

**13. Jahrestagung
der Gesellschaft für Biologische Systematik
(GfBS)**

**vom 23.-25. Februar 2012
am Zoologischen Forschungsmuseum
Alexander Koenig
in Bonn**

– Programm und Abstracts –

Ausgerichtet und erstellt von J. Wolfgang Wägele & André Koch

Mit freundlicher Unterstützung von:



Herzlich Willkommen !

zur 13. Jahrestagung der GfBS vom 23.-25. Februar 2012 am Museum Alexander Koenig in Bonn

Wir begrüßen alle Teilnehmer der 13. Jahrestagung der Gesellschaft für Biologische Systematik (GfBS) ganz herzlich am Zoologischen Forschungsmuseum Alexander Koenig (ZFMK). Damit tagt die GfBS bereits zum zweiten 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). Somit war die erste Jahrestagung der GfBS ein voller Erfolg und auch die diesjährige Veranstaltung ist mit 150 Teilnehmern sowie über 100 Postern und Vorträgen auf großes Interesse – vor allem von Nachwuchswissenschaftlern – gestoßen, was uns sehr erfreut.

Nachdem die GfBS in den vergangenen Jahren stets mit anderen Organisationen und Gesellschaften zusammen getagt hat, findet die diesjährige Jahrestagung wieder in "familiärem" Kreis statt, bevor 2013 erneut in Wien in einem größeren internationalen Rahmen getagt werden wird (Infos unter www.nobis-austria.at).

Ein bestimmtes Motto der Tagung gibt es diesmal nicht. Alle Themen aus der biologischen Systematik sind willkommen und die zahlreichen Vorträge und Poster zeigen das breite Spektrum der verschiedenen Themen aus der biologischen Systematik, die in der GfBS repräsentiert sind. Besonders aufgefordert hatten wir jedoch zum Einreichen von Beiträgen zu den Themen "Beschleunigte Erfassung von Biodiversität" und "EU-Netzwerke und Projekte für Forschung und Kooperation".

Dementsprechend findet zum ersten Thema am Donnerstagmorgen ein Eröffnungsvortrag von Rodolphe Rougerie von der Université de Rouen, Frankreich, statt. Diesem folgt eine Session von Vorträgen über DNA-Barcoding.

Am Mittwochabend zuvor 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 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.

Daneben können die Tagungsteilnehmer während der Mittagspausen im Rahmen einer begleiteten Führung die Räume des Biohistoricum 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) gegründete Forschungsarchiv des Biohistoricum 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 und Junge Systematiker (JuSys) während der Tagung treffen. Dies ist nach den Vorträgen am späten Donnerstagnachmittag geplant. Für Freitagnachmittag ist die ordentliche Mitgliederversammlung der GfBS mit der Verleihung des Bernhard-Rensch-Preises vorgesehen. Außerdem werden auch in diesem Jahr wieder die besten studentischen Poster und Vorträge ausgezeichnet. Der ereignisreiche Tag wird mit einem gemeinsamen Abendessen in einem ausgewählten Bonner Restaurant abgerundet (nicht in den Tagungsgebühren enthalten, also nach individuellem Bedarf gestaltbar).

Als weiterer besonderer Programmpunkt werden im Anschluss an die beiden Vortragstage am Samstag Software-Workshops über neu entwickelte Programme des Zentrums für Molekulare Biodiversitätsforschung des ZFMK durchgeführt, die für die Analyse von Sequenzdaten relevant sind. Weiterhin werden Einführungen in Softwarelösungen zur Sammlungsverwaltung, 3D-Rekonstruktion und MorphDBase angeboten.

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 oder Beethovens Geburtshaus, ist Ihnen dabei freigestellt. 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. Wer bereits ein paar Tage vor der Konferenz anreist ist, konnte sogar den rheinischen Karneval mit seiner ganzen Lebensfreude und den bunten Umzügen miterleben.

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 & André Koch, Bonn

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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 Abstracts nachzukommen, werden die **Vorträge** in zwei parallelen Sessions stattfinden. Neben dem Hörsaal auf der ersten Etage des Hauptgebäudes oberhalb der Empfangshalle, wird hierfür der Kursraum im Erdgeschoss des Clas-M.-Naumannbaus genutzt. Dieser liegt hinter dem Haupthaus und ist über eine Brücke auf der ersten Etage gegenüber dem Hörsaal schnell zu erreichen. Der Weg dorthin ist gut ausgeschildert.

Die **Poster** werden im Festsaal auf der zweiten Etage des Haupthauses gleich oberhalb des Hörsaales aufgestellt. Statt einer üblichen

Postersession werden die Poster in Form von Kurzvorträgen im Hörsaal präsentiert. Diese Präsentationen finden am Donnerstagnachmittag und Freitagmorgen 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 22. 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 **Vorträge** und **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 Museum. Das Bistro im Museum bietet jeden Tag ein günstiges Mittagsmenü an.

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 Mittagspausen am Donnerstag und Freitag 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 Uhr im Kursraum (Neubau) statt. 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 Uhr im Seminarraum des Hauptgebäudes auf der zweiten Etage. Neben der ODE-Sonderedition der JuSys werden weitere Aktionen (z.B. Workshops, nächstes JuSys-Treffen) und Themen besprochen. 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. Neben dem Bericht des Vorstandes finden Neuwahlen statt. 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 20 Uhr im italienischen **Restaurant „Tuscolo“** (ehemals „Aktuell“) in der Bonner Innenstadt hinter dem Münster 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. Achtung: Das Lokal ist bekannt für seine riesigen Pizzen. Bei kleinem Hunger eventuell besser zu zweit bestellen!

Workshops:

Nach der Tagung werden am Samstag drei parallele Workshop-Sessions zu unterschiedlichen Themen stattfinden. Einzelheiten entnehmen Sie bitte dem Plan auf Seite 21 und den Beschreibungen ab Seite 87.

Wichtige Telefonnummern:

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

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

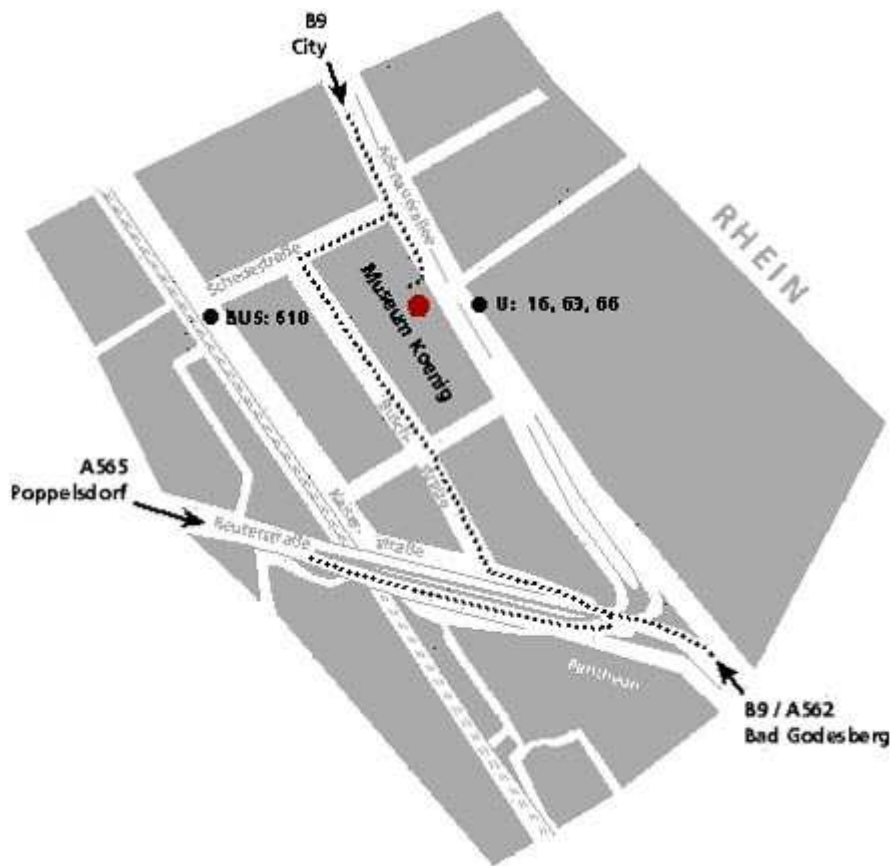
Biohistoricum: 0228-9122-269

ZFMK-Sekretariat: 0228-9122-201

Taxi: 0228-55 55 55 oder 19410

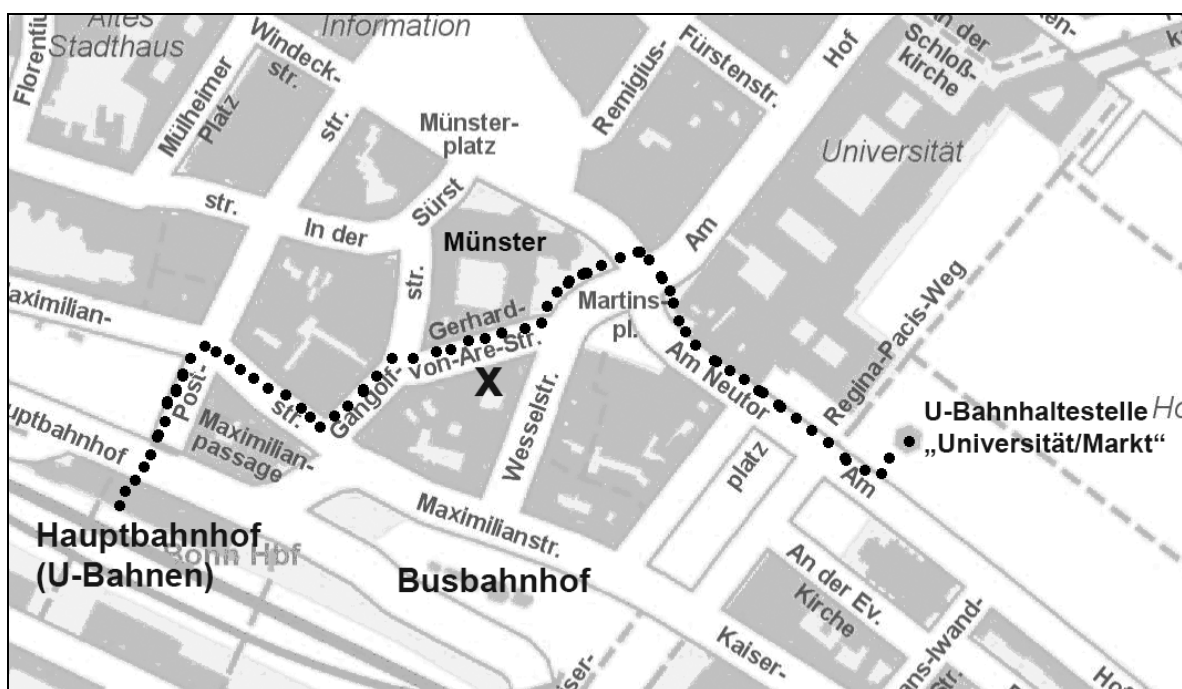
Sollten Sie noch offene Fragen haben, wenden Sie sich bitte an das Organisationsteam an der Registrierung. Dort empfangen und beraten Sie gerne Rebecca Ray, Isabella Terpkovic, Hossein Rajaei, Yannick Bucklitsch und André Koch.

Anfahrtsskizze zum Museum Koenig (Adenauerallee 160):



Wegbeschreibung zum Restaurant Tuscolo:

(Adresse: Gerhard-von-Are-Straße 8, schräg gegenüber dem Spielwarenladen „Puppenkönig“; Telefon: 0228-42976605)



Das Restaurant „Tuscolo“ befindet sich am Beginn der Fußgängerzone der Bonner Innenstadt. Parkmöglichkeiten in nächster Nähe stehen daher nur sehr begrenzt zur Verfügung. Es ist jedoch sehr gut mit den öffentlichen Verkehrsmitteln und zu Fuß zu erreichen.

Mit dem Auto:

- Lassen Sie Ihren PKW entweder am Museum stehen und fahren mit der U-Bahn in die Innenstadt oder benutzen Sie eines der zahlreichen Bonner Parkhäuser. Am nächsten gelegen sind die Uni-Tiefgarage unter dem Hofgarten gelegen und die Marktgarage. Beide erreichen Sie mit dem Autor in fünf Minuten über die Adenauerallee (B9) in Richtung Innenstadt. Folgen Sie der Beschilderung. Kurz bevor sich die Straße verengt und durch das Uni-Hauptgebäude führt, biegen Sie links ab in die Stockenstraße.
- Vor und hinter dem Hauptbahnhof befinden sich außerdem große Parkplätze.

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 direkt auf das Bonner Münster zu bis Sie an die T-Kreuzung gelangen. Nach dem Überqueren der Ampel halten Sie sich links und gehen nach kurzer Strecke rechts in die Gerhard-von-Are-Straße. Der Eingang zum Restaurant befindet sich nach wenigen Metern auf der linken Seite.
- Vom Bonner Hauptbahnhof (auch Busbahnhof) aus gehen Sie auf der Poststraße gerade aus in Richtung Innenstadt. Biegen Sie rechts in die Maximilianstraße ein

Programmübersicht der Tagung:

Mittwoch, 22. Februar:

- 18-22 Uhr Icebreaker und Registrierung in der Savanne im Lichthof des Museum Alexander Koenig
19-20 Uhr Führungen hinter die Kulissen des ZFMK

Donnerstag, 23. Februar:

- 8-9 Uhr Registrierung
9 Uhr Eröffnung und Begrüßung (W. Wägele, G. Haszprunar)
9.30 Uhr Eröffnungsvortrag (R. Rougerie)
10-16 Uhr Vorträge und Pausen
12 Uhr Besichtigung des Biohistoricums
16-17 Uhr Postervorträge (Session I)
17-19 Uhr Treffen der AG Junge Systematiker (JuSys)
17-19 Uhr Treffen der AG Kuratoren (offen für Interessenten)

Freitag, 24. Februar:

- 9-10.30 Uhr Postervorträge (Session II)
11-17 Uhr Vorträge und Pausen
12 Uhr Besichtigung des Biohistoricums
17 Uhr Mitgliederversammlung der GfBS
20 Uhr Konferenz-Dinner (Restaurant „Tuscolo“ in der Bonner Innenstadt gleich hinter dem Münster, Gerhard-von-Are-Straße 8)

Samstag, 25. Februar:

- 9-16 Uhr Workshops in drei parallelen Sessions
(Bitte beachten Sie hierfür das detaillierte Programm auf Seite 21)

Vortragsprogramm:

(Bitte kontaktieren Sie das Tagungsbüro für aktuelle Änderungen!)

	Zeiten	Veranstaltung	Redner	Thema	Chair	Raum	
Mi., 22.02.	18.00-22.00	Registrierung und Icebreaker	-	-	-	Empfangshalle/ Savanne	
	19.00-20.00	Führungen hinter die Kulissen	R. Hutterer, R. van den Elzen, D. Rödder, R. Peters	-	-	ZFMK-Sammlungen	
Do., 23.02.	8.00-9.00	Registrierung	-	-	-	Empfangshalle	
	9.00-9.30	Eröffnung	J. W. Wägele, R. Hutterer, G. Haszprunar	Begrüßung, Organisatorisches, Historisches	-	Hörsaal	
	9.30-10.00	Eröffnungsvortrag	<u>R. Rougerie</u>	Invertebrate diversity made easy? Rapid biodiversity assessment through DNA barcoding	J. W. Wägele	Hörsaal	
	10.00-10.15	2 Kurzvorträge: DNA Barcoding	<u>S. Pietsch</u> & J. Astrin	Launching the German Barcode of Life Project, GBOL	J. W. Wägele	Hörsaal	
	10.15-10.30		<u>A. Seah</u> & D. Ahrens	DNA barcodes and tree-based species delineation – how informative should DNA taxonomy marker be?			
	10.30-11.00-	Pause (30 min)					
	11.00-11.15	2x4 Kurzvorträge (parallel): DNA Barcoding	<u>M. J. Raupach</u> , M. Gossner, K. Hannig, T. Knebelsberger, S. Laakmann, I. Mohrbeck & L. Hendrich	Some thoughts about DNA barcoding	R. Rougerie	Hörsaal	
	11.15-11.30		A. Hausmann, M. Balke, G. Haszprunar, P. Hebert, <u>L. Hendrich</u> & S. Schmidt	BARCODING FAUNA BAVARICA: Taking Barcoding of Central European Animals to a new level			

Do., 23.02.	11.30-11.45	2x4 Kurzvorträge (parallel): DNA Barcoding	<u>J. Astrin</u> , P. Stüben & D. Ahrens	DNA Taxonomy in cryptic weevils	R. Rougerie	Hörsaal
	11.45-12.00		<u>S. Vargas</u> , A. Schuster, K. Sacher, G. Büttner, S. Schätzle, B. Läubli, K. Hall, J. Hooper, D. Erpenbeck & G. Wörheide	Barcoding sponges: an overview based on comprehensive sampling		
	11.00-11.15	2x4 Kurzvorträge (parallel): Evolution aquatischer Organismen	<u>M. Geiger</u> , C. Mayr & U. Schliewen	Evolutionary ecology of the Midas cichlid flock endemic to Crater Lake Apoyo, Nicaragua	J. Schwarzer	Kursraum Neubau
	11.15-11.30		<u>A. Kieneke</u> , P. Martínez Arbizu & D. Fontaneto	Geographic structure of intraspecific genetic diversity in marine Gastrotricha: Taxonomic consequences and possible historic reasons		
	11.30-11.45		<u>A. Ostmann</u> & A. Kieneke	3 D muscle structure and the evolution of remarkable planktonic Gastrotricha (Family Dasydytidae)		
	11.45-12.00		<u>F. Nitsche</u> & H. Arndt	Is there a phylogenetic separation of marine and freshwater choanoflagellates?		
	12.00-13.30	Mittagspause (90 min; zeitgleich Besichtigung des BIOHISTORICUMS mit K. Schmidt-Loske)				
	13.30-13.45	2x4 Kurzvorträge (parallel): Naturkundemuseen, Taxonomie und Artkonzepte	<u>K. Riede</u>	International Biodiversity Projects and Natural History Museums: current state and perspectives	G. Haszprunar	Hörsaal
	13.45-14.00		<u>V. Lohrmann</u> , K. Vohland, L. Chamsai, V. Firtzlaff, M. Ohl & C. Häuser	Taxonomische Forschung in Deutschland – Aufschwung oder Krise?		
	14.00-14.15		<u>A. Koch</u> , H. Wägele, A. Klussmann-Kolb, M. Kuhlmann, G. Haszprunar, D. Lindberg & J. W. Wägele	The Taxonomist – an endangered Race. A practical Solution for its Survival in the 21 st Century		
14.15-14.30	<u>B. Hausdorf</u>		Do we need a new species concept?			

Do., 23.02.	13.30-13.45	2x4 Kurzvorträge (parallel): DNA-Barcoding und Phylogeny	<u>F. Kilpert</u> , B. Beszteri, S. Frickenhaus & K. Valentin	PhyloAssigner – A software pipeline for rapid and reliable biodiversity determination using phylogenetic placement	M. Raupach	Kursraum Neubau
	13.45-14.00		<u>C. Mayer</u> & P. Kück	Very minor model violations can strongly affect the reconstruction success of maximum likelihood based tree reconstruction methods		
	14.00-14.15		<u>D. S. McLeod</u>	A Phylogenetic Reassessment of <i>Limnonectes kuhlii</i> Tschudi (1838)		
	14.15-14.30		<u>S. Agrawal</u> , C. Eberlein, F. Leese & C. Held	Higher regional diversity compared to what is known for an entire Antarctic continent in the genus <i>Antarctomysis</i> Coutière, 1906		
	14.30-14.45	kurze Pause (15 min)				
	14.45-15.00	2x3 Kurzvorträge (parallel): Systematik von Reptilien & Evolution von Riesenkuglern	<u>O. Hawlitschek</u> , Z. T. Nagy & F. Glaw	Comoran tree snakes: why and when subspecies still make sense	W. Böhme	Hörsaal
	15.00-15.15		<u>Y. Bucklitsch</u> , W. Böhme & A. Koch	Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)		
	15.15-15.30		<u>T. Wesener</u>	Origins of the Giant Millipedes – Microendemism and Multiple Speciation Processes on Madagascar (Diplopoda, Sphaerotheriida, Spirobolida)		
	14.45-15.00	2x3 Kurzvorträge (parallel): Biodiversity Data & 3D Software	<u>J. Hoffmann</u> & C. L. Häuser	OpenUp! – Opening Up the Natural History Heritage for Europeana	A. Blanke	Kursraum Neubau
	15.00-15.15		H. Scholz & <u>J. Hoffmann</u>	Biodiversity Heritage Library for Europe: Rapid assessment of taxonomic literature		
15.15-15.30	<u>B. Quast</u>		High throughput image registration with open source software			
15.30-16.00	Pause (30 min)					
16.00-17.00	Postervorträge I	Siehe Extraliste!	Siehe Extraliste! (Verschiedene Themen)	M. Ohl	Hörsaal	

Do., 23.02.	17.00-19.00	Treffen der AG Junge Systematiker (JuSys) (offen für Interessenten)		ODE-Ausgabe der JuSys etc.	A. Koch	Seminarraum (Hauptgebäude)
	17.00-19.00	Treffen der AG Kuratoren (offen für Interessenten)	<u>E. Gilissen</u>	Scanned museum collections and data sharing, some suggestions for best practice	P. Giere	Kursraum (Neubau)
			<u>A. Kroupa</u>	Digitisation of entomological collections – Three approaches at the Museum für Naturkunde Berlin		
<u>P. Giere</u>	Digitization of collection objects: an introduction					
Fr., 24.02.	9.00-10.30	Postervorträge II	Siehe Extraliste!	Siehe Extraliste! (Verschiedene Themen)	tba	Hörsaal
	10.30-11.00	Pause (30 min)				
	11.00-11.15	2x4 Kurzvorträge (parallel): Insekten Evolution & Phylogenie	<u>R. S. Peters</u> (on behalf of the 1KITE consortium)	Joining forces to unravel the evolution of insects – an introduction to the 1KITE project	B. Misof	Hörsaal
	11.15-11.30		<u>O. Niehuis</u> , G. Hartig, S. Grath, H. Pohl, A. Donath, C. Eisenhardt, J. Hertel, V. Krauss, J. Lehmann, C. Mayer, H. Tafer, R. Peters, K. Meusemann, R. G. Beutel, P. F. Stadler, E. Bornberg-Bauer & B. Misof	The first sequenced genome of a twisted-wing parasite (Insecta: Strepsiptera) and its phylogenetic implications		
	11.30-11.45		<u>H. O. Letsch</u> , K. Meusemann, B. Wipfler, K. Schütte, R. Beutel & B. Misof	Insect phylogenomics: results, problems and the impact of matrix composition		
11.45-12.00	<u>L. Krogmann</u>		New species of Lower Cretaceous Hymenoptera and the early evolution of the order			

Fr., 24.02.	11.00-11.15	2x4 Kurzvorträge (parallel): Verschiedene Themen	<u>M. Gerth</u> , J. Röthe & C. Bleidorn	Assessing brood parasitism as a potential mechanism for horizontal transmission of <i>Wolbachia</i> endosymbionts in bees (Anthophila)	tba	Kursraum Neubau
	11.15-11.30		<u>S. Krause</u> & M. Ohl	Die phylogenetische Signifikanz der Antennen und antennalen Sensillen der Grabwespen (Hymenoptera: Apoidea)		
	11.30-11.45		M. E. McNamara, D. E. G. Briggs, P. J. Orr, <u>S. Wedmann</u> , H. Noh & H. Cao	Fossilized structural colours in moths from the Eocene of Messel, Germany		
	11.45-12.00		<u>P. Giere</u> , M. Kuehbacher, O. Scharf, S. Bjeoumikova, R. Gubzhokov, M. Radtke, U. Reinholz, H. Riesemeier, G. Buzanich, R. Wedell, H. Soltau, I. Ordavo & N. Langhoff	Non-invasive chemical imaging: Color X-ray scanning for iron and calcium in the enamel of a red toothed shrew, <i>Sorex araneus</i> (Soricidae, Mammalia)		
	12.00-13.30	Mittagspause (90 min; zeitgleich Besichtigung des BIOHISTORICUMS mit K. Schmidt-Loske)				
	13.30-13.45	2x4 Kurzvorträge (parallel): Evolution von Insekten und Onychophoren	<u>A. Zwick</u> , H. Zhao & J. C. Regier	Molecular phylogeny of non-endopterygote Hexapoda	C. Bleidorn	Hörsaal
	13.45-14.00		<u>R. Mally</u> , C. Neinhuis & M. Nuß	Testing monophyly of megadiverse Spilomelinae (Insecta: Lepidoptera: Pyraloidea)		
	14.00-14.15		<u>L. Hering</u> , C. Bleidorn & G. Mayer	Opsins in Onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods		
	14.15-14.30		<u>G. Mayer</u>	Neuroanatomy of onychophorans and tardigrades: Implications for the phylogenetic position of Tardigrada		

