

16. Jahrestagung der Gesellschaft für Biologische Systematik (GfBS)

**vom 18.-21. März 2015
am Zoologischen Forschungsmuseum
Alexander Koenig
in Bonn**

– Programm und Abstracts –

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Mit freundlicher Unterstützung von:



Herzlich Willkommen!

zur 16. Jahrestagung der GfBS vom 18.-21. März 2015 am Museum Alexander Koenig in Bonn

Wir begrüßen alle Teilnehmer der 16. Jahrestagung der Gesellschaft für Biologische Systematik (GfBS) ganz herzlich am Zoologischen Forschungsmuseum Alexander Koenig (ZFMK). Damit tagt die GfBS bereits zum dritten Mal am Museum Koenig, dem Ort, an dem 1998 die erste Zusammenkunft der damals neu gegründeten Gesellschaft für Biologische Systematik ausgerichtet wurde. Vor vierzehn Jahren folgten über 200 Teilnehmer der Einladung des GfBS-Gründungsmitglieds und ZFMK-Direktors Clas M. Naumann (*1939 – †2004). Diesem für die GfBS historischem Ereignis folgten viele weitere Tagungen, mit denen schöne Erinnerungen verknüpft sind (u.a. Wien, Leiden, Berlin, München, Dresden, etc.). Die diesjährige Veranstaltung findet in gemütlicher Atmosphäre wieder am Museum Koenig in Bonn statt. Mit 75 Teilnehmern sowie über 55 Postern und Vorträgen – ist wieder ein hoher Anteil an Nachwuchswissenschaftlern vertreten.

Nachdem die GfBS in den vergangenen Jahren stets mit anderen Organisationen und Gesellschaften zusammen getagt hat, findet die diesjährige Jahrestagung wieder in "familiärem" Kreise statt. Das Thema der diesjährigen Tagung dreht sich ganz um Taxonomie. Unter dem Motto: „**Der Bedarf an taxonomischem Wissen: für wen und in welcher Form?**“ haben wir fünf Redner eingeladen, die uns aus aktuell laufenden Projekten berichten können. Daneben sind aber auch alle anderen Themen aus der biologischen Systematik vertreten und willkommen. Dementsprechend finden am Donnerstagmorgen die Hauptvorträge von Wolfgang Weisser (TU München), Florian Leese (Ruhr Uni Bochum) und HaJo Mader („Die Wildnisstiftung“ Brandenburg) statt. Am Freitag folgen dann Maximilian Weigend (Nees Institut Bonn) und Peter Zulka (Umweltbundesamt Wien). Am Mittwochabend werden die Tagungsteilnehmer bei einem traditionellen Icebreaker in der „Afrikanischen Savanne“ im Lichthof des Museum Alexander Koenig empfangen. An diesem Ort fand am 1. September 1948 die Eröffnungssitzung des Parlamentarischen Rates statt, der daraufhin das Grundgesetz der Bundesrepublik Deutschland erarbeitete. Zudem werden

Sie während der Tagung (Mittagspause am Freitag) die Gelegenheit haben, einen Blick hinter die Kulissen des Forschungsmuseums zu werfen, das heute etwa fünf Millionen Exemplare in seinen wissenschaftlichen Sammlungen beherbergt. Dabei werden die Teilnehmer der Tagung von Wissenschaftlern des Hauses begleitet.

Weiterhin können die Tagungsteilnehmer während der Mittagspause am Donnerstag (Anmeldung bei Dr. Katharina Schmidt-Loske) im Rahmen einer begleiteten Führung die Räume des Biohistoricums am ZFMK mit seinen einzigartigen Sammlungen von Büchern und Archivmaterial zur Geschichte der Biologie besichtigen. Dazu gehören Nachlässe, Briefe, Portraits und Illustrationen namhafter Naturwissenschaftler und Künstler sowie eine umfangreiche Bibliothek, deren wertvollste Bände im ehemaligen Arbeitszimmer von Alexander Koenig mit seinem besonderen Ambiente aufbewahrt werden, das schon Konrad Adenauer als erstem Bundeskanzler der BRD als Kanzlerbüro diente. Das 1998 von der Deutschen Gesellschaft für die Geschichte und Theorie der Biologie (DGGTB) gegründetes Forschungsarchiv des Biohistoricums befindet sich seit 2008 am ZFMK in Bonn und stellt eine große Bereicherung für die wissenschaftshistorische Arbeit am Museum Koenig dar.

Natürlich werden sich auch die AGs Kuratoren (3 Vorträge zum Thema: Preserving Tissues, Molecules, and other odd specimens – a practical look at special collections; offen für alle Interessierten) und Junge Systematiker (JuSys) während der Tagung treffen. Dies ist nach den Vorträgen am späten Donnerstagnachmittag gegen 17.30 Uhr geplant. Am Donnerstag um 16.00 wird außerdem die Ehrennadel der GfBS an Professor Horst-Kurt Schminke verliehen. Für Freitagnachmittag ab 17.00 Uhr ist die ordentliche Mitgliederversammlung der GfBS mit der Verleihung des Bernhard-Rensch-Preises an James Neenan vorgesehen. Außerdem werden auch in diesem Jahr wieder die besten studentischen Beiträge ausgezeichnet. Der ereignisreiche Tag wird mit einem gemeinsamen Abendessen im Restaurant „Ente“ am Kaiserplatz direkt in der Bonner City abgerundet (nicht in den Tagungsgebühren enthalten, also nach individuellem Bedarf gestaltbar).

Als weiterer Programmpunkt werden im Anschluss an die beiden Vortragstage am Samstag drei Workshops zu verschiedenen neuen Methoden angeboten (siehe Workshopplan).

Als Alternative zu den Workshops am Wochenende bieten Bonn und das nahe gelegene Köln zahlreiche Freizeitmöglichkeiten, um den Tagungsbesuch in der ehemaligen Hauptstadt und heutigen UN-Metropole ausklingen zu lassen. Ob Sie den Kölner Zoo mit seinem neuen Hippodrom,

rheinische Schlösser und Burgen, oder lieber eines der vielen renommierten Museen der Region besuchen möchten, wie zum Beispiel das Haus der Geschichte, das Rheinische Landesmuseum (Ausstellung: „Eiszeitjäger“), Bundeskunsthalle (Ausstellung: „DER GÖTTLICHE. HOMMAGE AN MICHELANGELO“) oder Beethovens Geburtshaus, ist Ihnen dabei freigestellt. Die Kunst und Ausstellungshalle Der Botanische Garten am Poppelsdorfer Schloss mit seinen großen Gewächshäusern ist außer samstags von Montag bis Freitag in der Zeit von 10-12 Uhr und 14-16 Uhr sowie am Sonntag von 10-17 Uhr geöffnet.

Fragen und Anregungen richten Sie bitte an das Organisationsteam, das Ihnen gerne behilflich sein wird.

Wir freuen uns auf eine ereignisreiche und interessante GfBS-Tagung!

Die Organisatoren am ZFMK,

Wolfgang Wägele & Johannes Dambach, Bonn

Inhaltsverzeichnis:

Begrüßung	1
Allgemeine Informationen	5
Programmübersicht	10
Vortragsprogramm	11
Liste der Posterkurzvorträge	17
Abstracts Vorträge	20
Abstracts Poster	59
Beschreibungen der Workshops	79
Platz für Notizen	82
Karten:	
Anfahrtsskizze zum Museum Koenig	8
Wegbeschreibung Restaurants ENTE.....	8

Allgemeine Informationen:

Um Ihren Aufenthalt am Museum Alexander Koenig in Bonn so angenehm wie möglich zu gestalten und eine reibungslose Tagungsteilnahme zu garantieren, haben wir einige nützliche Informationen für Sie zusammengestellt.

An- und Abreise:

Vom **Flughafen Köln-Bonn** bringt Sie der Shuttle-Bus SB60 schnell und unkompliziert in die Bonner Innenstadt.

Das Museum Koenig ist sehr gut mit **öffentlichen Verkehrsmitteln** zu erreichen. Vom Bonner Hauptbahnhof aus fahren Sie fünf Stationen mit den U-Bahnlinien 63/16 oder 66 in Fahrtrichtung Bad Godesberg bzw. Bad Honnef. Die Haltestelle heißt „Museum Koenig“. Beide Linien verkehren sehr regelmäßig. Außerdem können Sie die Buslinie 610 vom Bahnhof aus nehmen und bis zur Schedestraße fahren (siehe Plan).

Mit dem **PkW** fahren Sie aus nördlicher Richtung über die A 565, Abfahrt "Bonn-Poppelsdorf". Folgen Sie der Ausschilderung "Museumsmeile"; nach der Reuterbrücke ganz nach links einordnen, dann wie auf dem Lageplan dargestellt (siehe unten). Das Museum Koenig hat zwar einige Parkplätze, die jedoch auch von Angestellten und Besuchern des Museums genutzt werden. Die umliegenden Straßen sind meist Anwohnerparkzonen und werden sehr regelmäßig kontrolliert. Bitte parken Sie im Parkhaus in der Nähe der Kunst- und Ausstellungshalle, der Fußweg beträgt etwa 10 Minuten.

Vorträge und Poster:

Bitte geben Sie Ihre **Power-Point-Präsentationen** für Vorträge und Poster gleich nach der Anreise im Tagungsbüro ab, so dass wir sie problemlos auf die Rechner in den Vortragsräumen kopieren können. Während der Vorträge wird eine dreistufige Ampel den Rednern signalisieren, wie lange ihre Redezeit (noch) dauert.

Um den Wünschen aller eingereichten Vorschläge nachzukommen, werden die **Vorträge** am Freitag in zwei parallelen Sessions stattfinden. Neben dem Hörsaal auf der ersten Etage des Hauptgebäudes oberhalb der Empfangshalle, wird hierfür der Festsaal eine Etage über dem Hörsaal genutzt. Die **Poster** werden vor oder im Festsaal auf der zweiten Etage des Haupthauses gleich oberhalb des Hörsaales aufgestellt. Statt einer Postersession werden die Poster in Form von Kurzvorträgen im Hörsaal

präsentiert. Diese Präsentationen finden am Freitag um 11.00 Uhr statt. Jeder Autor hat maximal drei Minuten Zeit, um sein Poster kurz vorzustellen, das dann in den anschließenden Pausen genauer betrachtet und diskutiert werden kann. Die Reihenfolge der Kurzvorträge entnehmen Sie bitte der Auflistung ab Seite 20. Um einen schnellen Wechsel zu gewährleisten, empfiehlt es sich für die Vortragenden, während der Sessions die vorderen Sitzreihen zu benutzen.

Studenten-Preise:

Wie in den vergangenen Jahren werden die jeweils drei besten studentischen **Posterpräsentationen** mit Preisen ausgezeichnet. Die Gewinner werden während der Mitgliederversammlung am Freitagnachmittag bekannt gegeben. Dort erhalten sie auch die Urkunden und Preise. Darüber hinaus erhält jeder Student, der sich vorab für die Teilnahme angemeldet hat, einen kommentierten Bewertungsbogen ausgehändigt. Wir bedanken uns bei allen Juroren für ihre Mithilfe.

Catering:

Für das leibliche Wohl der Tagungsteilnehmer ist bestens gesorgt. Während der **Kaffee-Pausen** werden Getränke und Gebäck auf der zweiten Etage vor dem Festsaal serviert. Kleine Snacks können im Bistro auf der ersten Etage gleich neben dem Hörsaal erworben werden. Zum Mittagessen empfehlen wir das Restaurant „Da Dante“ im Hotel Kanzler gleich neben dem Museu oder das Bistro im Museum, das jeden Tag ein günstiges Mittagsmenü anbietet.

Biohistoricum:

Seit 2008 beherbergt das Museum Koenig das Forschungsarchiv der Deutschen Gesellschaft für die Geschichte und Theorie der Biologie (DGGTB). Die Bibliothek kann während der Mittagspause am Donnerstag unter Begleitung durch Frau Dr. Katharina Schmidt-Loske besichtigt werden (K.Schmidt-Loske@zfmk.de). Treffpunkt ist um 12 Uhr neben dem Hörsaal.

AG Kuratoren:

Das Treffen der AG Kuratoren findet am Donnerstag nach den Vorträgen ab 17.30 Uhr im Festsaal statt. Das Thema lautet: „Preserving Tissues, Molecules, and other odd specimens – a practical look at special collections“. Das Vortragsprogramm entnehmen Sie bitte dem Plan ab Seite 14. Die Veranstaltung ist für alle Interessenten offen.

AG Junge Systematiker (JuSys):

Zeitgleich zur AG Kuratoren trifft sich die AG Junge Systematiker um 17.30 Uhr im Seminarraum des Hauptgebäudes auf der zweiten Etage. Im Anschluss werden wir gemeinsam das Bonner Nachtleben erkunden. Alle Studenten und Nachwuchswissenschaftler sind hierzu ganz herzlich eingeladen.

Mitgliederversammlung:

Die Mitgliederversammlung am Freitagnachmittag bildet den offiziellen Abschluss der diesjährigen GfBS-Jahrestagung am Museum Koenig. Geplant ist der Bericht des Vorstandes sowie die Prämierung des besten studentischen Beitrages. Außerdem wird der Gewinner des Rensch-Preises bekannt gegeben, der seine Dissertation in einem kurzen Vortrag dem Publikum vorstellen wird.

Konferenz-Dinner:

Das Konferenz-Dinner wird am Freitagabend ab ca. 20 Uhr im oberen Stock im **Restaurant „ENTE“** in der Bonner Innenstadt am Kaiserplatz (**in der Kaiserpassage**) stattfinden (siehe Beschreibung unten). Falls Sie sich noch nicht zuvor per Email für das Dinner angemeldet haben sollten, holen Sie dies bitte im Tagungsbüro nach. Die Bestellung erfolgt à la Carte. Es gibt eine vielfältige Karte mit kleinen und großen, frischen, regionalen Spezialitäten.

Workshops:

Nach der Tagung werden am Samstag drei parallele Workshop-Sessions zu unterschiedlichen Themen stattfinden. Einzelheiten entnehmen Sie bitte dem Plan auf Seite 19 und den Beschreibungen ab Seite 83.

Wichtige Telefonnummern:

Tagungsbüro: 0228-9122-253 (während der Tagung nur zeitweise besetzt!)

Museumkasse 0228-9122-102 (während der Tagung gut erreichbar)

Biohistoricum: 0228-9122-269

ZFMK-Sekretariat: 0228-9122-201

Taxi: 0228-55 55 55 oder 19410

Sollten Sie noch offene Fragen haben, wenden Sie sich bitte an das Organisationsteam an der Registrierung. Dort empfangen und beraten Sie gerne unsere Helfer vom Tagungsbüro.

- Am besten lassen Sie Ihren PKW entweder am Museum stehen und fahren mit der U-Bahn in die Innenstadt. Wenn sie mit dem Auto kommen (über B9) müssen sie eines der Innenstadt Parkhäuser aufsuchen oder gegenüber des Hauptbahnhofs einen der kleineren Parkplätze anfahren.

Mit öffentlichen Verkehrsmitteln:

- Vom Museum Koenig aus fahren Sie mit den U-Bahnlinien 63/16 oder 66 in Richtung Innenstadt bis zur Haltestelle „Universität/Markt“. Nehmen Sie beim Aussteigen den linken Aufweg zum Kaiserplatz. Dort biegen Sie bitte rechts in die Straße „Am Neutor“ ein und gehen in Richtung Bonner Münster, links neben ihnen sehen sie dann erst den Kaiserplatz und die Kaiserpassage und dann den Martinsplatz (gegenüber dem Münster) Sie betreten die Kaiserpassage und folgen den Schildern (mehrere Eingänge von verschiedenen Straßen aus).

Programmübersicht der Tagung:

Mittwoch, 18. März:

- 14.00-18.00 Treffen GfBS Vorstand
- 18.00-22.00 Icebreaker und Registrierung in der Savanne im Lichthof des Museum Alexander Koenig
- 19.00-20.00 Führungen hinter die Kulissen des ZFMK

Donnerstag, 19. März:

- 8.00-9.00 Registrierung
- 9.10 Eröffnung und Begrüßung (W. Wägele, U. Fritz)
- 9.30 Hauptvorträge
- 13.30-17.20 Vorträge und Pausen
- 12.00 r Besichtigung des Biohistoricums
- 16.00 Verleihung der Ehrennadel
- 17.30-19.30 Treffen der AG Junge Systematiker (JuSys)
- 17.30-19.30 Treffen der AG Kuratoren (offen für Interessenten)

Freitag, 20. März:

- 9.00-10.00 Hauptvorträge
- 11.00-12.00 Posterkurzvorträge
- 12.00 Tour durch die Sammlungen
- 17.00 Mitgliederversammlung der GfBS, Rensch Preis etc.
- 20.00 Konferenz-Dinner (Restaurant „ENTE“ in der Bonner Innenstadt, ENTE Bistronomie, Martinsplatz 2A, 53113 Bonn)

Samstag, 21. März:

- 9.00-18.00 Workshops in drei parallelen Sessions

Tagungsprogramm der 16. Jahrestagung der Gesellschaft für Biologische Systematik (GfBS)

(Änderungen bitte dem Tagungsbüro mitteilen)

	Zeiten	Veranstaltung (Redezeit)	Redner	Thema	Chair	Raum
Mittwoch						
	14.00-18.00	Treffen GfBS Vorstand				Seminarraum
Mi., 18.03.	18.00-22.00	Registrierung und Icebreaker		-	-	Empfangshalle/ Savanne
Donnerstag						
Do., 19.03.	8.00-9.10	Registrierung			-	Empfangshalle
	9.10-9.30	Eröffnung	J. W. Wägele, U. Fritz	Begrüßung, Organisatorisches, Historisches	-	Hörsaal
	9.30-10.15	Invited Speaker (40+5min)	Wolfgang Weisser	Ecology and Systematics – how to form a new partnership	J. W. Wägele	Hörsaal
	10.15-11.00	Invited Speaker (40+5min)	Florian Leese	Improvement of freshwater ecosystem assessment with DNA barcoding	J. W. Wägele	Hörsaal
	11.00-11.30-	Pause (30 min)				
	11.30-12.00	Invited Speaker(25+5min)	HaJo Mader	Monitoring in wilderness areas	J. W. Wägele	Hörsaal
	12.00-13.30	Mittagspause (90 min) oder Besichtigung des Biohistoricum/Sammlungstour				
	13.30-13.45	Kurzvortrag (12+3)	Alexander M. Weigand, Daniel Grabner, Martina Weiss, Daniel Hering, Bernd Sures, Ralph Tollrian & Florian Leese	DNA barcodes of freshwater amphipods as a springboard for investigating biological processes in natural and novel freshwater ecosystems	F. Leese	Hörsaal

Do., 19.03.	13.45-14.00	Kurzvortrag (12+3)	<u>Matthias Geiger</u>	Germany's freshwater fishes assessed by DNA barcoding - implications for natural resource management			
	14.00-14.15	Kurzvortrag (12+3)	<u>Elise Laetz</u> , Leif Moritz, André Haubrich & Heike Wägele	Photosynthate Production in Kleptoplasts - Understanding How a Sea Slug Survives Starvation			
	14.15-14.30	Kurzvortrag (12+3)	<u>Jahn R.</u> , Abarca N. , Enke N. , Kusber W.-H. , Skibbe O. & Zimmermann J.	Linking morphological and molecular data in reference libraries for diatoms – challenges for taxonomy			
	14.30-14.50	kurze Pause (20 min)					
	14.50-15.05	3 Kurzvorträge (12+3min)	<u>Caroline Ring</u> & Michael Ohl	The Color Varieties of the Wasp - Mimicking Mantispid <i>Climaciella brunnea</i> (Insecta: Neuroptera): Single Species or Species Complex?	T. Töpfer		
	15.05-15.20		Constantin Zohner	Biogeographic history of Limonium (Plumbaginaceae), inferred with the first model that includes a parameter for speciation with dispersal			
	15.20-15.35		<u>Alexander Rockinger</u> & Susanne S. Renner	Making progress on the mega-diverse genus <i>Crotalaria</i> (Fabaceae) - major groupings of the 650 species, their biogeography, and ages			
	15.35-16.00	kurze Pause (25 min)					
	16.00-16.20	Verleihung der Ehrennadel					Hörsaal
	16.20-16.35	3 Kurzvorträge (12+3min)	Rachel C. M. Warnock, <u>Jonas Eberle</u> & Dirk Ahrens	Does morphological divergence anticipate genetic lineage sorting in Pleophylla chafers (Coleoptera)? – Evidence from integrating morphometric and molecular data	T. Wesener	Hörsaal	
	16.35-16.50		<u>Dirk Ahrens</u> , Tomochika Fujisawa, Hans-Joachim Krammer, Jonas Eberle, Silvia Fabrizi & Alfred P. Vogler	Sampling bias and species delimitation: Are rare species a problem?			
	16.50-17.05		Jan Phillip Oyen	Steps towards the phylogeny of pill millipedes (Diplopoda, Glomerida)			
17.05-17.30	Pause (25 min)						

Do., 19.03.	17.30-19.30	Treffen der AG Junge Systematiker (JuSys) (offen für Interessenten)		AG Treffen	CCF Schinkel	Seminarraum
	17.30-19.30	Treffen der AG Kuratoren (offen für Interessenten) Thema: Preserving Tissues, Molecules, and other odd specimens – a practical look at special collections	Peter Giere & Peter Michalik	New and uncommon collection types – an introduction	P. Giere	Festsaal
			Dirk Neumann	DNA and Tissue storage – from individual trials and chaos towards modern cross-linked Biorepositories		
			Brian Tindall			
Jonas Astrin	Biobank networks (mit anschließender Laborführung)					
ab 20.00		Konferenz-Dinner (!!verschoben von Fr. auf Do!!) Abendessen in gemütlicher Atmosphäre Individuelle Bestellung à la carte				Restaurant ENTE in der Bonner City
Freitag						
Fr., 20.03.	9.00-09.30	Invited Speaker(25+5min)	Maximilian Weigend	Mesoscale patterns of biodiversity in the Andes – setting conservation priorities based on detailed taxon distribution maps	J. W. Wägele	Hörsaal
	09.30-10.00	Invited Speaker(25+5min)	Peter Zulka	On subspecies, cryptic species and synonyms – taxonomic impediment in the national Red List assessment process.		
	10.00-10.15	Kurzvortrag (12+3min)	Omid Paknia, Hossein Rajaei Sh. & <u>André Koch</u>	Lack of well-maintained natural history collections and taxonomists in megadiverse developing countries hampers global biodiversity exploration		
	10.15-10.30	Kurzvortrag (12+3min)	Thomas Wesener	The GBOL - Myriapoda project: 1000 sequences reveal insights and shortcomings of the Barcoding of myriapods		
	10.30-11.00	Pause (30 min)				
11.00-12.00	20 Posterkurzvorträge (2-3min)					Hörsaal

Fr., 20.03.	12.00-13.30	Mittagspause 90 min				
	13.30-13.45	4 Kurzvorträge (12+3min) [parallel]	Thorleif H. Dörfel & Michael Ohl	The Australian digger wasps of the genus <i>Sphex</i> – a taxonomic revision	R. Peters	Hörsaal
	13.45-14.00		Ximo Mengual, Gunilla Ståhls & Santos Rojo	Systematics of pipizines (Diptera: Syrphidae) with implications for the evolution of aphidophagy		
	14.00-14.15		Ralph S. Peters, Oliver Niehuis & Lars Krogmann	Phylogenomic data and a strikingly rich fossil record illuminate the evolution of jewel wasps (Hymenoptera: Chalcidoidea)		
	14.15-14.30		Lena Lutz, Hannes Baur & Ralph S. Peters	Taxonomy of some common Western European jewel wasps (Hymenoptera: Chalcidoidea: Pteromalidae) - from integrative to desperate and back		
	13.30-13.45	4 Kurzvorträge (12+3min) [parallel]	Jonas Astrin	Trends in DNA barcoding and biodiversity research - a bibliometric perspective	J. Astrin	Festsaal
	13.45-14.00		Gerhard Haszprunar	Use, misuse, and criteria for „a DNA-barcoded species“		
	14.00-14.15		Harald Letsch, Brigitte Gottsberger & Jessica Ware	Differential diversification in anisopterous dragonflies (Odonata): a result of different habitat use and climate?		
	14.15-14.30		Werner Kunz	400 new bird species - the "Tobias-criteria" for species delimitation		
	14.30-15.00	Pause (30 min)				
	15.00-15.15	3 Kurzvorträge (12+3min) [parallel]	Till Töpfer	Acquisition, loss and re-activation of pathways of plumage colour synthesis in bullfinches (Aves: Fringillidae: <i>Pyrrhula</i>)	C. Koch	Hörsaal
	15.15-15.30		Markus Lambertz	Pulmonary complexity as the starting point for amniote evolution		
	15.30-15.45		Timo Hartmann, Flora Ihlow, Morris Flecks, Andreas Schmitz & Dennis Rödder	Underestimated diversity in <i>Calotes mystaceus</i> (Squamata: Agamidae) - An integrative approach to unravel a putative species complex		
	15.00-15.15	3 Kurzvorträge (12+3min) [parallel]	Anja C. Schunke & Anna Anschütz	Lost variation - The hyoid bone in rodents	T. Struck	Festsaal
15.15-15.30	Michael Weidhase & Christoph Bleidorn		Regeneration in annelids and its relationship to phylogeny			

Fr., 20.03.	15.30-15.45		Ekin Tilic & Thomas Bartolomaeus	Chaetae and chaetogenesis as a character complex to analyze annelid evolution		
	15.45-16.05	kurze Pause (20 min)				
	16.05-16.20	3 Kurzvorträge (12+3min) [parallel]	Morris Flecks, Lasse Lemm, Timo Hartmann, Jonas Astrin, Nikolay A. Poyarkov, Sebastian Steinfartz, Wolfgang Böhme & Dennis Rödder	How to identify species? An integrative approach to delimiting species in the threatened Middle Eastern mountain newts	C. Koch	Hörsaal
	16.20-16.35		Dennis Rödder, Eva Meyers, Flora Ihlow, Morris Flecks, Timo Hartmann, Tanja Ziesmann, Igor Oliveira, Faraham Ahmadzadeh & Ralph S. Peters	Identifying the gaps: status of molecular exploration of global amphibian diversity		
	16.35-16.50		Felix Pokrant & Wolfgang Böhme	Integrative Taxonomy of the Grass Snake (<i>Natrix natrix</i>)		
	16.05-16.20	3 Kurzvorträge (12+3min) [parallel]	Juliane Kretschmann, Marc Gottschling & Malte Elbrächter	The epitype - an important tool for reliable species identification in protists such as dinophytes	D. Ahrens	Festsaal
	16.20-16.35		Alexander Riedel, Thomas van de Kamp, Rene Tänzler & Michael Balke	A species description pipeline for the hyperdiverse weevil genus <i>Trigonopterus</i>		
	16.35-16.50		Natalie Cusimano & Susanne S. Renner	Does tree shape matters in ancestral state reconstructions?		
	16.50-17.00	kurze Pause (10 min)				
	ab 17.00	Mitgliederversammlung			- Bericht des Vorstands - Rensch-Preis Verleihung - Laudatio - Studenten Poster Preise	-
Ab 20.00	Abreise bzw. Abend zur freien Verfügung					
Samstag						

Sa., 21.03.	9.00- ca. 18.00	Workshops 1	Oliver Niehuis, Malte Petersen, Christoph Mayer, Vera Batista & Manuela Sann	Target DNA Enrichment – Methodology, Software, Practical Experience Report	Kursraum Neubau
	9.00- ca. 16.00	Workshops 2	Matthias Bernt & Alexander Donath	“MITOS” Mitogenom-Annotation	Seminarraum (Hauptgebäude)
	9.00- 18.00	Workshop 3	A. Blanke	3D-Rekonstruktion – High Quality 3D Reconstruction for Everyone: open-Source Solutions and their Workflow to analyse and publish MicroCT Data	Museumsschule (neben Seminarraum)

Liste der Poster-Kurzvorträge:

Session I: Donnerstag, 23.02.2012, 16-17 Uhr, Hörsaal

	Name	Titel
No	Alphabetische Reihenfolge	
1	<u>Dirk Ahrens</u> , Silvia Fabrizi, Erika Bazzato, Davide Cillo, Michele Rossini, Ignazio Sparacio, Jonas Eberle, Stella Columba Guido Sabatinelli, Marco Uliana & Giuseppe M. Carpaneto	Deep coalescence or cryptic species? Strong mtDNA divergence obscures species boundaries in <i>Pachypus</i> beetles with strong sex-biased dispersal
2	<u>Patrick Beckers</u> & Thomas Bartolomaeus	The evolution of the annelid nervous system in the light of current molecular phylogenies
3	<u>Arne Beermann</u> , Volodymyr Pushkar, Ximo Mengual, Björn Rulik & Florian Leese	Species diversity of selected aquatic dipteran families in two German stream ecosystems: a comparison of morphological and DNA-based assessments
4	<u>J. Chacón</u> , H. Hilger, S. Ovcinnikova, F. Luebert, M. Weigend	Molecular phylogenetics and systematics of the Boraginaceae s.str.
5	<u>Lars Dietz</u> & Florian Leese	Regional differentiation and extensive hybridisation between mitochondrial clades of the Southern Ocean giant sea spider <i>Colossendeis megalonyx</i>
6	<u>Jörn von Döhren</u> , Daria Krämer, Thomas Bartolomaeus	Analysis of a comprehensive data set on <i>Tubulanus polymorphus</i> Renier, 1804 leads to a separation of the species and to re-establishment of <i>Tubulanus (Carinella) ruber</i> (Griffin, 1898)
7	<u>Jonas Eberle</u> , Silvia Fabrizi, Dirk Ahrens	A phylogeny of Sericini chafers - Out of Africa and back again
8	Dirk Gassmann	Structural diversity and functional morphology of the damselfly ligula: implications for taxonomy, systematics and evolutionary biology
9	<u>Joachim Holstein</u> , Peter Grobe, Dagmar Triebel, and Anton Güntsch	The Biodiversity Network of the Humboldt-Ring (BiNHum): Joint Data Portal for Natural History Museums
10	<u>Flora Ihlow</u> , Morris Flecks, Timo Hartmann, Michael Cota, Sunchai Makchai, Pratheep Meewattana, Jeffrey E. Dawson, Long Kheng, Anja Rauh, Dennis Rödder, Uwe Fritz	Diversity in Southeast Asian Snail-eating Turtles (Geoemydidae: <i>Malayemys</i>): implications for phylogeography and taxonomy
11	<u>Carolin Kindler</u> , Henrik Bringsøe, Uwe Fritz	Phylogeography of grass snakes (<i>Natrix natrix</i>) all around the Baltic Sea: implications for the Holocene colonization of Fennoscandia
12	<u>Claudia Koch</u>	Cryptic reptile diversity in an isolated and gravely threatened habitat in Northern Peru

No	Fortsetzung Posterkurzvorträge	
13	Julia König, Jonathan-Philip Ruhm, Helena Römer, Mohan Siwakoti, Hartmut H. Hilger & Maximilian Weigend	Preliminary results of a revision of the family Boraginaceae for the Flora of Nepal
14	Daria Krämer, Thomas Bartolomaeus & Jörn von Döhren	A new monostiliferan species (Nemertea:Hoplonemertea) from the Mediterranean Sea in Italy
15	Juliane Kretschmann, Marc Gottschling	Generative ontogeny in <i>Cordia nodosa</i> Lam. (Cordiaceae, Boraginales)
16	Cathrin Schwarz, Jürgen Kriwet	Macroevolutionary patterns of the locomotor system in non-muraenoid eels (Teleostei: Elopomorpha)
17	Matthias Seidel, Michele De Palma, Martin Husemann	Molecular phylogenetics and subgeneric revision of the sub-Saharan genus <i>Eudicella</i> (Scarabaeidae: Cetoniinae)
18	J. Steckel, J. Nieschulze	Improving services for data quality and availability in environmental sciences
19	Vamberger Melita, Stuckas Heiko, Sacco Francesco, D'Angelo Stefania, Arculeo Marco, Cheylan Marc, Corti Claudia, Lo Volvo Mario, Marrone Frederico, Wink Michael & Fritz Uwe	Differences in gene flow in a twofold secondary contact zone of pond turtles in southern Italy (Testudines: Emydidae: <i>Emys orbicularis galloitalica</i> , <i>E. o. hellenica</i> , <i>E. trinacris</i>).
20	Tanja Weibulat, Martin Ebert, Martina Kölbl-Ebert, Markus Moser, Dieter Neubacher, Dirk Neumann, Henriette Obermaier, Wolfgang Reichert, Veronica Sanz, Markus Weiss, Dagmar Triebel	IDES: Making fish specimen data and images from natural history collections publicly accessible

ABSTRACTS

der

Vorträge & Poster

in alphabetischer Reihenfolge der Erstautoren

1. Vorträge:

Sampling bias and species delimitation: Are rare species a problem?

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In natural assemblages, and therefore also in most resulting taxonomic studies dealing with unknown taxa, the number of individual samples per species is highly skewed. The proportion of rare species (i.e. singletons) may exceed 30%. Therefore it was argued that DNA-based approaches for species delimitation and identification, which have enormous potential to accelerate studies of biodiversity, might strongly suffer under this bias. Therefore, we tested with empirical data and simulations the performance of the Generalized Mixed Yule Coalescent (GMYC) species delimitation, one of the currently most popular methods of DNA-based species delimitation. We studied species limits in southern African chafers (Coleoptera: Scarabaeidae: Sericini) (584 individuals of 101 morphospecies), building GMYC groups based on a Maximum Likelihood tree from *cox1* gene sequences. GMYC groups closely matched morphospecies defined by male genitalia, including 49 (48.5%) 'singletons', but the GMYC performance deteriorated greatly when subclades were analyzed individually. Subsequent simulations addressed the question, what sample size and sampling regime of species drawn from a tree randomly or in clade-specific fashion) affect the accuracy of the GMYC model. While GMYC estimates were accurate under even species sampling and high proportions of singletons alone (up to 52%), the GMYC model was sensitive to variable population size of species under investigation resulting in increased inaccuracy. Unbalanced species abundances (e.g. $\geq 50\%$ singletons) further aggravate the negative effects. A 'clade-wise' expansion of species sampling improved accuracy, in accordance with the empirical data. Therefore, if sampling is poor, estimates of species limits can be improved with data from a larger clade beyond the focal group. Extreme differences in population sizes, species abundance and localized geographic distributions of clade diversity limit the power of the method, but usually not within the parameter space of realistic data.

Trends in DNA barcoding and biodiversity research - a bibliometric perspective

Jonas Astrin

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Abstract

Does tree shape matters in ancestral state reconstructions?

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Reconstructing character states on a molecular phylogeny is a powerful tool for investigating trait evolution. Traits being “reconstructed” range from morphology and ancestral areas to ancestral ecologies and chromosome numbers. The factors determining state reconstructions are the statistical framework used, whether maximum parsimony, maximum likelihood, or Bayesian methods, the density of taxon sampling, and the extent of rate heterogeneity in a dataset. Over the past ten years, the mathematical, statistical, and biological difficulty, or indeed the impossibility, of ancestral state reconstruction (ASR) on trees has been explored and become increasingly clear. Nevertheless, trying to infer ancestral states remains an important activity in comparative biology and can set up strong hypotheses for further testing. An underappreciated problem is the influence of the branch length model used to reconstruct the tree for an ASR problem at hand. Traditionally, workers have preferred ultrametric trees, reflecting the notion that in living species we expect change to increase with time, not necessarily number of substitutions in the DNA regions sequenced for a particular study. Most ASR studies have acted on this expectation even when a few studies showed that phenotypic evolution and molecular branch length are sometimes positively correlated. Given this possibility, exploring the effects of doing ASR on either ultrametric trees or phylograms seems expedient. This talk will show how ASRs can be dramatically affected by the branch length depiction that is chosen. Since there is so far no statistical method for choosing the best branch length model for ASRs, reconstructions should always be carried out on both ultrametric and phylogram trees, with results then interpreted in the light of outside evidence.

The Australian digger wasps of the genus *Sphex* – a taxonomic revision

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Sphex is the second largest genus of digger wasps within the Sphecidae sensu stricto. With 118 described species and a cosmopolitical distribution, these large wasps can be found in almost any part of the world. Among the six ecozones, the Australasian region has the highest diversity of *Sphex*. Focusing on the Australian continent, over 20 morphological characters were thoroughly examined in pinned specimens from each of the 24 species known to occur there. Additionally, we were able to describe eleven new species by looking through incorrectly identified and unidentified material. From these results, a dichotomous key covering all known Australian species of the genus was generated. Locality records from all examined specimens were used to further assess the geographic distribution and species diversity among the federal states, with our results being supported by data about the Australian climate zones.

Does morphological divergence anticipate genetic lineage sorting in *Pleophylla* chafers (Coleoptera)? – Evidence from integrating morphometric and molecular data

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Abstract

Reconciliatory efforts of assessing morphological and molecular data in establishing species units are crucial for the success of an integrative approach to taxonomy. In this case study we investigate the evolutionary history of the scarab beetle genus *Pleophylla* (including 110 individuals of eight putative morphospecies, collected from eight localities in South Africa), and infer species boundaries through the integration of multiple lines of evidence. Traditional morphology-based species assignments were quantitatively assessed using Eigenshape analysis of the male genitalia. Phylogenetic relationships were reconstructed using likelihood and Bayesian methods, based on the nuclear ribosomal rRNA 28S gene, the nuclear internal transcribed spacer 1 (ITS1), and the mitochondrial cytochrome oxidase subunit 1 (*cox1*) and 16S rRNA (*rrnL*) genes. The Bayesian species tree resulted in strong support for the interspecific relationships estimated using the *cox1* data, and indicated that interspecific divergences may be extremely recent (the two youngest divergence events, were estimated to be no older than 0.17 Mya and 0.65 Mya, respectively). Species boundaries were estimated using statistical parsimony and the generalized mixed Yule coalescent (GMYC) model. Support of priorly assigned morphospecies was assessed in a Bayesian framework (iBPP), by evaluating morphological and molecular data simultaneously. While both the Eigenshape analysis and the ITS1-based species assignments were broadly congruent with the traditional morphospecies, the *cox1* data resulted in over-splitting, probably due to incomplete lineage sorting. We demonstrate the utility of characterizing phylomorphospace, to visualize and interpret patterns of divergence between different types of data sources, in particular among closely related species. All together, our findings suggest that *Pleophylla* has undergone a recent radiation, and that morphological divergence of their genitalia has proceeded complete lineage sorting of standard molecular markers.

How to identify species? An integrative approach to delimiting species in the threatened Middle Eastern mountain newts

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Abstract

The species plays a fundamental role in zoological fields such as ecology, evolution, biogeography, and conservation. Therefore, objective and clear-cut recognition of species is paramount. Molecular methods, especially barcoding, have become a popular tool to identify and delimit species and facilitated traditional morphology-based species recognition. However, following the plea for an integrative taxonomy, more lines of evidence should be incorporated when identifying species. While an increasing number of studies use ecological niche modelling (ENM) within an ecological and evolutionary framework, there are only few examples of ENM used to support taxonomy.

The Middle Eastern mountain newts (genus *Neurergus*) currently comprise six taxa whose status has been under debate. We aim to delimit species within this genus by combining different, independent lines of evidence. These include barcoding (using the two mitochondrial genes 16S rRNA and COI), multi-locus species trees evaluated using Bayesian species delimitation under different priors, morphological overlap analyses through n-dimensional hypervolumes of morphometric and colouration characters, and n-dimensional hypervolumes of the ecological niches using PCA-derived variables of environmental data obtained from occurrence records.

The consensus of all methods suggests four species within *Neurergus*. However, the conflicting results regarding species delimitation between the used methods underline the necessity of combining multiple methods within an integrative framework. Especially in threatened *Neurergus*, focussing on one method can mislead taxonomy and consequently hinder species-based conservation assessments. ENM provides a further, well applicable tool to test species hypotheses. Different realised niches indicate specific divergence, as physiological tolerances that define the niche evolve during or trigger speciation.

Germany's freshwater fishes assessed by DNA barcoding - implications for natural resource management

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This study represents the first comprehensive molecular assessment of freshwater fishes and lampreys from Germany. We analysed COI sequences for almost 80% of the species mentioned in the current German Red List. In total, 1056 DNA barcodes belonging to 92 species from all major drainages were used to (i) build a reliable DNA barcode reference library, (ii) test for phylogeographic patterns, (iii) check for the presence of barcode gaps between species and (iv) evaluate the performance of the barcode index number (BIN) system, available on the Barcode of Life Data Systems. For over 78% of all analysed species, DNA barcodes are a reliable means for identification, indicated by the presence of barcode gaps. An overlap between intra- and interspecific genetic distances was present in 19 species, six of which belong to the genus *Coregonus*. The Neighbour-Joining phenogram showed 60 nonoverlapping species clusters and three singleton species, which were related to 63 separate BIN numbers. Furthermore, *Barbatula barbatula*, *Leucaspius delineatus*, *Phoxinus phoxinus* and *Squalius cephalus* exhibited remarkable levels of cryptic diversity. In contrast, 11 clusters showed haplotype sharing, or low levels of divergence between species, hindering reliable identification. The analysis of our barcode library together with public data resulted in 89 BINs, of which 56% showed taxonomic conflicts. Most of these conflicts were caused by the use of synonymies, inadequate taxonomy or misidentifications. Moreover, our study increased the number of potential alien species in Germany from 14 to 21 and is therefore a valuable groundwork for further faunistic investigations.

Underestimated diversity in *Calotes mystaceus* (Squamata: Agamidae) - An integrative approach to unravel a putative species complex

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Calotes mystaceus DUMÉRIL & BIBRON, 1837 was commonly regarded as a widespread and relatively common species, occurring from north-eastern India in the West throughout Southeast Asia to the South China Sea in the East, to the Isthmus of Kra in the South and up to 27°N in the North. The recent discovery of a superficially similar but distinct species (*Calotes bachae*) by Hartmann et al. (2013) initiated a comprehensive investigation of the formerly recognized single species. A combination of morphometric, genetic and multivariate spatial methods was used to dismantle a total of five charismatic species.

To assess variation within the *Calotes mystaceus* complex, an extensive morphological dataset (23 meristic and eleven metric characters) of more than 100 specimens covering the distributional range of *C. mystaceus* was compiled. The dataset was analyzed using classical multivariate techniques. In addition, samples for molecular genetic analyses were collected from a representative subset of specimens. Samples were analyzed using the fast evolving mitochondrial genes cytochrome oxidase I (COI) and 12S rRNA to identify even minor genetic differences between different populations. Finally, we used multivariate spatial approaches to compare the environmental niches of the newly discovered taxa.

Including our discovery of *Calotes bachae* in 2013, we were able to dismantle four new species formerly included in the widespread species *Calotes mystaceus*. In conclusion, our integrative approach combining morphological, molecular and ecological data corroborate that diversity of this charismatic group of agamid lizards is highly underestimated.

Use, misuse, and criteria for „a DNA-barcoded species

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In many webpages, meetings and congresses (and probably also at the present one) researchers or institutions report that they have produced xxx barcodes representing xx species. A good number of these reports then conclude that these data now cover xx % of a fauna or of a group suggesting that a substantial part of the overall work is done. However, it is one point to produce a sequence of a/several standard marker/s of a species, but a different story to speak of a “barcoded species”. The latter requires a number of criteria such as a good number of independent samples with a geographic range (ideally including specimens from the type locality), analyses concerning species delimitation, freely available data and vouchers (for checks), and a cleared-up nomenclature. These criteria are mostly fulfilled in the global BOLD database and also educated there (www.boldsystems.org/index.php/SDP_Home). Unfortunately there are increasing numbers of smaller data-bases for particular taxa or regions or applied aspects being far from that standard, contributing to negative bias of DNA-barcoding as a methodology supporting taxonomy and biodiversity research as a whole. Barcoding is defined as a tool for re-identification of species in an accurate, effective (i.e. cheap and fast) and freely available manner, also to facilitate detection of new species – but not to replace the taxonomist. However, to fulfil these requirements, standards of “barcoded species” need to be upheld.

Linking morphological and molecular data in reference libraries for diatoms – challenges for taxonomy

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DNA Barcoding promises to be a fast method to assess the biodiversity of uni-celled organisms such as diatoms in environmental samples. If comprehensive and well curated reference libraries exist, DNA Barcodes can be used as identifiers of known species and indicators of cryptic or new species, even in taxonomic groups and geographic areas which have previously been under considerable morphological taxonomic scrutiny. Taxonomic reference libraries for DNA-Barcoding are crucial for a sound execution of metabarcoding in research. These reference libraries should be based on clonal diatom cultures from which sufficient amounts of DNA can be extracted and enough data (from the nucleus such as 18S, 28S, ITS; the chloroplast such as *rbcl*; and/or the mitochondrion such as CO1) can be produced. Furthermore, clonal cultures with their many valves of single origin provide the opportunity to study the morphology in LM and SEM – from morphometrics to the variability of valve shape and structure – of the respective strain. The identification of the strains, however, is turning out to be difficult since morphological features discovered – and established as characters for taxonomical concepts – in many decades of light microscopic investigation of mixed samples are not as stable and universal as expected. A well curated reference library will facilitate the linking of molecular data to the morphology of a specific strain as well as to a fitting name and taxon description. As more and more molecular data become available through DNA Barcoding, it becomes obvious that DNA sequence databases like EMBL-EBI/NCBI contain many unnamed and some named sequences which are neither linked to comprehensive information about their strains nor to vouchered specimens which is problematic for interpreting their taxonomical affiliation.

Lack of well-maintained natural history collections and taxonomists in megadiverse developing countries hampers global biodiversity exploration

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Recently, there have been controversial discussions regarding the decline in the number of taxonomists as the main bottleneck for the discovery and complete assessment of the global biodiversity. In addition, we here review and highlight the eminent role of natural history collections in exploring the global species diversity by discussing the current conditions of institutional infrastructure in biologically megadiverse developing countries (MDCs). To our knowledge, this is the first critical assessment, which primarily focuses on these biologically wealthy nations. We show that in addition to the taxonomists' shortage, the lack of well-maintained collection infrastructure represents the main bottleneck for biodiversity exploration in MDCs. No campaign to inventory biodiversity at national or global scale in a foreseeable timeframe can be successful without the creation of more positions for taxonomists and the expansion of existing or the establishment of new natural history collections in MDCs, respectively. Considering the lack of sufficient financial resources in many MDCs, we suggest that joint political priority of industrialized and developing countries should be given to the enduring maintenance and sustainable support of institutional infrastructures, if Convention on Biological Diversity (CBD) targets for 2020 are to be addressed expediently.

The epitype – an important tool for reliable species identification in protists such as dinophytes

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For unicellular organisms such as dinophytes, the biodiversity assessment started in the late 18th and early 19th century using light microscopy. Type material, particularly of older descriptions, mostly consists of specimens permanently mounted on glass slides (a historically important example is the Ehrenberg Collection curated at the Museum for Natural History in Berlin) or of an illustration only. In many cases, type material is ambiguous and makes reliable species determination problematic or impossible because of various sources of error (including imperfect documentation of subcellular diagnostic traits or insufficient morphological differentiation of cryptic species). To clarify the taxonomic identity of such ambiguous scientific names and for a correct application, the International Code of Nomenclature for algae, fungi and plants (ICN) provides the tool of designating an epitype. Epitypification has great potential for a stable taxonomy in the various unicellular organismal groups, but relatively few such studies have employed this approach in the past. In our ongoing research, we clarify the taxonomic identity of dinophyte species (some of them important and widely distributed such as *Scrippsiella erinaceus* comb. nov.; Thoracosphaeraceae, Peridinales) by collecting material at type localities. After establishing of living strains, the species are DNA-barcoded using rRNA sequences and investigated using modern light and scanning electron microscopy. Strains being morphologically consistent with corresponding protologues are used for designation of interpretative epitypes in form of permanent slides for light microscopy. The significant difference to the historical types is that they are linked to living material enabling the generation of DNA sequences as well as experiments in ecology and physiology. Thus, epitypification is a key tool for reliable species determination ensuring unambiguous links between a scientific species name, its protologue, morphology, ultrastructure, genetic characterisation and spatial distribution, all of which have importance, especially for character-poor, unicellular organisms such as the dinophytes.

400 new bird species – the “Tobias-criteria” for species delimitation

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The recent volume of the “Checklist of the Birds of the World”, published by “Handbook of the Birds of the World” and “BirdLife International” is the first taxonomic checklist of all the birds of the world, using uniform criteria for species delimitation applied consistently by the same experts. The basis for species delimitation are the so-called “Tobias-criteria”. Multiple phenotypic characters - including biometrics, plumage and voice – are used as a score to reassign species limits between birds. The authors argue that their system can be applied to the global avifauna to deliver taxonomic decisions with a high level of objectivity, consistency and transparency. As a consequence, the total number of Non-Passerines has been increased by 400 new species. For Passerines, the number is expected to increase even more. The scoring-method is in contrast to DNA-based taxonomies like the barcode approach. The authors legitimate their method by arguing that barcode-taxonomy is based on DNA sequences which have nothing to do with the genes that are responsible for the speciation process. But their opponents argue that the scoring-method ignores genotypic (hidden) differences among species and, therefore, it is a fall-back into the taxonomy of the 19th century. For bird species delimitation, several problems arise between the two taxonomic systems: the barcode-method would have to consider the Common Redstart in Germany to consist of several species due to large differences in barcodes, and it has to unite (“lump”) the Common Swift together with the Pallid Swift in Spain into one and the same species due to an almost complete lack in DNA differences. In several other examples of Eurasian bird species, differences in plumage, voice or reproductive compatibility in comparison to differences in DNA sequences do not line up with each other. This presentation tries to explain some basic problems in classification.

Photosynthese Production in Kleptoplasts – Understanding How a Sea Slug Survives Starvation

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Solar-powered sea slugs (Gastropoda: Sacoglossa) are well known due to their ability to steal chloroplasts (kleptoplasts) from their algal food and incorporate them. These kleptoplasts are said to sustain a slug for months during starvation periods although after a few months, they degrade and are probably digested. Previous research has focused on understanding the genetic and ecological basis behind this system, however little work has been done to understand the incorporation and retention processes on a cellular level. Our current work aims to clarify how chloroplasts are incorporated into digestive gland cells, and how the typical intracellular digestive processes are modified to allow kleptoplast retention. Using transmission electron microscopy, I will examine the initial endocytotic event and subsequent status within the cell. I will also use immunohistochemistry and fluorescent staining to examine the pH environment within the endosomal compartment during retention and digestion. Kleptoplast functionality has long been assumed due to a starving slug's prolonged life span, although little is known about when and how any photosynthetic products are made available to the slug. We demonstrate here that starch is produced and accumulated after kleptoplast incorporation and suggest that this starch is at least one nutritive product that allows slugs to survive months of starvation.

Differential diversification in anisopterous dragonflies (Odonata): a result of different habitat use and climate?

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A common pattern frequently occurring in phylogenetic trees is unbalanced clade size, i.e. the extent to which clades in a tree tend to differ in their diversity. While this can partially be expected simply by chance, several studies in the past have shown that imbalanced phylogenies are significantly more frequent than expected by models of diversification. As a consequence, the causes behind these patterns have become one of the central targets in evolutionary biology. In the present study, we explored the differential diversification among dragonfly families (Odonata: Anisoptera) and potential ecological traits that might have caused these patterns. We compiled a comprehensive molecular data set, based on eight ribosomal RNA and protein coding genes, representing all major dragonfly groups. Based on this data, tree reconstruction was conducted and divergence times of the anisopteran families were estimated. Our phylogenetic reconstruction proposes Aeshnoidea as the first branch in Anisoptera and Gomphoidea as sister group to Cavilabiata, the latter being subdivided into Cordulegastroidea and Libelluloidea. Stochastic character mapping further revealed lotic (flowing) fresh water systems as primary habitat, while lentic (still) fresh water bodies have been colonised independently in Aeshnidae, Corduliidae and Libellulidae. While the speciation rates in most lotic groups are uniform over time, speciation rate increased in lentic Aeshnidae and also in some libellulid clades. The timing of increased speciation rates indicates that the capability of using relatively ephemeral lentic habitats might be a prerequisite for radiations in times of warmer climate with high humidity.

Taxonomy of some common Western European jewel wasps (Hymenoptera: Chalcidoidea: Pteromalidae) – from integrative to desperate and back

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Parasitoid wasps are mostly small sized (few millimeters) hymenopterans whose larvae develop on or in various life stages of other arthropods, mainly insects, thereby killing the host immediately or after completion of development. The taxonomic knowledge of parasitoid wasps is scarce, and this even holds for many groups of our comparatively well-studied western European fauna, that can be commonly found in almost any habitat. These fundamental gaps in our understanding of species boundaries in one of the most species-rich and numerically most abundant insect groups which arguably includes pivotal parts of our terrestrial ecosystems hamper thorough biodiversity assessments and ecological community studies as well as correct decisions on the conservation of the biodiversity heritage of our “backyard”.

One of the difficult and diverse groups of parasitoid wasps is the genus *Pteromalus*, with approximately 250 species recorded in Germany. Most parts of the genus are in unrevised state ever since the descriptions of species in the 19th and 20th century, and available information is restricted to classical external-morphology-based taxonomy and fragmented biological data. In a *status quo* report, we exemplarily show how we approach such a huge taxonomic problem, integrating molecular and morphological/morphometric data, and which problems and promises arise, and how we plan to overcome the problems and extend the promises.

Systematics of pipizines (Diptera: Syrphidae) with implications for the evolution of aphidophagy

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The tribe Pipizini (Diptera: Syrphidae) has been treated as member of subfamily Eristalinae based on diagnostic adult morphological characteristics, while the larval feeding mode and morphology is shared with predatory members of subfamily Syrphinae. In this study, phylogenetic relationships and the taxonomic rank of the pipizine flower flies were estimated based on DNA sequence data from three gene regions (COI, 28S and 18S) and 111 adult morphological characters. We analysed each data set, both separately and combined, in a total evidence approach under parsimony and maximum likelihood. To evaluate the influence of different alignment strategies of rDNA 28S and 18S genes on the resulting topologies, we compared the topologies inferred with a MAFFT alignment with those topologies resulting from aligning the secondary structure of these rDNA genes. Total evidence analyses resolved pipizines as sister group of the subfamily Syrphinae. The homogenous morphology of the Pipizini clade in combination with their unique combination of biological characteristics among the Syrphidae suggest a change of rank to subfamily, Pipizinae stat. rev.

Steps towards the phylogeny of pill millipedes (Diplopoda, Glomerida)

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The pill-millipedes of the order Glomerida (Myriapoda, Diplopoda) are small enigmatic animals, occurring in the holarctic ecozone, which can roll up into a perfectly closed ball when threatened. The relationships of the genera within the Glomerida are still up to debate, as the current system is typological and based on a single character, namely the male telopods. To test the current system and explore the morphological diversity of the pill-millipedes, using an unprecedented taxon sampling, two nuclear and two mitochondrial marker genes were analyzed and 2355 high resolution SEM images of 17 separate structures were recorded and examined. Here we show that the current system of the order Glomerida does not provide a subdivision in monophyletic units. The molecular phylogenetic analyses failed to recover any of the currently proposed groups above genus level, such as the suborder Glomeridelloidea or the family Protoglomeridae. Problems could be found even on genus level, as *Haploglomeris multistriata*, which belongs to the sub-family Haploglomerinae was recovered within the genus *Glomeris* of the sub-family Glomerinae. Additionally, based on two exemplary morphological character systems, it is shown that the morphological diversity of the pill-millipedes is highly underrated and that numerous potentially phylogenetically informative characters can still be found by studying the external morphology with SEM-microscopy. Furthermore, it is shown that Europe is the most likely origin of the current distribution of the order and that the hitherto hypothesized close relationship between the American and Asian genera is unlikely. The results clearly demonstrate that there is still much work to be done to establish a robust phylogenetic system for the order and that the current focus on the male telopods needs to be shifted to include a wider spectrum of characters.

Phylogenomic data and a strikingly rich fossil record illuminate the evolution of jewel wasps (Hymenoptera: Chalcidoidea)

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Jewel wasps (Chalcidoidea) are a group of predominantly parasitoid wasps. They are among the most species rich, ecologically important and biologically diverse groups of terrestrial organisms. An estimated 500,000+ species are currently provisionally classified in 23 families and 83 subfamilies. Major patterns in the evolution of Chalcidoidea include their extreme morphological diversification, shifts in mode of parasitoid lifestyle and host specificity, and multiple secondary returns to phytophagy. A robust dated phylogeny is needed to address the question how and when this enormous diversity of species and biological and morphological traits has evolved.

In the framework of the Hymenoptera subproject of 1KITE (www.1kite.org), we sequenced and phylogenetically analyzed the transcriptomes of 36 Chalcidoidea species from 16 families. In addition, we are studying the rich fossil record of the group, which consists of more than 1,000 specimens from various amber deposits that span more than 100 million years of history, from the Early Cretaceous to the Miocene.

First results show that all early branching lineages of Chalcidoidea are egg parasitoids, which is in congruence with the fossil record, and that convergent evolution of some rather obvious phenotypic characters has happened more frequently than previously thought. This includes, for example, the ability to jump and associated morphological characters, the appearance of large-bodied taxa with enlarged and toothed hind femora and the development of exposed ovipositors. Also, we found further evidence that the superfamily requires revised classification, with numerous traditional families being apparently non-monophyletic. The minimum age of the group can be set at about 130 million years, based on previously unrecognized specimens from Lebanese amber. The new fossils, which cover all extant families and most subfamilies, provide important calibration points for the Chalcidoidea tree allowing us to date important biological and morphological transitions.

Integrative Taxonomy of the Grass Snake (*Natrix natrix*)

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The intraspecific phylogeny of the grass snake (*Natrix natrix*) has been under discussion since many decades. Various morphological and genetic attempts yielded often conflicting results and enhanced the need for a taxonomical revision. The aim of this study was to shed more light into this topic by analyzing phylogenetic relevant differences in osteology and other morphological characters to eventually support previously published mtDNA based phylogenies.

The deep phylogenetic split between African and Iberian grass snakes could indeed be supported by significantly lower ventral scale counts compared to all other *Natrix natrix* clades and several structural differences in basicranial morphology. Based on these morphological divergence, a large genetic distance due to a long term separation in the Miocene, the lack of confirmed hybridization with neighboring grass snakes, and the distinct coloration, we recommend species status for Iberian and North African grass snakes and suggest *Natrix astreptophora* (SEOANE, 1884), stat. nov., to be the new valid name for this taxon. On the other side, phylogenetic relationships between the other lineages remain highly cryptic and statistical verifiable morphological support for these clades could not be found in this study.

A species description pipeline for the hyperdiverse weevil genus *Trigonopterus*

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Trigonopterus weevils are flightless, yet they are widely distributed throughout Southeast Asia and Melanesia exhibiting a complex biogeographic history. They are hyperdiverse in New Guinea and a dominant feature of its natural forests, but the usefulness of these beetles for community ecology research has been precluded by their external similarity and the near absence of taxonomic data.

The majority of species are morphologically very difficult to distinguish, even for expert taxonomists. DNA barcoding proved as an effective tool for rapid discovery and identification of species, both locally and over a wider geographic range. Despite of their external similarity genetic divergence between the species is amazingly high (4.7-27.5%).

Here, we demonstrate the functionality of a species-description pipeline: we use cox1 sequence data, concise morphological descriptions compiled by an expert taxonomist, and high-resolution digital imaging to describe and formally provide large numbers of new species with scientific names. Together with web-publication and automated journal-wiki content pushing this creates the most efficient and sustainable taxonomy to date. Within two years the number of described species has been brought from 95 to 313; hundreds of additional new species await formal description and naming. Our studies on biogeography and functional morphology of *Trigonopterus* benefit from this newly created taxonomic foundation.

The Color Varieties of the Wasp-Mimicking Mantispid *Climaciella brunnea* (Insecta: Neuroptera): Single Species or Species Complex?

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Representatives of the mantispid *Climaciella brunnea* are characterized by distinct color varieties. The species appears widespread in North and Central America, while its occurrence depends on that of harmfully stinging wasps. Together they form a complex of Batesian mimicry. Today, the color forms of *C. brunnea* are considered to be representatives of one highly polymorphic species. Here, genetic differences between specimens are investigated. The appearance of model species and the occurrence of the according color mimic are closely linked. A phylogenetic analysis of the mitochondrial COI fragment of four different color morphs, however, reveals no direct correlation between genetic diversification and color forms. Phylogenetic clusters seem to be linked to their geographic origins. From this, two species are inferred within *C. brunnea*: One occurring in North America and one in Central America. Within the North American group, a distinct split between two populations can be observed, resulting in a western and an eastern group.

Making progress on the mega-diverse genus *Crotalaria* (Fabaceae) – major groupings of the 650 species, their biogeography, and ages

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Crotalaria L. has about 650 species of which some 480 occur in Africa and Madagascar, 110 in Asia, mostly in India, 54 in Australasia, and 60 in the Americas. Due to economic importance as fiber crops, green manure and cattle fodder, some species are distributed pantropically. Within Crotalariaeae (11 genera with together c. 1200 species), the African *Bolusia* (5 spp.) and *Euchlora* (1 sp.) appear to be the closest relatives of *Crotalaria*. The infrageneric classification of *Crotalaria* largely stems from the African species and is mainly based on flower and fruit morphology. Our current matrix includes 300 ITS sequences, representing 294 *Crotalaria* (46% of the total), with roughly proportional sampling of the main distribution regions, plus six outgroups. We also sampled a few pan-continentially distributed *Crotalaria*. The genus is monophyletic, and each of the geographic regions was occupied several times. The talk will present first results on the geological times during which the main clades evolved and on leaf morphological traits (simple, unifoliolate, trifoliolate, multifoliolate) that are revealed as unexpectedly conserved.

Status of molecular exploration of global amphibian diversity

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Herein, we assess the historical dimension of our knowledge on global amphibian species diversity and illustrate how our recognition of species diversity has changed through more than 250 years of discoveries based on range estimates of 7,038 species (95.8% of all amphibian taxa). Global coverage of amphibian diversity is estimated based on the twelve most common molecular markers, including 174,371 sequences. We hypothesize that (i) integrative taxonomy utilizing genetic information has accelerated the recognition of endemic, often cryptic taxa and ultimately led to a boost in discoveries of species. While the delimitation of early-described species relied on morphological (and ecological) characters, molecular data potentially allows a much finer distinction between taxa, which ultimately leads to a boost in species descriptions and a higher percentage of identified cryptic, often endemic taxa as new techniques become available. If so, the average minimum genetic distance between newly recognized species and the known set of species at a given time step will decrease. However, (ii) as the availability of molecular methods is not equally distributed around the globe, this translates in an uneven temporal and spatial detection rate. While marker selection predominantly depends on applicability for certain systematic studies, preferences for established genetic markers also result in an uneven global coverage causing a spatial bias in the coverage of the local amphibian fauna affecting the likelihood to detect new species via molecular methods. At the same time large scale phylogenies may suffer from this spatial bias as specific groups are underrepresented.

Lost variation – The hyoid bone in rodents

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The hyoid is a small bone derived from a branchial arch and consisting of several elements. Due to its tiny size and the fact that it is as a rule connected to the skull only by soft tissue it usually gets lost during preparation, particularly in small animals like rodents. Hence, very little information concerning its variability in small mammals is available.

We analysed a data set of 121 hyoid bones from 65 rodent species, including amongst others mice, gerbils, guinea pigs, and squirrels. Our analyses showed tremendous differences in size, shape, position, and number of bony elements. A remarkable degree of variation can be found between and even within species, but major changes seem to have occurred mostly between rodent suborders, with a strong tendency towards reduction of elements and rotational shifts.

Chaetae and chaetogenesis as a character complex to analyze annelid evolution

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Chaetae are one of the most studied structures of annelids, due to their enormous structural diversity that provide an important source of information for taxonomists and insights into annelid evolution. Recent reconstructions indicate that early annelids only had simple capillary chaetae, so complexity and diversity of chaetae increased during annelid evolution. In order to test this idea, we studied the chaetal pattern in Eunicida and were able to show that chaetal diversity increases within the radiation of this taxon, and provide sound explanations for the transformation of chaetae within the group. Annelid chaetae are formed within an ectodermal pouch (chaetal follicle). Dynamic microvilli of its basalmost cell determine the chaetal structure. In order to substantiate hypotheses of structural homology we compare the developmental processes that generate these structures, since homologous structures should result from similar morphogenetic processes. A comparative analysis of hooded hook chaetogenesis in the distantly related taxa Eunicida, Spionida and Capitellida reveals numerous differences that support the independent evolution of their hooded hooks. Not only the study of chaetogenesis itself but also the comparative analysis of its topological position supports homology hypotheses. By studying the chaetal formation in Echiura, we were able to present a phylogeny based evolutionary scenario for their origin. According to this, the paired neuropodia of the annelid ancestor were transformed into a pair of ventral chaetae in the echiruan stem lineage, while the ancestral notopodia were reduced. The caudal ring of chaetae in *Echiurus echiurus* and other derived species evolved once within Echiura and morphologically support a monophylum that has thus far only been substantiated by molecular data. All of these studies not only exemplify the informative value and significance of chaetae as a character, but also demonstrate the necessity of having robust phylogenies as a backbone for any evolutionary consideration.

Acquisition, loss and re-activation of pathways of plumage colour synthesis in bullfinches (Aves: Fringillidae: *Pyrrhula*)

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The red, orange and orange-brown colours of the body plumage of male *Pyrrhula* bullfinches are primarily based on carotenoids. Females and both sexes of monomorphic bullfinch species generally lack such pigmentation. Most likely, all feather carotenoids are metabolised from only two substrate (i.e. food-borne) pigments: lutein and β -carotene. These pigments are each transformed via three enzymatic pathways into different plumage carotenoids.

According to the available phylogenetic and plumage carotenoid distribution data, there is no particular carotenoid pathway unique to bullfinches. Instead, there is a mixed pattern of active and inactive metabolic pathways, leading to the presence of intermediate products and incomplete metabolisations of substrate pigments within *Pyrrhula* and among other finches (Fringillidae). Nonetheless, it is likely that the ability to metabolise food carotenoids to feather pigments was lost secondarily in those bullfinch lineages without carotenoid-coloured plumages. This is supported by frequent losses or gains of plumage carotenoids across the whole finch tree. Thus, regarding the variety of feather carotenoids found in fringillid birds, it appears plausible that the respective enzymatic cascades or parts of them were activated or inactivated several times during phylogenesis.

By combining data on carotenoid synthesis pathways with the molecular tree, hypotheses on the evolutionary development of carotenoid-based colouration patterns in bullfinches can be made. Considering the specificity of enzymes (or the lack thereof) to alter the structure of pigments, reconstructions of different complexity can be made. Reporting from a work in progress, this talk addresses perspectives and difficulties during the phylogenetic reconstruction of multi-component biochemical pathways.

Monitoring of opisthobranch biodiversity in Indonesia – where is the applied aspect?

####leider ausgefallen#####

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Coastal areas of Indonesia are considered as the most diverse marine habitats in the world. This comprises also opisthobranch taxa (Gastropoda, Mollusca), which exhibit highest species numbers and also highest diversity with regard to life styles in these tropical areas. Not only scientists are interested in opisthobranch diversity. Tourists, a major economic factor in these areas, are highly attracted by these beautiful gastropods. Actually, many diving centers advertising during the International Exhibition BOOT in Düsseldorf use large pictures of slugs for attraction. Less known is their importance in the search of new drug leads. Antibiotic resistance to traditional products is one of the biggest threats in human health and therefore these organisms have come into focus as novel producers of bioactive metabolites. Mollusk-derived molecules are most promising drug leads and especially opisthobranchs contribute already to several new medical therapies. When the Bundesministerium für Bildung und Forschung (BMBF) advertised their program in spring 2014 (Identifikation und Nutzung in Indonesien natürlich vorkommender Substanzen für die Arzneimittelentwicklung), the authors successfully applied and we will start with our project (*Indonesian Opisthobranchs and associated microorganisms -From biodiversity to drug lead discovery*) in 2015. Here we present our knowledge on opisthobranch diversity from that region, their use in medicine and finally the overall goal of our project.

Regeneration in annelids and its relationship to phylogeny

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Annelids possess extensive regenerative ability, from regeneration of appendages up to complete body regeneration from single segments. Since the first investigations of annelid regeneration in the middle of the 19th century, several hundreds of reports and studies have been published under this topic. However, due to an unsettled phylogeny, reliable hypotheses concerning evolution of regeneration ability within annelids were difficult. With the improvement of our knowledge in annelid phylogeny during the last years, there is now the possibility to reconstruct evolutionary traits for regeneration in annelids. In general, regeneration in annelids can be distinguished, e.g., by its context, namely during reproduction or after traumatic loss, by its direction, either anterior or posterior, or by its extent. Based on a comprehensive literature review, complemented by own investigations, we categorized annelid regenerative abilities and present the most complete summary, including all major subgroups. We address general evolutionary trends, like the presumably complete loss of regeneration ability in leeches, as well as unique occurrences, like the combination of sexual reproduction and regeneration during schizogamy in the Syllidae or the compensatory opercula regeneration in *Hydroides*. Our preliminary findings support the idea of high level regenerative ability in species reproducing asexually by fission, e.g., the Cirratulidae. In contrast, in several taxa of the Errantia, anterior regeneration is extremely limited to parts of the prostomium, antenna or palps, whereas posterior regeneration is unaffected, which indicates a relationship to their way of life. Moreover, we hypothesize that stem cell generation during regeneration by dedifferentiation of tissue cells represents the ancestral stage, whereas the involvement of pre-existing stem cells in regeneration, like in many clitellates, is a derived character. These outcomes provide essential knowledge for further studies as well as for identifying new model species for regeneration studies.

DNA barcodes of freshwater amphipods as a springboard for investigating biological processes in natural and novel freshwater ecosystems

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Amphipod crustaceans are ecosystem engineers in aquatic habitats and as such ideal model taxa for addressing research questions about biological processes in natural compared to novel ecosystems. We here provide an overview of how DNA barcodes of Amphipoda can be utilized as a springboard to e.g. i) environmental diagnostics identifying non-native or invasive species, ii) biodiversity research unveiling cryptic species, iii) parasitology linking host and parasite species dynamics, and iv) phylogeography unravelling dispersal and invasion histories of species.

Specifically we highlight the value of DNA barcodes in an ongoing collaborative project of the Mercator Research Center Ruhr (MERCUR) on the restoration of a heavily modified, urban freshwater ecosystem: the Emscher River (North Rhine-Westphalia; Ruhr Metropolis). As a former waste water channel, the Emscher River and some of its tributaries were biologically dead. Today, many of the already restored freshwater sections provide novel habitats for both indigenous and invasive species. An improved knowledge about these recolonization processes is not only important to control restoration programs but to maintain ecosystem function and services.

The GBOL - Myriapoda project: 1000 sequences reveal insights and shortcomings of the Barcoding of myriapods

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The German 'Barcode of Life' (GBOL) project aims at creating a genetic library of all species of animals, plants and fungi occurring in Germany. The Myriapoda are jointly managed by the Museum Koenig in Bonn and the Bavarian State Collection in Munich (Jörg Spelda), in association with the Senckenberg Museum Görlitz. The project aims to collect, determine and sequence the COI gene of at least 10 specimens for all 200 German myriapod taxa. A key to the success of this goal are voluntary 'faunal experts' who are reimbursed for their efforts with 5-10 € per specimen. Each specimen is photographed and stored in a natural history collection as a voucher under a unique collection code before a fragment of the COI gene is sequenced. After almost three years, most German millipede and centipede species could be obtained, including slightly more than 1000 sequences, mainly from Germany and Austria. The COI standard primer sets (HCO/LCO, HCOoutout/LCO, Nancy/LCO) only amplified the gene in 60% of the geophilid centipede and many millipede taxa, often because of genus- or species-specific mutations in the primer regions. First results are promising, with Diplopoda and Chilopoda species being generally well-distinguishable based on high differences of the COI. On the other hand, surprisingly high intraspecific variation could be observed in the Lithobiida and Geophilida centipedes, as well as in a few julid millipedes (e.g. *Ommatoiulus sabulosus*) and pill millipede (Glomerida) species. Specimens of some centipede species, are not grouping together, hinting to the presence of currently unrecognized species in Germany. Morphological studies or nuclear genes are now necessary to evaluate the observed genetic discrepancies and find potential cryptic species or synonyms. The COI study, especially of the widespread centipede and millipede species, should be expanded to populations all across Europe in order to gain further insights into the evolutionary history, which shaped the current distribution of European myriapod taxa.

Biogeographic history of *Limonium* (Plumbaginaceae), inferred with the first model that includes a parameter for speciation with dispersal

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Limonium L. has 200-350 species worldwide, most of them adapted to saline, coastal environments. As facultative halophytes most species are not dependent on high salt contents, but instead inhabit saline areas because they are outcompeted in other habitats. The extreme range in species number estimates is due to apomictic groups and frequent hybridizations. Most of the named species occur in the Mediterranean basin and West Africa. Twenty-three species are found on the Canary Islands of which 19 are endemic. That *L. dendroides* is endemic to La Gomera provides the possibility to either calibrate a molecular clock (although this makes the assumption that the species is younger than the island) or to use the island age as outside evidence to cross-validate divergence times obtained with other calibrations, e.g., rate calibrations. If this species evolved on La Gomera, the island age (10 my) provides a maximum age for *L. dendroides*. I will present results from a phylogenetic analysis of 100 *Limonium* species, including the 19 Macaronesian endemics. The biogeographical history of *Limonium* was inferred with a new approach (implemented in BioGeoBEARS), which for the first time incorporates the possibility of founder event speciation, a plausible mechanism in clades with island-endemics, such as *Limonium*. I inferred four Pleistocene colonizations of the Canary Islands, all from Morocco. These results confirm the close connection of the Canary Island flora with West Africa, while more northern islands, such as the Azores, are more closely connected to the European flora.

Pulmonary complexity as the starting point for amniote evolution

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An effective respiratory system for air breathing was one of the key elements in the course of vertebrate terrestrialization: i.e., the rise of amniotes. The traditional textbook view on this crucial evolutionary transformation is that the early amniotes exhibited lungs similar to those of extant amphibians: sac-like, single-chambered organs. Although mammals, turtles, crocodiles and birds have a rather complex, multichambered/branched pulmonary anatomy, this scenario seems to be confounded by the fact that the majority of lepidosaurs indeed have single-chambered lungs. We show that also lepidosaurs develop such pulmonary complexity during early ontogeny but that this complexity eventually becomes secondarily reduced and obscured. Our results consequently will require a rethinking of the hypothesis about early evolution of the respiratory apparatus among amniotes. Terrestrialization apparently was accompanied from the very beginning not only by aspiration breathing but also by complex lungs, and the single-chambered lungs of lepidosaurs represent a derived condition. We provide an evolutionary scenario for the evolution of lungs among amniotes that is based on extensive comparative anatomical and embryological data and acknowledges the fossil record and the biophysical constraints that act on pulmonary structure.

Hauptvorträge

Ecology and Systematics – how to form a new partnership

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Ecology cannot carry out research without Biological Systematics but Systematics as a science appears to be largely independent of Ecology. This perceived asymmetry is the cause of many past misunderstandings and has hampered successful cooperation. In my talk I will argue that both fields of science have more common interests than is generally perceived and that there is an urgent need for cooperation. I will point out several examples where ignorance, on both sides, has significant costs. Using examples from projects on the role of land use on biodiversity, and the consequences of biodiversity change for ecosystem functioning I will point out mutual fields of interest and current research needs where a new partnership between Ecology and Biological Systematics will be fruitful.

Improvement of freshwater ecosystem assessments with DNA barcoding: Promises and pitfalls

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Human activity has dramatically altered and degraded stream ecosystems and poses a threat to global freshwater biodiversity. The loss of biodiversity threatens ecosystem functioning, with direct negative consequences for the provision of ecosystem services. The Water Framework Directive of the European Union explicitly obliges its member states to counteract degradation of freshwater ecosystems and demands a good ecological and chemical status of surface waters by 2015, and for heavily modified water bodies by 2027. Many management and restoration activities have been launched to implement this ambitious Directive. Assessment of the ecological status for a given water body is hereby achieved by comparing species lists for selected taxon groups against those of natural (unmodified) reference water bodies and quantification of the mismatch. Benthic macroinvertebrates are a particularly important indicator group in the assessments. Identification of many species, however, is difficult or impossible due to the lack of diagnostic characters. This frequently leads to 1) incorrect species identification, 2) determination only to family or genus level, and 3) inconsistency of the data between collecting institutions. Recent studies have proven that these problems can lead to incorrect assignment of the ecological status and thus suboptimal management. DNA barcoding has been proposed as a possible solution to this problem, in particular when coupled with novel high throughput sequencing techniques. Yet, analytical and conceptual challenges remain prior to the integration of DNA barcoding in assessments programs. In this talk I will outline potential and pitfalls of novel DNA-based techniques in the context of large scale freshwater ecosystem monitoring programs.

Monitoring wilderness areas

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What is wilderness, what is *not* wilderness? A definition and criteria are proposed. What is the reason for the recently growing interest in wilderness? Since the influence of mankind is ubiquitous, the question "how realistic are wilderness concepts in the global industrialised world" must be answered. The target for wilderness in Germany, as decided by the federal government of Germany is 2 % of the total land area or 5 % of all forests. However, worldwide wilderness areas are on the retreat. Some information on the Foundation of Natural Landscapes in Brandenburg, the "wilderness" foundation, is presented. The wilderness foundation owns 13 000 ha of land in southern Brandenburg. Most wilderness areas in Germany are in an early stage of their development, especially those, which develop on former military training grounds. A continuous change in species composition, plants as well as animals, is already taking place. There is a need to monitor this change systematically and to document it. How can this be done without or with least disturbance?

Mesoscale patterns of biodiversity in the Andes – setting conservation priorities based on detailed taxon distribution maps

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The overall, global patterns of biodiversity and endemism have been compiled based on floras and checklists and can be considered as largely understood. They also incorporate all the taxonomic and systematic inaccuracies of the data they are based on, but at a global scale they provide a good and reliable basis for comparing levels of diversity and endemism at a country-by-country scale, or for identifying major hotspots of biodiversity. However, at the regional and landscape level, these global maps lack the required resolution and a lack of taxonomic and systematic accuracy becomes more relevant. Under-collecting and under-reporting of taxa are major issues at this level and may so grossly distort patterns as to render the formulation of rational conservation priorities impossible. Our study focused on a bottom-up approach, using detailed specimen data to pin-point centers of diversity and endemism in the Andes. Raw data are based on specimen records and field studies of a total of four plant groups with ca. 200 species overall. Previously published taxonomy and distribution records and the available data in international databases can be shown to be grossly wrong. Our results clearly indicate that overall Andean diversity in these groups centers around the Amotape-Huancabamba Zone and that much of it is concentrated in isolated and highly threatened relic forests. The bulk of the endemic species have been reported for the first time in the last 20 years in the groups under study, new taxa are described nearly each year. Most other plant groups are still very incompletely known, both in their taxonomy and distribution. However, the emerging mesoscale patterns are now opening the way to subsequent landscape-level studies for the identification of priority areas for conservation.

On subspecies, cryptic species and synonyms – taxonomic impediment in the national Red List assessment process

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Using new IUCN categories with a self-developed risk assessment method, Austria has been updating its Red Lists of threatened animals during the past years. Three Red List volumes have appeared, covering all vertebrate and 13 invertebrate groups. Currently, Red Lists of spiders, ground beetles and xylobiontic beetles are being prepared for publication. However, even with the inclusion of these groups, the fate of more than 85% of Austrian animal biodiversity still remains unclear.

Several obstacles related to zoological systematics have been encountered during the assessment process. The large number of synonyms in every taxon requires a synonymy database and still implies the risk that important assessment-related information is overlooked. Besides, synonyms hamper the accessibility of biodiversity for non-specialists and create an information overload, since multiple names have to be managed throughout the assessment process. Another recurring problem are subspecies and their inclusion in Red Lists. Ignoring them might lead to a severe underestimation of the true extent of biodiversity loss. In many cases, however, subspecies are simply the result of typologically defined names being passed on for decades and having almost no biological meaning. In other cases, subspecies reflect important genetic differentiation or are, in reality, cryptic species. Cryptic species are the worst taxonomic problem for species conservation, as the aggregate under which they are lumped together might appear safe, while several of the true species contained are on the brink of extinction. In a particularly sad example, poor fish taxonomy contributed to the extinction of *Coregonus gutturosus* in Lake Constance.

Modern systematic zoology could alleviate many of these problems. DNA barcoding is an important additional tool to properly delineate species and clarify relationships at the subspecific level. In times of rapid biodiversity erosion, these additional tools are increasingly needed.

2. Poster:

Deep coalescence or cryptic species? Strong mtDNA divergence obscures species boundaries in *Pachypus* beetles with strong sex-biased dispersal

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Mitochondrial markers (Cox 1, 16S) revealed a huge cryptic diversity in *Pachypus* beetles, an ancient lineage (Pachypodini) of scarab beetles endemic to the Tyrrhenian archipelago, the Tyrrhenian coast of Italy and NW Africa. These beetles, known so far with 6 species, are characterized by extreme sex biased dispersal, with females having the fore and hind wings completely reduced. Species entities determined from mtDNA using statistical parsimony, GMYC and PTP modeling are strongly incongruent with currently recognized species and with the tree topology of the nuclear markers (28S, ITS1) and would result in 42 putative species. Therefore, we investigated patterns of morphological variation (distance measures of external morphology and shape of male copulation organs) in order to infer their match with the alternative potential molecular species entities. While the shape of the genitalia results very little informative, body measurements allowed to differentiate between putative species, showing a good fit with a scenario of 11 species. However, principal component axes from body measurements analysis showed a correlation with species clades of the nuclear tree topology but also an elevated correlation with several (not all) GMYC clusters from mtDNA tree topology or even some more ancestral nodes, revealing some significant ambiguity for resolving the taxonomy in this way of integrated approach. The failure of these standard data and approaches call for more sophisticated analyses comprising more data and an iterative analysis pipeline.

The evolution of the annelid nervous system in the light of current molecular phylogenies

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Annelids are a taxon of segmented vermiform spiralian and one of the best studied animal groups. However, their phylogeny is still uncertain and a matter of debate since the first comparative morphological works appeared in the middle of the 19th century and the discussion continues since the advent of molecular phylogenies in the late 20th century. Investigations on the nervous system have a long tradition in comparative animal morphology. Characteristics of this organ system are still used to infer phylogeny of animal taxa. Annelids have been investigated in this context most notably by Holmgren and Fauvel in the early 20th century and Orrhage since 1960. Most of these publications focused on the innervation patterns of the different body appendages like antenna, tentacles and palps and neglected the overall anatomy of the nervous system. Additionally all of these studies have one big disadvantage: the transparency of the data, since the original data (stained slices), which were used to describe and reconstruct the nervous systems are not available to other researchers. Nowadays microscopical techniques as well as software solutions allow a fast acquisition of morphological data at a high resolution. We therefore generated Azan stained serial sections (aligned stacks) of currently 30 Annelid species and publish these in a morphological data base (MorphDbase) from which they can be downloaded and reinvestigated by other researchers. The aligned stacks are used to infer the entire anatomy of the central nervous systems and to reconstruct the evolution of this organ system based on the most recent molecular phylogeny published by Weigert et al. (2014).

Species diversity of selected aquatic dipteran families in two German stream ecosystems: a comparison of morphological and DNA-based assessments

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Biodiversity of freshwater ecosystems is in rapid decline globally. Coordinated national and international efforts aim at preserving and restoring freshwater biodiversity. The European Water Framework Directive (WFD) commits European Union member states to achieve good qualitative and quantitative status of all water bodies. Detailed species lists generated from benthos samplings are the basis for monitoring the restoration success, and among this fauna, insect species are the most abundant and species rich bioindicators in this context. However, for many insect species such as the Diptera, species-level determination is difficult or almost impossible from immature stages. Here, DNA barcoding could be an important tool complementing and improving ongoing monitoring efforts. As a first step, good reference databases linking DNA barcodes to correctly identified vouchers are a prerequisite for such endeavors. We collected adult insects with emergence traps over a whole year from two well-studied central European stream ecosystems (Breitenbach, Hesse & Kleine Schmalenau, NRW, Germany). We focused on the three dipteran families Dolichopodidae (330 specimens, 19 morphospecies), Empididae (517 specimens, 24 morphospecies) and Simuliidae (1,111 specimens, 6 species), and compared results of morphology-based species assessments to the DNA-based assessments based on the 'barcoding fragment' of the gene cytochrome c oxidase subunit I. This project is a contribution to the German Barcode of Life Project (GBOL).

Molecular phylogenetics and systematics of the Boraginaceae s.str.

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Recent studies all indicated that the subdivision of Boraginaceae s.str. is still unsatisfactorily resolved. Major open issues like the placement and affinities of Boraginaceae s.str. in Boraginales have been already solved. However, the monophyly and relationships among groups such as the Trichodesmeae, the *Mertensia*-group, the *Omphalodes*-group, the Core-Cynoglosseae (including *Amsinckia*, *Bothriospermum*, *Cryptantha*, *Cynoglossum*, and *Microula*) and various problematic genera such as *Afrotysonia*, *Anoplocaryum*, *Craniospermum* are still unclear. The present study addresses these questions using three plastid markers (*trnL-trnF*, *rps16*, and *trnS-G*) and a comprehensive sampling with 14 outgroup taxa and 162 ingroup species from 63 genera. The phylogeny shows high statistical support for most nodes on the backbone and on the individual clades. In Boraginaceae s.str. the Echiochileae are confirmed as sister to the remainder of Boraginaceae s.str., which, in turn, fall into two well-supported clades, the Boragineae-Lithospermeae and the Cynoglosseae s.l. (including Eritrichieae). Cynoglosseae s.l. is highly resolved with an expanded Trichodesmeae (*Chionocharis*, *Microcaryum*, *Lasiocaryum*, *Caccinia*, and *Trichodesma*) sister to the remainder of the group. Eritrichieae s.str. (*Eritrichium*, *Hackelia*, and *Lappula*) form a poorly supported polytomy together with the *Omphalodes*-clade and the *Mertensia*-clade (with *Mertensia* and *Anoplocaryum* as sister groups). The enigmatic genus *Craniospermum* is retrieved as sister to an expanded Myosotideae (incl. *Brachyobotrys*, *Trigonotis*, *Myosotis*, and *Pseudomertensia*) and this clade is in turn sister to the core-Cynoglosseae. Overall, the bulk of generic placements are now resolved satisfactorily and the remaining research questions can be clearly delimited. The key remaining problem is the resolution of the highly poly- and paraphyletic genus *Cynoglossum*, which will need to be addressed with a dual approach, including a complete revision of the confused alpha-taxonomy of this group and – based on this – near-comprehensive sampling, since clade specific morphological characters remain elusive.

Regional differentiation and extensive hybridisation between mitochondrial clades of the Southern Ocean giant sea spider *Colossendeis megalonyx*

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The giant sea spider *Colossendeis megalonyx* is one of the most widespread Southern Ocean pycnogonid species. Based on mitochondrial data it was recently suggested that *C. megalonyx* is a complex of at least six cryptic species with mostly small and non-overlapping distribution ranges. Here we expand the sampling to include over 500 sequences of specimens from around the Antarctic for the mitochondrial Cytochrome Oxidase subunit 1 gene (COI). Additionally, we have sequenced the nuclear ITS region for a subset of these specimens.

Using distance-based and general mixed Yule-coalescent species delimitation approaches, the number of distinct mitochondrial OTUs increased from six to 15-19 with our larger data set. Using various methods, we find evidence for population structure and past expansions in several of these clades. In contrast to earlier studies, many of these mitochondrial clades show a circumpolar distribution. The nuclear data are incongruent with the mitochondrial results in that some specimens from the same region group together in the ITS data although they were assigned to different COI OTUs. These mito-nuclear discordances can be reconciled by inferring that some OTUs characterized by divergent mitochondrial lineages can hybridize and should thus not be interpreted as cryptic species. The results of this study confirm that the presence of cryptic species should not be inferred based on mitochondrial data alone.

Analysis of a comprehensive data set on *Tubulanus polymorphus* Renier, 1804 leads to a separation of the species and to re-establishment of *Tubulanus (Carinella) ruber* (Griffin, 1898)

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Nemertea constitutes a spiralian clade of soft-bodied, vermiform animals that are encountered in all marine habitats. *Tubulanus polymorphus* Renier, 1804 (Palaeonemertea), much like most of the long known species is reported to be widely distributed in the northern hemisphere including the west coasts of both Europe (Atlantic Ocean) and North America (Pacific Ocean). Specimens from the Pacific coast of the US and Canada had been originally described as a different species, *Tubulanus (Carinella) ruber* (Griffin, 1898) mainly based on differing coloration. *Tubulanus (Carinella) ruber* was later synonymized with *Tubulanus polymorphus* attributing the differences between Atlantic and Pacific specimens to intra-specific variation. Analysis of comprehensive data sets, including life-history traits like habitat and reproductive period, ultrastructure of sperm cells, and gene sequence data on *Tubulanus polymorphus* samples from both locations confirms that the two populations are definitely distinct. As these differences cannot be explained by intra-specific variation the validity of *Tubulanus ruber* (Griffin, 1898) as a separate species distributed on the Pacific coast of North America is re-established. We are confident that the majority of widely distributed nemertean species prove to be unrecognized species assemblages with considerably narrower distribution ranges.

A phylogeny of Sericini chafers - Out of Africa and back again

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Robust phylogenetic hypotheses are indispensable for addressing a variety of systematic and evolutionary questions about classification, delimiting species and genera, inferring mechanisms of speciation, or the biogeographic history of species. Especially in hyper-diverse groups like they often occur in insects, serious sampling issues often hinder scientists from gaining satisfactory results. After more than a decade of sampling efforts, we present the most comprehensive tree of Sericini chafers (Coleoptera: Scarabaeidae) and its sister taxon Ablaberini to date, spanning a quarter (more than 800) of the currently described species from all over the world. Innovative DNA-sequence alignment methods with simultaneous tree estimation (SATé) were applied on the dataset of the nuclear ribosomal rRNA 28S, and the mitochondrial cytochrome oxidase subunit 1 (*cox1*) and 16S rRNA (*rrnL*) genes. Phylogenetic relationships were inferred using partitioned data with Maximum Likelihood in RAxML. Divergence times were assessed in a Bayesian framework, using BEAST for estimating branching rates under a lognormal relaxed clock with one fossil and one secondary calibration point. The age of the tribe Sericini was found to be 103 My (± 10 My). The most basal split of the group, separating Neotropical and Old World species, is therefore concordant with the breakoff of Gondwana. Ancestral ranges were reconstructed by Likelihood methods (ape in R), revealing repeated emigrations from Africa ranging from around 90 My to 40 My ago, and a reinvasion from Asia at 34 Mya (± 1 My) by a lineage of the subtribe Sericina that established itself with a large radiation all over Africa.

Structural diversity and functional morphology of the damselfly ligula: implications for taxonomy, systematics and evolutionary biology

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The diversity and the evolution of animal genitalia have intrigued systematists and evolutionary biologists for a long time. Especially in arthropods, male genitalia often provide the only reliable diagnostic characters available for distinguishing between species suggesting that they evolve much more rapidly than other morphological characters.

The ligula or secondary penis of the male damselfly (Odonata: Zygoptera) is a multifunctional structure designed for sperm transfer and – in many cases - sperm removal. Since Waage (1979) first provided evidence for the occurrence of sperm competition in calopterygid damselflies, several further cases and mechanisms of sperm competition in Odonata have become known. However, the diversity and variation of these functional morphological traits is largely unknown for many groups of Zygoptera, and the underlying mechanisms are poorly understood.

Scanning electron microscopic (SEM) studies of the male secondary copulatory apparatus in, among others, the damselfly families Coenagrionidae, Platycnemididae, Platystictidae and Argiolestidae provide new insights with regard to the amazing structural diversity of the zygopteran ligula. The implications for functional morphology, speciation, systematics and taxonomy of damselflies are discussed. Ultimately, it should be possible to predict the mating system and the behavioral ecology of a certain species based on its particular genital morphology.

The Biodiversity Network of the Humboldt-Ring (BiNHum): Joint Data Portal for Natural History Museums

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BiNHum (<http://wiki.binhum.net>) is a project of five natural history museums and research collections representing the Humboldt-Ring: the State Museum of Natural History Karlsruhe (SMNK), the State Museum of Natural History Stuttgart (SMNS), the Zoological Research Museum Alexander Koenig in Bonn (ZFMK), the Bavarian Natural History Collections in Munich (SNSB), and the Botanic Garden and Botanical Museum Berlin-Dahlem (BGBM).

The three-year project is funded by the German Research Foundation and deals with:

- data recovery and data mobilisation (SMNS, SMNK and the University of Ulm),
- implementation of modern search technologies and development of the data portal (ZFMK),
- data harvesting and data quality assurance (BGBM),
- deployment of Diversity Workbench (DWB) as a virtual environment for BiNHum (SNSB).

The BiNHum data portal will provide rich metadata content and multimedia data types like 3D images and audio files: The digitized fossil leaves database MORPHYLL (at SMNS) with ecophysiological relevant morphometry as well as ZFMK's acoustic multimedia databases will be accessible. For these purposes, the BiNHum portal will offer search options for complex data features (such as sound frequencies or geometric shapes) in addition to autocorrection, autocomplete, faceting, "shopping cart" and other harvesting features. The implemented AnnoSys tool enables users to make annotations to every dataset, which can highly improve data quality and offers new applications such as a digital loan system. A first version of the portal is available (<http://demo.binhum.net/>) using a scalable full-text search indexing server (SOLR 4.4.0) and a relational database (MySQL). Currently the database contains 1,757,221 searchable entries of natural history objects from 68 collections.

All partners use the Biological Collection Access Service (BioCASE) to provide their data to GBIF and to the BiNHum portal. For BiNHum the transformed data sources are harvested by GBIF's Harvesting and Indexing Toolkit (HIT), which has been extended to fulfill project-specific purposes (e.g. identification history, organismic associations).

Diversity in Southeast Asian Snail-eating Turtles (Geoemydidae: *Malayemys*): implications for phylogeography and taxonomy

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Severe over-collection, habitat loss, and other anthropogenic hazards contribute to tremendous population declines in Asian turtles. As a result, most Southeast Asian chelonian species are threatened by extinction. Taxonomic research on widely distributed taxa is considered a priority for future research to identify hitherto unrecognized cryptic species. Southeast Asian Snail-eating Turtles of the genus *Malayemys* are heavily exploited geoemydid turtles inhabiting a variety of natural and artificial freshwater habitats across Southeast Asia.

While individuals from the western portion of the distributional range (Chao Phraya and Mae Klong River Basins in central Thailand) were recently recognized as a separate species (*Malayemys macrocephala*), the eastern populations inhabiting eastern Thailand, southern Laos, Cambodia, and southern Vietnam retained the name *M. subtrijuga*. However, distinction of the two species is solely based on few morphological differences and is still controversial.

We combined molecular and morphometric data to assess the phylogenetic diversity and re-assess the taxonomy within this widely distributed genus.

Comprehensive analyses of the mitochondrial ND4 and cytochrome *b* genes revealed three distinct lineages, which do not match any geographic pattern. However, these lineages are concordant with results of morphological analyses using 30 morphometric characters. Our preliminary findings suggest the existence of three distinct taxa corresponding to the two previously recognized species *M. macrocephala* and *M. subtrijuga*, and a previously unrecognized third taxon.

Phylogeography of grass snakes (*Natrix natrix*) all around the Baltic Sea: implications for the Holocene colonization of Fennoscandia

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Using phylogenetic analyses of mtDNA sequences of approximately 100 grass snakes from the Baltic region, we show that Fennoscandia was invaded in the Holocene by three distinct mitochondrial lineages of *Natrix natrix*. Two of these lineages arrived from the south, and one from the east. One of the 'southern lineages' is confined to Gotland, where also the second 'southern lineage' is found. The latter is widely distributed in the southwestern Baltic region, western Fennoscandia and on the Åland Islands, while the other lineage present on Gotland is only known from a few sites in the Baltic region (northern Germany, central Poland). The island of Gotland, which was never connected by land bridges after the last glacial, must have been colonized twice by overseas dispersal. In addition, we recorded a third mitochondrial lineage in southern continental Finland, which was previously unknown from Fennoscandia. This lineage also occurs in the southeastern Baltic region and further east, suggesting that southern Finland was colonized from the east. Thus, the phylogeography of *N. natrix* matches a general paradigm for Fennoscandia, with Holocene invasions from the south and east.

Cryptic reptile diversity in an isolated and gravely threatened habitat in Northern Peru

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The equatorial dry forest in southern Ecuador and northern Peru is part of a global biodiversity hotspot and is thus home to a large number of floral and faunal species with a high proportion of endemics. Nevertheless, large parts of this ecosystem have never been surveyed in herpetological terms.

The present study was organized to contribute to the knowledge of the herpetofauna of this peculiar dry forest habitat and to provide a basis for further studies as well as for the development of conservation strategies. Field surveys to Peru were conducted between July 2005 and November 2010. During a total period of 13 months, 22 different localities along a stretch of more than 350 km of the Marañón River and some of its tributaries were surveyed.

The study revealed that the herpetofauna of this part of the equatorial dry forest is highly diverse and about half (29 of 59 species) of the recorded species seem to be endemic to this region. Many species discovered during the survey were new to science with a high portion of cryptic species.

Due to deforestation for firewood, agriculture and narcotics plantation, and due to mining activities and above all recent dam construction activities for 20 hydroelectric projects that will lead to floodings of great parts of the interandean dry forest valleys, it is mostly likely that the populations of many of the endemic species will decline in the near future. If no conservation strategies will soon be developed and implemented the destruction of this unique habitat will proceed and the decline of its diversity will be irreversible.

A new monostiliferan species (Nemertea:Hoploneurtea) from the Mediterranean Sea in Italy

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Nemertea is a spiralian taxon consisting of unsegmented, softbodied, vermiform animals, predominantly inhabiting marine environments. It comprises about 1,280 described species of mainly marine, epibenthic predators. The Mediterranean Sea is one of the best documented regions concerning species diversity of Nemertea with about 60 known species. A considerable number have been described based on external characters. However, these descriptions do not often include details on their internal morphology. This makes the description and systematic assignment of new species problematic. The last two decades have shown that a combination of molecular barcoding and detailed morphological descriptions can accurately assess systematic affinities of species identified as being new to science. In this study, we are reporting a new monostiliferan hoploneurtean from the Island of Giglio, Italy. So far, no description fits the specimens from Giglio, indicating that they represent a species new to science. We provide a comprehensive data set containing information about habitat, life cycle, outer and inner morphology, and sperm ultrastructure. In combination with molecular markers (COI, 16S, 18S, 28S) we will give a detailed characterization of the species. First results on sperm ultrastructure hint at an affiliation to Amphiporidae (Monostilifera, Hoploneurtea). This study shows that even in well studied areas, species diversity in Nemertea is underestimated.

Generative ontogeny in *Cordia nodosa* Lam. (Cordiaceae, Boraginales)

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Cordiaceae (Boraginales) are a monophyletic group as inferred from both molecular phylogenies and morphological apomorphies such as the undivided endocarp, a twice-bifid style and plicate cotyledons. Anatomical studies particularly of generative organs are rare in Cordiaceae, although they contribute to a better knowledge about species and may render important traits for phylogenetic analyses. We investigated morphology and anatomy of flower through fruit development of *Cordia nodosa* that is a widely distributed species in the Neotropics. Principle generative architecture of is rather homogenous in Cordiaceae: Flowers are tetracyclic and pentamerous, with a bicarpellate gynoecium. The characteristic architecture of the ovary with four loculaments results from the development of a apical sept and two false septa. The ovary is surrounded by intensely blue-stained tissue that has not been described for any other species of *Cordia* at this moment in time (we discuss whether it is a multilayered epidermis or derives from a well developed disc). After fertilization, the ovary develops to an asymmetrical drupe including (by abortion) a single seed. The results of the study are phylogenetically interpreted in comparison to the literature and the latest molecular trees available for the Boraginales.

Macroevolutionary patterns of the locomotor system in non-muraenoid eels (Teleostei: Elopomorpha)

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Living eels (Teleostei, Anguilliformes) are characterized by a high diversity in cranial morphology indicating shifts in morphospace occupation during their evolution and multiple divergence events. However, changes in the locomotion performed by the musculotendinous system of the trunk indicating shifts in swimming performance still have not been evaluated up to now because exceptionally preserved fossils displaying delicate soft-tissues are rare in the fossil record. Here, we present non-muraenoid anguilliforms from Late Cretaceous, Palaeogene and Neogene conservation Lagerstätten allowing a definitive assessment of their musculotendinous system and interpretation of their swimming performance in a phylogenetic framework. The increase of the myoseptal length follows largely the evolutionary arrangement of taxa with stem anguilliforms displaying the shortest lateral tendons, which are characteristic for CH-fishes while the lateral tendons in anguilloids and congroids are longer. Our results in comparison with an Eocene muraenoid from Monte Bolca support that non-muraenoid crown anguilliforms are IH-fishes conversely to previous assumptions, in which anguillids were considered CH-fishes. The macroevolutionary changes in the musculotendinous system from short to long tendons indicate a continuous adaptation of non-muraenoid anguilliforms to open water habitats, which occurred in the aftermath of the third oceanic anoxic event (OAE3) during the Coniacian-Santonian age.

Molecular phylogenetics and subgeneric revision of the sub-Saharan genus *Eudicella* (Scarabaeidae: Cetoniinae)

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Eudicella White (1839) is a genus of fruit chafers (Scarabaeidae: Cetoniinae) distributed broadly in sub-Saharan Africa. It contains more than 150 described taxa, which have been split by different authors into either two or three subgenera. These beetles are sexually dimorphic and exhibit furcate horns in males and burrowing legs in females. While the main structural characters appear relatively conserved, the high levels of intraspecific variation – mainly in body colour and shape of the clypeal horn – has led to the splitting of the valid species into a remarkable number of dubiously identified subspecies. *Eudicella* has been traditionally split into three subgenera: *Eudicella s.str.* (White), *Cyprolais* Thomson, and *Ceratorhina* Westwood (*sensu* Allard), the latter being invalid as it lacks a type species. Holm (1993) recently addressed the subgeneric classification of *Eudicella* and lumped *Ceratorhina* (*sensu* Allard; *nec* Westwood) into *Cyprolais*. However, *Cyprolais sensu* Holm appears morphologically heterogeneous and incoherent. Furthermore, a recent revision of *Eudicella s.str.* (De Palma, 2009 and 2011) based on morphological analysis lumped the number of valid taxa from ca.70 to 14(12 species and 2 subspecies). Here we revised the taxonomic status of *Eudicella* by performing a molecular phylogenetic analysis of several representatives of the three former subgenera. The new data suggest that the synonymies recently established (De Palma, 2009) are overall valid; however, unexpected findings were also obtained. In particular, *Eudicella* seem to form four well-defined taxonomic groups, which we propose as subgenera, whose main characters and distinguishing features will be presented.

Improving services for data quality and availability in environmental sciences

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There is a huge need to integrate **taxonomic data** to answer questions of global interest regarding earth's ecosystems and climate dynamics. Thus, integrative research builds on a diversity of data, like genetic, ecological, environmental or collection data. To integrate and organize this scattered knowledge base, GFBio provides a coherent infrastructure to improve scientific data integration and preservation.

GFBio is 'The German Federation for Biological Data' and consolidates important stakeholders in functional biodiversity and environmental science from 19 institutions within Germany. Based on proven infrastructures and tools like PANGAEA (Data Publisher for Earth and Environmental Science), Bexis++ (Biodiversity Exploratory Information System), DWB (DiversityWorkbench) and SILVA (high quality ribosomal RNA databases) GFBio offers a central portal for added-value-services concerning data intensive research. These services will integrate into the research cycle and include easy-to-use tools to create a data management plan, to assure the quality of the data, to analyze and visualize datasets or to save and re-use data for the long term.

To address researchers in the field of environmental sciences, but also National History Collections as well as larger national and international research projects and institutions, GFBio dynamically builds up a diverse training environment including e-modules, manuals, screencasts and videos. Further support will be offered by a helpdesk by FAQs and 'How Tos' to guide the user through data management issues. Moreover, GFBio offers personal training at workshops during conferences and assemblies or on command.

Differences in gene flow in a twofold secondary contact zone of pond turtles in southern Italy (Testudines: Emydidae: *Emys orbicularis galloitalica*, *E. o. hellenica*, *E. trinacris*).

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Using virtually range-wide sampling for three pond turtle taxa (*Emys orbicularis galloitalica*, *E. o. hellenica*, *E. trinacris*), we analyse gene flow across the southern Italian contact zone, where the ranges of all three taxa abut. Based on population genetic analyses of 15 highly polymorphic microsatellite loci and a mitochondrial marker, we show that the general genetic pattern matches well with the current taxon delimitation. Cline analyses reveal that the major genetic break between *E. o. galloitalica* and *E. o. hellenica* corresponds well with the currently accepted intergradation zone in southern Italy. However, introgression is largely unidirectional from *E. o. galloitalica* into *E. o. hellenica*. Gene flow between *E. orbicularis* and *E. trinacris* is negligible, with the Strait of Messina matching well with the narrow cline centre between the two species. The differences between the two taxon-pairs *E. orbicularis*/*E. trinacris* and *E. o. galloitalica*/*E. o. hellenica* support their current taxonomic classification and make them attractive objects for follow-up studies to elucidate the underlying mechanisms of speciation by comparing their properties.

IDES: Making fish specimen data and images from natural history collections publicly accessible

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The DFG-funded research infrastructure project IDES (<http://ides.snsb.info>) was designed to set up a high performing information infrastructure to be used by the institutions belonging to the Staatliche Naturwissenschaftliche Sammlungen Bayerns (SNSB). Project partners are the Bayerische Staatssammlung für Paläontologie und Geologie (BSPG), the Jura-Museum Eichstätt (JME), the Staatssammlung für Anthropologie und Paläoanatomie München (SAPM), the Zoologische Staatssammlung München (ZSM) and the SNSB IT Center. IDES is mobilising data of natural history collection specimens. It focuses on the fish group Actinopterygii from Europe and adjacent seas, starting from the Mesozoic era (Trias) until collections of extant fishes. Innovative imaging facilities were established and adapted to the specific requirements of the various kinds of collection objects, like dried collections of skeletons, wet collections, micro- and macrofossils, DNA and tissue collections, otoliths and fish scales. Paper documents with location data, species descriptions, drawings etc. are photographed. All images are processed, archived, transformed to various formats, transferred to a SNSB web image server and managed together with the contextual data in the Diversity Workbench (DWB, <http://www.diversityworkbench.net>). Several new working processes and data pipelines are established (http://ides.snsb.info/wiki/IDES_Digitalisierungsstationen_und_Arbeitsprozesse). The clients and databases of the DWB are extended and adapted to special requirements in the IDES context, e. g. parallel access to litho-, chrono- and biostratigraphy thesauri. Until now, more than 28,000 IDES data and 49,000 IDES images are managed in the DWB. The majority of this data and images will be accessible via several national and international search portals including those of GBIF and BiNHum. In the future, IDES data will also be available via other portals like GFBio (<http://www.gfbio.org>), GeoCASE, FishBase and FishNet 2.

Preliminary results of a revision of the family Boraginaceae for the Flora of Nepal

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Nepal is known for a very high plant diversity, but has been investigated only sparingly in the recent past. A group of institutions, led by the Royal Botanical Gardens Edinburgh (E), is currently elaborating a new “Flora of Nepal”, addressing this gap in our knowledge of global phytodiversity. The first product was a working checklist of families, genera and species. For the family Boraginaceae a total of 20 genera and 52 species are reported. The most species-rich genera are *Onosma*, *Maharanga* and *Cynoglossum*, all of which are very poorly understood across their range. These genera have now been revised for Nepal, recognizing a total of only 12 instead of previously 15 species. The study is based on the extensive use of herbarium material but – in *Cynoglossum* – also cultivation at Bonn Botanical Gardens. In *Cynoglossum*, all the species present can be shown to be very widespread, at least across the Himalayas, often considerably beyond: Thus, *Cynoglossum furcatum* is shown to extend from Georgia in the West to western China in the East and the Philippines in the South. Numerous names across that range can be shown to represent synonyms. The situation is similar in *Onosma* and *Maharanga*, where only 3 (instead of 5) respectively 4 (instead of 5) species are accepted. Overall, the Nepalese species largely seem to represent widespread taxa. At the same time, collection density is clearly still unsatisfactory and more extensive collections, esp. from eastern Nepal, might well turn up novel and previously unrecorded species.

Beschreibungen der Workshops:

Workshop 1: Target DNA Enrichment – Methodology, Software, Practical Experience Report

Ort: Kursraum, Neubau

Oliver Niehuis (1), Malte Petersen (1), Christoph Mayer (1), Vera Batista (1), Manuela Sann (2): Target DNA Enrichment – Methodology, Software, Practical Experience Report

1 Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig Bonn, Adenauerallee 160, 53113 Bonn

2 Leibniz Institute for Evolution and Biodiversity Science at the Humboldt University in Berlin, Invalidenstraße 43, 10115 Berlin, Germany

In this workshop, we will outline the method of target DNA enrichment (a.k.a. exome capture, hybrid enrichment) as a method of obtaining nucleotide sequence data for phylogenomics. Topics covered will include probe design, software to use for bait design, laboratory procedures, and we will demonstrate how enriched DNA sequences can be reliably assigned to target genes.

Workshop 2: "MITOS" Mitogenom-Annotation

Ort: Seminarraum, Hauptgebäude

Matthias Bernt (1), Alexander Donath (2): "MITOS" Mitogenom-Annotation

1 Professur für Parallelverarbeitung und Komplexe Systeme Fakultät für Mathematik und Informatik Universität Leipzig

2 Zentrum für Molekulare Biodiversitätsforschung /Zoologisches Forschungsmuseum Alexander Koenig

The analysis of mitochondrial genomes is a standard method in phylogenetic and phylogeographic studies. Manual annotation of mitochondrial genes, however, is often time consuming and cumbersome. MITOS (MITOchondrial genome annotation Server) is a free web server for the automated annotation of metazoan mitochondrial genomes. It uses state-of-the-art methods for a consistent annotation of protein and non-protein-coding genes.

We will give an insight in the methodology behind MITOS and present the latest improvements that lead to MITOS v2.

Participants are given the chance to analyze a metazoan mitochondrial genome of their choice and to discuss the results and their interpretation together with the workshop lecturers.

Workshop 3: 3D-Rekonstruktion – High Quality 3D Reconstruction for Everyone: open-Source Solutions and their Workflow to analyse and publish MicroCT Data

Ort: Museumsschule, 2. Etage Hauptgebäude

Alexander Blanke: High quality 3D reconstruction for everyone: open-source solutions and their workflow to analyze and publish microCT data.

Zentrum für Molekulare Biodiversitätsforschung /
Zoologisches Forschungsmuseum Alexander Koenig

3D reconstruction of morphologic structures is an increasingly used method. Correct specimen preparation and data handling presupposed, it delivers precise information about the spatial distribution of structures, volumetric information, functional characteristics etc.

At the same time figures can be generated in an easy way and 3D models deposited as electronic supplements in addition to the raw data.

The majority of scientists use expensive programs and workstations to access this methodological field. The aim of this workshop is to introduce several method pipelines which are completely open source and do not need workstations.

Participants will learn:

- how to segment (manually and semi-automatic and fully automatic) microCT data with various levels of detail
- export them into rendering software
- create 3D models ready for publication
- create figures with open source desktop publishing

Pros and cons of 3D reconstruction will be discussed.

If time permits, some post-processing options for 3D reconstructions will be presented.

For example:

- generating 3D PDFs
- generating videos / animations
- prospects for functional analyses (only in brief)

Participants are invited to use their own datasets. Of course example data sets will be provided, if needed.

Prerequisites for this workshop:

- bring your own laptop (WITH a mouse!), preferably a Windows machine (use WINE in case you are an Apple user, but don't expect too much)
- if you have your own dataset, contact the organizers WELL IN ADVANCE (meaning several weeks before the workshop starts!)

Notizen:

