah. Two weeks later, the remnants of Hurricane Rosa swept across the state, resulting in torrential rains which triggered debris flows and flash-floods, especially in the burned catchment. The compounded impact of these two events caused massive ecosystem disturbances throughout the Utah Lake Watershed. Because Trichoptera is one of the orders of macroinvertebrates primarily used as bioindicators of ecosystem health, we used environmental DNA to trace change in caddisfly populations to understand the impact of these mega-disturbances on the biodiversity and recovery of aquatic ecosystems. We compared samples from the summers of 2019 and 2020 to investigate how the progression of biogeochemical and biological succession compare following large ecological disturbance events. We also compare the data for Trichoptera with data from other macroinvertebrate organisms and bacteria. Understanding the impacts of extreme disturbance events and the post-disturbance succession will protect native species, effectively facilitate habitat and species restoration, and ensure continued water security for communities in semi-arid regions.



Session Assessment

Poster AS2

Iva Kokotović¹, Marina Veseli, Zrinka Karačić, Ivana Grgić, Marko Rožman, Ana Previšić
University of Zagreb, Faculty of Science, Croatia

Effects of climate change and pollution on caddisflies: insights from a multiple stress experiment

Water pollution and climate change negatively affect freshwater ecosystems, impairing their normal functions and balance. Various pollutants co-occur and interact, changing the way aquatic insects cope with stress. Accordingly, the aim of the current study was to investigate the single and combined effects of emerging contaminants (ECs); pharmaceuticals (PhACs) and endocrine disrupting compounds (EDCs) and elevated water temperature on aquatic insects at the aquatic-terrestrial habitat linkage. A laboratory microcosm experiment was conducted with a simplified freshwater food web containing nonvascular macrophytes and *Micropterna nycterobia*, Trichoptera larvae feeding mainly as shredders. Sampling included initial and several consecutive collections including all life stages (larvae, pupae and adult stage). Analyses such as total protein content, total lipid content, non-target metabolome and lipidome profiling were conducted in order to evaluate the response of *M. nycterobia* to selected stressors at molecular level. Increased water temperature had an impact on phenology causing earlier emergence of adults and a decrease in lipid mass. Furthermore, treatments with ECs lowered the protein mass in larvae and pupae, irrespective of the water temperature. Multiple stressor effect was noticed in treatments with combined ECs and elevated water temperature as the highest decrease in total protein content in larvae and pupae, and total lipid content in adults. Metabolome was more affected by ECs, while increased temperature had a greater effect on lipidome.



Session Assessment

Talk AS3

Kelly M. Murray-Stoker, Shannon J. McCauley

University of Toronto

Assessing effects of urbanization on Trichoptera assemblages within a regional context: A caddisfly community science project

Historical processes, landscape characteristics, and the distribution of biodiversity form the context in which local community interactions occur. We are studying the influence of regional context on urban stream communities of lotic caddisflies. To address this topic and increase geographic sampling coverage, we formulated a community-science project in the summer of 2021. Participants were recruited through social media and other online forums. We mailed collecting kits consisting of a USB-powered ultraviolet LED light, a collecting container, one bottle of preservative per collecting site, data sheets, and collection labels to each participant; participants mailed back their sample bottles with collected specimens and completed data sheets. More than 60 participants set up light-traps near urban and non-urban streams in seven different North American geographic regions, collecting adult caddisflies at over 130 sites across the US and Canada. Our goal is to evaluate community structure to assess whether the variation in Trichoptera diversity across regions can be best predicted by local, landscape-level, or historical patterns. Additionally, we aim to assess whether caddisfly communities in certain areas are better equipped to tolerate the effects of urbanization because of the historical distribution of taxonomic, ecological, and phylogenetic diversity. Studying this question will help researchers understand how much to consider the region-specific characteristics of a community in order to mitigate detrimental effects of urbanization and preserve the integrity of freshwater ecosystems.



Session Assessment

Video talk AS4

V. H. Resh, B. Higler, B. Statzner
University of California, Berkeley, USA

Species versus generic identifications in water-quality monitoring and ecological studies of Trichoptera: Is this still unresolved after half a century?

Species-level identifications of the larval stages of caddisflies and other aquatic insects are available for a very small proportion of the taxa used in water-quality monitoring and ecological studies. This has been a long-lamented condition but the proportion of associations of larval and adult caddisflies hasn't increased in over 50 years of documented advantages that species-level identifications add value to these studies. What is the information content that is lost when caddisfly larvae are identified to generic or even family level in such studies? Approaches to examining this question have ranged from anecdotal accounts of pollution-tolerance or behavioral differences among species within a genus to detailed statistical analyses comparing information available through different hierarchical levels. Justifications for higher-level taxonomic resolution have ranged from financial considerations to acceptance that higher levels are equally as valid as species identifications. Can compositional metrics such as tolerance values and species-trait indices assume there is little or no variability between species and generic levels of identification? Genetic techniques offer some promise of aiding larval-adult associations but an expansion of larval-taxonomic studies would quickly increase the value of information collected in water quality and ecological analysis.



Session Assessment

Talk AS5

Marina Veseli, Iva Kokotović, Mira Petrović, Marko Rožman, Ana Previšić

Department of Biology, Zoology, Faculty of Science, University of Zagreb, Croatia

Cross-ecosystem transfer of pharmaceuticals and endocrine disruptors through emerging caddisflies

Presence of emerging contaminants in freshwaters worldwide is recognized as growing threat for freshwater ecosystems, and its impacts on biota remain largely unknown. Emerging contaminants, like pharmaceuticals (PhACs) and endocrine disrupting compounds (EDCs), can be transferred from aquatic to terrestrial environments through emergent aquatic insects, which bioaccumulate them during their aquatic life stages. In the current study, we aim at investigating the role of caddisflies in transport of pharmaceuticals and endocrine disruptors from aquatic to terrestrial ecosystems and food webs. More precisely, we focused on examining bioaccumulation patterns of PhACs and EDCs in aquatic life stages of the caddisfly *Silo nigricornis* (Pictet, 1834), collected at two sites in the NW Croatia affected with wastewater pollution and extremely high abundance of this species. Moreover, with the aim to determine trends in ECs concentrations during different life stages, we calculated bioamplification factors (BAMFs) between larvae (LV) and pupae (PU), as well as between pupae and adults (IM). Results show that 17 ECs bioaccumulated in caddisfly tissues. Seven compounds' concentrations showed significant differences between life stages, all having highest values in adults compared to larvae and/or pupae. Accordingly, BAMFs showed increase in concentrations during at least one stage of the metamorphosis (LV to PU and/or IM) for 13 compounds. Moreover, for six compounds bioamplification was inferred (BAMFs ≥ 1) through both metamorphosis stages. Elevated concentration of ECs in adult caddisflies is mostly result of reduced body mass occurring during metamorphosis. Such increased body burden of PhACs and EDCs in adult caddisflies could greatly impact their riparian predators, such as spiders, birds and bats, which are consequently exposed to elevated concentrations of contaminants originating from aquatic pollution. Results of this research provide new insights on the behaviour and fate of PhACs and EDCs on the aquatic-terrestrial ecosystem boundary.



Session Assessment

Video talk AS6

Bindiya Rashni

SAGEONS, the University of the South Pacific, Laucala Campus, Fiji

Architects of the Fijian streams: a small island system Trichopteran tale

Indigenous communities of Pacific Island countries are culturally connected to their environments, natural resources and biodiversity. Because of this, biomonitoring that builds upon commonly held knowledge and cultural values has the greatest opportunity for success. Fijian freshwater ecosystems are wet, tropical, ecologically diverse and ethnobiologically rich. They support rich biological diversity and unique species of plants and animals that hold biocultural significance for the indigenous (Itaukei) communities. Many species are already recognized by indigenous communities as traditionally important, and they are already used as focal organisms in Fiji for freshwater conservation and biomonitoring that is building upon Traditional Ecological Knowledge. The rivers, creeks and streams that make up the lotic wetlands of Fiji support a rich diversity of Trichopteran fauna favoring a high diversity of case-caddis and island endemics. However, due to the absence of Plecopterans, the globally accepted EPT Indices are not easily applicable in Fiji and Melanesia. Despite that, owing to their bioindicator potential the Trichopterans have been widely used in the Fijian community based biomonitoring tools and the Fiji River-Invertebrate game. However, the description and understanding of aquatic stages and morpho-molecular fusion of aquatic larvae and aerial adults are still at an infancy stage. Thus, there is the potential for studies across the Fijian archipelago that are directly comparable for monitoring environmental trends across spatial and ecological gradients.



Room for notes