Fr., 24.02.	13.30-13.45	2x4 Kurzvorträge (parallel): Systematik und Evolution von Vögeln	<u>T. Töpfer</u>	Systematics of nightjars (Aves: Caprimulgidae) and the evolution of crypsis	R. van den Elzen	Kursraum Neubau
	13.45-14.00		<u>D. T. Tietze & M. Päckert</u>	Evolutionary history of swifts (Aves: <i>Apus</i> , <i>Tachymarptis</i>)		
	14.00-14.15		<u>A. Manegold</u>	Vocal learning in parrots and songbirds – synapomorphy or underlying synapomorphy?		
	14.15-14.30		<u>A. Bauer, H. Sauer-Gürth & M. Wink</u>	Genetische Analysen bei <i>Ficedula hypoleuca</i> in Tomsk, Westsibirien		
	14.30-15.00	Pause (30 min)				
	15.00-15.15	2x4 Kurzvorträge (parallel): Mollusken Phylogenie	<u>G. Haszprunar</u>	Molecular Phylogeny of Mollusca – Bringing Chaos into the Order?	H. Wägele	Hörsaal
	15.15-15.30		<u>A. M. Weigand, A. Jochum & A. Klussmann-Kolb</u>	Why DNA barcoding complements microgastropod taxonomy		
	15.30-15.45		<u>T. Huelsken, J. Keyse, L. Liggins, E. A. Treml & C. Riginos</u>	Parallel cryptic divergence among giant clams (Cardiidae: <i>Tridacna</i>) from the eastern Indian and western Pacific oceans		
	15.45-16.00		<u>D. Obermann, U. Bickmeyer & H. Wägele</u>	New pH-sensitive fluorescent dye Ageladine A proves incorporated nematocysts in <i>Aeolidiella stephanieae</i> (Opisthobranchia, Nudibranchia) to mature by acidification		
	15.00-15.15	2x4 Kurzvorträge (parallel): Verschiedene Themen Botanik	<u>M. Mittelbach, C. Kurth, S. Mitulla & D. Begerow</u>	Evolution of <i>Petrocoptis</i> A. Braun ex Endl. (Sileneae, Caryophyllaceae)	R. Jahn	Kursraum Neubau
15.15-15.30	<u>M. Weigend, M. Gottschling, V. Barreda & L. Palazzesi</u>		Andean lineages as descendants of the “Old South” - fossil Ledocarpaceae from Patagonia and the historical biogeography of Geraniales			
15.30-15.45	<u>T. Henning & M. Weigend</u>		Floral behaviour taken to extremes – pollen presentation and floral longevity in Loasaceae are modulated by light, temperature and visitation rates			
15.45-16.00	<u>G. Brokamp, C. Isaza, J.-C. Pintaud, R. J. Montúfar, S.</u>		Detecting adulteration and population differentiation by PCA and Cluster analysis			

Fr., 24.02.			Dussert & M. Weigend	with fatty acid composition data of <i>Oenocarpus bataua</i> (Arecaceae) mesocarp oil from NW South America		
	16.00-16.15	kurze Pause (15 min)				
	16.15-16.30	2x3 Kurzvorträge (parallel): Verschiedene Themen	<u>D. Brandis</u>	Abgeleitet oder basal? Das Receptaculum seminis der Maskenkrabbe <i>Ethusa mascarone</i> – eine bei Brachyuren bislang nicht bekannte Spermienspeicherstruktur	K. Meuseman n	Hörsaal
	16.30-16.45		<u>T. H. Struck</u> , N. Hill, A. Weigert & C. Bleidorn	The importance of appropriate outgroup taxon sampling in phylogenomic studies		
	16.45-17.00		<u>J. Schyra</u> & J. Korb	Phylogenetic analysis of the community structure of southern African termites		
	16.15-16.30	2x3 Kurzvorträge (parallel): Verschiedene Themen Arthropoden	<u>A. L. Schönhofer</u>	Versteckte Signale – Genitalmorphologie und Verbreitung als systematische Merkmale bei Weberknechten (Arachnida: Opiliones)	B. M. von Reumont	Kursraum Neubau
	16.30-16.45		<u>D. Gassmann</u>	Biogeography of tropical damselflies (Odonata, Zygoptera) of New Guinea and the Bismarck Archipelago – the role of Tertiary island arcs		
	16.45-17.00					
	ab 17.00	Mitgliederversammlung	G. Haszprunar, H. Schminke (Laudator) L. Menzel (Rensch- Preisträgerin)	- Bericht des Vorstands - Neuwahl des Vorstands - Rensch-Preis Verleihung - Laudatio - Studentenpreise	G. Haszprunar	Hörsaal
	ab 20.00	Konferenz-Dinner	-	-	-	Restaurant Tuscolo in der Bonner City

Zeitliche Gliederung* der Workshops:

(* Änderungen vorbehalten.)

Inhaltliche Beschreibungen der einzelnen Workshops finden Sie am Ende dieses Bandes ab Seite 87.

Sa., 25.02.	Workshops Session 1 (Sequenzanalyse-Tools)	9.00-10.30	B. Misof	ALISCORE	Kursraum Neubau
		10.30-11.30#	K. Meusemann	MARE – Matrix Reduction	
		11.30-13.00	W. Wägele, C. Mayer, S. Meid	SAMS – Split Analysis Methods	
	Workshops Session 2 (Sammlungs- verwaltungssysteme)	9.00-10.00	S. Ingrisch	Species File Software (Orthoptera Species File Online)	Seminarraum (Hauptgebäude)
		10.00-12.00	D. Triebel, M. Weiss, T. Schneider	Diversity Workbench – Software Components for Building and Accessing Bio- and Geodiversity Information	
		12.00-13.00	Mittagspause		
		13.00-14.30	G. Dröge, J. Astrin	DNA Bank Network – Manage and reference your DNA samples by using GBIF infrastructure	
		14.30-16.30	M. Tuerkay, A. Allspach, L. Menner	SeSAM – das Senckenbergische Sammlungsmanagement-System	
	Workshops Session 3 (verschiedene Themen)	8.30-11.30	P. Grobe, L. Vogt	MorphDBase – Utilization of the Character Matrices Module in MorphDBase: Learn how to increase the Quality of morphological Matrices	Museumsschule (Hauptgebäude)
		11.30-12.30	Mittagspause		
		12.30-16.00	A. Blanke	3D-Rekonstruktion – High Quality 3D Reconstruction for Everyone: open-Source Solutions and their Workflow to analyse and publish MicroCT Data	

Falls von den Teilnehmern gewünscht, kann eine Mittagspause von 11.30-12.30 gemacht werden.

Liste der Poster-Kurzvorträge:

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

No	Name	Titel
Thema: Botanik		
1	<u>Markus Ackermann</u> & Maximilian Weigend	Floral rewards and pollinator guilds in Nasturtiums (<i>Tropaeolum</i> , Tropaeolaceae)
2	<u>Antje Donner</u> , Lisa Moosmann & Frank Kauff	Phylogenetic and morphological analysis of <i>Chroococcidiopsis</i> , the Pleurocapsales, and related heterocyte-forming Cyanobacteria
3	<u>Nur Gokce Cetiner</u> , Eike Myland Quellhorst & Dirk C. Albach	Genetic Diversity of Some <i>Lupinus</i> (<i>Fabaceae</i>) Species using AFLP Fingerprint and DNA Data Sequencing
4	<u>Almila Ciftci</u> , Osman Erol & Volker Wissemann	Micromorphological Studies on Inflorescence and Seeds of Some <i>Plantago</i> L. (Plantaginaceae) Taxa in Turkey
5	D. Lauterbach, M. Ristow & <u>B. Gemeinholzer</u>	Population genetics and fitness in fragmented populations of the dioecious and endangered <i>Silene otites</i> L. (Caryophyllaceae)
6	<u>Angela Maria Schäfer</u> , René Prior, Martin Kemler & Dominik Begerow	Molecular studies on the genus <i>Saponaria</i> L.
7	<u>Sascha Lotze-Engelhard</u> , Martin Kemler & Dominik Begerow	What is <i>Urocystis</i> ?
8	<u>Christoph Carl-Friedrich Schinkel</u> , Birgit Gemeinholzer & Volker Wissemann	Investigations into a putative hybrid complex of <i>Sorbus</i> L. (Rosaceae)
9	<u>Natalia Tkach</u> , Martin Röser & Matthias H. Hoffmann	Parallel colonisation of the Arctic by plants
10	<u>Regine Jahn</u> , Jonas Zimmermann, Névida Abarca, Sabine von Mering & Wolf-Henning Kusber	Diatom research: towards cybertaxonomy
11	Jonas Zimmermann, Regine Jahn, Gernot Glöckner & <u>Birgit Gemeinholzer</u>	DNA barcoding of diatoms: establishment of routine laboratory protocols
12	<u>Alexandra Wölk</u> , Elke Döring, Julia Schneider & Martin Röser	A molecular phylogenetic and biogeographical analyses of <i>Helictotrichon</i> and related genera of oat grasses (Poaceae: Aveneae)
Thema: Insekten		
13	<u>Marc Beckett</u> & Dirk Ahrens	Distribution patterns and distribution modeling in the South African chafer genus <i>Pleophylla</i> (Coleoptera: Scarabaeidae)
14	<u>Carina Eisenhardt</u> , Jörg Lehmann, Peter F. Stadler & Veiko Krauss	Near intron pairs (NIPs) and the phylogeny of beetles and related insects

No	Thema: Insekten (Fortsetzung)	
15	<u>Christoph D. Schubart</u> , Thomas Sparrer, Markus Luber & Jörn A. Pützschler	Examples of barcoding and phylogeny reconstruction of native aquatic insect larvae: Heptageniidae (Ephemeroptera) and Hydropsychidae (Trichoptera)
16	Sebastian Büsse, <u>Alexander Blanke</u> , Bernhard Misof & Thomas Hörnschemeyer	The nymphal head of <i>Epiophlebia laidlawi</i> (Insecta: Odonata)
17	<u>Hans Peter Katzmann</u> , Joachim T. Haug, Andreas Maas & Dieter Waloßek	The hypostome-labrum complex in Euarthropods – different names for different structures!
18	<u>Martin Kubiak</u> & F. Friedrich	Beyond the haustellar complex – unexpected morphological complexity in adult head structures of caddisflies (Insecta: Trichoptera)
19	<u>Jennifer Nolzen</u> , Rüdiger Wagner, Jan Macher & Florian Leese	Species status of <i>Sericostoma personatum</i> and <i>Sericostoma schneideri</i> (Insecta: Trichoptera): Molecular and morphological evidence

Session II: Freitag, 24.02.2012, 9-10.30 Uhr, Hörsaal

No	Thema: Diplopoda, Onychophoren & Anneliden	
20	Cathrin Conrad & <u>Thomas Wesener</u>	The status of enigmatic, microendemic pill millipede species of the genus <i>Glomeris</i> in northern Italy (Diplopoda, Glomerida)
21	<u>Ivo de Sena Oliveira</u> & Georg Mayer	Novel and neglected structures useful for unravelling the taxonomy and phylogeny of Onychophora (velvet worms)
22	<u>Stefan Schaffer</u> , Lars Hering, Christoph Bleidorn & Georg Mayer	Phylogeny of Onychophora (velvet worms) based on mitogenomics
23	<u>Franziska Anni Franke</u> , Lars Hering & Georg Mayer	Evolution of the <i>Wnt</i> family genes in Onychophora (velvet worms)
24	<u>Patrick Beckers</u>	Nemertean nervous system: A phylogeny based on the morphological elements of the nervous system
25	<u>Conrad Helm</u> , Anne Weigert, Georg Mayer & Christoph Bleidorn	Organization of the muscular system in <i>Myzostoma cirriferum</i> (Annelida): Implications for the evolution of the myzostomid anatomy
26	<u>Anja Golombek</u> , Günter Purschke & Torsten H. Struck	The phylogenetic positions of the former archiannelidan taxa Protodrilidae and Polygordiidae within Annelida
27	<u>José Horacio Grau</u> & Fernando Carbayo	A new land planarian (Platyhelminthes, Tricladida, Geoplanidae) from southern Chile, with a discussion of its systematic position
28	<u>Sandy Richter</u> , Jörg Hetmank, Lars Hering, Giampietro Schiavo & Christoph Bleidorn	Analyses of the genomic structure of α -glycerotoxin

No	Thema: Anneliden (Fortsetzung)	
29	<u>Christian Schmidt</u> , Jörn von Döhren & Thomas Bartolomaeus	<i>Lineus ruber</i> and <i>Lineus viridis</i> – one, two, or more species of Heteronemertea (Nemertea)?
30	<u>Jörn von Döhren</u> & Thomas Bartolomaeus	New Standards in the Taxonomy of Nemertea
31	<u>Anne Weigert</u> , Torsten H. Struck & Christoph Bleidorn	A survey of <i>Hox</i> gene expression in adult <i>Owenia</i> cf. <i>fusiformis</i>
32	Lena I. Wolff, Verena Wilkens, <u>Christine Lehmacher</u> , Günter Purschke, Patricia A. Ramey-Balci & Dieter Fiege	Ultrastructure of photoreceptor-like sense organs in <i>Polygordius</i> (Annelida: Polychaeta): a possible character for species distinction?
No	Thema: Süßwasser-Organismen, Crustaceen & Gastropoden	
33	<u>Matthias Geiger</u> , Jörg Freyhof, Katharina Kurzrock, Sereina Rutschmann, Michael Monaghan, Thomas v. Rintelen, Matthias Glaubrecht, Bernhard Misof & Fabian Herder	Freshwater Diversity Identification for Europe (FREDIE)
34	<u>Kai Horst George</u>	Argestinae Por, 1986, the first recognized suprageneric monophylum within Argestidae sensu Por, 1986 (Crustacea, Copepoda, Harpacticoida)
35	<u>Meike Seefeldt</u> , Tim Feldkamp, Myriam Schüller & Florian Leese	Genetic and morphologic data unveil two overlooked Southern Ocean lysianassoid species (Crustacea, Amphipoda)
36	<u>Thomas Huelsken</u> , John Healy, Michael Hollmann & Cynthia Riginos	Genetic connectivity of sand-associated marine snails (Gastropoda) in the Great Barrier Reef, Australia
37	Bettina Scheel & <u>Bernhard Hausdorf</u>	Survival and differentiation of subspecies of the land snail <i>Charpentieria itala</i> in mountain refuges in the Southern Alps
No	Thema: Säugetiere, Frösche & Schildkröten	
38	<u>M. Liebe</u> , O. Zierau & P. Giere	The course of the Nervus facialis as a possible signal in mammal phylogeny
39	<u>Anja C. Schunke</u> & Diethard Tautz	Verschiedene Wege, das Gleiche zu tun – Die Mandibelform von Nagetieren mit gleicher Ernährung aus verschiedenen Unterfamilien
40	<u>Michael Barej</u> & Mark-Oliver Rödel et al.	Torrent Frogs and Slippery Frogs in West Africa – living close but being different
41	<u>Markus Lambertz</u> & Steven F. Perry	Lung morphology and systematics of the Kinosternidae (Testudines: Cryptodira)

No	Thema: Management von Biodiversitätsdaten & weitere Themen	
42	<u>Renate van den Elzen</u> , Peter Grobe & Zdravko Colic	Innovative Methoden zur Schnellerfassung von Sammlungsdaten
43	<u>Gleisberg, M.</u> , Güntsch, A., Fichtmüller, D., Kirchhoff A.	Where have all the data gone? The reBiND Project provides workflows and software for archiving biodiversity data
44	S. von Mering, W.-H. Kusber & <u>R. Jahn</u>	Open access to biodiversity data for botanists via GBIF
45	<u>M. Gleisberg</u> , Ch. Häuser, R. Jahn, W. Kiessling, R. Melzer, J. Overmann, D. Triebel, M. Türkay, R. van den Elzen & W.G. Berendsohn	GBIF-D enables free access to Biodiversity Data: How to contribute?
46	<u>Michael Laumann</u> & Reinhard Gerecke	DNS-Isolation aus einem Holotypus? Der Fall einer außergewöhnlichen Wassermilbenlarve aus Nord-Madagaskar
47	<u>N. U. Szucsich</u> , A. Böhm, M. Resch, D. Bartel, G. Timelthaler & G. Pass	Morphological study of NDE-vouchers: Confocal Laser Scanning Microscopy (CLSM) of Diplura and Protura after Non-destructive DNA extraction
48	<u>Yannick Bucklitsch</u> , Wolfgang Böhme & André Koch	Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)
49	Heike Wägele, Annette Klussmann-Kolb, Michael Kuhlmann, Gerhard Haszprunar, David Lindberg, <u>André Koch</u> & J. Wolfgang Wägele	The Taxonomist – an endangered Race. A practical Solution for its Survival in the 21 st Century

ABSTRACTS

der

Vorträge & Poster

in alphabetischer Reihenfolge der Erstautoren

1. Vorträge:

Higher regional diversity compared to what is known for an entire Antarctic continent in the genus *Antarctomysis* Coutière, 1906

Shobhit Agrawal¹, Chris Eberlein^{1,2}, Florian Leese² & Christoph Held¹

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The Antarctic benthos is characterized by endemic species which were generally believed to be circumpolar in distribution. Recent molecular studies using DNA barcoding, especially on taxa with limited mobility due to their benthic and brooding lifestyle, have proven that there are indeed a large number of cryptic species in the Antarctic marine realm underlining the fact that much of the biodiversity of the region is undiscovered. This study focussed on the highly abundant and ecologically important mysids belonging to the genus *Antarctomysis* which are as yet believed to consist of 3 species (*A. ohlini*, *A. maxima* and *A. profunda*) from a relatively understudied region (Terre Adelie). Using three molecular genetic markers (two mitochondrial: cytochrome oxidase subunit 1 and 16S rDNA and one nuclear: 18S rDNA) in addition to traditional morphological techniques we find surprisingly high inter- and intraspecific diversity in this taxon in a relatively small geographic region. We challenge the idea that the genus *Antarctomysis* consists of only three species by using state of the art species delimitation methods and unravel two new species which were hitherto unknown to science. Furthermore, it is shown how speciation within *Antarctomysis* might have a vertical and temporal scale wherein the evolutionary history of this genus is discussed in the light of the climatic history of the Antarctic continent. Our results show that even on a relatively fine geographical scale the number of species found were more than what was known for the entire continent leaving the question of “how many species are there” open requiring extensive research.

DNA Taxonomy in cryptic weevils

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2 Curculio-Institut, Mönchengladbach

An ongoing barcoding and integrative taxonomy project on western Palaearctic (mostly European and Macaronesian) cryptorhynchine weevils (Coleoptera: Curculionidae: Cryptorhynchinae) is presented. 'Traditionally' identified morphospecies are compared with species inferred through distance-based clustering and the tree-based Generalized Mixed Yule-Coalescent (GMYC) approach, based on two variable fragments of mitochondrial DNA (CO1 and 16S).

The different species inferences show overall similar, but low degrees of congruence with morphospecies, and composition of clusters partially varies. This initially low match between morphospecies and the different molecular species delineations shows the necessity of combining the output of various methods in an integrative taxonomy approach. Thereby we obtain an idea about the reliability of the different results and signals, which enables us to fine-tune sampling, delineation technique and data collection, and to identify species that require taxonomic revision.

Genetische Analysen bei *Ficedula hypoleuca* in Tomsk, Westsibirien

Andreas Bauer¹, Hedwig Sauer-Gürth¹ & Michael Wink¹

1 Institut für Pharmazie und Molekulare Biotechnologie (IPMB) der Ruprecht-Karls-Universität Heidelberg, Abt. Biologie, Im Neuenheimer Feld 364, D-69120 Heidelberg

Die in der Region Tomsk (Rußland) vorkommende Population des Trauerschnäppers *Ficedula hypoleuca* gilt als die östlichste im Verbreitungsgebiet und wird der Unterart *F. h. tomensis* (Syn. *F. h. sibirica*) zugerechnet, welche morphologisch von den anderen Unterarten unterschieden werden kann und durch den Ural von den Brutgebieten der Nominatform getrennt ist. Im Jahre 2005 wurden im Stadtgebiet des westsibirischen Tomsk sowie in einem gesondertem Beprobungsareal in den Waldgebieten der Stadt 2.431 Blutproben (1.970 aus den Waldgebieten, 342 aus dem Stadtgebiet) zumeist kompletter Bruten inklusive der beiden Elternvögel genommen. Alle Familien waren mit Beprobungsdatum, morphologisch bestimmtem Geschlecht bei den Altvögeln und Lage des Nestes gut dokumentiert. Zusätzlich waren noch 49 Vergleichsproben von *Ficedula h. hypoleuca* aus Moskau vorhanden. Zuerst wurde aus den Blutproben DNA extrahiert, danach wurden alle Individuen genetisch gesext mithilfe hochauflösender PAGE. Es wurden zwei Multiplex PCR-Sets mit jeweils vier Mikrosatellitenloci, bei denen jeweils ein Primer fluoreszenzgelabelt war, entworfen. Anschließend wurden die PCR-Produkte über Kapillarelektrophorese aufgetrennt. Mit diesen genetischen Markern wurde die komplette Probensammlung (Tomsk Stadt, Tomsk Waldgebiete, Moskau) untersucht. Das Hauptaugenmerk lag in erster Linie auf einer Familienanalyse der besonders gut dokumentierten Waldgebiete bei Tomsk. Hierbei wurden extrapair paternities aufgedeckt und eventuellen Alttieren zugeordnet. Daneben konnten auch bigyne Männchen erkannt und zum Teil aufgrund der genetischen Information der Marker ihrer „Zweitfamilie“ zugeteilt werden. Ein besonderer Blickpunkt lag dabei auf den Abständen der einzelnen Nester und der Distanz, die von den Männchen zwischen den beiden Nestern zurückgelegt werden mußte. Ausbreitungstendenzen innerhalb der Waldgebiete bzw. von den Waldgebieten in die Stadt Tomsk hinein wurden ebenso untersucht wie Unterschiede zwischen der Tomsker Population und der Nominatform, von der Vergleichsproben aus Moskau vorhanden waren. Sämtliche Auswertungen wurden mit der üblichen Software für Mikrosatellitenmarkern in Populationsgenetik und Phylogenie durchgeführt.

Abgeleitet oder basal? Das Receptaculum seminis der Maskenkrabbe *Ethusa mascarone* – eine bei Brachyuren bislang nicht bekannte Spermien-speicherstruktur

Dirk Brandis¹

1 Zoologisches Museum Kiel

Brachyuren oder Kurzschwanzkrebse weisen im Gegensatz zu den meisten anderen dekapoden-Krebsen eine innere Befruchtung der Eier auf. Bei der Kopulation werden Spermatotheken vom Männchen mit den ersten beiden stark abgewandelten Pleopodenpaaren, den so genannten Gonopoden in die weiblichen Geschlechtsgänge der Weibchen übertragen. Weibliche Krabben speichern die Spermien in einem Receptaculum seminis, der Spermiothek. An oder in den Spermiotheken findet auch die Befruchtung statt, Spermien können teilweise mehrere Jahre gespeichert werden. Spermiotheken sind sehr komplex gebaut, und folgen nach bisherigen Kenntnissen einem allgemeinen Bauplan-Schema. Alle Spermiotheken bestehen aus zwei Abschnitten, einem ventralen Epithel, das

von Cuticula ausgekleidet ist und einem dorsalen Drüsenepithel, die eine gemeinsame kompakte Kammer bilden. In diese Kammer mündet der Ovidukt, in diesem Bereich findet auch die Befruchtung statt.

Nach histologischen Untersuchungen an Weibchen der Maskenkrabbe *Ethusa mascarone* kann erstmals ein Spermathekentyp dargestellt werden, der grundlegend von dem bisher bekannten Schema aller bisher untersuchten Krabben abweicht: Drüsenepithel und Cuticula-Epithel bilden hier zwei weitgehend getrennte, nebeneinander liegende Kammern, die nur im Bereich der Oviductmündung miteinander verbunden sind, dorsal über ein komplexes Ventil, ventral über zahlreiche flexible Gänge.

Da Feinstruktur und Histologie der Spermatheken gegenwärtig noch von zu wenigen Brachyuren-Taxa genau bekannt ist, können die Ergebnisse zurzeit noch nicht abschließend eingeordnet werden. Die Befunde lassen aber zumindest Hypothesen zur Entwicklungsgeschichte der Brachyuren-Spermathek zu.

Detecting adulteration and population differentiation by PCA and Cluster analysis with fatty acid composition data of *Oenocarpus bataua* (Arecaceae) mesocarp oil from NW South America

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Many native palm species from NW South America bear oil-rich fruit (up to 73 % oil in dry fruit weight). Palm oil is generally extracted either from the mesocarp or the endosperm. In the majority of cases the mesocarp oils of palms from NW South America are characterized by their high concentration of monounsaturated fatty acids, while endosperm oils mainly consist of saturated fatty acids. More than 60 data sets on FA composition of *Oenocarpus bataua* var. *bataua* (hungurahua, majo) mesocarp oils and data of the genera *Attalea*, *Bactris*, *Euterpe*, and *Elaeis*, were analyzed in a PCA (principle component analysis) and based on that with a cluster analysis (agglomerative hierarchical clustering). These data included 38 samples collected in the course of field studies and 19 commercially available oils obtained from indigenous communities, street markets, alternative health shops, and small enterprises in Bolivia, Colombia, Ecuador, and Peru, and were complemented with data from the scientific literature. The analyses revealed that FA composition of native South American palm oils appears to be species-specific and FA composition can therefore be used to identify adulterations. This also permits the identification of five of the commercially obtained samples of "hungurahua oil" as soy oil (*Glycine max*). FA composition of *Oenocarpus bataua* var. *bataua* populations in French Guiana clearly differ from samples of the same species from Brazil, Bolivia, Colombia, Ecuador, Peru, and Venezuela. *Oenocarpus* appears to represent a very promising resource for oil extraction and is already marketed at a local and regional scale for food and cosmetics. Domestication of the species appears promising and data here presented provide the basis for the selection of adequate source populations for improved cultivars and show the genetic differentiation of oil quality within the species. Future studies should address questions of fruit/oil yield, growth rates and

resistance in order to provide a solid basis for agricultural or silvicultural development in the countries under study.

Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)

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Monitor lizards (Varanidae: *Varanus* spp.) are a relatively small group of squamate reptiles, which comprise the largest living lizards of the world. Being mainly carnivorous, monitor lizards are the top predators in most environments they inhabit. In Africa, Asia and Australia, monitor lizards inhabit a variety of different ecosystems from deserts to rainforests. They show specific ecological and morphological adaptations and can be strictly terrestrial, semi-aquatic or arboreal.

Across all nine recognized subgenera of the genus *Varanus* including 37 different species, scale shape and structure were analyzed using scanning electron microscopy (SEM). Results show that a microornamentation (ultradermatoglyphics) as seen in various squamate groups is also partly present in monitor lizards. However, only in few, albeit unrelated, monitor species examined the dorsal scales exhibit a specific honeycombed microstructure. The ecological meaning of this microstructure remains unknown. Nevertheless, scale shape as well as extent and size of granula rows around the main scales allow differentiation between single species, even among closely-related monitor lizard species such as the members of the *Varanus indicus* species group.

In addition, the systematic affiliation of *V. spinulosus*, a rare monitor species from the Solomon Islands with a unique scale structure, is discussed in the light of current hypotheses about its phylogenetic position within the Varanidae. Due to its unique scale structure, in combination with other morphological evidence, a monotypic subgenus for this enigmatic monitor species seems justified. Also for the members of the *V. prasinus* group from New Guinea within the subgenus *Euprepiosaurus*, erection of new subgenus seems justified based on the autapomorphic scale shape in concert with further morphological, molecular and ecological evidence.

Biogeography of tropical damselflies (Odonata, Zygoptera) of New Guinea and the Bismarck Archipelago – the role of Tertiary island arcs

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Damselflies (Odonata, Zygoptera) of the Southeast Asian and Indo-Pacific tropics have been studied with regard to their distributional history during the past years. Special focus is currently laid by the author on the rich odonate fauna of New Guinea, which combines Oriental and Australian elements and at the same time harbors a considerable number of endemic radiations. The feather-legged damselflies (Platycnemididae) are speciose in the region and provide suitable subjects for historical biogeographical studies. The subfamily

Calicnemiinae is absent from the Wallacea, i.e. from Sulawesi, the Moluccas and the Lesser Sunda Islands but highly diverse in the Himalayas and across mainland SE Asia and Sundaland as well as in the Philippines and in New Guinea. The phylogenetic reconstruction of the Calicnemiinae allows for the postulation of biogeographical pathways from SE Asia to New Guinea via former island arc systems in the Late Cretaceous to mid-Eocene. The central terranes of New Guinea, which have a complex history related to oceanic and continental rifting, probably served as the center of origin for the Papuan Platycnemididae as well as for the Philippine and Solomon genera which may be assumed to have secondarily reached the Philippines and Solomons via the South-Caroline-Melanesian Arc system in the Oligocene or Miocene. Recent odonatological survey work in New Guinea and the Bismarck Archipelago provide new records of, among others, species in the families Lestidae, Protoneuridae, Rhinocyphidae, which indicate a common biogeographical history of dragon- and damselflies from the (former) Tertiary island arcs to the north (South Caroline Arc) and to the east (Melanesian Arcs) of the island. The odonate fauna of New Britain island (Papua New Guinea), which recently has been the subject of a Rapid Biodiversity Assessment, will be discussed in more detail.

Evolutionary ecology of the Midas cichlid flock endemic to Crater Lake Apoyo, Nicaragua

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A comprehensive data set of population genetic (mtDNA, AFLPs), morphological (body shape) and ecological (isotopic signatures) proxies of species level differentiation for a representative set of individuals of all six endemic *Amphilophus* species occurring in Crater Lake Apoyo (Nicaragua) was established. Signatures of divergence were extracted from each data set to identify system specific factors potentially contributing to the sympatric speciation process. AFLP genetic differentiation was partitioned into a neutral and non-neutral component applying outlier-loci detection approaches and patterns of correlation between divergence proxies tested using Mantel tests and Canonical Correspondence Analysis. Significant eco-phenotypic covariance with AFLP data suggests a role of both, divergent natural, and sexual selection for shaping species divergence in Lake Apoyo. Breeding coloration was identified as potential key character for maintaining species cohesion, while ecological selection deduced from isotopic niche segregation displayed a much weaker signature. Bayesian clustering methods revealed substantial levels of admixture between species, but despite incomplete reproductive isolation, all six species apparently evolve as morphologically and genetically coherent units. Analysis of neutral genetic variation revealed several *A. zaliosus* as being introgressed by an unknown allochthonous contributor, hereby rendering the sympatrically evolving Lake Apoyo flock polyphyletic.

Assessing brood parasitism as a potential mechanism for horizontal transmission of *Wolbachia* endosymbionts in bees (Anthophila)

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Wolbachia infect a wide range of hosts and may be the most common bacterial endosymbionts of arthropods. Much research has been focussed on how *Wolbachia* manipulate their hosts' reproduction and thereby promote their own vertical transmission. Furthermore, frequent horizontal transfer of the endosymbionts has been demonstrated. The mechanisms responsible for this transmission and therefore the patterns that led to the worldwide distribution of *Wolbachia* are not well understood. In general, it has been proposed that *Wolbachia* spreads predominantly among closely related hosts or among hosts that are linked by their ecology.

In our study, we aim to test whether brood parasitism is a potential mechanism of horizontal *Wolbachia* transmissions in bees. Brood parasites or cuckoo bees infiltrate nests of solitary bees for oviposition. The cuckoo larva then feeds on the provisions provided by the bee host, thereby taking up salivary gland secretions of the bee host. If *Wolbachia* are transmitted this way, one would expect cuckoo bees and their corresponding hosts to share similar or identical *Wolbachia* strains. We tested for this pattern by sampling the German bee fauna with a focus on kleptoparasite-host pairs that bear *Wolbachia*. We then strain-typed the infections with various molecular markers, including five MLST genes, *wsp* and other bacterial genes.

Our results show that most bees bear quite similar *Wolbachia* strains, although there is no monophyletic clade comprising all *Wolbachia* strains from bee hosts. In five of 13 cases, kleptoparasite-host pairs carried near identical strains, suggesting that horizontal transfer of infections between bees and their kleptoparasites may occur. However, other pathways do not seem unlikely and need further exploration.

Non-invasive chemical imaging: Color X-ray scanning for iron and calcium in the enamel of a red toothed shrew, *Sorex araneus* (Soricidae, Mammalia).

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Chemical analysis of elements incorporated in biological or other materials mostly rely on the destruction or alteration of the specimen sampled. For unique or invaluable specimens – especially in museums – research may be hampered by resistance to allow sampling for reasons of conservation. These reservations may be diminished by a new method of spatial analysis using non invasive surface mapping of elements such as iron and calcium with an experimental compact pnCCD-based Color X-ray camera at the BAMline at the BESSY II synchrotron. This novel device was setup in collaboration with the Institute for Scientific Instruments GmbH, the Federal Institute for Materials Research and Testing, the Institut für Angewandte Photonik e.V, and PNSensor GmbH. Without physical contact, the Color X-ray

camera is capable of elemental analysis of the sample's surface, rendering it in an innovative tool for material and biological research. This device was used for the detection of iron and calcium in the enamel of a common shrew, *Sorex araneus* (Soricidae, Lipotyphla). It is known, that the enamel of a variety of vertebrate taxa (e.g. teleosts, amphibians, mammals) contains iron on or below the tooth's surface. This is related to enhanced wear-resistance of areas exposed to increased stress. In mammals, red enamel containing iron is found in rodents and red toothed shrews (Soricinae), where it occurs on dental cusps and shearing surfaces. In all but the outermost layer, red enamel containing iron is harder than the white enamel found in white toothed shrews (Crociturinae). Based on these findings, a macerated skull of the common shrew *Sorex araneus* was used as a biological sample to demonstrate the suitability of the new non-invasive approach in surface mapping of iron and calcium for biological research, especially for unique and invaluable museum specimens.

Molecular Phylogeny of Mollusca – Bringing Chaos into the Order?

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During the last century morphological studies and cladistic analyses have created less than a handful of hypotheses on deep molluscan phylogeny. These hypotheses mainly disagree upon the monophyly (clade) versus paraphyly (grade) of the shell-less taxa Aculifera and Aplacophora and on the position of the Scaphopoda. Within the last two years several, molecular analyses based on sequence analyses of few to several hundred genes have been published in very high-ranked journals and are based on sophisticated kinds of tree statistics. Despite of this the authors produced no less than five very different trees: indeed there is not a single node which occurs in all these trees, some of which even violate the monophyly of Conchifera. New clades have been proposed for Mono- and Polyplacophora (Serialia-concept) as well as for Gastropoda and Bivalvia (Pleistomollusca-concept), both hypotheses have not received support by any morphological analysis.

At the current state of the art the first conclusion is that at least four of these five trees (but maybe even all five) must be at least partly erroneous as such, since there is only a single true phylogenetic history. Only one study tried to correlate the results with any kind of morphology resp. the fossil record. The latter, however, is highly controversial concerning possible molluscan representatives of the Early Cambrian, which may be true Mollusca, or Polychaeta or represent an extinct clade of Lophotrochozoa.

An integrative way of phylogenetics is proposed where morphological, palaeontological and molecular data (in particular so-called rare genomic events rather than regular sequences) are combined to resolve the mystery of the molluscan tree.

Do we need a new species concept?

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New insights in the speciation process and the nature of 'species' that accumulated in the past decade demand adjustments of the species concept. The impact of the growing evidence that reproductive barriers are semipermeable to gene flow, that species can

differentiate despite ongoing interbreeding and that uniparental organisms are organised in units that resemble species of biparental organisms on the biological species concept is discussed. As a synthesis of ideas in existing concepts and the new insights a generalization of the genic concept is proposed that defines species as groups of individuals that are reciprocally characterized by features that would have negative fitness effects in other groups and that cannot be regularly exchanged between groups upon contact. The benefits of this differential fitness species concept are that it classifies groups that keep differentiated and keep on differentiating despite interbreeding as species, that it is not restricted to specific mutations or mechanisms causing speciation, and that it can be applied to the whole spectrum of organisms from uni- to biparentals.

BARCODING FAUNA BAVARICA:

Taking Barcoding of Central European Animals to a new level

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Despite a long tradition and intensive previous work in faunistics and zootaxonomy, Germany still lacks a comprehensive faunistic monograph for its more than 40,000 animal species. As DNA barcoding is a rapid, cost-effective alternative strategy for the identification of described species, for challenging existing species concepts, and for the discovery of new species, the Zoological Collection of the State of Bavaria activated the project 'Barcoding Fauna Bavarica' (BFB) in January 2009, representing the first program to create a DNA barcode library for all animal species in a whole country. The project is performed in close cooperation with the Biodiversity Institute of Ontario under the framework of the International Barcode of Life Project and currently supported by a 5-year grant from the Bavarian State Government. Research activities involve an active network of private collectors, entomological associations, Nature Reserve authorities and other cooperating institutions. The DNA Bank facility at the ZSM holds DNA extracts for spin-off research projects.

In 2012, BFB will have generated sequence data for more than 10.000 species, making it one of the most successful barcoding initiatives to date. Coverage is nearing completion for butterflies and moths (Macrolepidoptera), bees, grasshoppers and fishes. More than half of the known species total have been analyzed for the large groups of beetles and Microlepidoptera. Our analyses have led to the discovery of unexpected faunal elements, and have also revealed interesting cases of barcode similarity, barcode sharing, and deep intraspecific splits.

Comoran tree snakes: why and when subspecies still make sense.

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Species delimitation and species concepts have been a matter of debate among biodiversity researchers in the last decades, resulting in integrative taxonomy approaches. The discussion on subspecies status and concepts has been led much less extensively, with some researchers completely refraining from recognizing subspecies. However, particularly

differentiated allopatric island populations have traditionally been assigned subspecies status. We studied the molecular phylogeny and morphology of Comoran tree snakes of the genus *Lycodryas* Günther, 1879 (Serpentes: Lamprophiidae: Pseudoxyrhophiinae), hitherto classified as a single species (*Lycodryas sanctijohannis* Günther, 1879), endemic to the four major islands of the archipelago, Grand Comoro, Anjouan, Mohéli and Mayotte. This snake is remarkable for its strong sexual dichromatism unique among its genus and related genera. In an integrative taxonomical approach, we used the concept of independent lines of evidence to discriminate between evidence for species and subspecies status. We found that molecular (mtDNA) and morphological data provide sufficient evidence to support four different taxa within Comoran *Lycodryas*. We propose a taxonomic revision with the resurrection of two taxa and description of each one new species and one new subspecies, resulting in a split of Comoran *Lycodryas* into two species with each two subspecies. Finally, we discuss the subspecies concept, its application and its significance in integrative taxonomy, and emphasize that molecular or morphological characters should be accepted to support species and subspecies delimitation in lines of evidence only if sufficient and significant levels of divergence are detected.

Floral behaviour taken to extremes – pollen presentation and floral longevity in Loasaceae are modulated by light, temperature and visitation rates

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Anther movements are observed in several plant families and may be understood as a mechanism influencing pollen presentation and increasing outbreeding success of hermaphroditic flowers via optimized male function. Loasaceae show a complex floral behaviour, centered on autonomous and thigmonastic stamen presentation (triggered by flower visitors). Little is known about the regulation of these anther movements. We experimentally analyzed the factors regulating stamen movement in eight species of Loasaceae. Both autonomous and thigmonastic movement are found to be positively influenced by light and temperature and come to a virtual standstill in the dark and at low temperatures (12° C): Pollen presentation is discontinued during periods of pollinator absence. Contrary to expectation, no geometrical correlation between the floral scale stimulated and the stamen fascicle reacting could be detected, indicating that the stimulus is transmitted over the receptacle and stamen maturation dictates which and how many stamens react. Thigmonastic stamen presentation is dramatically accelerated compared to autonomous movement (3-37 times), indicating that the rate of stamen maturation can be adjusted to different visitation schedules. Flowers can react relatively uniformly down to stimulation intervals of 10-15 min., consistently presenting comparable numbers of stamens in the flower ca. 5 min. after the stimulus and can thus keep the amount of pollen presented relatively constant even under very high visitation frequencies of 4-6 visits/h. Thigmonastic pollen presentation dramatically reduces the overall duration of the staminate phase (to 1/3rd in *N.*, macrothyrsa). Similarly, the carpellate phase is dramatically reduced after pollination, down to 1 d from 4 d. Overall flower longevity is thus reduced by more than 2/3rds under high visitation rates and pollen depleted and pollinated flowers are rapidly removed from the pool. Complex floral behaviour in Loasaceae thus permits a near-total control over pollen dispensation schedules and floral longevity of the individual flower by an extraordinary fine-tuning to both biotic and abiotic factors.

Opsins in Onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods

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Multiple visual pigments, prerequisites for colour vision, are found in arthropods, but the evolutionary origin of their diversity has remained obscure. We explored the opsin genes in two distantly related species of Onychophora, the putative sister group of Arthropoda, using deep transcriptome sequencing techniques. Surprisingly, our data reveal the presence of only one opsin gene (onypsin) in each onychophoran species. In our phylogenetic analyses, the onypsins represent the sister group to the monophyletic clade of visual r-opsins of arthropods. These findings provide evidence for monochromatic vision in velvet worms and in the last common ancestor of Onychophora and Arthropoda, suggesting that the diversification of visual pigments and colour vision evolved in arthropods, along with the evolution of compound eyes – one of the most sophisticated visual systems known. Thus, we assume that the Early Cambrian stem-lineage arthropods without compound eyes, such as *Opabinia regalis*, displayed no colour vision.

OpenUp! – Opening Up the Natural History Heritage for Europeana

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Despite recent advances in the digitisation of our natural heritage, the vast majority of multimedia objects from the natural history domain are still difficult to discover and access for scientific users and the general public.

To address this problem, the OpenUp! project aims to improve the availability of over 1 Million specimen related multimedia objects, such as high quality specimen images, animal sound files, natural history art work, and movies from the domains of zoology, botany, palaeontology, anthropology and mineralogy. They will all be made easily accessible through Europeana, a convenient portal allowing free access to digitised multimedia objects from all over Europe. OpenUp! will enable a steady stream of multimedia objects to Europeana through the well established technical infrastructure provided by the Global Biodiversity Information Facility (GBIF). In addition, OpenUp! aims to extend the network of content providers of multimedia objects for Europeana.

OpenUp! project partners and the scientific community will benefit from this initiative in several ways. With the Collections Data Quality Toolkit, a software package developed by the project integrating reliable (web) services for references, natural history data providers will be able to assess the completeness, correctness, and compliance of their information and will be able to correct and enrich their data. Furthermore, object related metadata will be enhanced for a facilitated search in Europeana by semantic enrichment, including the common names of species in various languages. This will greatly improve the user's experience while conducting a search in Europeana. Finally, the search results in Europeana will be directly linked to the original source (digital object) on the institutional websites. As a consequence, the visibility of European natural history institutions will increase for both the

public and the scientific community, which will lead to a better understanding of the value of natural history collections throughout Europe.

Parallel cryptic divergence among giant clams (Cardiidae: *Tridacna*) from the eastern Indian and western Pacific oceans

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Giant clams of the genus *Tridacna* are some of the most iconic animals on coral reefs due to their large size and brilliantly colored soft tissue. All *Tridacna* species are CITES listed, reflecting their commercial and cultural value. Giant clams have provided raw material for tools, containers, and ornaments and more recently have been cultured for the international aquarium trade and many populations are locally harvested for both shells and meat. Despite local management efforts and international trade regulation, wild stocks of clams are much depleted and some species have become locally extinct (e.g. *T. gigas* in Fiji, Guam, New Caledonia and Vanuatu). For this reason, the presence of adult *Tridacna* on corals reefs can be considered indicative of effective management. There are currently eight described species within the genus *Tridacna*, differentiated by morphology and habitat preference. Although molecular phylogenetic investigations support accepted species delineations, they have included few individuals with limited geographic scope.

Here we use phylogenetic analyses to infer the species' history of *Tridacna* in the eastern Indian and western Pacific oceans. Distinct groupings consistent with cryptic lineages are evident for both a previously unrecognized group and within named species, with parallel divergence between Indian and Pacific Ocean taxa apparent in three distinct groups. Thus, when placed in the context of a broad scale phylogeographic study, we are able to distinguish between regional patterns and local endemism. North Papua appears to be a location of admixture between western and eastern clades for both *T. crocea* and *T. maxima*, although how far that area of intermixing extends to the east is not known, as no samples from eastern Papua or northern Papua New Guinea have been described. Thus, our finding of cryptic biodiversity within *Tridacna* species indicates that biodiversity in the western Indian and eastern Pacific oceans may be significantly underestimated.

Geographic structure of intraspecific genetic diversity in marine Gastrotricha: Taxonomic consequences and possible historic reasons

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A substantial fraction of marine meiobenthic taxa such as Gastrotricha are known to lack active or passive dispersal stages and thus assumed to be characterized by a poor dispersal capacity. This should be displayed by low levels of gene flow between geographically separated populations and lead to a distinct spatial structure of genetic diversity. However, most traditional and phenotypically defined species are widely (globally) distributed, and this creates a paradox situation. To shed light on this apparent paradox, we test (1) whether such

wide distribution may be due to misidentification and lumping of cryptic species with more restricted distributions and (2) whether spatial structures exist for the within-species genetic diversity of marine gastrotrichs at a regional spatial scale. As a model, we used a number of species of the genus *Turbanella* from different European shorelines of the NE Atlantic and adjacent shelf regions.

DNA taxonomy by means of mitochondrial plus nuclear sequence data, and statistic tests support distinctness of four traditional species (*Turbanella ambronensis*, *T. bocqueti*, *T. cornuta*, and *T. mustela*). Furthermore, we found evidence for two cryptic species within *T. hyalina* that occur sympatrically at different sites. An effect of geography on the intraspecific genetic structure of the most sampled species *T. cornuta* and *T. hyalina* is indeed present, with the potential for performing phylogeographic inference and for understanding past colonization processes of these microscopic animals. Holocene coastline transformations of the studied area much likely had an influence on the present-day distribution of distinct genetic variants. On the other hand, the discovery of a widely distributed haplotype indicates long-distance dispersal as well, despite the assumed low dispersal ability of gastrotrichs. Is this an indication for recent human-mediated dispersal?

PhyloAssigner – A software pipeline for rapid and reliable biodiversity determination using phylogenetic placement

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High throughput metagenomic surveys yield rapidly increasing amounts of sequence data. Using the phylogenetic placement approach it is now possible to quickly assign quality taxonomic labels to unknown reads and contigs. We therefore developed a comprehensive script-pipeline, PhyloAssigner, written in Perl extending the placing capabilities of the software pplacer. The pipeline integrates all necessary steps starting from a reference phylogeny and a user-defined reference alignment yielding a taxonomic label for every query sequence in a fully automated process. One particular innovation is that the pipeline allows LCA (last common ancestor) label assignments reflecting the uncertainty of the maximum-likelihood placement in the tree. In essence, the pipeline creates OTUs (operational taxonomic units) that are related to a known sequence. These NTUs (nodal taxonomic units) have the particular advantage of relating query reads to specific nodes on the phylogenetic tree, which helps comparing data from different studies more easily. The pipeline has been applied e.g. to 18S Sanger sequences from Antarctic sea ice and also to 16S pyrosequences from the open water column of the Bermuda Atlantic Time-series Study (BATS). Parallel processing allows handling of even largest amounts of input sequences.

The Taxonomist – an endangered Race. A practical Solution for its Survival in the 21st Century

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Taxonomy is the basic scientific discipline of biology recording the rich global biodiversity and postulating hypotheses of identity and systematic relationships, on which all other sciences dealing with organisms rely. However, the scientific contributions of taxonomists are largely neglected when using species names in scientific publications by not citing the authority and original description on which they are based. Consequences of this neglect are reduced recognition of the importance of taxonomy, which in turn results in diminished funding, lower interest from journals in publishing taxonomic results, and a reduced number of young scientists entering the field. This has led to the so-called taxonomic impediment at a time when the assessment of the biodiversity on earth is of critical importance for the viability of the human race.

Here we emphasize a simple solution to this dilemma, which has recently been published by Wägele et al. (2011). We merely propose that whenever a species name is used in any kind of publication, the author(s) of the original species hypothesis be included in the literature cited, including also newer taxonomic revisions and identification keys. This means nothing more than what is routinely done for any other hypothesis or assumption included in a scientific publication. In addition, we postulate that journals primarily publishing taxonomic studies should be indexed in ISISM to enhance the recognition and impact of taxonomy.

The practical proposal outlined above would make visible the true contributions of taxonomists within the scientific community, and would provide a more accurate assessment for funding agencies deciding about taxonomic studies, thus helping to alleviate the taxonomic impediment by supporting the recruitment of more young scientists into the field of taxonomy.

Wägele, H., A. Klussmann-Kolb, M. Kuhlmann, G. Haszprunar, D. Lindberg, A. Koch & J. W. Wägele (2011). The Taxonomist – an endangered Race. A practical Proposal for its Survival. *Frontiers in Zoology*, 8:25.

Die phylogenetische Signifikanz der Antennen und antennalen Sensillen der Grabwespen (Hymenoptera: Apoidea)

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Für das Reproduktionsverhalten (einschließlich Nestbau- und Beutefangverhalten) hat die Antenne aculeater Hymenopteren insbesondere als sensorisches Körperteil eine essentielle Bedeutung: Sie ist mit zahlreichen Sinnesorganen (Sensillen) bedeckt, die als Chemo-, Hygro-, Thermo- und Mechanorezeptoren dienen. Die kutikularen Anteile der Sensillen bilden komplexe Strukturen, auf denen die morphologische Unterscheidung verschiedener Sensillentypen beruht. Obwohl die Anatomie und Morphologie der antennalen Sensillen aculeater Hymenopteren Gegenstand zahlreicher veröffentlichter Studien sind, behandelt die Mehrheit dieser Publikationen jedoch nur eine oder sehr wenige Arten. Das Fehlen einer einheitlichen Klassifikation der antennalen Sensillen erschwert die vergleichende Untersuchung und ihre Homologisierung innerhalb der Aculeata. Auch über die spezifischen Funktionen der verschiedenen Typen ist bisher nur wenig bekannt. Das Vorkommen bestimmter Sensillentypen, ihre spezifische Morphologie, ihre Dichte und ihre Verteilung

sowohl entlang der Antenne als auch auf den einzelnen Flagellomeren variieren zwischen übergeordneten Taxa, interspezifisch und selbst zwischen den Geschlechtern. Damit stellen die antennalen Sensillen (wie auch die Antenne) umfangreiche Merkmalssysteme dar, die potentiell für phylogenetische Analysen von Bedeutung sind. Da die Antenne und ihre Sensillen jedoch in enger Assoziation mit ihren spezifischen biologischen Funktionen evolvierten, können ihre Ausprägungen nicht ausschließlich in einem phylogenetischen Kontext verstanden werden. Wichtigste Ziele des laufenden Projekts sind daher die vergleichende morphologische Untersuchung und Beschreibung der Antennen und antennalen Sensillen der aculeaten Hymenopteren sowie die Untersuchung ihrer phylogenetischen und adaptiven Signifikanz. Der Schwerpunkt der Arbeit liegt dabei auf der mit fast 10.000 beschriebenen Arten größten Gruppe solitärer Wespen, den Grabwespen (*Sphecidae sensu lato*). Innerhalb dieser morphologisch heterogenen Gruppe konnte eine Vielfalt an Reproduktionsstrategien nachgewiesen werden, unter anderem Brutparasitismus und pseudoparasitoide Verhaltensweisen. Da ihnen bei Nestbau und Beutefang die entscheidende Rolle zukommt, konzentriert sich die Studie zunächst auf adulte Weibchen.

New species of Lower Cretaceous Hymenoptera and the early evolution of the order

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The evolutionary history of Hymenoptera, which represents one of the largest species radiations of hexapods, is still poorly understood. The early evolution of hymenopteran taxa is of general biological interest, as it was accompanied by a dramatic change in biology from phyto- and xylophagy (i.e. sawflies and woodwasps) to parasitoidism (Euhymenoptera). This talk briefly outlines the phylogeny of Hymenoptera based on recently published morphological and molecular data sets (Vilhelmsen et al. 2010, Sharkey et al. 2011). The second half of the talk focuses on two recently discovered fossils from the Lower Cretaceous Crato Formation of Brazil, which provide new insights into the past diversity of Hymenoptera (Krogmann & Nel 2012, Krogmann et al. in press). A new fossil sawfly species with bilabellate antennae is placed within Tenthredinoidea and indicates that long distance mate finding behaviour (as exhibited by recent Diprionidae and some Pergidae and Tenthredinidae) was already well established in the Lower Cretaceous. The phylogenetic position of a second fossil, the woodwasp *Cratoenigma articulata* gen. et. sp.n., is discussed on the basis of relevant thoracic, abdominal and wing venation characters. The fossil cannot be placed in any existing superfamily and most likely forms the sister group of the clade Xiphydriidae + Euhymenoptera. This would place it well within Unicalcarida, the clade in which the transition from endophytic to parasitoid lifestyle evolved.

Krogmann L., Engel M.S., Bechly G. & Nel A. (in press): Lower Cretaceous origin of long-distance mate finding behaviour in Hymenoptera (Insecta). *Journal of Systematic Palaeontology*.

Krogmann L. & Nel A. (2012): On the edge of parasitoidism - a new Lower Cretaceous woodwasp forming the putative sister group of Xiphydriidae + Euhymenoptera. *Systematic Entomology* 37: 215-222.

Sharkey M.J., Carpenter J.M., Vilhelmsen L., Heraty J., Liljeblad J., Dowling A.P.G., Schulmeister S., Murray D., Deans A.R., Ronquist F., Krogmann L. & Wheeler W.C. (2012): Phylogenetic relationships among superfamilies of Hymenoptera. *Cladistics* 28: 80-112.

Vilhelmsen L., Mikó I. & Krogmann L. (2010): Beyond the wasp-waist: structural diversity and phylogenetic significance of the mesosoma in apocritan wasps (Insecta: Hymenoptera). *Zoological Journal of the Linnean Society* 159: 22-194.

Insect phylogenomics: results, problems and the impact of matrix composition

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The emergence of recent insect orders can be seen as a prominent example of an "ancient rapid radiation" process, extremely difficult to assess in phylogenetic tree reconstruction, as only few informative molecular and morphological characters are available. Phylogenomic data (EST: "Expressed Sequence Tags") has been used to assess the relationships among insects with a main focus on Polyneoptera (lower Neoptera: roaches, earwigs, grasshoppers etc.) and Paraneoptera (true bugs, lice etc.). As recent EST data sets are generally characterised by a heterogeneous distribution of genes across taxa, we tried to optimise the data matrix composition. Our results suggest a monophyletic origin of Polyneoptera and Eumetabola (Paraneoptera + Holometabola). However, obvious artefacts of tree reconstruction were identified (human louse *Pediculus humanus* assigned to Odonata or Holometabola; mayfly genus *Baetis* nested within Neoptera), which were most likely rooted in a matrix composition bias due to the inclusion of sequence data of entire proteomes. Until entire proteomes will be available for each species in phylogenomic analyses, this potential pitfall should be carefully considered.

Taxonomische Forschung in Deutschland – Aufschwung oder Krise?

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Sterben Taxonomen wirklich aus oder erlebt die Taxonomie mit den neuen Methoden und Publikationsmöglichkeiten eine Blüte? Dieser Frage geht die Studie zur aktuellen Lage der taxonomischen Forschung in Deutschland im Rahmen des Projekts „Netzwerk-Forum zur Biodiversitätsforschung Deutschland“ (www.biodiversity.de) nach, welches von DIVERSITAS initiiert und vom BMBF finanziert wird. Dafür werden die Akteure und Strukturen sowie die Breite des Forschungsfeldes untersucht. Taxonomische Forschung findet zwar überwiegend in naturkundlichen Museen und botanischen Gärten statt, ist aber aufgrund innovativer Forschung durch molekulare Methoden, evolutionsbiologische Fragestellungen und aufgrund der politisch relevanten Ziele zur Erhaltung der Biodiversität in viele Disziplinen eingebunden. Um diesen Trend zur integrativen Taxonomie als Chance zu nutzen, werden verschiedene Maßnahmen, die von der verbesserten Anerkennung in Publikationen bis hin zu einem Tenure-Track für Kuratoren reichen, vorgeschlagen.

Testing monophyly of megadiverse Spilomelinae (Insecta: Lepidoptera: Pyraloidea)

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Spilomelinae represent one quarter of the 16,000 described species of Pyraloidea, making it the most speciose subgroup of the snout moths. Spilomelinae are world wide in distribution with highest diversity in the tropics. They contain many species of economic importance, including invasive pests like the box tree moth *Cydalima perspectalis*. So far, Spilomelinae are exclusively defined by typological means and have repeatedly been claimed to be polyphyletic. A morphology-based cladistic analysis failed to find autapomorphies for the group. As an initial step towards a stable, phylogenetically justified nomenclature, we present first results of our test on the monophyly of Spilomelinae.

Our taxon sampling comprises representatives of most of the 15 genus groups defined by Munroe (1995) (though he did not give a diagnosis for any of these groups) as well as several Pyraustinae taxa. We compiled molecular data of mitochondrial *cox1* gene and nuclear genes *EF1a*, *GAPDH*, *IDH* and analysed them phylogenetically using MrBayes. Our preliminary results indicate a sister-group relationship of Spilomelinae and Pyraustinae. Spilomelinae only form a natural group with the inclusion of Wurthiinae, confirming the results of Mitter *et al.* (in prep.). None of the genus groups but the *Samea* group appear monophyletic. However, several enigmatic taxa (e.g. *Euclasta*) and genus group representatives are still missing from the sampling and may provide further insights, once they are included.

Apart from enhancing the taxon sampling, the next major undertaking is the generation of a morphological data matrix based on anatomical characters of the adults. By this, we intend to get insights into character evolution within Spilomelinae and Pyraustinae, to constitute a phylogenetically well-founded circumscription of Spilomelinae, and to establish the groundwork for the further investigation of its 317 genera.

Vocal learning in parrots and songbirds – synapomorphy or underlying synapomorphy?

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Recent DNA-sequence based studies on the phylogeny of birds found support for a sister-group relationship between parrots (Psittaciformes) and passerines (Passeriformes) (Hackett *et al.* 2008. *Science* 320:1763; Suh *et al.* 2011. *Nature Comm.* 2:443). These findings are the more remarkable, because such a sister-group relationship was never supposed before, and morphological evidence for a parrot-passerine clade is still lacking. It is nevertheless striking that parrots and certain Passeriformes, i.e. the songbirds (Oscines), are capable of vocal learning, a behaviour which is otherwise only known for hummingbirds (Trochilidae) and few mammals (human, cetaceans, and presumably certain bats). In fact, Suh *et al.* (2011) supposed that vocal learning is synapomorphic for parrots and passerines. Available comparative neuroanatomical data indicate, however, that neuroanatomical features related to vocal learning in parrots, songbirds, and hummingbirds are not homologous, but homoiologous. Although the same brain areas underwent neuroanatomical specialisations in

all three lineages, differences in cytochemistry and neuronal pathways suggest convergent evolution of these song systems. Furthermore, vocal learning seems to be part of the stem species pattern of Psittaciformes, but not of that of Passeriformes. Vocal learning actually evolved once in the ancestral lineage of songbirds, but is primarily lacking in the sister group of Oscines, i.e. the Suboscines, and unknown for New Zealand wrens (Acanthisittidae), the sister group of both Oscines and Suboscines. Two species of distantly related Suboscines are supposed to be vocal learners, but again available neuroanatomical data indicate that these birds evolved this behaviour independently. Provided that parrots and passerines are indeed each other closest relatives, vocal learning could only be regarded as an underlying synapomorphy of these taxa.

Very minor model violations can strongly affect the reconstruction success of maximum likelihood based tree reconstruction methods

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Maximum likelihood (ML) and Bayesian tree reconstruction methods rely heavily on a specified model of sequence evolution. It is well known that violations of the model or of other assumptions made by the method can lead to the reconstruction of wrong phylogenetic trees. It is however widely believed that ML based methods are robust to modest violations of the model or its underlying assumptions.

We present a set of very minor model violations, which on some topologies can have a strong effect on the reconstruction success of ML based methods. These model violations have not been analysed in the literature before and unfortunately are difficult to avoid when analysing real data sets with today's reconstruction methods.

Neuroanatomy of onychophorans and tardigrades: Implications for the phylogenetic position of Tardigrada

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Onychophora (velvet worms) and Tardigrada (water bears) are key groups for understanding the evolution of arthropods, but their exact phylogenetic relationship remains unresolved. In particular, the position of tardigrades is discussed controversially since in different studies they are regarded as the sister group of: (1) Onychophora, (2) Arthropoda, (3) Onychophora plus Arthropoda, or (4) Nematoida. Onychophorans and tardigrades share some ancestral features with Cambrian fossils called lobopodians, such as the unjointed limbs and the soft body (missing exoskeleton). Notably, segmentation of the body is less advanced in these animals as compared to arthropods. Hence, analysing the features associated with body segmentation in onychophorans and tardigrades may play an important role for resolving their relationships. In this talk, I present new neuroanatomical data from onychophorans and tardigrades and discuss their implications for the phylogenetic position of Tardigrada.

A Phylogenetic Reassessment of *Limnonectes kuhlii* Tschudi (1838)

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For nearly 200 years, *Limnonectes kuhlii* Tschudi (1838) has been regarded as a single, widely distributed, and relatively common species of Southeast Asian stream frog. Recent phylogenetic analyses have clearly indicated that this “species” represents a remarkably diverse species complex within which individual species that are not each other’s closest relatives exist in syntopy. Moreover, many species in this complex seem to be regionally endemic. These results have provided the impetus to re-evaluate the status of *Limnonectes kuhlii* and the IUCN categorization of “Least Concern”.

Fossilized structural colours in moths from the Eocene of Messel, Germany

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Structural colours are widespread among animals and form the basis of diverse inter- and intra-specific communication strategies. Butterflies and moths (Lepidoptera) exhibit the widest diversity of colour-producing photonic nanostructures. Structural colours are generated by scattering of light by variations in the basic components of the lepidopteran scales, which include longitudinal ridges and transverse crossribs upon a basal lamella that is supported by columnar trabeculae in the scale lumen. The evolution of structural coloration in lepidopterans, however, is poorly understood. First examples of structurally coloured scales in fossil lepidopterans were investigated in fossil moths from the 47-million-year old Grube Messel oil shale. These specimens exhibit bright, non-iridescent metallic hues which are generated by a multilayer reflector comprised of a stack of perforated laminae in the scale lumen. The original colours were altered during fossilisation but are reconstructed based upon preserved ultrastructural detail. Colouration is brightest on the dorsal forewing surfaces, it probably served as a dual-purpose defensive signal, i.e. aposematic during feeding and cryptic at rest. This visual signal was enhanced by reduction of iridescence (change in hue with viewing angle), achieved via two separate optical mechanisms – extensive perforation and concave distortion – of the multilayer reflector. The fossils show that plastic scale developmental processes and the use of complex optical mechanisms for interspecific signalling had evolved in lepidopterans by the mid-Eocene.

McNamara, M.E., Briggs, D.E.G., Orr, P.J., Wedmann, S., Noh, H., Cao, H. (2011). Fossilised biophotonic nanostructures reveal the original colors of 47 million-year-old moths. *PLoS Biology* 9(11): e1001200. doi:10.1371/journal.pbio.1001200.

Argestidae Por, 1986 (Copepoda, Harpacticoida) in the deep sea: systematics and geographical distribution

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Meiofauna-Organismen sind in allen Lebensstadien stark sedimentassoziiert, daher gelten ihre Ausbreitungsmöglichkeiten traditionell als eingeschränkt. Dennoch wurden einzelne Arten verschiedener Meiofauna-Taxa an weit voneinander entfernten Orten gefunden. Dies trifft auch zu für Arten der Copepoda Harpacticoida in Sedimenten aus der Tiefsee, welche nach Nematoda das zweithäufigste Meiofauna-Taxon stellen. Umfangreiche biogeographische Studien (113 beprobte Stationen in verschiedenen Meeresregionen mit insgesamt 717 Einzelproben) basierend auf Arten der Familie Aegistidae Por, 1986, eines der häufigsten Taxa der Harpacticoida in der Tiefsee, lassen auf eine sehr weite, vermutlich sogar weltweite Verbreitung vieler Arten schließen. Dementsprechend scheinen geologische Strukturen die Ausbreitung von Tiefseearten nicht zu verhindern. Dieses Ergebnis ist insofern verblüffend, als dass es der bisherigen Annahme widerspricht, dass z.B. die unterseeischen Gebirgszüge im Südostatlantik zwischen dem Kap-, Angola- und Guineabecken die Verbreitung meiobenthischer Tiefseearten unterbinden.

Meiofaunaproben aus der Tiefsee enthalten zu etwa 95% unbeschriebene Arten. Daher ist die Beschreibung sechs neuer, geographisch weit verbreiteter Arten aus der Tiefsee und die phylogenetische Charakterisierung zweier abundanter Gattungen grundlegend für meine faunistischen und geographischen Analysen anhand von Aegistidae auf Artebene. Umfassende morphologische Studien der Art *Mesocletodes elmari* Menzel, 2011 zeigen eine hohe intraspezifische Variabilität, wie sie bislang nur für wenige Tiefsee-Harpacticoida beschrieben wurde und erlauben darüber hinaus zukünftig die Artbestimmung zusammengehöriger Männchen und Weibchen für die meisten *Mesocletodes* Arten, welche im Gegensatz zu anderen Gattungen der Aegistidae außerordentlich umfangreiche Geschlechtsdimorphismen zeigen. Ferner ist, basierend auf Untersuchungen von Copepodiden derselben Art, die zuverlässige Artbestimmung von Aegistidae ab dem dritten Copepodidstadium möglich. Weil Copepodidstadien bis zu 50% aller Harpacticoida in Tiefseesedimenten stellen, steht dadurch mehr Material aus den verhältnismäßig individuenarmen Tiefseeproben für Studien zur Verfügung. Die Berücksichtigung von Copepodidstadien zusätzlich zu den Adulten erlaubt eine genauere Schätzung über die Verbreitungsgebiete einzelner Arten und die tatsächliche Diversität in einer Region, als es anhand von ausschließlich adulten Aegistidae möglich ist.

Evolution of *Petrocoptis* A. Braun ex Endl. (Sileneae, Caryophyllaceae)

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Morphological and molecular data clearly retrieve the Sileneae (Caryophyllaceae) as a monophyletic group within the carnation family. Nonetheless, several phylogenetic relationships within this tribe still remain unresolved. *Petrocoptis* is a small genus of chasmophytic plants within the Sileneae and endemic to the Iberian Peninsula. Populations are wide spread and fragmented due to their restriction to calcareous rocks. Its taxonomic history, based on morphological and ecological characters, has been very complex, resulting

in treatments of 7 to 11 taxa in 5 to 9 species, according to the respective author. In addition, the group has recently been placed as a subgenus into the large genus *Silene* L.. However, molecular phylogenetic studies consequently place the only sampled species *Petrocoptis pyrenaica* (Bergeret) A. Braun ex Walp (= *Silene pyrenaica* (J. Bergeret) Mayol & Rosselló) as sister-group to core Sileneae genera *Silene*, *Lychnis* L., *Heliosperma* Rchb., *Eudianthe* Rchb., *Agrostemma* L., and *Atocion* Adans..

In this study we sampled 22 specimen of 9 taxa and use sequences of the Internal Spacer Region of the ribosomal DNA, the plastid intron *rps16*, and the *trnH-psbA* spacer region to investigate intra- and intergeneric relationships of the *Petrocoptis* group.

The results consistently support a monophyletic placement of *Petrocoptis* within the Sileneae, which remains constantly separated and distant from the other sampled Sileneae genera. Molecular intrageneric clades refer to geographical patterns, contradicting recent morphological subdivisions. Nonetheless, genetic distances among taxa are very small, showing close relatedness and a probably ongoing radiation.

The first sequenced genome of a twisted-wing parasite (Insecta: Strepsiptera) and its phylogenetic implications

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Twisted-wing parasites are endopterygote insects with a highly derived morphology and life history and whose phylogenetic relationship to other endopterygote insects has proven notoriously difficult to resolve (“The Strepsiptera problem”). We sequenced the genome of a newly discovered twisted-wing parasite from the Tunisian Sahara. The new taxon belongs to the family Mengenillidae, whose species are plesiomorphic in many aspects. The aim of the genome sequencing was (1) to clarify the phylogenetic affinities of this intriguing and enigmatic group of insects, (2) to provide the most detailed description of a newly discovered insect species up to this date that includes both comprehensive morphological and molecular data, and (3) to assess problems associated with sequencing a veritable non-model organism. The genome was sequenced to an estimated $\geq 14\times$ coverage using 454-pyrosequencing technology and the genomic sequences assembled into 100,940 scaffolds and contigs (N50 = 8.7 Kb). The large number of comparatively short scaffolds/contigs is possibly a consequence of the genome’s unusually high AT content (72.9 %). Polymorphism, introduced by pooling specimens collected in the field, may represent another confounding parameter. Using a combination of *ab initio* and evidence-based gene prediction, we annotated ~13,000 genes with high confidence. Roughly 4,500 of these proved to be orthologous or inparalogous among endopterygote and paraneopteran insects. After removing ambiguously aligned sites, the compiled dataset of orthologous and inparalogous genes consisted of 1.8 million codon sites. To minimize a confounding impact of inhomogeneous nucleotide or amino acid frequencies among sequences in the phylogenetic analysis, we analyzed RY-recoded second codon positions only. Maximum likelihood

estimates overwhelmingly suggest a close phylogenetic relationship of twisted-wing parasites and beetles. Hadamard conjugation indicates no plausible conflict in the phylogenetic signal. We are currently analyzing genomic meta-characters, such gene order and the position of introns within genes, to obtain additional, independent phylogenetic estimates.

Is there a phylogenetic separation of marine and freshwater choanoflagellates?

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Choanoflagellates are supposed to be a sister group to metazoans. Nevertheless not even the phylogeny within this group is well resolved except for the loricated acanthoecids. We examined the rDNA of several freshwater and marine choanoflagellate species regarding the hypothesis whether there is a phylogenetic separation between the two habitats or not. In addition we present for the first time data on one of the earliest described choanoflagellates, *Codosiga botrytis* and its unexpected phylogenetic position.

New pH-sensitive fluorescent dye Ageladine A proves incorporated nematocysts in *Aeolidiella stephanieae* (Opisthobranchia, Nudibranchia) to mature by acidification

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Sequestration of cnidocysts from their prey with subsequent use in defence is known from few metazoan phyla. Especially members of the taxon Aeolidioidea (Nudibranchia, Gastropoda) are well known for this. One of the still unanswered questions is why nematocysts do not explode while feeding on the cnidarian, and why these same unexploded cnidocysts can be transported along the digestive tract into the specialized morphological structures, the cnidosacs, to finally be armed for putative defence against predators.

The most plausible explanation for this phenomenon would be to have a certain amount of immature and therefore non-functional nematocysts in the food. A recent study of Berking & Herrmann (2005) on cnidarians suggests the nematocysts to mature by acidification/enrichment of protons in the nematocyst's capsule. After this hypothesis only immature nematocysts are transported into the cnidosac and then have to be made functional by accumulation of protons. In this study we present a new fluorescence staining method to test the hypothesis of Berking & Herrmann (2005) and detect changes in the pH values of kleptocnides, interpreted as changes in maturation stages. Ageladine A is a new fluorescent dye which turned out to be the first marker to stain the nematocysts' capsule properly dependent on its pH value. With this marker we could show that kleptocnides indeed change their pH value after incorporation into the aeolidioidean cnidosac.

Berking, S., Herrmann, K., 2005. Formation and discharge of nematocysts is controlled by a proton gradient across the cyst membrane. *Helgoländer Marine Research* 60, 180-188.

3 D muscle structure and the evolution of remarkable planktonic Gastrotricha (Family Dasydytidae)

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The musculature of two species of the freshwater family Dasydytidae *Dasydytes* (*Dasydytes*) *goniathrix* and *Haltidytes crassus* was studied using phalloidin staining, confocal microscopy and computer aided 3D reconstruction. The species of this family show conspicuous adaptations to a semi planktonic lifestyle, which is quite uncommon among the usually bottom-dwelling gastrotrichs. Similar to other dasydytid species, *D. (D.) goniathrix* and *H. crassus* have paired groups of movable spines with an associated system of somatic oblique and segmented lateral muscles that bring about spine action.

Data of these and further species were collected in a species-character matrix for the use of phylogenetic inference. A parsimony analysis of dasydytid species supports a split into *Anacanthoderma* and Dasydytidae *sensu stricto*. There is further evidence for a clade including *Dasydytes*, *Setopus* and *Ornamentula*. Different evolutionary transformations within Dasydytidae are much likely related to changes in the functioning of musculature and motile spines. An active antagonistic abduction of spines induced by oblique and adduction by segmented lateral muscles was hypothesized in two former studied species. This is contrasted by the alternative hypothesis of active abduction and passive adduction due to relaxation of muscles in *D. (D.) goniathrix* and *H. crassus*.

The muscle-spine-system as such evolved at the latest within the stem lineage of Dasydytidae *s. str.* It represents for sure a prerequisite for a successful development of new ecological niches for freshwater gastrotrichs. This has obviously stimulated an impressive radiation of these micrometazoans in the tropical region.

Joining forces to unravel the evolution of insects – an introduction to the 1KITE project

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1KITE (1K Insect Transcriptome Evolution) is an international initiative started in 2011 that aims to study the transcriptomes of 1,000 insect species encompassing all recognized insect orders (www.1kite.org). The expected sequence data will allow inferring for the first time a robust phylogenetic backbone tree of insects, one of the most species-rich groups of metazoan organisms.

Scientists involved include not only experts in molecular biology, but also experts in insect morphology, taxonomy, paleontology, embryology, bioinformatics, and scientific computing. Overall, scientists from eight nations (Australia, Austria, China, Germany, Japan, Mexico, New Zealand, and the US) are collaborating in 1KITE. From Germany are involved: the University of Bonn, the Zoologisches Forschungsmuseum Alexander Koenig, Bonn, the University of Jena, the University of Hamburg, the Staatliches Museum für Naturkunde Stuttgart, and the Heidelberger Institut für Theoretische Studien (HITS). All transcriptome sequence data will be collected by the Beijing Genomics Institute (BGI), Shenzhen, China.

Preliminary analyses of the already available sequences show that the obtained data are of yet unparalleled size and quality. We aim to generate a 1,000-gene data set with virtually no missing data. 1KITE is divided into several subprojects, each of which focusing on specific phylogenetic groups. There are subprojects on, for example, apterygote hexapods, Odonata,

Polyneoptera, Hymenoptera, Trichoptera, and Antliophora. Additionally, 1KITE includes the development of new software for data quality assessment, phylogenetic reconstruction, and molecular dating that will allow for advanced and accelerated analyses of such large amounts of sequence data.

Sequencing will be completed by the end of 2012. The results are expected to have an extraordinary and long-standing high impact on entomological and phylogenetic research.

Launching the German Barcode of Life Project, GBOL

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The GBOL (German Barcode of Life) project is a large-scale DNA barcoding campaign designed to capture the biodiversity of Germany. GBOL has been granted a funding of approximately 5 million Euros by the German Federal Ministry of Education and Research (BMBF) for an initial period of 3 years. Launching the GBOL project is a step towards collecting, processing, data sharing and deposition of samples in conventional and molecular collections in order to facilitate the compilation of an open, validated DNA barcode database for German eukaryotic species.

GBOL is a national consortium of natural history museums and other research institutions which will provide their professional taxonomic expertise and existing infrastructure (e.g. dry and wet collections, frozen tissue and DNA collections, databases, and laboratories) to perform the German biodiversity inventory.

Involved institutions:

ZFMK, Zoologisches Forschungsmuseum Alexander Koenig, Bonn (project speaker, zoology coordinator),

ZSM, Zoologische Staatssammlung München (zoology coordinator),

SMNS and SMNK, Staatliches Museum für Naturkunde Stuttgart and Karlsruhe,

SMNG, Senckenberg Museum für Naturkunde Görlitz (soil organisms coordinator),

BGBM, Botanischer Garten und Botanisches Museum, Berlin,

Universität Bonn, Nees-Institut (botany coordinator),

Senckenberg am Meer, Wilhelmshaven,

and cooperation partners at several German universities.

High throughput image registration with open source software

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The registration of images in virtual image stacks is a very crucial and time consuming step when generating 3D reconstructions from histological or electron microscopical serial sections. Recent research by an open community of biologists working on 3D reconstruction have lead to new robust algorithms for image registration that often outperform commercial products in this field. On the other hand, most algorithms or software packages are of restricted usability only, because they rely on special kinds of image data. Thus, most commercial and open source programs fail to handle large image stacks with gigabytes of data or image stacks with color channels. Additionally, intrinsic problems in microscopical data sets can prohibit computer aided registration completely in some cases. To circumvent

these problems it is crucial to explicitly know the disadvantages and benefits of the available software packages and to use the right package for each task. In order to do registrations of huge colored and grayscale image stacks I developed a pipeline that uses the freely available IMOD software package from the Boulder Laboratory for 3D Electron Microscopy of Cells. A graphical user interface allows for fast automated registration with little manual intervention. The registration of an image stack with more than 30 gigabytes of rgb-colored data usually takes about one to two hours of work and can be performed on cheap computer hardware.

Some thoughts about DNA barcoding

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In spite of the fact that DNA barcoding is still criticised, feared and/or simply not understood, DNA barcoding has become an established and quite efficient method to understand and assess biodiversity during the last few years. All around the world numerous projects have been started to compile reference libraries from specimens of various taxa whose identity is already firmly established. However, in the case of animals, the use of a mitochondrial gene fragment for valid species identification is not without problems: limitations of the COI barcoding approach can arise from its single-locus identification system, the effect of introgression events, incomplete lineage sorting, numts, heteroplasmy, recent speciation events and maternal inheritance of intracellular endosymbionts. Nevertheless, the effectiveness of DNA barcoding for the identification of animal species has been proven in a high number of publications/presentations, analysing both vertebrate and invertebrate taxa, and new insights into ecology and species biology have already emerged from various pioneering DNA barcode studies. In this context, results of various case studies, including both terrestrial and marine taxa, will be presented and discussed.

International Biodiversity Projects and Natural History Museums: current state and perspectives

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The 21st century started with an impressive number of international biodiversity initiatives, such as the International Year of Biodiversity (2010) and the recently launched United Nations Decade on Biodiversity (<http://www.cbd.int/2011-2020/>). Most nations are now members of the Convention on Biological Diversity and expressed a strong commitment for safeguarding Earth's biodiversity through their National Biodiversity Action Plans and work programs supporting taxonomy, such as the Global Taxonomy Initiative. Internet projects such as the Global Biodiversity Information Facility (www.gbif.org) provide unprecedented opportunities for taxonomists and Natural History Museums to make their efforts visible

through the federation of separate museum databases: users can search for species, visualise localities on a map and recall pictures of museum specimens made available by “Virtual Museums”. However, availability of multimedia data is still limited, particularly for type specimens. Taking European museums as an example, I demonstrate the potential of successful virtual museum projects and analyse priorities and needs for further digitisation, which is a pre-requisite for repatriation of biodiversity data from tropical countries. Improved access to collections is also among the main tasks of the recently established CETAF secretariat in Brussels (Consortium of European Taxonomic Facilities - <http://www.cetaf.org/>). This new institution will function as a European voice for taxonomy and systematics, and hopefully helps to sustain orphaned EU activities from former projects supporting taxonomy, such as the European Distributed Institute of Taxonomy (www.e-taxonomy.eu).

Invertebrate Diversity Made Easy? Rapid biodiversity assessment through DNA barcoding

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Documenting and describing the diversity of invertebrates are very challenging tasks for biologists. Invertebrates are generally small, cryptic, with complex life-cycles and biology. Species, whose identification is generally reserved to a few (if any) specialists, number in the millions, of which only a small portion – possibly as little as 20% – has been formally described so far. DNA barcoding is a species identification tool based on the use of a short and standardized species-diagnostic genetic marker. As a technically fast and high-throughput method, it was proposed as a promising way for assessing species diversity at a pace unequalled by classical taxonomy.

Using examples from studies in different taxa and at a scale ranging from local to global, I will present how DNA barcodes can quickly and effectively produce basic diversity metrics for biodiversity assessments in invertebrates. Pitfalls, limitations and difficulties will be discussed, highlighting the importance of reference libraries and the seemingly subtle though important distinction between DNA barcoding and molecular taxonomy. From a specific example in Amazonian Lepidoptera, I will also present the potential of Next Generation Sequencing techniques which enable the sequencing of environmental samples for biodiversity assessment.

Finally, I will briefly discuss some of most exciting perspectives resulting from the empirical, rapid and massive accumulation of DNA barcode data in invertebrates.

Versteckte Signale – Genitalmorphologie und Verbreitung als systematische Merkmale bei Weberknechten (Arachnida: Opiliones)

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Innerhalb der weltweit verbreiteten Spinnentiergruppe der Weberknechte (Arachnida: Opiliones) etablierte sich relativ spät eine moderne Systematik basierend auf den Strukturen der männlichen Genitalmorphologie. Molekulargenetische Methoden ermöglichen erst in diesem Jahrtausend eine alternative Prüfung dieser Theorien, integrierten jedoch

morphologische Merkmale nicht immer konsequent oder beurteilten ihre phylogenetische Aussagekraft innerhalb einzelner Gruppen sehr unterschiedlich.

Eine erneute Betrachtung zeichnet die männliche Genitalmorphologie als eines der Schlüsselmerkmale innerhalb der Weberknechte aus. Sie ermöglicht die sichere Abgrenzung höherer Taxa und der meisten Arten. Phylogenetische Signale liefern hierbei in hierarchischer Reihenfolge die Grundorganisation der Penes mit verschiedenen Muskeln oder Hydraulik, prinzipielle Strukturmerkmale die eine Funktionsänderung während der Paarung vermuten lassen bis hin zu artspezifischen Unterschieden. Besonders in Gruppen mit geringem morphologischem Freiheitsgrad stößt diese genitalmorphologisch basierte Systematik jedoch an ihre Grenzen. Para- und polyphyletische Gruppen scheinen vor allem innerhalb der langbeinigen Sclerosomatiden die Regel. Das Zusammenspiel relativ primitiver Grund-Organisation der Genitalien mit anscheinend komplexen aber möglicherweise Art- und Individuen-spezifische Strukturen verhindert in dieser und in verwandten Gruppen eine verlässliche genitalmorphologische Einteilung. Erste molekulargenetische Untersuchungen zeigen dass die geographische Verbreitung ein deutlich besseres Merkmal für Monophyla innerhalb dieser Gruppen liefert als die offenbar konvergente Morphologie. Monophyletische, geographische Gruppen lassen sich auch in Taxa mit klarer genitalmorphologischer Abgrenzung nachvollziehen und zeigen in Gruppen mit disjunkter Verbreitung historische Biogeographische Verbindungen auf.

Der Vortrag zieht eine vorläufige Bilanz aktueller molekulargenetischer Studien und unterstreicht den bleibenden Wert der genitalmorphologisch begründeten Systematik innerhalb der Weberknechte. Zusätzlich wird die Biogeographie als Merkmalskomplex hervorgehoben und bestätigt Weberknechte als Modelorganismen für Biogeographische Studien.

Biodiversity Heritage Library for Europe: Rapid assessment of legacy taxonomic literature

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Large and well-curated natural history libraries are a very important pre-requisite for biodiversity-related research. The library work, however, has several serious limitations that slow down the work significantly. The natural history library corpus is highly fragmented and scattered. In particular much of the early published literature is rare or is only available in a very few libraries. A lot of time and effort is involved to collect all scientific works that are necessary for a specific project. Digital libraries facilitate the search and retrieval of publications online and thus improves the efficiency of research.

Since 2009, the *eContentplus* project Biodiversity Heritage Library for Europe (BHL-Europe) is developing several access routes to the biodiversity literature digitised by many European and global partners over the last years. With the Global References Index to Biodiversity (GRIB, <http://grib.gbv.de/>), BHL-Europe provides in collaboration with the EDIT project a union catalogue of library holdings of libraries. This will facilitate the search for literature and facilitate the management of digitisation projects. For an effective access to already digitised literature, BHL-Europe is building a multilingual portal. This portal will also have functionalities to search for taxonomic names, for example. The backbone of this portal is a preservation and archive system built on a customised storage infrastructure housed by the Natural History Museum in London. We are currently collecting digitised literature from 28 different content providers including the GfBS (ODE) on our servers, and collect all the content that is currently available under <http://www.biodiversitylibrary.org>. In addition, we are

working on solutions to mirror the European content to the partners of the growing network of a Global BHL. In order to serve a broader audience, the digitised literature available by BHL-Europe is also accessible by Europeana, Europe's digital library, archive and museum (<http://www.europeana.eu/>) and the Biodiversity Library Exhibition.

Phylogenetic analysis of the community structure of southern African termites

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Studying community assembly and structure of species allows insights into the fundamental mechanisms that dictate how species assemble and why communities are structured the way they are. In recent years there have been several improvements in this field, especially because phylogenetic data has been included into the analysis of community ecology and diversity, which has made it possible to explore theories about the influence of historical and ecological factors in structuring communities.

There are two theories of coexistence that can apply to community structure. The niche theory, which states that species have to differ in their niches to coexist, and the neutral theory, which says that species are demographically equivalent and niche differences are not essential for coexistence. Here species distribution is due to random chance. We tested whether southern African termite communities are niche-assembled or if they are assembled randomly and which processes and traits are responsible for structuring communities (habitat filtering or competition). Because there are many cryptic termite species, barcoding was used for species identification.

We could show that there is a regional species pool of 11 species in semiarid to arid regions of Namibia. No phylogenetic overdispersion or clustering could be identified, implying random assemblage of species. The analysis of 'spatial phylogenetic structure' showed that co-occurring species are distantly related to each other.

This seemingly contradictory pattern can be explained by opposing ecological forces. Phylogenetic overdispersion generated by interspecific competition cancels out phylogenetic clustering generated by habitat filtering. This suggests that niches play an important role in termite community assembly in Namibia.

DNA barcodes and tree-based species delineation – how informative should DNA taxonomy marker be?

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DNA barcodes are widely used for species identification, integrative taxonomy and rapid biodiversity assessments. However, most approaches for species estimates from DNA sequences rely on another piece of evidence (e.g. morphospecies delineations) to calibrate match of specimens or cut-off thresholds for the species delineations. The only method free of such assumptions is so far the General Mixed Yule Coalescence (GMYC) modeling that infers species limits directly from a phylogenetic tree with multiple specimen sampling, i.e. the transition from speciation to coalescence. Since the tree structure and in particular the distribution of nodes are highly determinant for the significance of species estimate of the GMYC model, we performed an empirical case study on how informative (or long) a barcode

fragment has to be to allow one to infer sufficiently good trees that permit a reliable species delineation based on a given sampling. Based on various datasets of mtDNA data with morphospecies assignments, we found that the performance of GMYC modeling rapidly deteriorates with a shortening of the fragment. The deterioration of performance of GMYC modeling, however, seems not to be correlated with the length of the marker.

Our findings should be of a great importance not only for the barcoding community but also for future developments in rapid biodiversity assessment research, since we yield exclusively short DNA fragments in next generation sequencing (i.e. environmental sequencing).

The importance of appropriate outgroup taxon sampling in phylogenomic studies

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Phylogenomic data in the form of EST databases or nuclear genomes and the wealth of information they provide has been successfully used to address the relationships of and within metazoan taxa. Nonetheless, compositional biases, missing data and artifacts such as long-branch attraction can also affect studies based on these data. Another aspect, which may mislead traditional phylogenetic studies, are inappropriate representations of outgroup taxa. While the influence of outgroup taxa on phylogenomic reconstructions has been shown for small datasets with respect to the number of taxa, for large-scale analyses as are more common nowadays this has yet to be thoroughly investigated. Herein, we show an empirical example of annelid relationships, which is affected by outgroup representation. Analyses based on only a small number of outgroup taxa strongly placed both Oweniidae and Myzostomida outside Annelida. In case of Myzostomida this misplacement can be attributed to increased substitution rates and, hence, long-branch attraction. We will also explore and discuss the potential factors influencing the placement of Oweniidae. Substantially, increasing the representatives of outgroup taxa alleviated these problems and both Oweniidae and Myzostomida were resolved as part of the annelid radiation. Interestingly, increasing the amount of available data for Oweniidae did not overcome the misplacement given a small number of outgroup taxa. Therefore, even in large-scale phylogenomic studies outgroup representation is crucial.

Evolutionary history of swifts (Aves: *Apus*, *Tachymarptis*)

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We provide a molecular phylogeny for Old World swifts of genera *Apus* and *Tachymarptis* (tribe Apodini) with a complete taxon sampling at the species level. Phylogenetic reconstructions were based on two mitochondrial and three nuclear markers while another nuclear standard marker did not show any intergeneric variation or phylogenetic signal among the target taxa at all. In contrast to previous hypotheses, the two genera *Apus* and *Tachymarptis* turned out to be reciprocally monophyletic in all reconstructions, however with

no support from nuclear markers alone. *Apus* was consistently divided into three major clades: 1) East Asian clade (two species), 2) African-Asian clade (five species), 3) African-Palearctic crown clade (eight species including European *A. apus* and *A. pallidus*). Swifts spend almost their entire life in the air. These birds are well adapted to that lifestyle in physiological and morphological respect (e.g. long pointed wings). Therefore morphological differentiation among species is much less pronounced. Based on the dated phylogeny for our focus clade, we reconstruct ancestral distributional areas and discuss morphological adaptations and emergence of long-distance migration accompanying dispersal and vicariance events. 13 species occur in tropical Africa or on islands off the African coast, making the Afrotropic the most likely area of the most recent common ancestor. Only nine species can be found outside this ecozone, but none outside the Old World. Furthermore, only four of these nine species are the only long-distance migrants in the study group. In general the investigated species show rather dull coloration. 14 species have at least a white chin and five of these furthermore a white rump. We will consider such traits in spatial and temporal respect. The study was substantially funded by Sächsisches Staatsministerium für Wissenschaft und Kunst, AZ4-7531.50-02-621-08/1.

Systematics of nightjars (Aves: Caprimulgidae) and the evolution of crypsis

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Nightjars are a distinctive group of crepuscular or nocturnal birds with particular secretive habits. Being mainly ground-breeders, they rely heavily on visual crypsis, maintained by various shape-blurring plumage patterns. Thus different nightjar species may strikingly resemble each other without being related very closely. Owing to their relatively uniform appearance and a similar lifestyle, the systematics of nightjars has long been misconceived and was influenced by misinterpretations of intergeneric convergence. Consequently, recent molecular studies challenge traditional taxonomic arrangements.

Whereas crypsis is discussed mainly in ecological respect, considering cost-benefit argumentations, the phylogenetic background of the phenomenon remains often neglected. In particular, meaningful examples from vertebrates are still lacking. Because crypsis is a strong response to predator pressure, it also reflects the connection between evolutionary diversification and adaptative constraints within lineages.

Thus, I hypothesise that the development of cryptic protective plumages in nightjars is strongly correlated with the evolutionary history of every lineage. Although far from being complete, molecular data indicate the need for substantial alterations, particularly at the genus level (traditionally 89 species in 15 genera). In order to enable a comprehensive re-assessment of nightjar systematics, it is aimed to complete the molecular tree of nightjars (incl. sample processing from preserved specimens) and to discuss conclusions on the evolutionary development of crypsis in this bird family. Since much of this study depends on museum specimens, it also emphasises the importance of museum collections for up-to-date biosystematic research.

Barcoding sponges: an overview based on comprehensive sampling

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Phylum Porifera includes ~8,300 valid species distributed world-wide in aquatic ecosystems ranging from fresh-water bodies to coastal environments and deep-sea. The taxonomy and systematics of sponges is complicated, and morphological identification can be time consuming. DNA barcoding can provide sponge biologists with a simple and rapid method for the identification of samples of unknown taxonomic membership. The Sponge Barcoding Project (www.spongebarcoding.org), the first initiative to barcode a non-bilaterian metazoan phylum, aims to provide a comprehensive DNA barcode database for the Phylum Porifera. ~7,500 sponge specimens have been extracted, and amplification of the standard COI barcoding fragment has been attempted for approximately 3,300 museum samples with ~25% mean amplification success. Based on this comprehensive sampling, we present the first report on the workflow and progress of the sponge barcoding project, and discuss some common pitfalls inherent to the barcoding of sponges. A DNA-barcoding workflow capable of processing potentially large sponge collections has been developed and is routinely used for the Sponge Barcoding Project with success. Sponge specific problems such as the frequent co-amplification of non-target organisms have been detected and potential solutions are currently under development.

Why DNA barcoding complements microgastropod taxonomy

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Terrestrial microgastropods of the taxon Carychiidae inhabit zones of permanent humidity of aphotic epigeal (*Carychium* spp.) or subterranean habitats (*Zospeum* spp.). Members of both taxa demonstrate a Holarctic distribution and possess a general shell of two millimeters in height. They are consistently described by conchology alone, with characters such as shell length, shell width, ratios of shell dimensions, number of whorls, striation and form and position of the folds comprising the columellar apparatus frequently investigated. Several of the historic taxonomic first descriptions backdate more than 120 years and are far away of being accurate for modern taxonomy. Finally, within the taxon of the Carychiidae, we are faced with the evolutionary mechanisms of phenotypic plasticity (i.e. environment-dependent shell variability for *Carychium* spp.) and morphological stasis (for *Zospeum* spp.) further hampering taxonomic classifications.

We integrated DNA barcodes, 650 bp fragments of the Cytochrome C Oxidase Subunit I (COI), to identify and delineate carychiid microgastropods. DNA barcodes for members of the Carychiidae are highly informative and separate most (>90%) of the taxa. The remaining cases are likely results of cryptic and incipient speciation. The origin of genetic diversity underlying DNA barcodes will be discussed. In a retrospective morphometric approach, we analyzed historically established conchological characters of DNA barcoded individuals of

two *Carychium* species thereby revealing a continuum of intraspecific conchological variability and broad zones of overlap between taxa. Conclusively, we propose the revision of historic taxonomic descriptions by the complementary application of discrete (genetic) data and plea for an integrative taxonomic approach – not only for microgastropods.

Andean lineages as descendents of the “Old South” - fossil Ledocarpaceae from Patagonia and the historical biogeography of Geraniales

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Geraniales comprise ca. 900 species in 13 genera, mostly distributed in South Africa and South America. The evolutionary history of Geraniales, especially its smaller genera, is incompletely known because of a limited fossil record and incomplete phylogenies. Here, we present the discovery of five new fossil pollen types from the Miocene of Patagonia (southern South America) that can be confidently assigned to Ledocarpaceae. The fossils show that the crown nodes of *Balbisia* and *Viviania* have to be placed at, or before 10 Ma. We also provide a molecular phylogeny including all extant groups in Geraniales. Our results support the hypothesis that Geraniales include four well-supported lineages: [Hypseocharitaceae (monogeneric), Geraniaceae (*Erodium*, *Geranium*, *Monsonia*, *Pelargonium*)], Melianthaceae (*Bersama*, *Melianthus*), Greyiaceae (*Francoa*, *Greyia*, *Tetilla*), and Ledocarpaceae (*Balbisia*, *Rhynchotheca*, *Viviania*). We estimate the earliest and most significant divergences to have occurred during the late Eocene [37 to 35 million years ago (Ma)] following a significant global cooling event and increased seasonality. Diversifications in *Melianthus* and *Greyia* closely correspond to paleoclimatic changes and are much more recent than previously assumed. However, divergence of the Andean *Hypseocharis*-lineage much predates main Andean uplift: current distributions evidently go back to northward migrations and subsequent extinctions in the South. Similarly, *Rhynchotheca*, *Balbisia* and *Viviania* have their current southern distribution limit >10° N of the fossil finds, indicating a massive northward displacement. Fossil data and phylogenetic data thus confirm a considerably warmer and more humid climate of the Patagonian late Miocene and indicate that warm-temperate Miocene Patagonia may have been an important source area for the current flora of the Andes.

Origins of the Giant Millipedes – Microendemism and Multiple Speciation Processes on Madagascar (Diplopoda, Sphaerotheriida, Spirobolida)

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The millipede fauna of Madagascar is unique, enigmatic and colourful. Its origins are still unclear, evidence for both dispersal from Africa and Gondwanan vicariance exists. More than 14 new genera and 90 species of millipedes were discovered and described in the last five years alone, 36 of them giant pill-millipedes. Several species of giant pill-millipedes show gigantism and striking colour patterns only on Madagascar. In a recent study focusing on the taxonomy and biogeography of the millipede fauna of the island, an unusual distribution pattern in numerous millipede species was detected, indicating the occurrence of microendemism. 10–50% of the species were only found in areas smaller than 10x10 kilometres. Microendemism may be attributed to the limited dispersal abilities of millipedes and their adaptation to life in cryptic habitats. My research focuses, in addition taxonomic revisions and inventories, on the phylogeny of giant pill-millipedes. My current work addresses whether the ancestors of the enigmatic Malagasy genera drifted from Africa to the island or are of vicariant origin, as well as larger evolutionary questions, like the origins of Island gigantism in invertebrates, and why species only occur in such restricted areas.

Molecular phylogeny of non-endopterygote Hexapoda

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The higher phylogeny of Hexapoda has been a topic of intense debate for decades, in particular the interordinal relationships. Despite great advances with morphological and molecular data, many relationships essentially remain unresolved, typically due to lack of strongly supported hypotheses, conflict between competing weaker hypotheses, and/or limitations of taxon sampling.

Here we present new data from up to 27 nuclear, protein-coding genes (23kbp) for 58 taxa, representing most orders of non-endopterygote Hexapoda and expanding a published arthropod data set to a total of up to 64 genes (42kbp) for 77 hexapods and 61 outgroup taxa. Maximum likelihood and Bayesian analyses of non-synonymous nucleotide substitutions robustly resolve most interordinal relationships. The resulting topology is congruent with those higher taxa that were well supported in previous studies, but provides additionally supported hypotheses for previously unresolved groupings. Particular attention is paid to the placement of Odonata and Ephemeroptera relative to Neoptera, of the "living fossil" *Tricholepidion gertschi* to other Zygentoma, and to the phylogeny of Polyneoptera.

2. Poster:

Floral rewards and pollinator guilds in Nasturtiums (*Tropaeolum*, Tropaeolaceae)

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The genus *Tropaeolum* (Tropaeolaceae) is a neotropical genus of herbaceous plants with complex, brightly coloured, spurred, zygomorphic flowers. Most of the ca. 100 species are growing in and along the Andes. Nectar is secreted into the spur, and flower colour and – size, and spur size and shape vary dramatically between species. Surprisingly, little is known about floral function and pollination in these intriguing plants, but literature data and own observations indicate that taxa are mainly visited by bees and hummingbirds, while butterflies and beetles have also been observed. To test a possible correlation between nectar production and observed pollinators, nectar amounts and concentrations in ten species were measured and the nectar sugar amount/flower calculated. Spur length was measured as a proxy for nectar accessibility. Pollen of some species was counted and P/O-ratio calculated. Three major groups can be distinguished based on nectar characters. I, low nectar production (0.3-3.3 µl nectar/flower resp. 0.2-2.0 mg sugar/flower) with highly concentrated nectar (53-64 %), II, similar amounts of nectar and sugar (2.7-4.9 µl nectar/flower resp. 1.0-2.0 mg sugar/flower) but lower concentration (37-40 %), III, copious amounts of nectar and sugar (13.2-15.3 µl nectar/flower resp. 3.8-6.3 mg sugar/flower) and nectar concentrations similar to group II (29-40 %). Nectar groups largely coincide with differences in spur length [I: 2-12(-19) mm, II: 24-32 mm, III: 14-19 mm]. P/O-ratios range from 3,348 to 111,855 and thus indicate obligate xenogamy compared to Crudens' classification (1977) of breeding systems. Observations in cultivated plants confirm that without pollination no fruits develop, but geitonogamous selfing is possible. Pollinator observations indicate that the three "nectar groups" correlate to visitor guilds: small flowers with a short spur are visited by beetles, bees and butterflies (I), larger flowers with small amounts of nectar by bees, but also by some hummingbirds (II) and those with large amounts of nectar only by hummingbirds.

Torrent Frogs and Slippery Frogs in West Africa – living close but being different

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As part of larger phylogenetic analyses of the African genera *Petropedetes* Reichenow, 1874 and *Conraua* Nieden, 1908, a focus has been laid on their western most representatives: *Petropedetes natator* Boulenger, 1905 and *Conraua alleni* (Barbour & Loveridge, 1927) are two species of conservation concern hence, a better knowledge on their status is necessary as presence of unrecognized taxa have been assumed. The two species inhabit lotic habitats in forested areas from Sierra Leone to Ivory Coast, West Africa, and often even co-occur sympatrically. However, they differ in their biology, especially tadpole biology (rapids vs. stagnant water), as well as shifted altitudinal preferences.

Samples extending the currently known distribution range have been analyzed, resulting in recognition of distinct evolutionary lineages within the two taxa. While recognized lineages in the genus *Petropedetes* indicate presence of hitherto unrecognized species, the situation is more ambiguous in *Conraua*. We herein provide the current stage of this project.

Nemertean nervous system: A phylogeny based on the morphological elements of the nervous system

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Nemerteans are a taxon of spiralian of which most described species are marine benthic hunters. The majority of the animals are nocturnal predators which are able to follow actively their prey and catch it with a unique structure the eversible proboscis. Superficially seen, nemertean nervous system appears quite uniform in being composed of a four lobed brain and two lateral medullary cords which originate in the ventral lobes of the brain and extend the whole length of the animal. The two dorsal and ventral lobes of the brain are interconnected by commissural tracts above or below the rhynchocoel, respectively. But the fine structure of the nervous system differs considerably among higher taxa and sometimes closely related species.

In the classical view nemerteans fell into three higher taxa: Palaeo-, hetero- and hoplonemertea. This classification is among other things, based on the anatomy of the nervous system. In this study I describe the structure of the nervous system of members of different nemertean taxa order to create a data matrix based on the morphological elements present in nemertean nervous system. Classical Azan staining was chosen to get an entire view of the elements present in the nervous system and to be able to infer the position of the central nervous system in relation to the body wall layers. Immunocytochemistry was chosen to reveal the fine structure of the elements of the nervous system. A number of 61 characters concerning the morphological elements of the nervous system arose of this investigation. The analysis resulted in 1 most parsimonious tree. Hoplonemerteans and heteronemerteans are monophyletic with good support and together form a monophyletic taxon called neonemertea. Palaeonemerteans are paraphyletic. Compared to other recently published results the nervous system, although being just one organ system turned out to be a reliable morphological system to infer nemertean phylogeny.

Distribution patterns and distribution modeling in the South African chafer genus *Pleophylla* (Coleoptera: Scarabaeidae)

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The species of the beetle genus *Pleophylla* (Scarabaeidae) are as far as known restricted to the eastern escarpment of South Africa, and in particular its forest relicts. The genus includes a variety of species of which only a small part (8) have been described and nothing is known about their distributions. A first molecular phylogeny of the species *Pleophylla* indicates a recent species radiation of an old lineage with lack of monophyly for a number of morphologically well-defined species probably due to incomplete lineage sorting and/or hybridisation. Although there is little information on the biology of *Pleophylla* species, we investigate the hypothesis whether habitat fragmentation, such as native forests of the South

African highlands, might be one of the causes of the recent diversification in this group of beetles. In course of this project we gain a detailed overview on the distribution of the *Pleophylla* species based on collection specimens of various Natural History Museums, to reconstruct their distribution, biogeography and infer niche divergences between the putative species.

So far, for around 700 male specimens classified to 18 morphospecies species genitalia were dissected and analysed. Their distribution was analysed and visualized in maps, and based on the geo-referenced records the distribution of the species is modeled. Differences in the ecological 'niches' are inferred between the different morphospecies using multidimensional analysis of climatic parameters of record sites.

Systematic and evolutionary implications of monitor lizards' (Varanidae) scale structure using scanning electron microscopy (SEM)

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Monitor lizards (Varanidae: *Varanus* spp.) are a relatively small group of squamate reptiles, which comprise the largest living lizards of the world. Being mainly carnivorous, monitor lizards are the top predators in most environments they inhabit. In Africa, Asia and Australia, monitor lizards inhabit a variety of different ecosystems from deserts to rainforests. They show specific ecological and morphological adaptations and can be strictly terrestrial, semi-aquatic or arboreal.

Across all nine recognized subgenera of the genus *Varanus* including 37 different species, scale shape and structure were analyzed using scanning electron microscopy (SEM). Results show that a microornamentation (ultradermatoglyphics) as seen in various squamate groups is also partly present in monitor lizards. However, only in few, albeit unrelated, monitor species examined the dorsal scales exhibit a specific honeycombed microstructure. The ecological meaning of this microstructure remains unknown. Nevertheless, scale shape as well as extent and size of granula rows around the main scales allow differentiation between single species, even among closely-related monitor lizard species such as the members of the *Varanus indicus* species group.

In addition, the systematic affiliation of *V. spinulosus*, a rare monitor species from the Solomon Islands with a unique scale structure, is discussed in the light of current hypotheses about its phylogenetic position within the Varanidae. Due to its unique scale structure, in combination with other morphological evidence, a monotypic subgenus for this enigmatic monitor species seems justified. Also for the members of the *V. prasinus* group from New Guinea within the subgenus *Euprepiosaurus*, erection of new subgenus seems justified based on the autapomorphic scale shape in concert with further morphological, molecular and ecological evidence.

The nymphal head of *Epiophlebia laidlawi* (Insecta: Odonata)

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Due to its unique combination of characters, which are otherwise characteristics of dragonflies (Anisoptera) or damselflies (Zygoptera), respectively, species of *Epiophlebia* are often called "living fossils". *Epiophlebia superstes* Selis, 1889, *Epiophlebia laidlawi* Tillyard, 1921 and the lately discovered *Epiophlebia sinensis* Li & Nel, 2011 are the only recent representatives of this group. Publications focused on the phylogeny of Odonata arrange *Epiophlebia* in a sistergroup relationship with the Anisoptera, forming the so-called Epiprocta (e.g. Bybee 2008). One substantial problem of most studies concerning *Epiophlebia* was the lack of specimens of *E. laidlawi*. Due to our Nepalese colleagues some specimens of *E. laidlawi* nymphs are available since 2010. Nymphs of *E. sinensis* are not available yet. The insect head has been repeatedly shown to be a phylogenetically instructive character system (Beutel et al. 2010). The adult head of Odonata has been well investigated (e.g. Asahina 1954 for *E. superstes*), compared to the nymphal head, which is poorly studied. Therefore, the aim of the present study is to investigate nymphal heads of Anisoptera, Zygoptera and *Epiophlebia* to fill this gap of knowledge. Furthermore, our study might facilitate the use of morphological characters for subsequent phylogenetic analyses. This poster presents the head morphology of *Epiophlebia laidlawi* as a first step of the investigation.

Asahina, S. (1954) A morphological study of a relic dragonfly *Epiophlebia superstes selys* (Odonata, Anisozygoptera). 153pp., Tokyo (The Japan Society for the Promotion of Science).

Beutel, R. G., Zimmermann, D., Krauß, M., Randolph, S. & Wipfler, B. (2011) Head morphology of *Osmylus fulvicephalus* (Osmylidae, Neuroptera) and its phylogenetic implications. *Organisms, Diversity and Evolution* 10:311-329.

Bybee, S. M., T. H. Ogden, M. A. Branham, and M. F. Whiting. 2008. Molecules, morphology and fossils: a comprehensive approach to odonate phylogeny and the evolution of the odonate wing. *Cladistics* 23:1-38.

Genetic Diversity of Some *Lupinus* (*Fabaceae*) Species using AFLP Fingerprint and DNA Data Sequencing

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The *Lupinus* (*Fabaceae*) genus includes a number of important crop species. Beside the diversity centre in America there exist *Lupinus* species in Europe. The use of defined nucleotide sequences for the analysis of genetic diversity among this species has revealed modest levels of diversity. Also morphological characters can not solve all systematic problems. Therefore, the diagnose of different molecular characters is necessary. The aim of this study is revealing genetic diversity among some *Lupinus* (*Fabaceae*) species using AFLP fingerprint and sequencing data of the nrITS locus. We used 30 different *Lupinus* (*Fabaceae*) species with totally 42 samples in this study. DNA extraction from herbarium material and silica-gel dried samples was performed using Analytic Jena DNA extraction kit. For AFLP fingerprint we used six different primer combinations in two Multiplex sets. Finally, the analysis of the AFLP and sequence data was done with PAUP* using Parsimony, Maximum Likelihood, UPGMA and Neighbor-Joining algorithms.

Micromorphological Studies on Inflorescence and Seeds of Some *Plantago* L. (Plantaginaceae) Taxa in Turkey

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Plantago L. is one of the largest genera of the family Plantaginaceae and probably the most widely distributed genus within the family. The here presented study includes all except one species from Turkey, in total 24 *Plantago* taxa. Apart from previous studies based on seed micromorphology of *Plantago*, this study is the first using micromorphological characters of the inflorescence to test for species delimitation. Observations were made by using light microscopy and scanning electron microscopy (SEM). Most of the source materials are derived from air dried herbarium specimens from various herbaria in Turkey. The study showed that hairs and glands as well as epidermal cell arrangement is very variable across species. Therefore, inflorescence parts provide no useful characters to make certain distinction between different species; however it can be used to differentiate sections. For example, the section Lamprosantha Decne. can clearly be delimited from section Oreades Decne. by granulate surface characters.

The status of enigmatic, microendemic pill millipede species of the genus *Glomeris* in northern Italy (Diplopoda, Glomerida)

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Of the Holarctic pill millipede order Glomerida, the European genus *Glomeris*, commonly encountered by European field zoologists, is by far the most species-rich. The species of *Glomeris* are unevenly distributed across Europe, with only a single species present in northern Germany, Scandinavia and Great Britain, but a hotspot of diversity present in Italy, where 34 species, of them 20 country-endemics, were recorded. However, many of these species are only known from their first description, often dating back more than 100 years, and were only recorded from a single locality. Furthermore, many of these species seem, according to their first description, to be similar to widespread species of variable colouration, such as *G. undulata* Koch, 1844 or *G. connexa* Koch, 1847. To find out whether the species richness of the pill millipedes in Italy is the result of taxonomic inflation combined with a total lack of revisions, or whether it is the result of a more natural process was the aim of this study.

Six of the little-known Italian *Glomeris* species, *G. genuensis*, *G. ligurica*, *G. euganeorum*, *G. primordialis*, *G. schubarti*, *G. oropensis*, were recently collected at their type localities, allowing the undertaking of a molecular analysis. The sequences of their cytochrome *c* oxidase I gene (COI) of six endemic species were compared with those of other, more widespread pill millipede species. Surprisingly, significant differences (4-10% uncorrected distances) were found between the species. The distribution limits and evolutionary history of the six analysed Italian pill millipede species remain unknown.

Phylogenetic and morphological analysis of *Chroococcidiopsis*, the Pleurocapsales, and related heterocyte-forming Cyanobacteria

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The classification of Cyanobacteria is still largely based on morphological data, which does not necessarily reflect their evolutionary history. The order Pleurocapsales, for example, is characterized by a unique mode of reproduction, and traditionally include the genus *Chroococcidiopsis*. Recent studies indicate that *Chroococcidiopsis* may be a sister group to the heterocyte-forming Cyanobacteria instead. We analysed three genes (16S rDNA, *rpoC1*, *gyrB*) with a focus on the Pleurocapsales, *Chroococcidiopsis* and heterocyte-forming cyanobacteria. The available data from GenBank and completed genomes were combined with new sequences and analysed for approx. 100 strains using Maximum Likelihood and Bayesian methods. In addition, scanning electron microscopy was used to examine the thylakoid structures as a morphological character of selected taxa. Our results support the hypothesis that *Chroococcidiopsis* is related more closely to heterocyte-forming Cyanobacteria, and confirm the non-monophyly of the Pleurocapsales.

Near intron pairs (NIPs) and the phylogeny of beetles and related insects

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Today, the reconstruction of the organismal evolutionary tree is based mainly on molecular sequence data. However, the resolution is sometimes insufficient, particular in deep branches. We found a new phylogenetic marker class which we called near intron pair (NIP). This marker is derived by insertion of a novel intron located less than 50 nt from an evolutionary older intron position. Since correct splicing is impeded by very small exons, such near intron pairs (NIPs) very rarely coexist. The gain of the novel intron is nearly always associated with the loss of the old intron. In cases of intron migration both events are directly connected. Therefore, it should be possible to characterize one of the introns as ancient (plesiomorphic) and the other as novel (derived or apomorphic).

The suitability of NIPs as a phylogenetic marker was demonstrated by analysis of the evolutionary positions of Hymenoptera and Coleoptera in relation to Lepidoptera and Diptera using genome project and genomic PCR data.

Now the resulting phylogenetic informative intron distributions are investigated in representative species of other holometabolic insect orders in order to expand the genome-scaled studies of holometabolic insects. Additionally, we evaluate the two hypothetical pathways to NIPs (consecutive intron loss and intron gain versus intron migration) and determine the relative age of the novel intron positions.

Evaluating 38 NIPs localized in 23 genes, we found one case, where the Neuropterida share a synapomorphic intron position with coleopterans exclusively. This supports a sistergroup-relationship between Neuropterida and Coleoptera (Neuropteriformia).

In addition, we found one common derived intron of Strepsiptera with Polyphaga excluding the Adephaga. This suggests a position of the Strepsiptera inside the Coleoptera.

Furthermore, we found that all derived intron positions are of moderate age. Some evidence

point out that at least two of these novel intron positions resulted from intron migration and did not involve the insertion of novel introns.

Evolution of the *Wnt* family genes in Onychophora (velvet worms)

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Organisation of the body into serially repeated units or segments is found in several distantly related animal groups, including chordates, annelids and arthropods. The evolutionary origin of body segmentation in these groups is under debate and it is unclear whether segmentation has evolved once, twice, or several times among bilaterians. Gene expression studies in one of the closest relatives of arthropods, the Onychophora, might help to clarify this issue since the onychophoran body shows both segmental and non-segmental features. Previous studies have shown that the *Wnt* family genes, including *wingless* (*Wnt1*), play a crucial role in the segmentation process of the arthropod embryo. However, the function of these genes in onychophoran development remains obscure. To assess whether onychophorans and arthropods share a common segment patterning mechanism, we have identified the complete set of *Wnt* genes in the embryonic transcriptomes of two onychophoran species using Next Generation Sequencing methods. Our phylogenetic analysis of the obtained sequences shows that two genes, *Wnt8* and *Wnt3*, are missing from the onychophoran transcriptomes. Ongoing expression studies of the identified *Wnt* orthologs will help to understand the function of these genes and clarify their involvement in the segmentation process of the onychophoran embryo.

Freshwater Diversity Identification for Europe (FREDIE)

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DNA barcoding encompasses molecular genetic approaches of assigning samples of unknown or uncertain origin to reference sequences. In recent years this technique has increasingly gained importance as it offers the possibility to accelerate detection and monitoring of biodiversity. Nevertheless, quality and significance of automatized barcoding routines are strictly bound to availability and quality of underlying reference data. Within the FREDIE network project, resources and expertise of three Leibniz institutes are combined to create a reliable and sustainable reference system for European freshwater fishes, molluscs and mayflies. Representatives of nearly all between Portugal and Ural living species of the three groups will be collected, identified by experts and sequenced to become barcode references. In cases where conventional (mitochondrial) DNA markers do not lead to unambiguous identifications a stratified identification system will be developed. Based upon the barcodes, the potential of high-resolution DNA melting analysis as alternative technique for species identification will be evaluated. This rather new method is fast, low priced and promising but currently almost exclusively used in adjacent areas. Efficiency and cost-value ratio of both methods will be compared in a case study. Additional to DNA sequence data,

FREDIE will provide the respective voucher specimens and a DNA collection as permanent references that will be made available to the scientific community via the infrastructure of the involved museums. Altogether, this strategy delivers beside the reference data and complementary collection vouchers for the first time molecular and morphological based estimations of species numbers of the three organism groups for Europe as well as new insights into their geographic structuring on a large scale. The important networking idea is not only to guarantee realization of this ambitious major project but also to evolve long-term cooperation and perspectives through jointly supervised postgraduates and the collected data from remote European areas.

Argestinae Por, 1986, the first recognized suprageneric monophylum within Argestidae sensu Por, 1986 (Crustacea, Copepoda, Harpacticoida)

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The family Argestidae (Copepoda, Harpacticoida) was established by Por, 1986. It is commonly considered as typical representative of deep-sea meiobenthos, playing an even dominant role within deep-sea harpacticoid copepods. In the past years, an increasing number of faunistic and biogeographic studies related to deep-sea Harpacticoida focused on Argestidae because of their ubiquity and high relative abundance in deep-sea samples. Thus, it is expected that results from faunistic and biogeographic investigation on Argestidae might perhaps be generalized and assigned to at least all deep-sea Harpacticoida and perhaps even to other meiobenthic deep-sea taxa. Nevertheless, the monophyly of the family is far from being verified; recent Argestidae are united because of diagnostic rather than phylogenetic characteristics. The missing phylogenetic characterization of Argestidae is for instance one reason for the remarkable difference of both genus and species numbers (15-20, and 77-96, respectively) provided by several authors, staying those taxa side by side but absolutely disordered and neglecting any phylogenetic relation. Furthermore, it is obvious that without previous phylogenetic elucidation, meaningful investigations on Argestidae remain impossible and even dispensable.

Recently, several studies aimed to clear up the systematic relationships inside Argestidae. While some authors concentrate on relations within single genera, others started discovering those between different genera. Here, evidences for a monophylum that is formed by two genera, namely *Argestes* Sars, 1910, and *Fultonina* T. Scott, 1902, are presented. Both genera are represented by four species each, all of which sharing the following derived characteristics: 1) body densely covered with small cuticular spinules; 2) female antennula with very strong seta terminally on 6th segment; 3) sensilla arising dorsally at thoracic somites remarkably elongate. As these features and their combination are unique inside Argestidae, they are regarded as autapomorphies for a suprageneric monophylum compound by *Argestes* and *Fultonina* and named Argestinae Por, 1986.

Where have all the data gone? The reBiND Project provides workflows and software for archiving biodiversity data

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Usually, biodiversity data generated by studies and projects stay with the authors of a scientific publication and the data holders often don't have the capacity to transform data files into standardized, contemporary and well documented formats. Only a small part of it is used for publications and thereby available for the scientific community. The rest of the data stays in unpublished files or databases and a growing volume of valuable but poorly documented scientific data are stored on outdated media and software platforms. Thus these data are in danger to be lost for the scientific community.

At the same time, access to primary biodiversity research data is urgently needed to address pressing scientific questions in a rapidly changing environment. In July 2011 the reBiND project (<http://rebind.bgbm.org/>) funded by the Deutsche Forschungsgemeinschaft (German research foundation) started. It builds on a survey and assessment of existing threatened biodiversity databases with a focus on collection and observational data. The project aims to establish an archive for such primary biodiversity data. Therefore cost-efficient workflows to rescue legacy databases are developed. reBiND workflows will combine software tools for transforming data stored in outdated database systems into well-documented, standardized, and commonly understood XML-formats (e.g. ABCD) with a system for storing, documenting, and publishing the information as a web service. The workflow will be thoroughly tested, refined and documented in a best-practice handbook.

Find the idea of the project also in a stop motion video: http://rebind.bgbm.org/rebind_movie.

GBIF-D enables free access to Biodiversity Data: How to contribute?

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The Global Biodiversity Information Facility (GBIF) is an initiative of 56 countries and 47 international organizations. GBIF has the overall mission of mobilizing the world's primary biodiversity data via the Internet. The GBIF network currently provides access to more than 317 million records. This includes specimen as well as observation data from a large variety of data sets.

GBIF was established in 2001 and Germany is one of the founding nations. Currently GBIF Germany (GBIF-D, www.gbif.de) is funded as a 3-year project by the Federal Ministry of Education and Research (BMBF, 01LI 1001 A-F).

Eight institutional nodes form the backbone of GBIF-D. The Botanic Garden and Botanical Museum Berlin-Dahlem is responsible for general coordination as well as for plants and protists; the German Collection of Microorganisms and Cell Cultures in Braunschweig for bacteria and archaea. In Munich, the Botanische and Zoologische Staatssammlung are in charge of fungi, lichens and invertebrates (molluscs and myriapods). The Museum fuer Naturkunde in Berlin is responsible for insects and fossils, the Senckenberg Forschungsinstitut in Frankfurt for invertebrates (marine invertebrates) and the Forschungsmuseum Alexander Koenig in Bonn for vertebrates.

Main objective of GBIF-D is the mobilization of data from Germany's research community, focussing on "species occurrence data", i.e. specimens and observations. GBIF-D also offers expertise on technical aspects of data capture and database networking. Stable workflows from data entry to open and free online access are established in support of providers. Managing the sharing of global biodiversity data is a complex task – but essential to solve the growing environmental crises. GBIF is far more than the mobilization of natural history collections data. We will call on the scientists present to integrate their data into the GBIF network and to start using GBIF data for their own work, in order to benefit from the global GBIF effort.

The phylogenetic positions of the former archiannelidan taxa Protodrilidae and Polygordiidae within Annelida

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The interstitium in marine sediments is a typical habitat for certain annelid taxa. Because of their small body size and an apparently simple body organisation some of them have been considered as primitive annelids and as part of the basal grade "Archiannelida" (e.g., Dinophilidae, Protodrilidae, Saccocirridae, or Polygordiidae). Conversely, these taxa were regarded as a polyphyletic assemblage of secondarily simplified annelids adapted to the interstitial realm. Due to this adaptation, these annelids lack several features which are characteristic for larger annelid taxa, making it difficult to differentiate between primary absence and secondarily simplification. Therefore, the phylogenetic position of the former archiannelidan taxa as such still remains controversial. Based on anatomical and ultrastructural similarities of the pharyngeal organs and of the palps, Protodrilidae, Protodriloidae, and Saccocirridae were grouped together as Protodrilida, with an eventual origin within Spionida based on corresponding structural peculiarities of the palps and the nuchal organs. In case of Polygordiidae morphological similarities of the cuticle, the musculature, and the locomotory pattern suggested a closer relationship to Opheliidae. However, these similarities could also reflect convergent adaptations to coarse gravel sediments. Molecular analyses based on nuclear 18S- and 28S-rDNA neither support a monophyletic taxon Protodrilida nor a sister group relationship of Polygordiidae and Opheliidae, and instead indicate a possible sister group relationship of Saccocirridae and Polygordiidae as well as these taxa being part of a basal radiation although with weak support. To get a better resolution and probably a higher depth of information, we are trying a mitogenomic approach based on complete mitochondrial genomes of these taxa. Herein, we report the preliminary results based on the mitochondrial genome data of Polygordiidae, Protodrilidae and other non-archiannelid annelid taxa with respect to the phylogenetic position of these taxa.

A new land planarian (Platyhelminthes, Tricladida, Geoplanidae) from southern Chile, with a discussion of its systematic position

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Land planarians are predatory platyhelminthes inhabiting the forest floor which are believed to have colonized land hundreds of millions of years ago. Today there are over 800 known species worldwide. Most of the Neotropical land planarians belong to the subfamily Geoplaninae, which contains over 280 species. This is the only subfamily having dorsal testes and numerous eyes. In Chile there are approximately 26 known species of land planarian, 9 of which remain in a 'bucket' genus, *Pseudogeoplana*, for species whose internal morphology remains unknown. Recently a unique specimen of land planarian was collected in the Chonos archipelago of southern Chile. Externally the animal has a yellow-brownish appearance, with a median longitudinal line and pigment stripes on most of the dorsal surface. The ventral surface is light yellow in color, with a pale yellow median line. The eyes are numerous and dorsal. The subcutaneous and parenchymal musculature lacks cephalic specializations. The parenchymal longitudinal muscles are present as a ventral plate intermixed with parenchymal diagonal fibers. The testes are located underneath the transversal supra-intestinal parenchymal muscle layer and the prostatic vesicle receives ramified multicellular secretion ducts. The male copulatory apparatus features a small cone-shaped penis papilla, located in the top anterior corner of the male atrium and slightly orientated ventrally. The female atrium is dislocated sideways, and bears a secondary glandular cavity. The ovovitelline ducts approach the female canal ventrally and shell glands open into a common ovovitelline duct. Accommodating this specimen into the current taxonomic categories remains a delicate task as sets of morphological features do not match any of the existing Geoplaninae genera. Interestingly, the uncommon arrangement of the parenchymal musculature is similar to that of other Chilean Geoplaninae species. This would imply the convergent evolution of the general anatomy of the muscular system of cis-Andean, Chilean, species, and trans-Andean species.

Organization of the muscular system in *Myzostoma cirriferum* (Annelida): Implications for the evolution of the myzostomid anatomy

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Myzostomids have been shown to be part of the annelid radiation based on rare genomic changes marker systems whereas phylogenomic analyses indicate an early divergence of this group in the annelid tree of life. Due to their parasitic/symbiotic lifestyle associated with echinoderms, myzostomids show a highly derived morphology and a lack of characters typically found in annelids, such as external body annulation, coelomic cavities, and segmental ganglia of the nervous system. Detailed analyses of the myzostomid muscular system are missing, thus constraining conclusions on the evolution of their anatomy. To clarify whether the myzostomid musculature shows typical annelid features, we analyzed the

distribution of f-actin, a common component of muscle fibers, in adult specimens of *Myzostoma cirriferum* using phalloidin-rhodamine labeling in conjunction with confocal laser scanning microscopy. Our data show that the musculature of the myzostomid body comprises an outer circular layer, an inner longitudinal layer, numerous transverse muscles, and prominent muscles of the parapodial complex. Thus, the muscular system of myzostomids corresponds with the organization assumed for the annelid ground pattern. This finding is consistent with the phylogenetic placement of myzostomids as part of the annelid radiation.

Genetic connectivity of sand-associated marine snails (Gastropoda) in the Great Barrier Reef, Australia

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The marine benthic soft-sediment zone is the most widespread connected habitat in the world, reaching from shallow waters to the deep sea and from Arctic to Antarctic. The widely distributed sand-associated gastropods are mainly known from tropical coral reefs and the sea bed, but are also found in other sandy habitats, such as sea weeds, esutarine areas, and mangrove forests. Because sand-associated gastropods inhabit a more continuous habitat than reef-associated species their genetic connectivity is predicted to be higher. Here we present preliminary results of phylogenetic analyses of the sea bed associated *Tudivasum armigera* (Turbinellidae), the strictly reef-associated *Polinices mammilla* and the habitat generalist *Notocochlis gualtieriana* (both Naticidae) in the Great Barrier Reef. The benthic developing *T. armigera* occurs in deeper muddy/sandy areas of the sea bed (> 15 m depth). The species forms three distinct clades which overlap in the central Great Barrier Reef (Townsville). Each one clade extends into the northern and southern GBR following the Eastern Australian Current. The coral reef associated lecithotrophic developing *P. mammilla* shows two divergent GBR clades which co-occur on Lizard Island. One clade is more closely related to Vanuatu and Indonesia which in turn also show strong genetic divergence to any other clade indicating geographic isolation. By contrast, the lecithotrophic developing *N. gualtieriana* shows high genetic variability with haplotypes shared between the GBR, the central Indo-Pacific and even the Red Sea. The genetic connectivity of sand associated snails is therefore more variable than expected. Given the depth of genetic divergence, the distinct clades in *T. armigera* and *P. mammilla* could represent cryptic species indicating that the gastropod biodiversity in the GBR may be underestimated. The presented results demonstrate the need for further research in the biology of sand-associated gastropods.

Diatom research: towards cybertaxonomy

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Cybertaxonomy comprises aspects of availability of primary biodiversity data, digitisation of data as well as taxonomic research in an electronic environment. The Global Biodiversity Information Facility (<http://data.gbif.org>) fits to the needs of cybertaxonomy, providing standardised biodiversity data open access via the Internet. GBIF-D *Plants, Algae and Protists* (www.gbif.de), funded by the Federal Ministry of Education and Research (BMBF, grant 01 LI 1001 A-F), is engaged in extending the quantity of data and datasets of German providers and in solving data quality issues. Aim of this initiative is to raise the usability of those data for taxonomy and cybertaxonomy.

Databases on primary biodiversity data, such as *AlgaTerra* (www.algaterra.org), are providing researched data on specific taxonomic organism groups to GBIF. The *AlgaTerra* Information System for micro algal biodiversity comprises type information, specimen data as well as images, videos, and molecular data for terrestrial and limnic micro algae. One focal area of *AlgaTerra* is the publication of images from diatoms field observations as well as specimen and types data of African, American, and European diatoms.

As a repository of primary biodiversity data *AlgaTerra* publishes voucher images of the research projects, such as of diatom DNA barcoding. These records are linked to or cross-referenced with research papers (see Zimmermann et al. 2011, Barcoding diatoms: evaluation of the V4 subregion on the 18S rRNA gene, including new primers and protocols. – *Organisms Diversity & Evolution* 11: 173-192, and http://www.gbif.de/botany/barcoding_3).

The hypostome-labrum complex in Euarthropods – different names for different structures!

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Little of the head of Euarthropoda is more heavily debated than the nature of the pre-oral hypostome-labrum complex. Various terms for structures associated with the hypostome and labrum exist and cause considerable confusion in the literature. For example, different terms are used for the same structures and vice versa the same term has been applied to different structures. The term 'hypostome' is quite well established in trilobite terminology, restrictedly used for a sclerotized plate that bears the mouth opening at its rear. In contrast, the use of 'labrum' is more confusing. In the literature about (Eu)crustacea, 'labrum' is used either for the labrum alone or for the compound of hypostome and labrum. For Chelicerata and Insecta own terminologies, like 'epistome-labrum', 'clypeo-labrum', but also 'labrum' alone, have become established for plates covering the mouth, but their relation to the hypostome and labrum of other euarthropods remained undiscussed. Morphological data on the hypostome-labrum complex exist but are inconsistent, hardly interpretable, and a clear definition of the terms is still missing. Gene-expression data on this topic are available, but these point into different directions and do not allow a definite interpretation. Accordingly, a consistent comparative morphological investigation of the hypostome-labrum complex of Euarthropoda appears essential. Aiming at demonstrating that hypostome and labrum are two different structures with different origins and different tasks, we will investigate a wider range of euarthropod taxa including fossil representatives, applying modern documentation methods including 3D imaging. Our aims are the homologization of the different structures around the mouth opening, a standardized terminology and the reconstruction of the evolution of the hypostome-labrum complex within the Euarthropoda.

Beyond the haustellar complex – unexpected morphological complexity in adult head structures of caddisflies (Insecta: Trichoptera)

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With about 13.000 described species Trichoptera (caddisflies) is the most diverse group of insects with aquatic larvae. Together with Lepidoptera (butterflies and moths) they form Amphiesmenoptera - arguably the best supported supraordinal clade of Hexapoda. In contrast to the undisputed position of the group, the intraordinal relationships of Trichoptera are still unclear and the basal branching pattern is unresolved. The monophyly of the two large lineages Annulipalpia and Integripalpia is well founded, but the placement of four families traditionally assigned to “Spicipalpia” is unclear. These four taxa include species with highly specialized life habits (e.g., feeding strategies, case building behavior) and are apparently crucial phylogenetically, and also for the understanding of the evolution of morphological structures and patterns of behavior. Here we present a description of the adult head of *Philopotamus ludificatus* McLachlan, 1878 (Annulipalpia, Philopotamidae). For data acquisition micro-computed tomography, histology and scanning electron microscopy in combination with 3-dimensional computer-based reconstruction were used. We provide an overview of external and internal structures (muscles, nervous system and digestive tract). The main goal was to provide morphological data for a representative of Annulipalpia, which was assumed to be close to the groundplan of the group. Plesiomorphic features retained in the head of *Philopotamus* are for instance the moderate size of the mandibles (smaller in the spicipalpien groups and strongly reduced in Integripalpia) and the comparatively small, granulose haustellum, which is distinctly modified in Integripalpia. Morphological data of this presumably “basal” representative of Annulipalpia (and Trichoptera) will provide a solid backbone for a broad comparative study of cephalic structures of caddisflies in our ongoing project on trichopteran evolution.

Lung morphology and systematics of the Kinosternidae (Testudines: Cryptodira)

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Turtles are an enigmatic taxon of amniotes, whose phylogenetic position has been under discussion ever since the dawn of systematic biology. In addition to their overall position, their ingroup relationships also are often very controversial. Especially the rise of molecular approaches to phylogeny yielded many hypotheses that are in strong contrast to earlier morphology-based ones. The traditional character complexes used in morphological turtle phylogenetic research are osteological, focusing on cranial aspects, while very little attention has been paid to soft-tissues. We focused the present study of a relatively small taxon of turtles, the Kinosternidae or mud and musk turtles, using a respiratory-related character complex. The total of 25 currently recognized kinosternid species is usually grouped into two distinct lineages, the Kinosterninae (*Kinosternon* spp. and *Sternotherus* spp.) and Staurotypinae (*Claudius angustatus* and *Staurotypus* spp.). We examined specifically lung morphology in representatives of all four extant genera and based on this discuss the current concepts in kinosternid systematics.

DNS-Isolation aus einem Holotypus? Der Fall einer außergewöhnlichen Wassermilbenlarve aus Nord-Madagaskar

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Mit fortschreitender Entwicklung der molekularen Techniken nimmt ebenso deren Bedeutung in der Systematik stark zu: neben der phylogenetischen Auswertung molekularer Daten zur Verwandtschaftsanalyse von Taxa oder zur Populationsanalyse auch zur Differenzierung und Abgrenzung von Spezies. Vor allem bei kryptischen Spezies gewinnt die molekulare Beschreibung neben der morphologischen Beschreibung an Gewicht, so zum Beispiel durch das Barcoding-System. Während es im Fall größer dimensionierter Organismen möglich ist, Fragmente eines Individuums zur DNS-Isolation zu verwenden und den Rest des Tieres mit anderen Methoden weiterzubearbeiten, bereiten kleine Organismen, die zu großen Teilen oder sogar vollständig zur DNS-Analyse eingesetzt werden müssen, ausgesprochene Probleme. Falls mehrere Exemplare vom selben Fundort vorliegen, ließe sich in solchen Fällen eine Mischanalyse, die auf mehreren Exemplaren (zum Beispiel der Typus-Serie) basiert, in Betracht ziehen, doch ist ein solches Vorgehen naturgemäß problematisch. Wir beschreiben hier anhand der Larve eines höchstwahrscheinlich unbeschriebenen höheren Taxons der Hydrachnidia (Acari, Parasitengona) eine Technik, die die molekulare und morphologische Analyse eines bedeutenden Einzelexemplars ohne dessen Zerstörung ermöglicht. Zur Isolation der DNS können kommerziell erhältliche Kits herangezogen werden, wobei die Protokolle je nach Hersteller und Probenmaterial etwas modifiziert werden müssen, aber gute Ergebnisse erreichen und eine molekulare Charakterisierung ermöglichen.

Nach chemischer Isolation der DNS konnte das Einzelexemplar wie eine Exuvie vollständig für die morphologische Beschreibung eingesetzt werden. Bei Vergleichsanalysen an Vertretern der Oribatida (Acari) zeigten diese nach DNS-Isolation auch in REM-Darstellungen keine äußeren morphologischen Änderungen im Vergleich zu unbehandelten Individuen. Die beschriebene Technik bietet sich vor allem für kleine Arthropoden-Spezies an, die nur in wenigen Individuen vorliegen und könnte sogar für Taxa angewandt werden, die nur vom Holotypus-Exemplar bekannt sind.

Population genetics and fitness in fragmented populations of the dioecious and endangered *Silene otites* L. (Caryophyllaceae)

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In fragmented dry grasslands in north-eastern Germany, we analysed genetic structure, fitness, and habitat quality of the endangered, dioecious, insect pollinated plant species *Silene otites* (Caryophyllaceae). Population fragmentation is often correlated with loss of genetic diversity and reduced fitness, while obligate out-crossing (dioecy) is expected to enhance genetic diversity reduce genetic differentiation, and avoid inbreeding depression through frequent gene flow. However, in highly fragmented populations dioecy has only

diminishing effects upon genetic structure as pollination limitations (e.g. flight distance of pollinators) most often restricts inter-population gene flow.

We screened 10 populations by AFLP analysis and detected a high level of differentiation among populations ($F_{st} = 0.36$), while the intra-population genetic diversities ($H_E = 0.165\text{--}0.240$) were similar as compared to hermaphroditic species. Neither a correlation between geographic and genetic distance nor between genetic diversity and population size could be detected, which is indicative for reduced gene flow among populations and random genetic drift. Higher total coverage resulted in reduced plant fitness, and the number of juveniles was negatively correlated to cryptogam cover. Our results indicate that on a regional geographic scale dioecy does not necessarily prevent genetic erosion in the case of habitat fragmentation, especially in the absence of long distance seed and pollen dispersal capacity.

The course of the Nervus facialis as a possible signal in mammal phylogeny

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For morphologists, the recent changes in mammal phylogeny caused by molecular data has led both to the quest for morphological evidence of the new taxa such as Afrotheria or Afrosoricida and the re-examination of characters once used to establish taxa that are no longer valid in their original meaning (e.g. Lipotyphla). However, since only little morphological evidence supporting these recently introduced taxa is available, new characters are examined for suitability in this search. In this context, the course of the Nervus facialis is examined. It emerges from the Cavum cranii through the Porus acusticus internus in the posterior part of the Canalis facialis. The Canalis facialis leads through the petrosal and ends in the Recessus epitympanicus through the Foramen stylo-mastoideum. The interesting part is the contorted course through and over the petrosal which may hold a phylogenetic signal. To test this hypothesis selected species of Afrosoricida and Lipotyphla were examined, using *Dasypus novemcinctus* (Xenarthra) as an outgroup. Histological sections from *Erinaceus europaeus* (11 specimens), *Sorex araneus* (8), *Talpa europaea* (6), *Geogale aurita* (1), *Hemicentetes spinosus* (3), *Microgale dobsoni* (1), *Setifer setosus* (2), *Tenrec ecaudatus* (1) and *Dasypus novemcinctus* (4); were examined using light microscopy. Furthermore, museum specimens in ethanol of *Tenrec ecaudatus* were examined with micro-CT (1) and MRT (2). The resulting data was used to produce a 3D model of the course of the Nervus facialis and the adjacent structures. With this combined approach it is intended to contribute to morphological evidence for the Afrosoricida and the core insectivores (Lipotyphla).

What is *Urocystis*?

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The genus *Urocystis* RABENHORST, which belongs to the Urocystales (Ustilaginomycotina), comprises about 160 species and appears to be morphologically well defined. However, molecular phylogenetic studies have shown that the monophyly could be questioned, and that some other genera are at least closely related.

In the research summarised here, around 25% of the known species of the genus *Urocystis* have been studied by molecular phylogenetic methods and presented in a comprehensive analysis for the first time. The aim of this research was to elucidate the phylogeny of the genus *Urocystis*. Therefore we used the genetic markers ITS, LSU and TEF1. The sequence data formed the basis for the multi-gene analysis in which neighbour-joining, maximum parsimony, maximum likelihood and bayesian interference were applied.

Overall, the results were concise, showing several monophyletic groups representing *Urocystis* species on closely related host species. However, some genera that lack spore balls of the *Urocystis*-type were mixed within the genus *Urocystis* and the backbone was not always well resolved. As traditional genus description of spore balls did not support the molecular phylogeny, we analysed the morphology of the spore balls in more detail. The spores were categorized due to their number of fertile cells and checked against the phylogenetic hypotheses obtained in the various analyses. With our data it is not possible to resolve the phylogeny of the genus *Urocystis* completely, but it was clearly shown that the genus *Urocystis* is paraphyletic in its present circumscription because the genera *Melanoxa*, *Mundkurella*, *Ustacystis* and *Vankya* cluster within the genus *Urocystis*.

Thus the new results raise far-reaching questions about the systematics of the whole complex of genera *Urocystis*, *Melanoxa*, *Mundkurella*, *Ustacystis* and *Vankya*.

Species status of *Sericostoma personatum* and *Sericostoma schneideri* (Insecta: Trichoptera): Molecular and morphological evidence

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Inside the caddisfly genus *Sericostoma* the validity of several described species and their distribution ranges are subject of controversial discussions. Generally, the species descriptions are based on minor morphological differences of the male genitalia, mainly the shape of the lateral sclerites of the 10th abdominal segment. In this work, the two broadly distributed European species *Sericostoma personatum* and *S. schneideri* were studied using the mitochondrial gene marker Cytochrom Oxidase I and the nuclear 28S rRNA and wingless genes. The Iberian species *S. cf. baeticum* the species *S. siculum* from Sicily were used as outgroups.

None of the three genes supports a division of the species *S. personatum* and *S. schneideri*. However, mitochondrial polymorphisms revealed a distinct geographical pattern: one group of the *S. personatum* / *S. schneideri* complex was primarily found in Eastern Europe, another

group in central, western and northern Europe, and one group only located in the Alps and Black Forest above 700 m. The one outgroup species, *S. siculum*, was distinct to the other *Sericostoma* species. *S. baeticum*, however, shared haplotypes with *S. personatum* and *S. schneideri*. The haplotype patterns can be explained with the glacial history of Europe with lineage sorting in independent refugia and subsequent leading edge recolonization of northern regions. However, genetic data do not support that *S. personatum* and *S. schneideri* and possibly even *S. baeticum* are distinct species. Our results suggest that morphological characters currently used for the identification of species into *S. personatum* and *S. schneideri* may reflect ancestral polymorphisms or underlie phenotypic plasticity. Therefore, their use for species delimitation within the genus *Sericostoma* shall be used with caution.

Novel and neglected structures useful for unravelling the taxonomy and phylogeny of Onychophora (velvet worms)

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Onychophorans or velvet worms comprise a small group of invertebrates, which play an important role for studying biodiversity, biogeography and conservation. Recent molecular studies revealed a high degree of cryptic speciation and endemism among various onychophoran subgroups whereas morphological diversity has not been explored sufficiently thus far. Typically, onychophorans are regarded as uniform animals, which do not show much morphological variation. Here, we present new morphological data using scanning electron microscopy on moulted skins and preserved specimens of different onychophoran species (including both Peripatidae and Peripatopsidae). We detected a number of novel characters and character states associated with various papillae and structures with hitherto unknown functions, including volcano-like and bean-shaped papillae, modified sensillae, interpedal organs, embryonic foot projections, chemoreceptors, and tracheal pits. These findings suggest that the actual morphological diversity of Onychophora has been underestimated thus far. Exploitation of this diversity might assist in describing new species and performing reliable taxonomical revisions. In addition, the inclusion of the new characters in morphological data matrices will help clarify the phylogeny of Onychophora, in particular of Peripatidae, which is arguably the least studied major onychophoran subgroup.

Analyses of the genomic structure of α -glycerotoxin

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Glyceridae (bloodworms) are carnivorous polychaetes which use their eversible pharynx for prey catching. The pharynx is equipped with four teeth which are connected with venom producing glands. Venom systems evolved in a broad phylogenetic range of animals and are used for defense or predation. Venoms consist of mixtures of bioactive molecules, including proteins, organic molecules (such as neurotransmitters and amino acids), and salts. Active

components are usually described as toxins. The investigation of such toxins often leads to the discovery of agents which could be very relevant for the development of new medications in medicine. In a study (Meunier et al. 2002, EMBO J 21: 6733-6743) it has been found, that some bloodworm species are able to produce a currently unique neurotoxin. This α -glycerotoxin is characterized by its specific effect on the nervous system in stimulating $Ca_v2.2$ channels with a high specificity. Additionally its effects are completely reversible. The combination of the high specificity and reversibility of α -glycerotoxin could it make to an important tool in medicine.

We conducted mRNA-seq, as well as whole genome shotgun sequencing of gland tissue from *Glycera tridactyla* using Illumina sequencing technology. Using amino acid data from protein sequencing of short fragments of purified glycerotoxin we were able to identify a 3000bp coding sequence of the 3'end of α -glycerotoxin in our sequence data, which might span 30% of the 320kDA protein. Based on this data set, specific primers were designed which made it possible to amplify a nearly 6kb fragment from genomic DNA. So far, sequencing revealed the existence of at least three introns within our fragment. Moreover, we were able to identify a 1000bp coding region of α -glycerotoxin in other *Glycera* species. Using a phylogenetic approach we show that all currently identified glycerotoxin-bearing species form a monophyletic group.

Molecular studies on the genus *Saponaria* L.

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Within the core eudicotylous family Caryophyllaceae the genus *Saponaria* L. comprises species differing highly not only in their morphology but also in their geographical occurrence. E.g. *S. officinalis* L. is a herbaceous species growing up to 60 cm in height and is widespread distributed, while *S. lutea* L. is a small cushion plant growing in restricted areas of the Swiss alps. Even though species of this genus are common, and used economically for the extraction of saponin, and several new species were described during the last century, an up to date and all embracing phylogeny of this genus is still missing.

Thus, the aim of this study was to gain insight into the phylogeny of the genus *Saponaria*. The questions addressed were:

1. Are phylogenetic and morphological species concept congruent within this genus?
 2. Are common nuclear and chloroplast gene regions suitable for a phylogeny of this genus?
- 21 species and 3 hybrids out of the 61 species described in this genus were analysed. DNA was isolated out of fresh- and herbarium specimens. The used gene regions were ITS, trnk/matK, trnT-trnL-trnL-trnT and trnS-trnG-trnG.

Our results of the molecular analyses confirm the morphological species concept as all members of each species clustered together in monophyletic groups. The hybrid specimens clustered together with one of the parent species. Only one species out of 54 samples were identified wrongly. In contrast to other genera of the Caryophyllaceae the ITS region provided good resolution with high support values.

In addition, our data indicate that within the genus subdivisions occur reflecting the geography of the species. But this hypothesis has to be tested especially with more species of the Middle East region for final clarification.

Phylogeny of Onychophora (velvet worms) based on mitogenomics

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Currently, the phylogeny of Onychophora is unresolved and even the monophyly of the two major onychophoran subgroups, Peripatidae and Peripatopsidae, is uncertain. Previous studies of complete mitochondrial genomes have shown the utility of the mitochondrial data sets for clarifying the internal relationships of Onychophora. However, large-scale approaches, including species from different geographical regions, are still missing. We therefore conducted a phylogenomic approach based on whole genome shotgun libraries and nearly complete mitochondrial genomes of onychophoran species from Chile, South Africa, mainland Australia, Tasmania, New Zealand, Vietnam and Costa Rica. Assemblies of the raw data revealed large contigs spanning the mitochondrial genomes. Protein-coding gene sequences from these genomes were concatenated into a supermatrix and analysed using Maximum Likelihood. This approach recovered a tree with high support values for most nodes. The monophyly of Peripatidae and Peripatopsidae is strongly supported. Furthermore, the phylogeny within these two groups is in good concordance with the biogeographic distribution of taxa studied. An analysis of the mitochondrial gene order among onychophorans revealed that the gene arrangement is conserved in representatives of Peripatopsidae but highly diverse in the Peripatidae species.

Survival and differentiation of subspecies of the land snail *Charpentieria itala* in mountain refuges in the Southern Alps

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We studied 16S rDNA sequences and AFLP markers of the door snail *Charpentieria itala* in the Southern Alps to investigate the importance of mountain refuges for survival and differentiation of land snails during the Pleistocene. The occurrence of *Charpentieria ornata*, the sister species of *Charpentieria itala*, in the Eastern Alps as well as the decline of genetic diversity of the populations of *Charpentieria itala* as measured with AFLP markers from east to west indicate that *Charpentieria itala* colonized the study area from east to west. The basal position of some subspecies of *Charpentieria itala* that morphologically resemble *Charpentieria stenzii* in the mitochondrial gene tree and large genetic distances within *Charpentieria itala* indicate that the *stenzii*-like subspecies diverged before the ice ages. These subspecies are mainly restricted to higher altitudes in the Garda, Brescia and Bergamasque Prealps that remained unglaciated in the Pleistocene glacials. The range occupied by these subspecies was fragmented by glaciers during the Pleistocene. The genetic differentiation and the isolated distribution areas of the *stenzii*-like subspecies provide evidence for their survival in five separate mountain refuges in the Bergamasque, Brescia and Garda Prealps. In addition, the clustering of the *Charpentieria itala latestriata* populations from different valleys indicates a low altitude refuge. While the *stenzii*-like subspecies were separated from other subspecies of *Charpentieria itala*, partial reproductive barriers evolved. Gene flow between the two groups remained restricted locally when they

came in contact again when not *stenzii*-like subspecies colonized the lower altitudes of the Garda, Brescia and Bergamasque Prealps after the retreat of the glaciers.

Investigations into a putative hybrid complex of *Sorbus* L. (Rosaceae)

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The genus *Sorbus* L. in the subfamily Maloideae of the Rose family (Rosaceae) comprises 100 to 200 shrub- to tree-like deciduous species. *Sorbus* features natural hybridization with both diploid and polyploid progenies. *Sorbus* is an example of an agamic complex with seed formation without sexual reproduction in many polyploids. Apomictic species of *Sorbus* are in large part suspected to have arisen from hybridization events. Some hybrids and their parenthood are well known, likewise among the *Sorbus latifolia* aggregate.

In Bavaria (Germany) regional occurrence of the 3 potential hybrid species *S. pannonica*, *S. danubialis* and *S. subdanubialis* is observed. Previously delineated as aggregate of presumably fixed intermediate forms of *S. aria* and *S. graeca*, respectively *S. umbellata*, no molecular approaches have been performed to assign parenthood, yet.

The here presented molecular approaches test for the hypothesis if (1) these species are hybrids and (2) that *S. aria* is involved in these hybridization events.

The three putative hybrid species and references of *S. aria*, *S. aucuparia* and *S. torminalis*, together with *Malus sylvestris* as outgroup, were studied using nuclear ribosomal DNA internal transcribed spacer (ITS) and chloroplast DNA *trnL-F* sequences. Analysis of ITS and *trnL-F* revealed close relationships among the putative hybrids, forming a nearly monophyletic clustering in ITS networks and a monophyletic group in the *trnL-F* tree. In all cases *S. aria* is found to be closely related to the putative hybrids, while recent parenthood of *S. aucuparia* and *S. torminalis* can be excluded. Infra-specific nrDNA polymorphism is found in *S. pannonica*. Hypotheses explaining incongruent phylogenetic signals remain elusive, with a complex pattern of reticulate evolution as most attractive explanation.

***Lineus ruber* and *Lineus viridis* – one, two, or more species of Heteronemertea (Nemertea)?**

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Until the sixties most nemertean researchers regarded *Lineus viridis* and *Lineus ruber* as color variants of a single species. Studies in Roscoff (France) revealed differences in their development, so that both were considered as separate species. Since then color differences were assumed to be reliable species identifiers, with *L. viridis* having greenish and *L. ruber* having reddish body colorations. Beside dark-green and red individuals, however, all kind of green-brown and red-brown intermediates had been found along the North Sea coast. We therefore asked for the status of both species and started a comparative survey of the population structure of both species in the Brittany (France) and the German Bight (North Sea). We chose mitochondrial (COI) as well nuclear (ITS) markers to avoid data misinterpretation by analyzing mitochondrial data alone. The sequence data show that *L. viridis* is a complex of two species, while all *L. ruber* specimen analyzed belong to a single species. The data also show that *Lineus ruber* is not present in the North Sea, although some *L. viridis* collected on the Isle of Helgoland had the same red color as *L. ruber* from

Roscoff. Members of both *L. viridis* species were found at every sampling site; separating them by their coloration was impossible. The study shows that (1) mitochondrial and nuclear marker sequences successfully allow species delimitation and identification, (2) color patterns are not reliable for species identification, and (3) sequence data reveal a higher diversity than previously assumed.

Examples of barcoding and phylogeny reconstruction of native aquatic insect larvae: Heptageniidae (Ephemeroptera) and Hydropsychidae (Trichoptera)

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Ongoing studies on the diversity of invertebrate freshwater larvae in the wider surroundings of Regensburg prompted the use of molecular methods to characterize and identify representatives of Diptera, Ephemeroptera, Plecoptera and Trichoptera from different larval instars. In one instance, imagines were raised from mayfly larvae. In other cases, identifications were achieved with updated and detailed morphological keys or with the help of the corresponding taxonomic specialists. However, despite all these efforts of initial identifications, some larvae could only be assigned to the genus level, thus providing a useful scenario for a molecular barcode approach.

Three genera of aquatic insects were targeted with more detail: *Ecdyonurus* and *Heptagenia* (Ephemeroptera: Heptageniidae) and *Hydropsyche* (Trichoptera: Hydropsychidae), allowing to include all species occurring in Germany of the latter two taxa. Our dataset of *Hydropsyche* was furthermore enlarged with representatives from Austria, France, Romania, Bulgaria, and Greece. In these cases, it became of interest to reconstruct molecular phylogenies in order to understand lineage evolution, diversification patterns, and, in the case of *Hydropsyche*, to verify morphology-based taxonomic subunits by using mitochondrial and nuclear DNA markers.

Overall, we recommend the use of molecular barcoding for the identification of aquatic insect larvae and thus to improve biomonitoring methods for our freshwater systems. When applied consistently, this approach furthermore provides useful data for phylogenetic reconstructions and for the detection of cryptic species or range extensions into Central Europe, for which we provide examples.

Verschiedene Wege, das Gleiche zu tun – Die Mandibelform von Nagetieren mit gleicher Ernährung aus verschiedenen Unterfamilien

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Die Unterkiefer der Nagetiere zeigen bekanntermaßen sehr konsistent Formunterschiede, die mit der Ernährung korrelieren; so sind die Mandibeln von carnivoren Arten eher langgestreckt, die von herbivoren Arten eher kurz und hoch. In einer Analyse mehrerer Unterfamilien, in denen die verschiedenen Ernährungstypen unabhängig entwickelt wurden, haben wir getestet, ob sich die bekannten Formunterschiede auf den gesamten Unterkiefer gleichmäßig beziehen, oder ob bestimmte Stellen bevorzugt verändert werden, z.B. Muskelansatzstellen. Die Ergebnisse zeigen, dass es sehr wenige Einzelmerkmale gibt, die über alle Unterfamilien hinweg bei gleicher Ernährung eine identische Ausprägung haben.

Stattdessen gibt es innerhalb jeder Unterfamilie charakteristische Unterschiede zwischen den Arten mit verschiedenen Ernährungstypen. Für die Zukunft ist geplant, die Formveränderungen anhand besser aufgeklärter Verwandtschaftsverhältnisse und erweiterter Datensets noch genauer zu untersuchen.

Genetic and morphologic data unveil two overlooked Southern Ocean lysianassoid species (Crustacea, Amphipoda)

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Species diversity is difficult to assess for Southern Ocean taxa due to patchy sampling and the frequent occurrence of cryptic or overlooked species. The amphipod superfamily Lysianassoidea is the most abundant and diverse amphipod taxon in the Southern Ocean. However, correct identification is hindered by rudimentary descriptions and the lack of diagnostic characters, in particular for the genera *Tryphosella* and *Uristes*. Hence, the number of lysianassoid species described may not represent the true diversity of the group. In a genetic case study, analyses of the mitochondrial CO1 and the nuclear 18S and 28S rRNA genes of *Uristes murrayi* (Walker, 1903) revealed three well-supported clades. In this study, detailed morphological investigations (morphometric, light- and scanning electron microscopic analyses) were performed in order to search for yet overlooked diagnostic morphological characters. The results from this integrative taxonomic approach reveal the presence of two distinct new species within nominal *U. murrayi*.

Morphological study of NDE-vouchers: Confocal Laser Scanning Microscopy (CLSM) of Diplura and Protura after Non-destructive DNA extraction

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Non-destructive DNA extraction (NDE) of minute arthropods, such as Diplura and Protura, allows for utilisation of the autofluorescence property of the insect cuticle in subsequent morphological studies. The combination of two already established methods (NDE & CLSM) both (i) raises the confidence of determination of specimens used in molecular studies and (ii) permits to study and visualize cuticular structures used as taxonomic and/or phylogenetic characters. The destruction of specimens during conventional DNA extraction does not allow to determine the individuals used for molecular studies. Maintenance of the cuticular parts by NDE thus may prevent misidentifications or creation of unintentional chimeric sequences. Such advantages are especially important in Protura and Diplura, where determination is highly challenging. Additionally many exoskeletal features of these groups are poorly documented apart from simple line drawings.

Structures of the head, thorax and abdomen of Protura and Diplura will be visualized and discussed in the light of current phylogenetic hypotheses regarding the relationships among entognathous hexapods. Among others the first figures of the sternocoxal articulation of dipluran and proturan legs will be shown. The evolution of such an articulation was mentioned to represent one of the few potential morphological synapomorphies, supporting a sistergroup relationship between Protura and Diplura in a taxon called Nonoculata.

Parallel colonisation of the Arctic by plants

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The now treeless and cold region of the Arctic was covered throughout much of Tertiary with deciduous and coniferous forest. During the late Tertiary and Pleistocene cooling and the retreat of the forests this space became available for (re)colonisation and evolution of plants. The environmental conditions of the Arctic are very harsh. Nevertheless, c. 2500 vascular plant species occur presently in the Arctic. These species may be immigrants from southern areas or may have evolved *in situ*. To infer colonisation patterns and putative adaptations we study species occurring in the Arctic in a phylogenetic framework. Species of the genera *Artemisia* L., *Ranunculus* L., and *Pedicularis* L. were chosen as model groups. Additionally, many molecular phylogenetic studies available for other genera occurring in the Arctic were studied to infer the origin of the arctic flora. Multiple evolution of arctic taxa from non-arctic ancestors of different ages and places of origin and with various ecology preferences is the prevalent pattern detected for the arctic flora. Evolutionary radiations as found in arctic *Douglasia* (Primulaceae) are a rare exception. It turns out that arctic species have evolved from ancestors that may have occupied virtually all geographical areas and vegetation types of the adjacent non-arctic areas. A clear preference for habitat or vegetation type were seemingly not required for successful spread into the Arctic.

Innovative Methoden zur Schnellerfassung von Sammlungsdaten

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Seit 2002 ist der Wirbeltierknoten von GBIF-Deutschland am Zoologischen Forschungsmuseum Alexander Koenig, Bonn (ZFMK), angesiedelt. Er stellt Fund- und Beobachtungsdaten von Säugetieren, Vögeln, Fischen, Amphibien und Reptilien für Forschung, Lehre und die interessierte Öffentlichkeit frei zur Verfügung. Seit dem 01.11.2010 wird er vom Bundesministerium für Bildung und Forschung im Rahmen des Verbundprojektes „GBIF-D, Kompetenzzentren innovativer Datenmobilisierung“ (Förderkennzeichen 01 LI 1001 F) finanziell gefördert und unterstützt.

Die drei wesentlichen Ziele des Projekts sind:

- Mobilisierung bereits digitalisierter Wirbeltierdaten
- Schnellerfassung noch nicht digitalisierter Daten
- Optimierung des Webauftrittes und der Suchfunktionen im Webportal des Wirbeltierknotens

Das Poster stellt die ersten Ergebnisse im Projekt vor.

New Standards in the Taxonomy of Nemertea

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Nemertea (ribbonworms) is a group of unsegmented, nocturnal, mostly marine predators that are traditionally described from internal characters obtained from histology of serially sectioned animals. Descriptions done prior to the second half of the last century are often fragmentary and type species are lost or inappropriate for comparison. If serial sectioning of holotypes has been done, it is often difficult to get access to them. Because of this, identifying these animals is time-consuming so that in several ecological surveys and species inventories nemerteans are at best listed on higher taxonomic levels. On the other hand there are recent attempts to describe new nemertean species based on sequence data and color patterns only. Such an approach interrupts the taxonomic tradition, but provides the basis for rapid species identification by barcoding. To solve this potential conflict we started a standardized procedure for re-describing nemertean species, which includes collecting animals from the type locality or related areas and recording their environmental and metrical parameters. 15-20 individuals are photographically documented for color pattern, individualized and fixed for analyzing their COI sequence. Two of them are used for analyzing their 16S and 18S sequence, three of them for analyzing the internal morphology. Head to midgut region and median parts of these animals are serially sectioned, Azan stained, photographically recorded, aligned and deposited in MorphDBase, so that virtual series of sections are made accessible worldwide. The sequence data are deposited in genebank so that molecular and morphological data of the same individuals are connected. Species identification can be done by barcoding or by morphology with reference to a certain specimen. Linking sequence data to morphological data maintains the tradition in nemertean taxonomy and allows comparison with older type material. This standardized procedure allows surprising biogeographical insights that will be exemplified for thus far inadequately described species.

Open access to biodiversity data for botanists via GBIF

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The Global Biodiversity Information Facility (GBIF) is an international initiative providing free and open access to biodiversity data via the Internet for scientific research, conservation, and education. GBIF-mobilised primary biodiversity data include records based on specimens from natural history collections, field observations and multimedia resources. The Federal Ministry of Education and Research (BMBF, grant 01 LI 1001 A-F) is funding a 3-year-project to enlarge the German GBIF community (www.gbif.de).

GBIF Germany *Plants, Algae and Protists* currently delivers 5.8 million records to the global GBIF network, i.e. an increase by 17% in 2011. Mobilisation and digitisation of herbarium data is one of the core activities of the botanical projects of GBIF Germany. The range of datasets is now going to be extended by the inclusion of additional data from herbaria, from living collections (botanical gardens and algal cultures), and from field observations (e.g., floristic surveys and vegetation databases). Some organism groups with low representation in GBIF - such as algae and protists - are now receiving increased attention.

GBIF Germany supports the botanical community through the documentation, quality control, and storage of primary biodiversity data. Technologies developed in the context of BioCAsE (Biological Collection Access Services) are used to publish annotations to digitised herbarium vouchers and to network data providers, e.g. within the *DNA Bank Network* (www.dnabank-network.org). With respect to multimedia objects, GBIF Germany will provide the image server technology for a joint *German Digital Herbarium* and other services for the joint publication of multimedia data as well as metadata. Taxonomic information systems are increasingly based on the *Internet Platform for Cybertaxonomy* software developed by the European Distributed Institute of Taxonomy (EDIT).

The Taxonomist – an endangered Race. A practical Solution for its Survival

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Taxonomy is the basic scientific discipline of biology recording the rich global biodiversity and postulating hypotheses of identity and systematic relationships, on which all other sciences dealing with organisms rely. However, the scientific contributions of taxonomists are largely neglected when using species names in scientific publications by not citing the authority and original description on which they are based. Consequences of this neglect are reduced recognition of the importance of taxonomy, which in turn results in diminished funding, lower interest from journals in publishing taxonomic results, and a reduced number of young scientists entering the field. This has led to the so-called taxonomic impediment at a time when the assessment of the biodiversity on earth is of critical importance for the viability of the human race.

Here we emphasize a simple solution to this dilemma, which has recently been published by Wägele et al. (2011). We merely propose that whenever a species name is used in any kind of publication, the author(s) of the original species hypothesis be included in the literature cited, including also newer taxonomic revisions and identification keys. This means nothing more than what is routinely done for any other hypothesis or assumption included in a scientific publication. In addition, we postulate that journals primarily publishing taxonomic studies should be indexed in ISISM to enhance the recognition and impact of taxonomy.

The practical proposal outlined above would make visible the true contributions of taxonomists within the scientific community, and would provide a more accurate assessment for funding agencies deciding about taxonomic studies, thus helping to alleviate the taxonomic impediment by supporting the recruitment of more young scientists into the field of taxonomy.

Wägele, H., A. Klussmann-Kolb, M. Kuhlmann, G. Haszprunar, D. Lindberg, A. Koch & J. W. Wägele (2011). The Taxonomist – an endangered Race. A practical Proposal for its Survival. *Frontiers in Zoology*, 8:25.

A survey of *Hox* gene expression in adult *Owenia* cf. *fusiformis*

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Hox genes are known to play a key role in body plan formation and often show expression patterns along the anterior-posterior axis during larval development. Numerous studies have explored Hox gene expression in larval development and genome organization in various taxa, but little is known about expression patterns and their function in adult stages. We discovered that the segmented annelid *Owenia* cf. *fusiformis* (Oweniidae) expresses Hox genes not only during larval development but also in adult stages. We identified 9 out of 11 expected Hox gene transcripts in an Illumina mRNA-seq library of only adult stages of *Owenia* cf. *fusiformis* using local Blast algorithms. Using ML-based phylogenetic analysis including Hox genes from 23 additional taxa paralog groups have been identified for our transcripts. These results are a pre-requisite for further studies using in-situ-hybridization, to investigate hox gene expression patterns in adult and larvae stages.

Ultrastructure of photoreceptor-like sense organs in *Polygordius* (Annelida: Polychaeta): a possible character for species distinction?

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Members of Polygordiidae Czerniavsky, 1881 are typical and often dominant inhabitants of coarse sediments subjected to strong currents, "*Polygordius*-Schill". They occur worldwide and have mostly been reported from the intertidal and the continental shelf. Polygordiidae currently comprises only *Polygordius* with 18 nominal and two subspecies. These nematode-like animals are small and lack external signs of segmentation, parapodia and chaetae as well as external ciliation. Thus the number of morphological characters for species distinction is limited to the shape and structures of the prostomium and pygidium. In earlier descriptions, however, less reliable characters as size, color, presence/absence/color of "eyespot", and arrangement of blood vessels were also used. As a result identification of *Polygordius* species is difficult and some of the so-called cosmopolitan species may actually comprise several cryptic species whereas others appear to be invalid. For better distinction among species and understanding of the phylogeny, evolution and biogeography of the group we started an integrative approach using molecular and morphological methods, i.e. DNA-sequencing and LM, SEM, TEM, and cLSM. In order to evaluate whether the photoreceptor-like sense organs previously described for *Polygordius appendiculatus* Fraipont, 1887 provide additional characters of taxonomic value, the ultrastructure of these organs was studied in two other species, *Polygordius erythrophthalmus* Giard, 1880 and *Polygordius lacteus* Schneider, 1868. These organs occur in comparatively large numbers and comprise different types of sensory cells, one rhabdomeric and two ciliary, which are variously combined to form small sensory organs. Whereas structural differences are negligible between *P. erythrophthalmus* and *P. lacteus*, major differences can be observed for *P. appendiculatus*. These results are in accordance with our molecular and morphological studies indicating that *P. erythrophthalmus* represents a junior synonym of *P. lacteus*. Moreover, these preliminary results also show that ultrastructural data may significantly contribute to species distinction in morphologically similar taxa.

A molecular phylogenetic and biogeographical analyses of *Helictotrichon* and related genera of oat grasses (Poaceae: Aveneae)

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Helictotrichon s.str. is a genus with about 65 species. The genus is most diverse in the temperate regions of the northern hemisphere especially the Mediterranean area. A second center of diversity is located sub-Saharan in the high mountain regions of tropical Africa to South Africa. Sequences of the plastid *matK-psbA*, the nuclear ribosomal ITS and a part of nuclear single copy gene topoisomerase 6 (Topo6) were used to reconstruct the phylogeny of the genus *Helictotrichon* with focus on the Eurasian and South African species. In addition, the analysis contains a few species of the tropical mountains of Africa and Asia and a couple of genera of the *Koeleria* lineage. Plastid and nuclear sequences were analysed by maximum parsimony and Bayesian methods. The Topo6 sequences reveal a strong geographical pattern of genetic variation which allows for comprehensive phylogeographic analyses. The South African species and tropical *Helictotrichon elongatum* have two copy types (A and B) of the Topo6 fragment. These copy types are strongly different from that found in the Eurasian species of *Helictotrichon*. Copy type B probably descends from the *Koeleria* lineage and A from the South African *H. longum* or *H. rogerellisii*. Nuclear ITS and plastid *matK-psbA* analyses corroborate the separation of the Eurasian and the sub-Saharan African species as two different groups.

DNA barcoding of diatoms: establishment of routine laboratory protocols

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Diatoms are present in all types of water bodies. As environmental conditions influence species diversity, diatom presences, absences, and abundances are suitable indicators to detect water quality. As conventional morphological identification of diatoms demands specialised in-depth knowledge we establish DNA barcoding methods to develop an easy to use, quick, efficient, and standardised organism identification tool to serve routine water quality assessments. We developed standard laboratory procedures for DNA barcoding in diatoms. For this, we 1) identified a short segment (about 420 bp) of the ribosomal SSU (18S) which is applicable for the identification of diatom taxa, and 2) provide a routine protocol including standard primers for this group of microalgae. We tested the protocol on 29 diatom taxa, representing limnic diatom diversity, and received 100 % correctly identified taxa at species level. Earlier proposed DNA barcoding regions for diatoms are being discussed.

Beschreibungen der Workshops:

Die detaillierte zeitliche Gliederung der Workshops entnehmen Sie bitte dem Plan auf Seite 21. Eine Nachmeldung während der Tagung ist unter Umständen möglich. Bitte wenden Sie sich diesbezüglich an das Tagungsbüro.

Session 1: Neuartige Sequenzanalysen-Programme

Ort: Kursraum, Neubau

ALICSCORE

It has been demonstrated, that random similarity of sequences or sequence sections can impede phylogenetic analyses or the identification of gene homology. Additionally, randomly similar sequences or ambiguously aligned sequence sections can negatively interfere with the estimation of substitution model parameters. Phylogenetic studies have shown, that biases in model estimation and tree reconstructions do not disappear even with large data, but in fact can become pronounced. It is therefore important to identify possible random similarity within sequence alignments in advance of model estimation and tree reconstructions.

Different approaches have been already suggested to identify and treat problematic alignment sections. We propose an alternative method, which can identify random similarity within multiple sequence alignments based on Monte Carlo resampling within a sliding window. The method infers similarity profiles from pairwise sequence comparisons and subsequently calculates a consensus profile. In consequence, consensus profiles identify dominating patterns of non-random similarity or randomness within sections of multiple sequence alignments.

Referent: Bernhard Misof (ZFMK)

MARE – Matrix Reduction

Most approaches in multigene data sets are dealing with predefined thresholds or biclique/quasi-biclique solutions to decrease the amount of missing data. The software MARE delivers an alternative heuristics which (1) assesses tree-likeness of partitions ('genes') in supermatrices using extended geometry mapping and (2) reduces supermatrices with a simple hill climbing procedure to single quasi-bicliques with information content of the matrix. Formally, it reduces a super matrix to an incomplete edge-weighted bipartite graph, representing a subset of taxa and genes. It can be applied currently only on amino acid data. In the workshop, first principles of MARE will be introduced (LINUX and gcc compiler required).

The aim is to raise the awareness for a considered handling of large phylogenomic data sets with their challenges and pitfalls in terms of data quality.

Referent: Karen Meusemann (ZFMK)

SAMS – Split Analysis MethodS

SAMS is an interactive analysis program for molecular data. It implements several routines which, for a given set of aligned DNA sequences, estimate the phylogenetic signal present in the data that supports or contradicts putative splits, i.e. internal branches in putative phylogenetic trees. With this information it is possible to visualize the information content of the data set and the signal to noise relationship. This method does not refer to a tree topology or a model of sequence evolution, and is therefore an ideal tool for a priori estimation of information content of data sets.

Literatur:

Wägele, Johann Wolfgang, and Christoph Mayer. 2007. Visualizing differences in phylogenetic information content of alignments and distinction of three classes of long-branch effects. *BMC Evolutionary Biology* 7: 147. doi:10.1186/1471-2148-7-147.

Referenten: Wolfgang Wägele, Christoph Mayer und Sandra Meid (alle ZFMK)

Session 2: Systemvorführungen zur Sammlungsverwaltung

Ort: Seminarraum, 2. Etage Hauptgebäude

Species File Software (Orthoptera Species File Online)

Species File Software ist ein Werkzeug zur Verwaltung taxonomischer Daten nebst zugehöriger Informationen wie Status und Verbleib der Typen, Literaturzitate, Verbreitung. Specimen-Daten werden mit Fundorten verknüpft, die nach einem hierarchischen System geordnet sind. Medien-Dateien (z.B. Fotos, Tonaufnahmen) sind mit einer Specimen und mit der Art verknüpfbar und lassen sich in der Summe oder Individuen spezifisch präsentieren. Es bestehen drei verschiedene Möglichkeiten der Verknüpfung von anderen Datenbanken, um Species File als taxonomisches Rückrat für andere Webpräsentationen zu nutzen. Als Beispiel wird Orthoptera Species File Online vorgestellt mit eigenen Bearbeitungsmöglichkeiten anhand einer online Übungsversion.

Referent: Sigfrid Ingrisch (ZFMK)

Diversity Workbench – Software components for building and accessing bio- and geodiversity information

The modularized Diversity Workbench (www.diversityworkbench.net) represents a virtual research environment for multiple scientific purposes with regard to management and analysis of life sciences data. The framework is appropriate to store different kinds of bio- and geodiversity data and facilitates the processing of ecological, molecularbiological, observational, collection and taxonomic data. It is capable and flexible enough to be applied as data storage unit for institutional data repositories. The Diversity Workbench is set up on a xml-enabled relational database system. Clients of every database of the Workbench are used as stand-alone applications and provide supporting functions to clients of corresponding databases. This results in a high flexibility with regard to the conceptual design, enabling sophisticated user administration and a rapid setup of project-specific and user-adapted entry forms. Further, it facilitates the dynamic integration of web services

and external data resources. Functions for field data gathering are provided by the application DiversityMobile (DFG-funded project presented under <http://www.diversitymobile.net>), designed for monitoring ecological and biological data, using mobile devices. The database DiversityCollection provides the option to export data to GBIF via the BioCase-Wrapper by using the TDWG standard schema ABCD.

Referenten: Dagmar Triebel, Markus Weiss (beide SNSB) und Tobias Schneider (Universität Bayreuth)

DNA Bank Network – Manage and reference your DNA samples by using GBIF infrastructure

Access to genomic DNA collections becomes increasingly important, as fast progress in DNA based technologies continues to dramatically speed up research on the genetic diversity of life. Nevertheless, the scientific community has not yet made the storage of DNA material in natural history collections a matter of general routine. As a consequence, falsifiability of results and original data - the foundation of good scientific practice - is often neglected. Several countries and institutions are now tackling this deficit by establishing DNA banks and providing access through the DNA Bank Network. The DNA Bank Network is a non-commercial scientific service based on the infrastructure of the Global Biodiversity Information Facility (<http://www.gbif.org/>) and the Biological Collection Access Service (<http://www.biocase.org/>). Currently five research collections focus on different groups of organisms (bacteria, archaea, protists, plants, algae, fungi, and animals) and provide access to information associated with their DNA samples. This includes associated DNA, tissue and specimen information. Each institution operates independently, but the DNA and specimen databases of all partners are jointly accessible via a central web portal (<http://www.dnabank-network.org/>).

The Workshop will give an overview about the technical infrastructure of BioCASE, GBIF and the DNA Bank Network. Furthermore the workshop will propose best practice guidelines for referencing voucher specimens, DNA samples and GenBank accessions. The open source software DNA Module is an easy way of managing your DNA collection and referencing DNA samples with any GBIF compliant database worldwide. Attendees can try out the DNA Module and the web portal. In preparation of this workshop attendees are called upon to check if their own institutions are providing specimen data to GBIF already, and if data on DNA voucher specimens are being made available via GBIF. Please bring your own laptop if possible.

Referenten: Gabriele Dröge (Botanischer Garten und Museum Berlin-Dahlem) und Jonas Astrin (ZFMK)

SeSAM – das Senckenbergische SAMmlungsmanagement-System

Sammlungen enthalten Nachweise von Vorkommen bestimmter Arten an bestimmten Orten zu bestimmten Zeiten. Außerdem sind Sammlungen Archive für wissenschaftliche Anschauungen und Theorien zu einem bestimmten Zeitpunkt. Die Dokumentation der komplexen Zusammenhänge zwischen Objekt, Objektdaten und

Theorien gelingt optimal nur mit IT-Unterstützung. Das senckenbergische Sammlungsmanagementsystem SeSam ist eigens hierfür entwickelt worden.

Referenten: Michael Tuerkay, Andreas Allspach und Lothar Menner (alle Senckenberg Forschungsinstitut)

Session 3: Weitere Workshops

Ort: Museumsschule, 2. Etage Hauptgebäude

Utilization of the Character Matrices Module in MorphDBase: Learn how to increase the Quality of morphological Matrices.

MorphDBase is an online web portal and database. MorphDBase is the way to archive, share and disseminate data of biological species and morphological structures. Researchers can provide detailed documentation, and can efficiently collaborate with colleagues.

In the workshop the participants will learn how to increase transparency and reproducibility of their scientific workflow by working with the database and they will learn how to use the matrix module provided within MorphDBase. The workshop will be divided into the following sections:

- A brief introduction will give an overview of the interface and the idea behind the Project MorphDBase.
- In a "hands on" section the participants can use own material to upload and edit content into the Database, annotate it, and share it with other participants.
- In the last part the matrix module will be introduced and used by the participants. They will learn how to build a morphological character matrix from scratch, learn about the pitfalls of character matrix building and see how MorphDBase can help in increasing the quality of morphological character matrices.

Referenten: Peter Grobe (ZFMK) und Lars Vogt (Universität Bonn)

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

3D reconstruction of morphologic structures has become an increasingly used method in recent years. Correct 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. The majority of scientists use expensive programs and workstations to access this methodological field. The aim of this workshop is to introduce a method pipeline which is completely open source (Programs Reconstruct, Blender, Image J, and Scribus) and does not need workstations. Participants will learn:

- how to segment (manually and semi-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.

Referent: Alexander Blanke (ZFMK)

Notizen:

