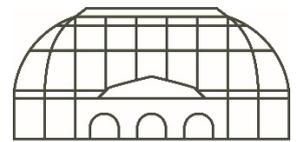


Caryophyllales 2015

Conference Programme and Abstracts

DFG



BG | Botanischer Garten &
BM | Botanisches Museum
Berlin

Freie Universität



Berlin

Caryophyllales 2015 – Conference Programme and Abstracts

Berlin September 14-19, 2015

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Botanic Garden and Botanical Museum Berlin-Dahlem

Freie Universität Berlin

Königin-Luise-Straße 6-8

14195 Berlin, Germany

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WLAN Name: conference

Key: 7vp4erq6

Programme overview

	Core conference			Workshops		
Time slot *	Pre-conference Sept 13, 2015 (Sun)	Sept 14, 2015 (Mon)	Sept 15, 2015 (Tue)	Sept 16, 2015 (Wed)	Sept 17, 2015 (Thu)	Sept 18, 2015 (Fri)
9.00-10.30		Opening session	Session 3: Caryophyllaceae (1)	Session 7: Floral morphology	EDIT Platform (Introduction)	Herbarium management: JACQ
10.30-11.00		<i>Coffee break & Poster session</i>	<i>Coffee break & Poster session</i>	<i>Coffee break & Poster session</i>	<i>Coffee break</i>	<i>Coffee break</i>
11.00-12.30		Session 1: Adaptive evolution	Session 4: Caryophyllaceae (2)	Session 8: A wider picture	EDIT Platform (hands-on)	Herbarium management JACQ Sileneae biodiversity informatics
12.30-14.00		<i>Lunch break</i>	<i>Lunch break</i>	<i>Lunch break</i>		
14.00-15.30		Session 2: Amaranthaceae s.l.	Session 5: Portulacinae	Session 9: Different lineages	EDIT Platform (hands-on)	Xper2 Sileneae biodiversity informatics
15.30-16.00		<i>Coffee break & Poster session</i>	<i>Coffee break & Poster session</i>	<i>Coffee break</i>	<i>Coffee break</i>	<i>Coffee break</i>
16.00-17.30		Tour: Garden & Dahlem Seed Bank	Session 6a/b: Caryophyllaceae (3) / Aizoaceae	Closing session	EDIT Platform (hands-on)	Xper2
17:30-18:45			Tour: Herbarium, Museum, Library			
	18:30 Ice-breaker		19:00 Conference dinner			
	* exact timing see programme					

Sunday, Sept. 13**18:30-21:00 Icebreaker**

Venue: The tropical greenhouses at the botanical garden

18:00 Registration desk open (at the greenhouses)

18:30 Reception

Monday, Sept. 14, morning

8:00 Registration desk open (at the botanical museum)

9:00-10:30 Opening

9:00 Welcome and logistics

9:05 T. Borsch An integrative and dynamic approach for monographing species-rich plant groups - building the global synthesis of the angiosperm order *Caryophyllales*9:35 P. Hernández Ledesma A taxonomic backbone for the global synthesis of species diversity in the angiosperm order *Caryophyllales*

9:55 W. Berendsohn A global synthesis: e-Taxonomy and the botanical research community

10:10 S. Brockington Lineage-specific gene radiations underlie the evolution of novel betalain pigmentation in the *Caryophyllales***10:30-11:00 Coffee break and poster session**(P01) I Castañeda & al. (S. Fuentes-Bazan) Distribution and evolution of *Coccoloba (Polygonaceae)* in the Antilles(P08) S. I. Rupp & al. What's inside? - Four anatomical leaf types in the *Amaranthaceae* s.str.(P13) J. A. Akopian Bio-morphological investigation of the *Chenopodiaceae* Vent. family in South Transcaucasia**11:00-12:30 Session 1: Adaptive evolution in the *Caryophyllales***11:00 A. Moore & al. Phylogeny of the *Portulacineae* from sequence capture data and perspectives on the evolution of CAM photosynthesis.11:15 E. Voznesenskaya & al. Evolution of C4 photosynthesis in *Caryophyllales*: the role of C3-C4 intermediate species11:30 M. Lauterbach & al. Development of the C4 pathway takes its time in *Salsola soda* – C4 leaves follow C3 cotyledons11:45 M. Doostmohammadi & al. (H. Akhiani) Is *Pteropyrum* a causeway to C4 evolution in *Polygonaceae*?12:00 R. Khoshravesh & al. Adaptive photosynthetic strategies in Old World *Salsoleae*: evolution of C4 photosynthesis and morpho-anatomical traits12:15 N. Koteyeva & al. Temporal and spatial transitions in development of C4 photosynthesis in C4 *Suaedoideae* plants**12:30-14:00 Lunch break**

Monday, Sept. 14, afternoon

14:00-15:15 Session 2: Systematics and diversity of *Amaranthaceae* s.l.

14:00	G. Kadereit	<i>Chenopodiaceae</i> – loving the extreme!
14:15	V. Di Vincenzo & al.	Evolutionary diversification of the African Achyranthoid clade (<i>Amaranthaceae</i>) in the context of sterile flower evolution and epizoochory
14:30	S. Fuentes & Thomas Borsch	Phylogeny and evolution patterns of <i>Chenopodium</i> sensu stricto
14:45	A. Sukhorukov & al.	Exact delimitation of the morphologically similar but phylogenetically distant genera <i>Blitum</i> and <i>Oxybasis</i> (<i>Chenopodiaceae</i> – <i>Amaranthaceae</i>): a case study of several enigmatic taxa
15:00	P. Kamau (Kenya)	Diversity and Conservation Status of the Family <i>Amaranthaceae</i> in East Africa
15:15	M. Keshavarzi & N. Khorsandiyar	Stem anatomical study of <i>Sarcocornia fruticosa</i> (<i>Amaranthaceae</i>)

15:15-15:45 Coffee break and poster session

(P02)	J. M. Acosta & al.	Architectural models in <i>Gomphrena</i> (<i>Amaranthaceae</i>)
(P09)	T. Chatrevoor & H. Akhani	An integrated morpho-molecular study of the genus <i>Salicornia</i> (<i>Chenopodiaceae</i>) in Iran

15:45-17:30 Guided tours to the botanical garden and Dahlem seed bank

Tuesday, Sept. 15, morning

9:00-10:30 Session 3: Systematics and diversity of *Caryophyllaceae* (1)

9:00	M. S. Dillenberger & J. W. Kadereit	How to achieve monophyletic genera in the <i>Caryophyllaceae</i> - a case study of <i>Minuartia</i> L. and related genera
9:15	B. Frajman & al.	Did environmentally induced phenotypic variation lead to recurrent speciation in the <i>Heliosperma pusillum</i> group (<i>Caryophyllaceae</i>)?
9:30	G. Mostafavi & al.	Morphology, diversity and micromorphology of the <i>Minuartia</i> species (<i>Caryophyllaceae</i>) in Iran
9:45	A. Nersesyan	Tribe <i>Caryophylleae</i> (fam. <i>Caryophyllaceae</i> , subfam. <i>Caryophylloideae</i>) in the Southern Transcaucasus and adjacent regions
10:00	M. Timaná de la Flor & al.	Predictive biogeography of high-Andean <i>Caryophyllaceae</i> in the context of climate change
10:15	A. García-Fernández & al.	<i>Silene ciliata</i> (<i>Caryophyllaceae</i>) as a model species in a climate change scenario: our multidisciplinary approaches

10:30-11:00 Coffee break and poster session

(P04)	N. Vlasova	Systematics and biogeography of <i>Stellaria</i> L. (<i>Caryophyllaceae</i>) of the Asian Russia and Mongolia
(P10)	E. Ataşlar & K. Yildiz	Seed morphology of West Anatolian <i>Gypsophila</i> L. species from Turkey
(P14)	T. R. Stoughton	Edaphic endemism and <i>Silene verecunda</i> (<i>Caryophyllaceae</i>): One taxon, or twenty?

11:00-12:45 Session 4: Systematics and diversity of *Caryophyllaceae* (2)

11:00	J. C. del Valle & al.	The Good, the Bad and the Ugly: Phylogeographic Evidence from Three Genomes in Iberian <i>Silene</i>
11:15	Y. Naciri & al.	A phylogenetic circumscription of the <i>Silene italica</i> group and its allied species (<i>Caryophyllaceae</i>) in the Mediterranean Basin
11:30	K. Yildiz & Z. Aydın	Biodiversity and systematics in the <i>Silene</i> (<i>Caryophyllaceae</i>) species occurring in Turkey
11:45	Z. Aydın & B. Oxelman	Cryptic diversity in <i>Silene</i> section <i>Atocion</i> (<i>Caryophyllaceae</i>)
12:00	A. Gholipour & F. Rahimi Pashakolai	Chromosome number variation in Iranian <i>Silene</i> (<i>Caryophyllaceae</i>) species
12:15	M. Keshavarzi & al.	Seed morphology of the <i>Silene commelinifolia</i> Boiss. complex (<i>Caryophyllaceae</i>) species
12:30	I. Casimiro-Soriguer & al.	Transcriptome analysis of the petal of <i>Silene littorea</i>
12:45	Bengt Oxelman	Sileneae.info: A continuously updated taxonomic revision of <i>Sileneae</i> , based on species tree phylogenies and morphological data

13:00-14:00 Lunch break

Tuesday, Sept. 15, afternoon

14:00-15:00 Session 5: Phylogeny, systematics and evolution of *Cactaceae*

14:00	S. Arias & T. Terrazas	A systematic approach to <i>Hylocereae</i> and <i>Echinocereae</i> (<i>Cactaceae</i>)
14:15	R. Nyffeler	Molecular phylogenetics and classification of <i>Cactaceae</i> : insights from exploring GenBank and applying a supermatrix approach
14:30	N. Korotkova	Phylogenetic study of the <i>Hylocereae</i> (<i>Cactaceae</i>)
14:45	D. Hunt	The CITES <i>Cactaceae</i> Checklist

15:00-15:45 Coffee break and poster session

(P03)	P. Hernández-Ledesma & R. Bárcenas	Microstructural organization of the psbA-trnH intergenic spacer in <i>Cactaceae</i> (<i>Caryophyllales</i>)
(P06)	K. Yildiz	Seed, pollen and chromosome morphology of <i>Silene</i> (<i>Caryophyllaceae</i>) in Turkey
(P12)	T. Shagholi & al.	Biodiversity of <i>Tamarix</i> in Iran

15:45-17:30 Session 6a: *Caryophyllaceae* (3) / Session 6b: *Aizoaceae*

16:00	S. Ghazanfar	Distribution patterns of the <i>Caryophyllaceae</i> in Iraq
16:15	I. Mehregan & al.	<i>Caryophyllaceae</i> in Iran, a band of mismatches
16:30	D. B. Montesinos-Tubée	Systematic update of <i>Caryophyllaceae</i> in Peru: Diversity and distribution
16:45	C. Klak & al.	Phylogeny and character evolution for the recently diversified <i>Ruschieae</i> (<i>Aizoaceae</i>) in southern Africa
17:00	K. Bohley	Phylogeny, leaf anatomical characters and biogeography of <i>Sesuvioideae</i> (<i>Aizoaceae</i>)
17:15	S. Liede-Schumann & H. E. K. Hartmann	Phylogeny of the genus <i>Drosanthemum</i> (<i>Aizoaceae-Ruschioideae</i>)

17:30-18:45 Guided tours to the herbarium, library and botanical museum

19:00- Conference Dinner

Wednesday, Sept. 16, morning

9:00-10:30 Session 7: Floral morphology and evolution in *Caryophyllales*

9:00	H. Flores & al.	Homology of floral structures in <i>Amaranthaceae</i> s.l.: a perspective from floral ontogeny.
9:15	A. Vrijdaghs & al.	The development from underlying intercalary meristems of the calyx and androecial tube in <i>Amaranthaceae</i> s.l.
9:30	I. Sánchez del Pino	Floral evolution and development in subfamily <i>Gomphrenoideae</i> (<i>Amaranthaceae</i> s.str.), preliminary data
9:45	P. dos Santos & L. Ronse de Craene	Floral development of <i>Lewisia</i> (<i>Montiaceae</i>): investigating patterns of perianth and stamen diversity
10:00	L. Ronse de Craene & P. dos Santos	Pleiomery and meiomery in <i>Montiaceae</i> : mechanical pressure as driver of floral diversification
10:15	D. D. Jolles	Hypothesis testing in circumscription-resistant lineages: morphometric methods for estimating patterns of floral evolution in species complexes

10:30-11:00 Coffee break and poster session

(P05)	J. M. de Vos	Ecological determinants of reproductive display: Evolution of flower number - flower size trade-offs.
(P07)	J. M. Burke	Towards a global checklist of <i>Rumex</i> (<i>Polygonaceae</i>), a species-rich genus with diverse sexual systems
(P11)	P. M. Gonella & al.	Advances in the taxonomy of the Brazilian-tetraploid clade of <i>Drosera</i> (<i>Droseraceae</i>)

11:00-12:45 Session 8: A wider picture

11:00	M. J. Moore & al.	What can "big data" tell us about <i>Caryophyllales</i> ? Resolving phylogeny, genome duplications, and ecophysiological evolution in a hyperdiverse clade
11:15	A. Barker & D. Kirkup	Plants of the World Online – building on the legacy of eMonocot
11:30	T. Hennig	Sample data processing in an additive and reproducible taxonomic workflow
11:45	H. Ochoterena	Cladistics using morphology and its impact on ontology and diagnosis
12:00	G. Droege	The Global Genome Biodiversity Network
12:15	T. R. Stoughton	Next-gen data for a next-gen problem: Resolving relationships and taxonomy of the tuberous, perennial <i>Claytonia</i> (<i>Montiaceae</i>)
12:30	G. A. Allen	Colonization of North America by alpine-arctic lineages of <i>Polygonaceae</i> and <i>Caryophyllaceae</i>

12:45-14:00 Lunch break

Wednesday, Sept. 16, afternoon

14:00-15:30 Session 9: Phylogeny and evolution of different *Caryophyllales* lineages

14:00	A. Fleischmann	Evolution of carnivory in <i>Caryophyllales</i> and diversification of <i>Drosera</i>
14:15	N. Douglas & al.	An expanded view of the phylogeny of <i>Nyctaginaceae</i> based on chloroplast data
14:30	S. Mosaferi & al.	Genetic diversity of <i>Persicaria minor</i> (<i>Polygonaceae</i>) in Iran
14:45	J. J. Ortiz Díaz & al.	Diversity and distribution of <i>Coccoloba</i> (<i>Polygonaceae</i> , <i>Eriogonoideae</i> , <i>Coccolobeae</i>) in Mesoamerica
15:00	D. Toere & al.	Molecular phylogeny of <i>Acantholimon</i> : a diverse Irano-Turanian genus of <i>Plumbaginaceae</i> (<i>Caryophyllales</i>)
15:15	M. Malekmohammadi & al.	Phylogenetic study of the genus <i>Limonium</i> (<i>Plumbaginaceae</i>) using four nuclear and chloroplast sequence data
15:30	C. F. Catarino de Sá	<i>Nyctaginaceae</i> in Brazil: species richness, herbarium collections and conservation status

15:45-16:15 Coffee break

16:15-17:30 Closing Session

16:15	C. Miller & W. G. Berendsohn	The World Flora Online – Achieving Target 1 of the Global Strategy for Plant Conservation
16:30	Discussion	The <i>Caryophyllales</i> Network – Quo vadis?
17:20	T. Borsch	Closing remarks

Thursday, Sept. 17: Workshops**9:00-10:30: The EDIT Platform for Cybertaxonomy, Introduction**

A. Güntsch, A. Müller, K.Luther	Introduction to the EDIT components, development perspectives and installation of the EDITor
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11:00-12:30 Workshop 1: EDIT Platform for Cybertaxonomy

A.Müller, K. Luther, C. Mathew, P.Plitzner, S. v. Mering, T. Henning, N. Kilian	EDITor hands-on with focus on taxonomy (taxa, synonyms, rebinations)
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14:00-15:30 Workshop 2: EDIT Platform for Cybertaxonomy

A.Müller, K. Luther, C. Mathew, P.Plitzner, S. v. Mering, T. Henning, N. Kilian	EDITor hands-on with focus on factual data, term editing and bulk editing
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16:00-17:30 Workshop 3: EDIT Platform for Cybertaxonomy

A.Müller, K. Luther, C. Mathew, P.Plitzner, S. v. Mering, T. Henning, N. Kilian	EDITor hands-on with focus on specimen editing
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Friday, Sept. 18

9:00-12:30 Workshop 4: JACQ

11:00-12:30 Sileneae biodiversity informatics

14:00-17:30 Workshop 5: Xper²

14:00-15:30 Sileneae biodiversity informatics

Saturday, Sept. 19

Post conference excursion to Schorfheide-Chorin

8:00 Start at BGBM

Abstracts

(listed in alphabetical order according to the last name of the first author)

Architectural models in *Gomphrena* L. (*Amaranthaceae*)

Juan M. Acosta, Mariel G. Perreta & Abelardo C. Vegetti
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The architecture of a plant depends on the nature and relative arrangement of each of its parts. Originally, architectural studies were focused with the analysis of the aerial vegetative structure of trees, so the plant architecture of herbs were poorly characterized in morphological and taxonomic studies. In our study, the concepts of architectural analysis were applied to species of the genus *Gomphrena* as a starting framework for understanding their structural characteristics in *Amaranthaceae* herbs. Based on this approach, different vegetative growth models were determined for 23 species included in this study. The most important architectural characters are: 1) number of axes categories for each model and 2) growth form of the epicotilar axis. The great variability in the vegetative morphology observed among the species included in this study can be summarized in nine different structural models. Despite the frequently stressed importance of considering plant morphology and/or architecture to understand their phylogeny, very few studies actually describe the link between phylogeny and architecture. Although here we probably require more data about the plant structure of the others *Gomphrena* species not included in our study, the architectural analysis allowed us to show different patterns of vegetative development in *Gomphrena* and these data could be useful to integrate morphological features with taxonomic and/or phylogenetic purposes.

Bio-morphological investigation of the *Chenopodiaceae* Vent. family in South Transcaucasia

Janna A. Akopian
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Chenopodiaceae Vent. family in South Transcaucasia (S) includes 90 species and subspecies from 36 genera and 8 subfamilies and is represented by the following biomorphotypes: phanerophytes (*Halostachys belangeriana*); xeromorphic orthotropic chamaephytes (*Atriplex cana*, *A. turcomanica*, *Caroxylon ericoides*, *C. nodulosum*, *C. vermiculatum*, *Halothamnus glaucus*, *Krashennikovia ceratoides*, *Suaeda microphylla*); orthotropic and plagiotropic nanochamaephytes (*Camphorosma lessingii*, *Caroxylon gemmascens*, *Noaea mucronata* ssp. *mucronata*, *N. mucronata* ssp. *leptoclada*, *Kaviria cana* ssp. *cana*, *K. cana* ssp. *futilis*, *K. tomentosa* ssp. *tomentosa*, *Kochia prostrata*, *Suaeda dendroides*); clump- or cushion-forming chamaephytes and nanochamaephytes with rooting plagiotropic shoots (*Camphorosma monspeliaca*, *C. monspeliaca* var. *pulviniformis*, *Halimione verrucifera*, *Halocnemum strobilaceum*, *Kalidium capsicum*); caudex-forming chamaephytes and nanochamaephytes (*Anabasis aphylla*, *A. eugeniae*, *Caroxylon dendroides*, *Kaviria tomentosa* ssp. *takhtadshanii*); hemicryptophytes with annual monocyclic monocarpic shoots and special type of storage roots (*Beta corolliflora*, *B. lomatogona*, *B. macrorrhiza*, *B. maritima*); vine-like hemicryptophytes with scrambling annual, monopodial, extremely elongated shoots and fleshy storage roots (*Hablitzia tamnoides*); therophytes (*Anthoclamys polygonoides*, *Atriplex* species, *Bassia*

hyssopifolia, *Bienertia cycloptera*, *Caroxylon nitrarium*, *Ceratocarpus arenarius*, *Chenopodium* species, *Climacoptera crassa*, *Girgensohnia oppositiflora*, *Halanthium rarifolium*, *H. kulpianum*, *Halimocnemis pilifera*, *Kali tamamschjanae*, *K. tragus*, *Kochia scoparia*, *Microcnemum coralloides* ssp. *anatolicum*, *Noaea minuta*, *Petrosimonia brachiata*, *P. glauca*, *Salsola soda*, *Salicornia perennans*, *Seidlitzia florida*, *Suaeda acuminata*, *S. altissima*, *S. gracilis*, *S. salsa* and others, including annuals/biennials with basal rosettes - *Beta maritima*, *Chenopodium foliosum*, *Spinacia tetrandra*). Therophytes (59 species) and chamaephytes (25 species) are the most numerous in ST, while hemicryptophytes - 5 species, phanerophytes - 1 species.

Colonization of North America by alpine-arctic lineages of *Polygonaceae* and *Caryophyllaceae*

Geraldine A. Allen

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The phylogeographic patterns of arctic-alpine plants have received much recent attention, though understanding of these patterns can be limited by insufficient sampling of geographic ranges, difficulties in delimiting species, or insufficiently resolved phylogenies. I describe recent collaborative studies in arctic-alpine species of three genera. *Bistorta* (*Polygonaceae*) comprises ~50 northern hemisphere species, of which three are native to North America. The alpine *B. bistortoides* and the Beringian arctic *B. plumosa* are genetically variable, with strong geographic differentiation. In contrast, the widely distributed arctic-alpine *B. vivipara* has low genetic diversity with little geographic structure, suggesting recent rapid spread. The three species arrived separately in North America via the Bering Strait at different times during the Pleistocene. *Oxyria* (*Polygonaceae*) contains only one species that is widespread, the arctic-alpine *O. digyna*, which originated in south-central Asia and migrated east and west to its present circumpolar range. It colonized North America primarily from the west via the Bering Strait, with additional more recent migrations from Greenland and Europe. In *Silene* (*Caryophyllaceae*), at least three or four lineages have independently colonized arctic-alpine North America; one of these is *S. acaulis*. In a range-wide study, we identified a complex history for *S. acaulis* with distinct European-centred and North-American-centred intraspecific lineages. We inferred a southern European origin of this species with subsequent spread to North America, possibly by multiple routes. For all of these genera, Beringia has provided a major migration corridor, but complex patterns indicate repeated colonization from multiple sources.

Seed morphology of West Anatolian *Gypsophila* L. species from Turkey

Ebru Ataşlar¹ & Kemal Yıldız²

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Seed morphology of 12 taxa (6 of them endemic) that belong to the genus *Gypsophila* L. were investigated using scanning electron microscopy (SEM). In this study the seed morphology of *Gypsophila sphaerocephala* Fenzl ex Tchihat var. *sphaerocephala* (Sect. *Capituliformes*), *G. arrostii* Guss. var. *nebulosa* (Boiss. & Heldr.) Barkoudah, *G. perfoliata* L. var. *perfoliata*, *G. perfoliata* L. var. *araratica* Kit Tan, *G. curvifolia* Fenzl, *G. eriocalyx* Boiss. var. *eriocalyx*, *G. eriocalyx* Boiss. var. *henrici* (Czecz.) Barkoudah (Sect. *Rokejeka*), *G. parva* Barkoudah, *G. viscosa* Murray (Sect. *Dichoglottis*), *G. tubulosa* (Jaub. & Spach) Boiss. (Sect. *Macrorrhizaea*), *G. pilosa* Huds., and *G. venusta* Fenzl (Sect. *Hagenia*) were investigated. Differences in seed morphology between these taxa were determined.

The purpose of this study was to use SEM to determine the extent to which morphological differences affect seed morphology in some species of *Gypsophila*.

A systematic approach to *Hylocereeae* and *Echinocereae* (Cactaceae)

Salvador Arias & Teresa Terrazas

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Climbing, epiphytic (*Hylocereeae* tribe) and columnar cacti (*Echinocereae* tribe) native to North and Central America form two natural groups related. Although most species have diversified across Mexico, Guatemala and Costa Rica, some extend from the SE United States (Florida) to the northeast of Argentina. Different genera have been included and excluded (*Hylocereeae*: 6-10; *Echinocereae*: 13-25), as well as the number of recognized species (*Hylocereeae*: 63-82 spp.; *Echinocereae*: 124-216 spp.). Our systematic study includes three stages. First, analyze the phylogenetic relationships of *Hylocereeae* and *Echinocereae* to recognize monophyletic genera, using information from cpDNA markers, morphology and anatomy. ***Hylocereeae*** is a monophyletic group where changes are observed in some characters: climber to epiphytic species; cylindrical and thick to flat and thin branches; from heavily armed to subinermes branches; large and nocturnal to short and sometimes daytime flowers. According to our results, *Echinocereae* (sensu stricto) is limited to North America and has some structural changes: erumpent areola, small shrubs to large trees. Second, we are developing taxonomic comparative studies for delimiting species with more comprehensive evidence (morphology, sequences, and distribution). Advances include genera *Aporocactus*, *Disocactus*, *Cephalocereus*, *Pachycereus* and *Peniocereus*. Third, integrate these results in their classification and regional floras (e.g. Tehuacan, Mesoamerica, Bajío).

Cryptic Diversity in *Silene* section *Atocion* (Caryophyllaceae)

Zeynep Aydin^{1,2} & Bengt Oxelman²

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Section *Atocion* Otth in the genus *Silene* includes a number of highly similar annual taxa that are distributed in the Eastern Mediterranean. Recently, and based on phylogenetic evidence, the section has been restricted to 3 - 5 species with several subspecies sometimes recognized. We have previously showed that none of these classifications is congruent with phylogenetic relationships inferred from DNA sequence data from multiple nuclear loci.

In this study, we investigate species delimitations and phylogenetic relationships in sect. *Atocion* using information from six potentially unlinked nuclear loci. Preliminary results indicate high species diversity, including several cryptic species that lack clear geographic or morphological distinctiveness.

Plants of the World Online, building on the legacy of eMonocot

Abigail Barker & Don Kirkup

The Royal Botanic Gardens, Kew; A.Barker@kew.org & D.Kirkup@kew.org

eMonocot was a successful collaborative project between the NHM, Oxford University and Kew, which aimed to link together monocot taxonomists by providing support and tools to enable communities to manage their taxonomic data online and in doing so, contribute to a portal. The portal was aimed at those studying the ecology or evolution of the monocot plants, or users who wanted to understand monocot biodiversity and conservation.

Kew published its science strategy in May 2015 and one of the nine strategic outputs is the Plants of the World Online - POWOP. POWOP reuses the eMonocot model but also extends it aiming to deliver an online global resource for plants not just monocots. This e-resource will be a single point of access for authoritative information on plant species, from anywhere in the world. It will provide a multi-dimensional catalogue of plant life, including information on identification, distribution, traits, threat status, molecular phylogenies and uses. It will use Kew's extensive data resources alongside images from the digitisation of the collections. This portal will enable dissemination of plant information at levels accessible to all. This will ultimately lead to a resource that has global coverage, linking directly through to the taxonomic framework provided by the World Flora Online (www.worldfloraonline.org), which aims to provide an online taxonomic resource for all known plants.

Phylogeny, leaf anatomical characters and biogeography of *Sesuvioideae* (*Aizoaceae*)

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The *Sesuvioideae* are sister to the remaining *Aizoaceae* and mainly consist of inconspicuous succulent herbs distributed in tropical and subtropical areas. The subfamily currently includes five genera —*Cypselea*, *Sesuvium*, *Trianthema*, *Tribulocarpus* and *Zaleya*—with about 60 species. Shared traits are circumscissile capsules, stipule-like appendages at the petiole and leaf base, and arillate seeds. Centre of diversity of the subfamily is southern Africa, but it is also found in Australia and the Americas. In contrast to the remaining subfamilies of *Aizoaceae*, the *Sesuvioideae* seem not to express CAM photosynthesis but are dominated by C_4 species.

We first present major results of molecular phylogenetic and biogeographical analyses as well as a leaf anatomical survey of the subfamily (Bohley et al. 2015). The subfamily likely originated in Africa/Arabia with *Tribulocarpus* as sister to a clade containing *Trianthema*, *Sesuvium* (incl. *Cypselea*) and *Zaleya*. Intercontinental dispersal occurred within *Trianthema* (to Australia and South America) and *Sesuvium/Zaleya* (to Australia and North/Central America). We found a high diversity in anatomical leaf types (two C_3 and four C_4 types) and frequent shifts in leaf anatomical traits with multiple losses or reduction of water storage tissue in the subfamily. The biochemical diversity of the C_4 syndrome in *Sesuvioideae* points to multiple origins of the C_4 pathway, however, ancestral character reconstruction favours a single origin of C_4 and two subsequent reversals.

Furthermore, we present preliminary results of ongoing studies on the systematics and photosynthetic pathway of *Sesuvium*. Particularly *S. portulacastrum* is an interesting species concerning its adaptability in extreme environments.

An integrative and dynamic approach for monographing species-rich plant groups – building the global synthesis of the angiosperm order Caryophyllales

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One of the major goals of systematics is to provide a synthesis of knowledge on the diversity of a group of organisms, such as flowering plants. Biodiversity conservation and management call for rapid and accurate global assessments at the species level. At the same time the rapid development of evolutionary biology with a spectrum of approaches to test species relationships and species limits, has revolutionized and is still revolutionizing the science of plant systematics including taxonomy. We explore the relevant scientific and technological developments with the aim to suggest a conceptual framework for an integrated monographic synthesis which can reach global coverage. Our exemplar group are the Caryophyllales, which are a lineage of worldwide distribution, comprising approx. 5% of flowering plant species diversity. The current situation of classification is marked by a transition from pre-phylogenetic treatments to taxonomic treatments increasingly evaluated in an evolutionary context. Structured data (both molecular and morphological), linked to well-documented specimens will be important as fundamental entities of information that can be subjected to evolutionary analysis. As a result, taxon concepts are established as hypotheses which then can be used as basis for a classification system in a second step. Global syntheses need to provide information and use a classification system that reflects the current state of knowledge. In order to accommodate the constantly improved understanding of the organisms, eventually also resulting in the change of taxon concepts, the treatments need to be dynamic. The workflow for a global monographic synthesis as outlined here is supported by currently available biodiversity informatics tools such as the EDIT Platform for Cybertaxonomy. The availability of electronic sources (names, protologues, type images, literature) greatly facilitates the access to information, but as our case shows, considerable efforts for data curation and research are still needed. The implementation of a global monographic synthesis such as the Caryophyllales requires the involvement of the global scientific community.

Lineage -specific gene radiations underlie the evolution of novel betalain pigmentation in *Caryophyllales*

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Betalain pigments are unique to the *Caryophyllales* and structurally and biosynthetically distinct from anthocyanins. Two key enzymes within the betalain synthesis pathway have been identified: 4,5-dioxygenase (DODA) that catalyzes the formation of betalamic acid and CYP76AD1, a cytochrome P450 gene that catalyzes the formation of cyclo-DOPA. We performed phylogenetic analyses to reveal the evolutionary history of the DODA and CYP76AD1 lineages and in the context of an ancestral reconstruction of pigment states we explored the evolution of these genes in relation to the complex evolution of pigments in *Caryophyllales*. Duplications within the CYP76AD1 and DODA lineages arose just before the origin of betalain pigmentation in the core *Caryophyllales*. The duplications gave rise to DODA-a and CYP76AD1-a isoforms that appear specific to betalain synthesis. Both betalain-specific isoforms were then lost or downregulated in the anthocyanic *Molluginaceae*

and *Caryophyllaceae*. Our findings suggest a single origin of the betalain synthesis pathway, with neofunctionalization following gene duplications in the CYP76AD1 and DODA lineages. Loss of DODA-a and CYP76AD1-a in anthocyanic taxa suggests that betalain pigmentation has been lost twice in *Caryophyllales*, and exclusion of betalain pigments from anthocyanic taxa is mediated through gene loss or downregulation.

Towards a global checklist of *Rumex* (Polygonaceae), a species-rich genus with diverse sexual systems

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Rumex is the second largest genus in the *Polygonaceae*. With ca. 200 species and a nearly cosmopolitan distribution across temperate regions, compiling a comprehensive list of all species is a daunting task. The last monograph was produced by Meissner in 1856. During the 20th century, Rechinger produced regional treatments for *Rumex*. These taxonomic works, along with other regional treatments, can also provide a wealth of information regarding sexual systems and natural history of *Rumex* species. This study synthesizes previous taxonomic work, to move towards a comprehensive global treatment for the genus. Subgeneric classification schemes, distribution patterns, and sexual system diversity are presented.

Transcriptome analysis of the petal of *Silene littorea*

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Silene littorea shows a flower color polymorphism, with white-flowered individuals coexisting with dark pink- and light pink-flowered individuals. Here we will use RNA-Seq to sequence and measure the expression of the anthocyanin biosynthetic pathway genes of the three color morphs across three developmental stages. We will also determine the biochemistry of the petal. We identified 29 putative paralogues for the 15 candidate genes, and assembled the complete coding sequences for 28 out of 29, including some tentative regulators. Among the 29 putative paralogues, we identified 622 SNPs, however only 9 SNPs in *Ans* differentiated the color morphs based on the allele frequencies. On the other hand, the expression analysis showed that F3h had more than 42x differential expression between pigmented and white petals. The biochemical profile revealed cyanidin as the primary anthocyanin and five flavonoid intermediates.

Diversity and evolution of the genus *Coccoloba* (*Polygonaceae*) in the West Indies

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Coccoloba is a Neotropical genus of about 120 species of trees and shrubs, of which 63 species with 81% endemism are found to occur in the West Indies. Based on a detailed comparative analysis used also for species descriptions, a matrix of 40 morphological and anatomical characters was generated and subjected to parsimony analysis. Taxon sampling includes 65 species of *Coccoloba*, one species of *Neomillspaughia* and outgroups are *Antigonon* and *Persicaria*. The results support the monophyly of *Coccoloba* and that its sister lineage is *Neomillspaughia*. Three clades are resolved within *Coccoloba*: clade A encloses *C. venosa* and *C. lehmannii* from South America and the Lesser Antilles (section *Campderia* and section *Coccoloba* pro part), where the synapomorphy is the presence of membranous and free perianth tepals in the fruit. Clade B encloses species from Cuba, Hispaniola and Puerto Rico (section *Rhigia* and section *Coccoloba* p.p.), where the synapomorphy is the extreme reduction of the inflorescence axis. Clade C encloses species from West Indies, Mesoamerica and S. America (sections *Coccoloba* p.p. and *Paniculatae*), where the synapomorphy is the absence inflorescences protective trichomes. Preliminary phylogeny reconstruction based on the plastid regions *trnL-F*, *matK/trnK* and *rpl16* and nuclear ITS also supports the monophyly of *Coccoloba* and the clade A. However, clades B and C are in a big polytomy. The low sequence diversity could be explained by a recent diversification of *Coccoloba* in the Neotropics and the West Indies, but in order to test this hypothesis work underway is to resolve the internal relationships of *Coccoloba* based on further sequence data of the plastid and nuclear genomes.

An integrated morpho-molecular study of the genus *Salicornia* (*Chenopodiaceae*) in Iran

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Species of *Salicornia* are hygrophalophytic plants widely occurring in inland and coastal salt marshes and saline river margins in most parts of Iran. The scarcity of constant characters, succulency of all parts which disappear important taxonomic features by drying and the phenotypic plasticity linked to habitat make this genus a nightmare for botanists. For a long time, only *Salicornia europaea* was assumed to occur in the area of Flora Iranica. However, long term studies by the authors associated with extensive field observation, cytological studies, co-cultivation experiments and molecular studies (ETS nuclear and *rpl16* plastid markers) revealed a great diversity in Iran. The cytological studies showed that diploid and tetraploid species are well distinguished by the morphology of floral units. The truncate central florets which reach to the upper segments, is a constant character in tetraploid species. In our molecular study ETS sequences of 101 accessions, *rpl16* sequences for 66 accessions (61 accessions having both markers) have been generated and analyzed using maximum likelihood and Bayesian analysis from all parts of Iran and some representatives of Eurasian taxa and *Sarcocornia perennis* as outgroup. The nuclear and plastid trees are not congruent. The tetraploid species grouped in a highly supported monophyletic clade in plastid tree. The diploid taxa are highly heterogenous and depending on individual or combined analysis form groups which support recent described taxa from Iran with two new taxa and improvements of previous interpretations. In conclusion, Iran is one of the main centers of diversity of the genus *Salicornia*.

The Good, the Bad and the Ugly: phylogeographic evidence from three genomes in Iberian *Silene*

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The genus *Silene* Section *Psammophilae* includes *S. littorea*, *S. adscendens*, *S. cambessedessi*, *S. stockenii*, and *S. psammitis* - all cross compatible endemic species restricted to the Iberian Peninsula and Balearic Islands. We investigated the phylogeographic relationships of these species using a genome skimming approach from genomic DNA sequences of 26 populations representing these species' distribution ranges. Reference-guided assembly of primarily 250-bp pair-end Illumina reads produced the complete plastid genome (cpDNA; 156 kbp), partial mitochondrial genome (mtDNA; 74 kbp), and the nuclear ribosomal cistron (nrDNA, 6.4 kbp). Portions of the cpDNA and mtDNA Next Gen assemblies were confirmed by Sanger sequencing 1650 bp which were more than 95% identical. Phylogenetic analysis of data from the three genomes are largely incongruent with current taxonomy, they do so with varying levels of support. The cpDNA tree has a number of nodes with bootstrap >70% (57.69%; "the Good"); the nrDNA cistron tree is largely unresolved with 30.75% of nodes supported ("the Bad"); whereas the mtDNA assembly was challenging (only 29.13% coverage) but also well supported (76.92% nodes >70%; "the Ugly"). *Silene cambessedessi*, restricted to the Balearic Islands, is the only species that forms a monophyletic clade. Another well supported clade of *S. littorea* and *S. stockenii* emerges from the southern region of the Iberian Peninsula (Cadiz). The widespread incongruence between taxonomy and phylogeographic results may arise from gene flow among these cross compatible species where only a speciation event like isolation to the Balearic Islands is necessary to produce agreement between taxonomy and phylogeography.

Ecological determinants of reproductive display: evolution of flower number - flower size trade-offs in *Lewisia* (*Montiaceae*)

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It is a common feature in Angiosperm flower evolution that among closely related species, the "size" of flowers (measured as e.g., diameter, mass, or number of parts) correlates negatively with the number of flowers per inflorescence and plant. It is poorly understood what drives evolution along such floral "trade-offs".

Here, we report results on correlations of ecological niches among *Lewisia* (*Montiaceae*) species, a group of species particularly variable in flower size and number, with morphological and phenological floral traits and plant-level patterns of resource allocation.

Floral traits are positively correlated with each other, and negatively correlated with flower number per plant. Species with few-but-large flowers occur in comparatively dry habitats, where precipitation is only briefly more than potential evapotranspiration. Anthesis length appears evolutionary constraint across species, but because small-flowered species open only few flowers

simultaneously, they flower longer than large-flowered species. These results suggest that the partitioning of reproductive effort over few-but-large flowers may function as an adaptation to short growing seasons, while limiting possibilities for among flower self-pollination. These results may help understand the common occurrence of comparatively large floral displays in environments where favourable conditions are temporally restricted, such as desert and alpine environments.

How to achieve monophyletic genera in the *Caryophyllaceae* - a case study of *Minuartia* L. and related genera.

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Caryophyllaceae Juss. are a middle-sized family with approximately 86 genera and 2200 species. The family is distributed worldwide, but centred in the northern hemisphere. Almost 80% of the species belong to eight genera, i.e., *Arenaria* L., *Cerastium* L., *Dianthus* L., *Gypsophila* L., *Minuartia* L., *Paronychia* Mill., *Silene* L. and *Stellaria* L. Molecular phylogenetic studies of the *Caryophyllaceae* or parts of it revealed that several genera, and especially these eight genera, are not monophyletic. These results were confirmed in different studies, but only little effort has been made to translate these results into a revised classification. Our study focused on *Minuartia* s.l. *Minuartia* traditionally contains 175 species distributed almost exclusively in the northern hemisphere. We sampled more than half of the species covering all infrageneric groups of *Minuartia* s.l. and sequenced nuclear and plastid markers. The phylogeny unambiguously showed that the genus in its broad circumscription is highly polyphyletic. Our molecular phylogeny of *Minuartia* s.l. was used to establish new circumscriptions of *Minuartia* and five other genera as well as to describe three new genera. These new or newly circumscribed genera are all supported by morphological and/or karyological characters. Similar work is needed for several other genera and we show which future changes are necessary in the classification of the *Caryophyllaceae* provided monophyly of taxa is accepted as the primary criterion.

Evolutionary diversification of the African Achyranthoid clade (*Amaranthaceae*) in the context of sterile flower evolution and epizoochory

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The Achyranthoid clade of the *Amaranthaceae* includes nearly all of the ca. 270 African species. Most members of this clade exhibit unique inflorescence structures with sterile flowers modified to hooks or spines serving for epizoochory. Considering that terrestrial herbivores started to become more abundant in line with the expansion of grassland and savannah ecosystems, sterile flowers

modified to adhesive appendages could have been an innovation boosting the diversification of Achyranthoids in open habitats with large animals serving dispersal.

We present a molecular phylogeny of Achyranthoids including 26 of the 31 genera, based on five plastid genomic regions and nuclear ITS, inferred by maximum likelihood and Bayesian methods. Divergence dates were estimated and we looked for diversification rate shifts and trait- or time-dependant increases of speciation rates. Ancestral character states for modified sterile flowers were estimated. The monophyly of the Achyranthoid clade was confirmed with maximum support. Internal relationships of Achyranthoids exhibit two main subclades and depict several genera such as *Cyathula* and *Psilotrichum* as polyphyletic. The Achyranthoid clade started to diversify c. 32 Ma ago, after the expansion of grassland and savannah ecosystems. While sterile modified flowers originated multiple times in Achyranthoids, no trait-dependant increase of species diversification rates could be found based on the BiSSE model. Further analysis in a Bayesian framework indicated that the Achyranthoids and its sublineages diversified without significant shifts of the diversification regime and independent of changes in dispersal mode across tropical Africa.

Is *Pteropyrum* a causeway to C₄ evolution in *Polygonaceae*?

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Pteropyrum has long been regarded as a small genus of *Polygonaceae* with four known species from arid regions of Iran and some adjacent countries. The species of *Pteropyrum* are not precisely delimited and intermediate characters makes them difficult to identify. On the other hand it has a close affinity to C₄ *Calligonum* and can be a suitable model for C₄ evolution studies. This study includes taxonomic and phylogenetic studies of *Pteropyrum* species using morphological, micromorphological, and molecular approaches. In addition, the leaf and cotyledon anatomical characters of the genera *Pteropyrum* (C₃), *Atraphaxis* (C₃) and *Calligonum* (C₄) were studied to elucidate the anatomical evolutionary trends of C₄ photosynthesis. Using nuclear ITS sequences and morpho-anatomical characters five new species are to be described which double the number of species. In phylogenetic tree based on ITS sequences, all of the species are classified in two highly supported clades. Convergent evolution and homoplasy caused some species to be morphologically very similar although belong to different phylogenetic clades. Leaf anatomical studies show that *Atraphaxis* has a multilayer and large volume of mesophyll tissue while *Calligonum* as a C₄ plant has only one layer of mesophyll cells. The volume and layer number of mesophyll tissue decreases while water storage tissue area significantly increases from *Atraphaxis* to *Pteropyrum* and *Calligonum*. This phenomenon shows that evolution in Salsoloid anatomy is related to an increase in water storage tissue and leaf succulency.

Floral development of *Lewisia* (*Montiaceae*): investigating patterns of perianth and stamen diversity

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The present study illustrates the complex floral development of *Lewisia* (*Montiaceae*) in an evolutionary context. Flowers are enclosed by two median bracteoles (involucrum), as most

Portulacinae. Unlike most other taxa of the *Montiaceae* (*Caryophyllales*), the petaloid perianth in *Lewisia* develops in two separate steps: two lateral petaloids arise immediately after bracteole initiation, while the median petaloids lag behind and develop only after the stamens. Stamen number fluctuates between five and more than twenty. The number of median petaloids is generally increased from three up to eleven organs, in close connection with the androecium. The involucre has a strong influence on the arrangement of organs in the flower, causing a delay on the growth and development of the petaloids, as well as an increase of petaloid and stamen number, independently of changes in carpel number. In addition, carpel number influences the position and number of stamens. Mechanical pressures of the enclosing involucre play a crucial role in the evolution of species of *Lewisia* and those species with fewer petaloids and stamens correspond to the ancestral condition. A well resolved phylogeny of *Montiaceae* is needed to assess floral evolution within *Lewisia* and among other *Montiaceae*.

An expanded view of the phylogeny of *Nyctaginaceae* based on chloroplast data

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The *Nyctaginaceae*, with nearly 400 species, are a very heterogeneous group that includes species with a diverse set of unusual features, and a number of characters that are uncommon in angiosperms, such as winged, and adhesive, fruits, and specialization to edaphically unusual soils. However, the simple flower, combined with substantial homoplasy and poor preservation in herbaria has caused this family to have a very difficult taxonomic history and many genera are still very poorly understood. We have collated chloroplast sequence data from nearly 200 species of *Nyctaginaceae*, including 59 full chloroplast genome sequences, and here present a combined phylogenetic analysis of the entire family, providing insight into the diversity contained within several complex genera. *Commicarpus* is found to have surprisingly low divergence among its species, despite its wide distribution. *Boerhavia*, contrastingly, consists of coherent morphological and geographic groups, although additional sampling from the Indo-Pacific region is needed. Several transitions to restrictive soils have occurred, resulting in some clades (especially in *Anulocaulis* and *Acleisanthes*) that are important in gypsum areas of North America. These results show increased resolution in tribe *Pisonieae*, corroborating earlier suggestions that *Neea* and *Guapira* are interdigitated, while *Pisonia* itself is also paraphyletic. Future efforts to understand the systematics of *Nyctaginaceae* are now focusing on greater sampling of nuclear data to resolve the phylogeny at the species level, and to place the remaining enigmatic taxa.

The Global Genome Biodiversity Network

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The Global Genome Biodiversity Network (GGBN, <http://www.ggbn.org>) is a global network of genomic samples from across the Tree of Life, benefiting society through biodiversity research, development and conservation. This network will foster collaborations among repositories of molecular biodiversity in order to ensure quality standards, improve best practices, secure interoperability, and harmonize exchange of material in accordance with national and international legislation and conventions. GGBN currently has 36 member institutions and is open to any biodiversity biobank or biorepository. Biodiversity biobank-holding institutions urgently need to set a standard of collaboration towards excellence in collections stewardship, information access and sharing and responsible and ethical use of such collections. GGBN meets these needs by enabling and supporting accessibility and the efficient coordinated expansion of biodiversity biobanks worldwide. The GGBN Data Portal bridges the gap between specimen databases and sequence portals and sets a global standard for exchanging and accessing biodiversity DNA and tissue sample data. Here I present an overview about GGBN and its components such as the Data Portal and its benefits for the botanical community, e.g. for research on *Caryophyllales* taxa.

***Nyctaginaceae* in Brazil: species richness, herbarium collections and conservation status**

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Nyctaginaceae in Brazil have 4 tribes, 11 genera and 48 species, the richest being the tribe *Pisonieae* with 33 species. A revision of this tribe (1996) revealed 30 species. Taxonomic and nomenclatural problems are extensive in this tribe (e.g. the genus *Neea*, limited mostly to the Amazon, has very few species with rare collections from remote areas). Collections of the *Bougainvilleae* tribe must be increased in order to define the area of distribution (*Belemia*) and to revise *Bougainvillea*. Limited almost strictly to Brazil, *Leucastereae* tribe raises concern because of species conservation while the *Nyctagineae* tribe is composed of naturalized species. Recently, a group was established (A.O.P.Coelho, C.F.C.Sá, D.S.Costa, E.F.S.Rosseto & F.S.Souza) to work on the *Nyctaginaceae* for the *Flora of Brazil On Line 2020*. Our aim is to make progress in the complex also on the species complexes (e.g. *Guapira opposita*) and improve identification. Research on *Nyctaginaceae* in SIBBr, GBIF and SpeciesLink revealed 16,300 herbarium specimens in Brazil (the largest at RB totaling 2,549), with 2,000 specimens in herbaria abroad. The collections are concentrated in areas where there are large herbaria and in the phytogeographic domains of the species, but are very sparse in the Amazon. Currently, 2,479 species of the total of 46,097 species of Flora of Brazil, are in a threat category of, with 94 *Caryophyllales*, especially *Cactaceae* and *Amaranthaceae*. *Nyctaginaceae* must be re-assessed, especially the *Leucastereae* and *Bougainvilleae* tribes and their endemic monotypic genera, because the populations do not lie within protected areas.

Evolution of carnivory in *Caryophyllales* and diversification of *Drosera* (*Droseraceae*)

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The genus *Drosera* comprises about 250 species, the centres of species diversity lie in the Southern Hemisphere. A robust phylogeny of the genus is supported by taxonomic, cytological, palynological and biogeographic data.

Homology of floral structures in *Amaranthaceae* s.l.: a perspective from floral ontogeny.

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Within Caryophyllales, *Amaranthaceae* s. l. has rather reduced flowers that have been subject to different interpretations. It is commonly accepted that though homoplasy can be caused by convergent evolution, an incorrect interpretation of the morphology of structures can also lead to erroneous conclusions. Studies on floral development are therefore ideal to postulate homology hypotheses in this group. With the aim to clarify the nature of problematic floral structures, we studied the floral development in several lineages of *Amaranthaceae* using SEM and LM. We focused on the nature of bracts/bracteoles and perianth parts, on the androecium modifications and on the ovary position. We not only propose evidence for their re-interpretation, but also introduce a new approach within this group for studying floral homology. In female flowers of *Atriplex* and *Spinacia* (*Chenopodioideae*), the perianth consists of two persistent acrescent sepals formerly interpreted as bracteoles. Flowers are usually initially hermaphroditic with the exception of *Spinacia* and the strictly female flowers in *Atriplex*, which are unisexual from the earliest developmental stages. In the case of *Gomphrenoideae*, 4-5 stamens are raised on a nectariferous floral cup formed below them, with the simultaneous formation of 4-5 appendages alternating with the stamens. This suggests that the reproduction is dependent on animal vectors rather than wind. We hypothesise that the androecial tube, the staminal ring in *Beta vulgaris* and the 'fused filaments' in some *Chenopodioideae* are morphological homologues. *Amaranthaceae* s. l. species provide ideal sources for evolutionary developmental studies related to inflorescence structure, merosity, and sex determination.

Did environmentally induced phenotypic variation led to recurrent speciation in *Heliosperma pusillum* group (Caryophyllaceae)?

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Variation in biotic and abiotic conditions in heterogeneous environments can lead to the formation of distinct populations adapted to their specific habitat. *Heliosperma pusillum* and *H. veselskyi* in the Alps are an example of morphological and functional adaptation to creeks and moist calcareous screes in the (sub)alpine belt and rock overhangs and shallow caves in the montane belt, respectively. Although phenotypic divergence remains stable in two consecutive generations in a common garden, both taxa are not divergent in their DNA sequence (RADseq data) and are able to interbreed as revealed by crossing experiments. Moreover, the genetic similarity is correlated with geography rather than taxonomy, suggesting recent and recurrent divergence of both types, resulting from middle- to short-term adaptive processes under the influence of the environment. We

also present preliminary results based on bisulfite RADseq to test for genome-wide differences in DNA methylation correlated with the striking phenotypic differentiation and discuss the possible role of epigenetics in the initial phase of divergent evolution.

Phylogeny and evolutionary patterns of *Chenopodium* s. str.

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The genus *Chenopodium* sensu stricto as recently re-defined to be a monophyletic entity, is a cosmopolitan lineage with more than 100 species. Its distribution is in temperate and subtropical dry regions from sea level to high altitudes. *Chenopodium* encloses species with different ploidy levels (diploids, tetraploids and hexaploids) and also cultivated species (e.g. *C. quinoa*). Using a dense taxon sampling and combined rapidly evolving plastid regions (*trnL-F*, *trnK/matK* and *rpl16*) as well as nuclear ITS we applied tree searches (MP, ML, BI) and network analyses. The plastid signal is considerably improved over previous analyses and revealed five well-supported internal clades: i) the *C. vulvaria* lineage (diploids from Europa), ii) *C. nutans* and allies (diploids from Australia and New Zealand), iii) *C. album* and allies (diploids, tetraploids and hexaploids from Eurasia), iv) *C. pallidicaule* and allies (diploids from South America) and v) a large clade of North American diploid species including a complex of New World tetraploids (*C. berlandieri*, *C. hircinum*, and *C. quinoa*). While nrITS congruently resolves *Chenopodium vulvaria* as sister of all remaining *Chenopodium* species, the Australian and North American diploids appear in a basal polytomy. The *Chenopodium album* complex except *C. ficifolium* is resolved as a well-supported clade comprising the polyploidy taxa. The hexaploid *C. opulifolium* lineage is distinct from the *C. album* complex in the nuclear topology and appears sister to a *C. berlandieri*, *C. hircinum*, *C. quinoa* lineage. The new world tetraploids including the Andean crop plant Quinoa apparently go back to a single polyploidization event, which does not involve the South American *C. pallidicaule* as previously thought. Overall, there may be three major polyploidization events in *Chenopodium*. The analysis of well-documented specimens from wild populations (for the non-cultivated species) that cover multiple localities of their ranges and the generation of complementary sets of character data is an important strategy for illuminating the origin of polyploid entities in *Chenopodium*, in line with the need of evaluating species concepts throughout the genus.

Silene ciliata (Caryophyllaceae) as a model species in a climate change scenario: our multidisciplinary approaches.

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Silene ciliata Poiret (Caryophyllaceae) is a perennial cushion plant, endemic of Europe that inhabits the Northern Mediterranean mountain ranges, from Portugal to Greece. In spite of its complex taxonomy, the existence of different subspecies and multiple ploidy levels, during the last decade, it has been used as a model species to develop ecological, population genetics and conservation studies related to the responses of high-mountain plants to climate change. Our research has been

mainly focused on plant adaptation responses under the current global change scenario and their consequences on the populations of Central Spain, which are at the southern range of the species distribution. Reciprocal transplants, common garden experiments, microsatellite analyses and effective dispersal studies are (among others) some of the approaches used with this species. Results have highlighted that *S. ciliata* populations are showing local adaptation responses to current climate change scenario along the mountain altitudinal gradient, a limitation of gene flow between populations or some pernicious effects of inbreeding depression in small populations. Ongoing research is also focusing on the use of NGS technologies and the unraveling of the phylogeographic patterns, to improve the knowledge of the species about their responses to past and current climate changes.

Distribution patterns of the *Caryophyllaceae* in Iraq

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The family *Caryophyllaceae* is one of the most species rich families in the flora of Iraq with 29 genera and 125 species. The largest genera include *Silene* (37 spp.) *Gypsophila* and *Minuartia* (14 spp. each), *Dianthus* (12 spp.), *Cerastium* (11 spp.) and *Acanthophyllum* (6 spp.). Other genera are represented by five or less than five species; nine genera are represented by a single species. One or possibly two species are endemic, found in the Mountains Region. The majority of the Iraqi *Caryophyllaceae* are found throughout the Middle East, especially eastern Turkey, western Iran, Syria and the Arabian Peninsula; in Iraq the *Caryophyllaceae* are mainly distributed in the Mountains and Upper Plains and Foothills Regions. The larger genera (*Silene*, *Gypsophila*, *Minuartia*, *Dianthus*, *Cerastium*) follow a similar distribution pattern, that is, being most abundant on the Mountains and Upper plains of Iraq. For *Silene*, most of the perennial species belong to the Irano-Turanian floristic region with distributions in Turkey, NW Iran and Syria, however the annual species of *Silene* show a wider distribution, extending from the Mediterranean region to Pakistan.

Chromosome number variation in Iranian *Silene* (*Caryophyllaceae*) species

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The change in chromosome number among organisms is an important phenomenon in the evolution of vascular plants. The information about chromosome number of any taxa is useful in taxonomical and phylogenetic studies.

There are about 750 species of the genus *Silene* in the world, out of which approximately 110 species grow in Iran. During the last decade, some cytological studies were done on the genus *Silene* in Iran. In general, chromosome number information of 113 populations of 52 species belonging to 7 sections was reported. Most of examined species (37) had $2n=2x=24$ diploid chromosome number. 10 species were found to be tetraploids ($2n=4x=48$). *Silene aucheriana* and *S. gynodioica* show two different ploidy levels; $2n=2x=24$ and $2n=4x=48$ chromosome number. *S. crispans* is an octaploids ($2n=8x=96$) while *S. indeprensa* shows two ploidy levels; diploid and octaploid ($2n=2x=24$ and $2n=8x=96$). *S. hirticalyx* is an interesting taxon regarding chromosome number which shows higher variation in ploidy levels, from diploid to octaploid.

Three types of variation in chromosome number of *Silene* species are observed: 1- Intra-population 2-Inter-population and 3- Intra and inter-section. Our findings show that the basic chromosome

number of Iranian *Silene* species is $x=12$. According to the available information, there is no logical relationship between chromosome number and the sections classification in this genus. Because of large variation in the diploid chromosome number of *Silene* species in Iran, such study on other species is necessary to get insight into the trends of variation in chromosome number of this genus in Iran.

Advances in the taxonomy of the Brazilian-tetraploid clade of *Drosera* (*Droseraceae*)

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Drosera (*Droseraceae*) comprises around 250 species distributed worldwide, 31 of which occur in Brazil. Among the Brazilian taxa, a group stands out for its morphology and cytology, being characterized by the circinate leaf vernation and chromosome number of $n=40$. In this work, we reviewed the taxonomy of these species, using morphological characters and ecological evidence to circumscribe the known taxa, re-establish old synonyms and describe new species. Four major groups were identified, and six new taxa were described, including *Drosera magnifica*, the largest species of the genus in the Americas, notorious by being discovered on Facebook. The group is now focus of a phylogenetic study, using morphological and molecular data.

Adding value to research data – development of a system for sustainable sample data processing

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The proper documentation of research samples in the biological sciences and their integration as collection items in scientific collections is still a downstream process usually left to the collections and their staff. The subsequent inclusion of samples into collections inevitably favours data- and sample loss and hampers the generally demanded reproducibility of research results. Large amounts of data are usually stored independently from their source samples, which in turn are often transferred into collections only selectively. All data (metadata and result data) of each scientific sample must ideally be integrated into databases during the scientific process to sustainably maintain the relationships between samples and related data. Ideally, all datasets can be stored in a single, generic database that hosts all data regardless of their format.

Based on the EDIT Platform for Cybertaxonomy, we have developed a software solution to permanently document and store both, the research objects with their metadata and the data(sets) gained from them during the research process. The software unites three basic functionalities: (1) a data repository with import and export services using globally standardised data formats (e.g. ABCD), (2) an editor (Taxonomic Editor) for the recording, integration and management of heterogeneous datasets (e.g. herbarium specimen, scans, molecular raw data) and (3) a data portal to present and provide the datasets. The software thereby is fully integrated in the existing functionalities of the EDIT Platform. The datasets can be incorporated into an existing classification

with all its scope and can be dynamically linked with taxa. The datasets can then be shown in this context in the data portal, presenting the current state of research

A taxonomic backbone for the global synthesis of species diversity in the angiosperm order *Caryophyllales*

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The *Caryophyllales* constitute a major lineage of flowering plants with approximately 12,500 species in 39 families. A taxonomic backbone at the genus level is provided that reflects the current state of

knowledge and accepts 749 genera for the order. A detailed review of the literature of the past two decades shows that enormous progress has been made in understanding overall phylogenetic relationships in *Caryophyllales*. Whereas the process of re-circumscribing families in order to be monophyletic appears to be largely complete, the phylogenetic evaluation of generic concepts is still well underway. As a result of this, the number of genera has increased by more than ten percent in comparison to the last complete treatments in the "Families and genera of vascular plants" series. A checklist with all currently accepted genus names in *Caryophyllales*, as well as nomenclatural references, type names and synonymy is presented. The database of "Names in Current Use 3" served as starting point for constructing the generic checklist. This was compared and emended by checking the treatments of Caryophyllales in "The Families and Genera of Vascular Plants". Further information from data bases (such as IPNI and Tropicos) was used to emend the list and check for consistency. The available literature as relevant for discussing the state of knowledge was revised in the context of refining the presentation on phylogenetic relationships and generic concepts and to add further taxa. In addition to the involvement of numerous authors working on Caryophyllales, considerable effort by a full time scientist dedicated to the work was needed for building up the resource, coordination, cleaning and completing data.

All data were gathered, edited and revised using the tools in the EDIT Platform for Cybertaxonomy, which also provided the output for print publication and now feeds the online data portal. This will facilitate continuous updates and outputs into further formats such as World Flora Online. This synopsis represents a first step towards the aim of creating a global synthesis of the species diversity in the angiosperm order *Caryophyllales* involving the work of numerous specialists around the world.

Microstructural organization of the *psbA-trnH* intergenic spacer in *Cactaceae* (*Caryophyllales*)

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The *psbA-trnH* non-coding intergenic spacer (IGS) of the plastid genome has been widely used at lower taxonomic level in several angiosperm groups for phylogenetic reconstruction. It has as well been proposed as a genetic barcode due its high variability. This IGS is located in the single-copy region between the *psbA* and *trnH* genes in the vicinity of the IRa. The *psbA-trnH* IGS consist of two main regions, a relatively conserved and small untranslated region (3'UTR) including a putative regulatory region followed by a stem loop that regulates the expression of the *psbA*, and the non-functional untranscribed *psbA-trnH* intergenic spacer. The architecture of the region has been widely studied in various angiosperms but in-depth analysis at the family level with a broad sample of species is still lacking. In *Cactaceae*, one of the most representative families of the arid regions of America, the *psbA-trnH* IGS has been broadly used in phylogenetic studies without concern of primary homology and alignment issues. With the goals of knowing the architecture and variability of this region through the different taxonomic levels in the family, we analyzed 752 *psbA-trnH* IGS sequences for various terminals of the family. The region length varies from 205 to 454 bp, the TTAGTGATA-Box in the 3'UTR is highly conserved in the terminals. The second part of the IGS, the non-functional untranscribed region, is a highly diverse mutational hotspot were primary homology issues are confounded and it is practically impossible to provide a solid hypothesis of molecular homology at higher taxonomic levels.

The CITES *Cactaceae* Checklist

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In addition to national laws governing the collecting and export of cacti, international trade in the plants is subject to CITES, the Washington Convention on International Trade on Endangered Species, to which 180 countries are signatory Parties. Compilation of a 'nomenclatorial reference' of the *Cactaceae* was called for by the 6th Conference of the Parties in 1987. A first edition, compiled by the speaker with the assistance of an international panel of nearly 50 advisers, was published in 1992, a second in 1999 and a third is in draft for approval by the next Conference of the Parties for publication next year.

From the point view of the CITES Plants Committee, and probably of researchers and users generally, nomenclatural stability is of prime importance, plant names being the language of taxonomy. Not everyone approves of committee-based taxonomy, but the publication of the CITES *Cactaceae* Checklist could be said to have provided the relatively stable benchmark or at least the 'Aunt Sally' that has helped to make research on the family an attractive option in recent decades. The speaker argues, however, that those publishing phylogenetic hypotheses in *Cactaceae* are tending to destabilize classification by favouring narrower rather than broader generic limits and by not employing traditional infrageneric categories such as subgenera as a means of delimiting minor clades without disturbing generic names in common usage.

Hypothesis testing in circumscription-resistant lineages: morphometric methods for estimating patterns of floral evolution in species complexes

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Understanding evolutionary patterns at the boundaries among populations and species is often challenging. For example, reproductive isolation may be weak among young species, producing admixture. Even when gene flow is sufficiently restricted to promote speciation, isolation may be evident only in genetic patterns at first, not morphology. In the broad sense, *Claytonia lanceolata* (*Montiaceae*) is a species complex, widespread along mountain systems of western North America (ca. 34N–52N). In the north, suitable habitat for these taxa is relatively continuous, promoting gene flow among populations of close relatives. At southern latitudes, including both Basin & Range and southern California desert mountains, plants are isolated in high elevation "sky islands". Members of the *Claytonia lanceolata* complex exhibit variation in leaf morphology, but leaves are typically more subject to environmental heterogeneity than flowers. The dogma to date is that *Claytonia* flowers reflect variations of a main theme, possibly an ancestral type. However, we notice considerable variation in petal shape and color markings in the flowers of *Claytonia lanceolata* s.l., both within and among populations and taxa. We applied morphometric techniques, including Elliptical Fourier Analysis, to images of flowers from multiple populations of *Claytonia* to determine whether intra- and inter-population (and taxa) differences in floral variation can be used to infer patterns of reproductive isolation. We found that populations of *Claytonia* maintain high levels of variation in floral morphology, but some populations and taxa exhibit patterns of floral

divergence. These patterns may be associated with geographic isolation or selection by insect visitors.

Chenopodiaceae – loving the extreme!

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Within *Caryophyllales* the goosefoot family (106 gen./c. 1500 spp.) belongs to the Caryophyllids and is closely related to *Amaranthaceae*. From their Early Tertiary cradle in West/Central Asia *Chenopodiaceae* spread worldwide in arid, saline and ruderal environments. In several lineages *Chenopodiaceae* seem to tightly follow the track of aridification since the timing of their geographical diversification is closely linked to the formation of arid environments in the respective areas. The family evolved a number of morphological, anatomical and physiological traits that make them successful colonizers and survivalists in harsh habitats. Complex traits such as C₄ photosynthesis and various mechanisms of salt and inundation tolerance originated early and multiple times in the family giving rise to a great diversity of C₄ types, halo-, hygrohalo- and xerophytes. Also striking morphological adaptations are found in many lineages. Especially within the hygrohalophytic *Salicornioideae* the extremely reduced leaf and flower morphology is the despair of taxonomists. While flowers of *Chenopodiaceae* are mostly inconspicuous their diaspores show some interesting features such as heterospermy and very fast seed germination in several lineages. Anatomical specialities are (apart from the striking diversity of C₄ leaf types, anomalous secondary growth and a fleshy cortex in succulents) for example found in the epidermis in terms of a multi-layered epidermis or salt trichomes. An overview of the phylogeny of *Chenopodiaceae* is given with special emphasis on intriguing specialities that evolved in the family.

Diversity and conservation of *Amaranthaceae* in East Africa

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Amaranthaceae is a tropical family with estimated 65 genera and over 1000 species which include weeds and some locally important vegetables. In East Africa there are 25 genera with 89 species according to herbarium records. The East African Herbarium (EA) hold 6232 specimens of which 3034 collections are Kenyan, the rest have been collected from Uganda, Tanzania, Ethiopia and Congo. This form a good representation of *Amaranthaceae* species collected over a long period of time. The family is well curated using recent publications e.g. Flora of Tropical East Africa (FTEA). *Celosia* and *Amaranthus* are the most species diverse genera with 12 and 11 species respectively. The species are widely distributed in tropical Africa but some have narrow distribution. Endemism in the family is low with Kenya and Tanzania each having 4 endemic species. The *Amaranthaceae* hotspots generated using herbarium data has been identified to be in the drylands of East African countries. These areas are characterized by open grassland, bushland, farmlands, and roadsides with erratic annual rainfall of less than 300mm. Overlaying the data with protected areas showed most of the species are found outside protected areas experiencing anthropogenic pressure. In additions, many areas in Kenya are under sampled and previous sampling seems to follow the road networks. Many species in *Amaranthaceae* particularly the genus *Amaranthus* are widely used as leafy vegetables and grain crops in most African homes due to their high nutritional contents.

Seed morphology of *Silene commelinifolia* Boiss. complex (*Caryophyllaceae*) species

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Eighteen *Silene* populations of four species (*S. commelinifolia*, *S. lucida*, *S. nurensis*, *S. eremicana*) are studied for their seed micro-morphology by stereo microscopy and SEM. It was done for the first time in Iran. Studied taxa show a great variation in seed shape and size, lateral and peripheral shape and shape of seed testa cells. Totally 19 quantitative and qualitative seed features were measured and evaluated. PAST and SPSS software were used and species relationships were evaluated. *Silene eremicana* and *S. lucida* are grouped near each other and show a close relationship which is concordant with their morphological similarities. Due to seed micro-morphological data it was evident that morphologically similar species to *S. commelinifolia* are clearly separated from each other. So seed morphology is of taxonomic value in the studied group.

Stem Anatomical study of *Sarcocornia fruticosa* (Amaranthaceae)

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Sarcocornia fruticosa (L.) A. J. Scott (*Amaranthaceae*) has cosmopolitan distribution. These halophytic and fleshy bushes have articulated stems. There is great similarity between *Sarcocornia*, *Arthrocnemum* and *Salicornia*. In present study anatomical observations were made on articulated stems of *Sarcocornia fruticosa* from seven localities of Europe. Stern cross sections were handmade and studied by light microscopy after double coloration with Congo red and methylene green. Results showed that there are 2-3 palisade layers under stem epidermis, S-8 aquifer parenchyma and a layer of endodermis cells. In the cortex elongated to cylindrical idioblasts are observed. Small vascular bundles are present under the idioblast zone and arranged in one or two concentric rings. The stele is comprised of 6-8 vascular bundles. The anatomical differences between stems of *Salicornia* and *Arthrocnemum* are discussed.

Adaptive photosynthetic strategies in Old World *Salsoloideae*: evolution of C₄ photosynthesis and morpho-anatomical traits

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It has been speculated that the evolution of C₄ photosynthesis is an adaptation to heat, aridity, and salinity. Despite the fundamental biochemical similarities in C₄ function, C₄ plants show remarkable diversity in photosynthetic structures. *Chenopodiaceae* comprise the highest variety of C₄ anatomy among the eudicots. *Salsoloidea* is the most morpho-anatomically diverse lineage in *Chenopodiaceae*, with the majority of genera performing C₄ photosynthesis. Here, we examine the extent of this

variation and the evolutionary and ecological significance of assimilating organs, including cotyledons, leaves, stems and tepals, in *Salsoloideae*, tribes *Salsoleae* (NADP-ME) and *Caroxyleae* (NAD-ME), using morphology, anatomy, phylogeny, life cycle and habitat information. *Caroxyleae* have flat cotyledons, germinate under moderate environmental conditions, and are usually adapted to salty and disturbed soils. In contrast, cotyledons of *Salsoleae* are succulent and filiform, advantageous for seedling establishment in xeric habitats. C₄ anatomy in tepals of *Caroxylon* species contributes to net photosynthesis and compensates partial defoliation of plants during the hot season. Stem photosynthesis is rare in *Caroxyleae*, but common in *Salsoleae*. Multiple transitions from leaf to stem photosynthesis have been observed in *Salsoleae*, facilitating their survival under extreme drought and high irradiation in gypsum hills, gravelly and sandy deserts. Our results highlight that development of Kranz anatomy from the early vegetative to late reproductive cycle outlines the ecological distribution of C₄ species of *Salsoloideae*, enabling them to grow successfully in highly dynamic macro and microhabitats.

Phylogeny and character evolution for the recently diversified *Ruschieae* (*Aizoaceae*) in southern Africa

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The *Ruschieae* is a large tribe of about 1600 species of succulent perennials, which form a major component of the arid parts of the Greater Cape Floristic Region. So far phylogenetic relationships within the tribe have been unresolved, largely through the paucity of variable molecular characters and this is ascribed to the tribe's recent and rapid radiation. Our phylogeny is based on ten chloroplast gene regions and represents a nearly complete sampling of the 100 currently recognized genera in the *Ruschieae*. For the first time, we provide well-supported evidence that taxa with mostly mesomorphic, often ephemeral leaves and weakly persistent fruits form a basal grade of lineages in the *Ruschieae*. These lineages subtend a large polytomy of taxa with almost exclusively xeromorphic, persistent leaves and strongly persisting fruits. Among the basal grade of lineages, those occurring within the winter-rainfall region typically shed their leaves. This contrasts with taxa of the basal grade from outside the winter-rainfall region, in which the leaves persist. Our results show that, in both strongly and weakly persistent fruits, specialized characteristics of the fruit evolved repeatedly and so these structures are highly homoplasious.

Deep relationships, circumscription and generic concepts in *Hylocereeae*, *Cactaceae*

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The *Hylocereeae* are a mainly central American-Mexican tribe of epiphytic, hemiepiphytic and climbing cacti. They are well known and popular due to their spectacular nocturnal flowers and have some importance as crop plants grown for their edible fruits.

The *Hylocereeae* are one of the last large *Cactaceae* tribes that have not been yet examined in detail phylogenetically. So neither the circumscription of the *Hylocereeae* nor the internal relationships within the tribe are currently known with confidence.

We present the first comprehensive phylogenetic study of the *Hylocereeae* and allies. All currently accepted species and subspecies were sampled and the study is based on the plastid regions trnK/matK, the rpl16 intron, rps3-rpl16, and trnL-F. The aims were to evaluate the delimitation of the *Hylocereeae* and to create a phylogenetic framework for the genera based on plastid data.

The clade containing the “traditional” *Hylocereeae*, including *Acanthocereus* and *Peniocereus* p.p., but excluding *Strophocactus* gains maximal support. The three species of *Strophocactus* fall outside and *Strophocactus wittii* is found unrelated to *S. testudo* and *S. chontalensis*. We suggest reinstating the genus *Deamia* as a taxonomic and nomenclatural consequence of these results.

Two main clades are resolved within the *Hylocereeae*: one clade contains the climbing, spiny, often hemiepiphytic genera *Hylocereus*, *Selenicereus* and *Weberocereus*. *Hylocereus* and *Selenicereus* cannot be separated from each other and some species of *Weberocereus* are additionally found intermixed within *Hylocereus/Selenicereus*. The second clade contains the largely flat-stemmed epiphytic genera *Pseudorhipsalis*, *Disocactus* and *Epiphyllum*. All of them are found polyphyletic; especially *Disocactus* and *Epiphyllum* are highly intermixed with each other.

The mostly well-resolved topology is used to reconstruct the evolution of growth forms and pollination syndromes. Selected morphological characters defining the genera are discussed.

This study represents a first step towards understanding the evolutionary history of the *Hylocereeae* and will serve as the basis for comparative analyses using nuclear genes in the future.

Temporal and spatial transitions in development of C4 photosynthesis in C4 *Suaedoideae* plants

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C4 photosynthesis requires spatial separation of phases of carbon assimilation which is achieved by development of mesophyll (M) and bundle sheath (BS) (dual-cell Kranz anatomy) or different cytoplasmic domains in individual chlorenchyma cells (single-cell non-Kranz anatomy). Both systems require spatial separation of the capture of atmospheric CO₂ by phosphoenolpyruvate carboxylase (PEPC) in C4 cycle and the donation of high levels of CO₂ by C4 decarboxylases to Rubisco. To establish this complex system structurally and biochemically, C4 photosynthesis requires a highly coordinated expression of many genes during leaf development.

The temporal and spatial patterns of photosynthetic enzyme expression were characterized in accordance with structural maturation across a leaf developmental gradient in representatives of two Kranz and two non-Kranz structural types of C4 Chenopods. The relative amounts of Rubisco large subunit and PEPC peptides in different cell compartments were evaluated at different stages of leaf development by immunohistochemistry. An in situ mRNA hybridization procedure was used to reveal temporal and spatial patterns of Rubisco gene expression. Inlet mass-spectrometry was used to evaluate the sensitivity of the CO₂ compensation point to oxygen concentration which provides a measure of functional C4 cycle development. Analysis shows two different ontogenetic programs

exist in species with non-Kranz and Kranz types anatomy which are suggested to have evolved independently in different *Suaedoideae* lineages with NAD-ME type C4 photosynthesis. The pattern of non-Kranz species development differs from Kranz in having a clear progression from a C3-default to intermediate to C4 state not only structurally but also biochemically and functionally.

Development of the C4 pathway takes its time in *Salsola soda* – C4 leaves follow C3 cotyledons

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Some species of *Salsola* (*Chenopodiaceae*) convert from C3 pathway during seedling stage to C4 pathway in adult leaves. This unique developmental transition of photosynthetic pathway offers the exceptional opportunity to follow the development of the derived C4 syndrome from the C3 condition at anatomical and molecular level within individual plants. By means of mRNA sequencing we examine C4 photosynthesis in an ontogenetic approach at the transcriptional level as the C4 syndrome develops. Additionally, we compare $\delta^{13}C$ values, anatomical sections, and expression patterns of C4 relevant proteins during up to ten developmental stages (from seed to adult plant) of the annual *Salsola soda* to reveal the mode of C4 syndrome establishment. We specifically ask the question if booting up the C4 syndrome in *Salsola soda* requires a gradual establishment of C4 components or follows an „all at once“ pattern.

The $\delta^{13}C$ values and anatomical sections clearly indicate a C3 phase during young and old cotyledon stages. During these two phases transcripts of C4 candidate genes like phosphoenolpyruvate carboxylase (PEPC), PEPC-related protein, and NADP-malic enzyme are expressed at low levels compared to a significant increase in leaf stages. Additionally, transcripts encoding transporter proteins functioning in phosphoenolpyruvate translocation (PPT, PPT2) and malate transport (Dit1, Dit2) are also up-regulated in leaves compared to cotyledons. In comparison, transcripts of Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase (RuBisCO) shows no significant differences in gene expression among all studied developmental stages, this latter pattern contrasts with the general understanding that less RuBisCO is needed in C4 plants.

Phylogeny of the genus *Drosanthemum* (*Aizoaceae-Ruschioideae*)

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Within core *Ruschioideae*, *Drosanthemum* inhabits a special position because it forms a separate clade placed as a sister group to the remaining c. 130 genera. The genus, which comprises c. 120 species, is distributed throughout South Africa and Namibia, with a center of diversity in the southwestern Cape. Eight geographically strongly overlapping subgenera have been identified based on differences in flowers and capsules, most of these were confirmed in molecular studies. The

latter suggest a union of two subgenera and the establishment of a new subgenus definitely including material that had been shifted between *Drosanthemum* and *Delosperma* until now. Furthermore, components of subgenera can now be re-assessed, resulting in a new arrangement of subgeneric taxa.

Phylogenetic study of the genus *Limonium* (*Plumbaginaceae*) using four nuclear and chloroplast sequence data

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In order to study the infrageneric relationships of the cosmopolitan genus *Limonium*, sequences of four nuclear and chloroplast markers (ITS, *trnK-matK*, *trnL-F* and *petD*) have been analyzed. Our ITS data set includes 143 accessions belonging to 70 species and the plastid matrix includes 89 accessions of 64 species. *Popoviolimon turcomanicum* and three species of *Psylliostachys* have been used as outgroup. Independent and combined analysis of nuclear and plastid data sets using Bayesian Inference method show similar topology. Our results confirm two major highly supported clades within the genus *Limonium* corresponding to the subgenera *Pterocladus* and *Limonium*. Within the subgenus *Limonium* four major clades are distinguishable: (1) a well-supported clade containing three Saharo-Sindian species of the section *Sarcophyllum* (*L. axillare*, *L. stocksii* and *L. paulayanum*) as sister clade to all other species of the subgenus *Limonium*; (2) a well-supported clade consisting of mostly West and Central Mediterranean species belonging to the sections *Polyarthrion* and *Schizhymenium* as well as sect. *Limonium* with some species of the subsections *Hyalolepidae*, *Densiflorae*, *Dissitiflorae* and *Steirocladae*; (3) a well-supported Irano-Turanian clade containing sections *Siphonocalyx*, *Nephrophyllum*, *Platyhymenium* and a large part of *Limonium* subsect. *Hyalolepidae*; (4) a large clade with two subclades including Irano-Turanian species of the section *Sarcophyllum* in one subclade and species of sect. *Limonium* subsect. *Genuinae* and sect. *Sphaerostachys* in the second subclade. Separation of the recently described genus *Miriolimon* from *Limonium* is highly supported. Two members of the sect. *Siphonocalyx* (*L. sogdianum* and *L. drepanostachyum*) are nested within the subgenus *Limonium*, thus corroborating the rejection of *Eremolimon* as a separate genus.

Caryophyllaceae in Iran, a band of mismatches

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In three separate studies, phylogeny and morphology of the genera *Minuartia*, *Cerastium*, *Stellaria*, *Myosoton* and *Lepyrodiclis* in Iran were studied using analysis of internal transcribed spacer (ITS) and

scanning electron microscopy. Tracing the characters on the obtained phylogenetic trees, we found that in most cases the given phylogenies do not accord with the present traditional taxonomy. Most of the traditionally defined groups especially at genus and infragenus levels seem to be artificial. In addition, despite the relative high similarity between the morphology of species, their ITS alignment showed to be interestingly variable (> 30 % of characters were parsimony informative). We also observed some differences in quantitative and qualitative palynological characters of similar species that could be useful. Despite the diagnostic value of palynological data at the species rank, it was not useful to circumscribe any taxonomic group at the higher ranks. We observed better results with micromorphology of seeds. Our results showed that a new grouping of taxa is highly required for the *Caryophyllaceae* using more molecular markers.

The World Flora Online – Achieving Target 1 of the Global Strategy for Plant Conservation

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In its decision X/17, the Convention on Biological Diversity (CBD) adopted a consolidated update of the Global Strategy for Plant Conservation (GSPC) for the decade 2011–2020 at its 10th Conference of the Parties held in Nagoya, Japan in October 2010. The updated GSPC includes five objectives and 16 targets to be achieved by 2020. Target 1 aims to complete the ambitious target of “an online flora of all known plants” by 2020. A widely accessible Flora of all known plant species is a fundamental requirement for plant conservation and provides a baseline for the achievement and monitoring of other targets of the Strategy. The previous (GSPC 2010) target 1 aimed to develop “a widely accessible working list of known plant species as a step towards a complete world flora,” and this target was achieved at the end of 2010, as The Plant List (<http://www.theplantlist.org>). Drawing from the knowledge gained in producing The Plant List, a project to create an online world Flora of all known plant species is now underway. A World Flora Online (WFO) Council has been formed with twenty seven participating institutions world-wide and supporting Technical and Taxonomic Working Groups who are diligently working to achieve the 2020 Target. The importance of integrated expert networks providing taxonomic treatments to WFO as one of the products of their research was explicitly recognised by the Council. We hope that input from the Caryophyllales network will be piloting that strategy. An information portal is online at <http://www.worldfloraonline.org>. The structure of the WFO will be a framework capable of accommodating regional floristic information (at national or lower level) that can provide answers in both regional and global contexts. Enhancements will include more complete synonymy; geographic distributions to at least country level, drawing on national floras, checklists, and monographs; habitat data; identification tools, principally interactive keys, images, and descriptions; conservation status; and other enhancements as practicable, e.g., vernacular names. Rapid progress is now being made toward publication of a beta WFO public portal. This presentation will describe the vision, technical approach, progress to date and plans for this new and significant global project.

Systematic update of *Caryophyllaceae* in Peru: diversity and distribution

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The family *Caryophyllaceae* in Peru is represented by 19 genera, 143 species, 7 subspecies and 20 varieties. The information about its distribution comes from numerous collections at different herbaria from which 800 specimens were examined since 2009 at CPUN, CUZ, HSP, HUSA, HUT, K, L, MO, MOL, UPCH and USM. Among endemics, 47 (27.6%) were identified comprising 11 genera. Considering the Peruvian departments that host the highest number of species (analyzed from literature citations and herbarium collections) are: Lima (55 spp.), Ancash (52 spp.), Junín (40 spp.), Cusco (37 spp.) and Cajamarca (34 spp.). This numbers are high considering the large amount of plant collections provided by different scientific projects. In contrast, several departments have few or no collections or species reports (less than 6 spp.) such as Amazonas, Apurímac, Huancavelica, Ica, Lambayeque, Loreto, Madre de Dios, Piura, Tacna and Tumbes. This study demonstrates how important it is to provide herbarium material from such regions that may host significant species distribution and endemics. One example is the department of Moquegua where I am studying the flora for over 10 years. Previous reports (before 2005) were of three species, today, the number has increased to 17 species which includes two new ones in the group of *Arenaria* and *Paronychia*. Unidentified material have been found at different herbaria which include new species yet to be described, especially in the *Arenaria* and *Paronychia* group. The *Arenaria* complex deserves much attention; over 200 herbarium specimens remain unidentified at several herbaria; this is also true for *Stellaria*, *Paronychia* and *Drymaria*.

What can "big data" tell us about Caryophyllales? Resolving phylogeny, genome duplications, and ecophysiological evolution in a hyperdiverse clade

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The *Caryophyllales* (sensu APG III) inhabit all terrestrial ecosystems and all seven continents, and have experienced a rich and complex evolutionary history that includes multiple gains and losses of several fundamental ecophysiological traits including salt tolerance, C4 photosynthesis, betalain vs. anthocyanin pigmentation, carnivory, and extreme cold and drought tolerance. As part of a US NSF-funded collaborative project, we are exploring the molecular evolution of many of these traits across the *Caryophyllales* by generating and analyzing transcriptomes for hundreds of taxa representing the phylogenetic breadth of the clade. We are also using these data to test phylogenetic hypotheses at deeper levels of *Caryophyllales* and to explore genome duplications. To understand ecophysiological trends at a finer scale across *Caryophyllales*, we are also reconstructing niche evolution using a phylogenetic hypothesis of 3,000+ *Caryophyllales* taxa derived from a supermatrix of all available sequences for several commonly generated plastid and nuclear loci, including matK, rbcL, and ITS. This talk provides a brief overview of these efforts.

Phylogeny of the *Portulacineae* from sequence capture data and perspectives on the evolution of CAM photosynthesis.

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The *Portulacineae* are a group composed of the *Cactaceae* and seven other major clades that have diversified in desert and dryland areas worldwide: *Anacampserotaceae*, *Basellaceae*, *Didiereaceae*, *Halophytaceae*, *Montiaceae*, *Portulacaceae*, and *Talinaceae*. Different clades within the *Portulacineae* appear to have adapted to grow in dry habitats at least semi-independently, so the group gives us a chance to examine the repeated evolution of many traits associated with drought-tolerance in a similar genetic background. We are particularly interested in the evolution of CAM photosynthesis. The members of the *Portulacineae* show all stages in the evolution of CAM from full C₃ photosynthesis to facultative CAM photosynthesis to constitutive CAM photosynthesis, which appears to have arisen multiple times. In addition, the *Portulacaceae* have also evolved C₄ photosynthesis in a CAM photosynthetic background. This is very unusual, as most groups are either exclusively C₃ and C₄ or exclusively C₃ and CAM.

We are using targeted sequence capture to reconstruct the phylogeny of the *Portulacineae*. This technique allows us to use dry material, including herbarium material, so we can sample broadly in the group and understand the evolution of clades that have been poorly studied in the past, such as the *Anacampserotaceae*. In addition to sequencing a variety of genes for phylogenetic reconstruction, we are targeting genes involved in photosynthesis in particular, in order to look for sequence changes and gene duplications associated with the evolution of CAM and C₄ photosynthesis.

Genetic diversity of *Persicaria minor* (*Polygonaceae*) in Iran

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Persicaria minor (Huds.) Opiz. is an annual herb of *Polygonaceae* from Southeast Asian countries. It grows in damp areas, river banks and near of rice fields up to 2000 meter of sea level. This species can be distinguished from other species of *Persicaria* by features such as slender stem, linear to linear-lanceolate leaves, brownish or greenish cylindrical ochrea and lax inflorescence.

Today, conservation of biological diversity is an important concern for most of countries especially for those that are rich in Flora. To conserve biodiversity, the most important step is to analyze genetic diversity. It provides valuable data on patterns of species diversification, population size and inbreeding. Results of these analyses may have positive effect on conservation strategy and future breeding of medicinal or endangered plants.

Persicaria minor is a medicinal plant that grows in different geographical regions of Iran and forms several local populations. In this study, we investigated the genetic diversity using ISSR marker as well as population structure and gene flow in 92 plants from 11 geographical population of *Persicaria minor* in Iran.

Genetic diversity analysis revealed high within population genetic variability. The AMOVA test

produced significant genetic difference among the studied populations. The Mantel test revealed significant correlation between genetic distance and geographical distance of the populations. STRUCTURE analysis and K-Means clustering revealed population genetic fragmentation and the presence of two gene pools for this species. The results suggested that genetic divergence, gene flow and local adaptation have played role in diversification of *Persicaria minor*.

Morphology, diversity and micromorphology of the *Minuartia* species (*Caryophyllaceae*) in Iran

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In the present study, morphology diversity and micromorphology of all Iranian *Minuartia* species belonging to two different subgenera (i.e. *Minuartia* subgen. *Spergella* and *Minuartia* subgen. *Minuartia*) were investigated. According to the latest results 22 species and one subspecies were detected for the country. The distribution map, identification key and taxonomic description are presented. Morphological studies led to the recognition of two new species, *M. khorassanica* (with limited distribution in E Iran) and *M. sabalanica* (in NW Iran) and one new subspecies, *Minuartia lineata* subsp. *litwinowii*. Due to some morphological similarities, *M. sabalanica* was placed in sect. *Acutiflorae*. Moreover, a new section (sect. *Khorassanicae*) was added to the sections of subgen. *Minuartia* based on many morphological differences seen in *M. khorassanica* especially in floral parts. Therefore, seven sections are recognised for the subgen. *Minuartia*. The results of seed micro-morphology were useful in differentiating some closely related taxa at the species level. Some species such as *M. hamata* and *M. khorassanica* were quite different from other species nested in sect. *Minuartia* micro-morphologically.

A phylogenetic circumscription of the *Silene italica* group and its allied species (*Caryophyllaceae*) in the Mediterranean Basin

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Silene L. is the largest genus of *Caryophyllaceae* with about 700 species occurring naturally in temperate and alpine habitats. They are particularly well represented around the Mediterranean Basin where about 350 species are recorded and with main known centres of endemism in Greece and Turkey.

The taxonomy of *Silene* remains controversial due to many diagnostic characters being homoplastic (e.g. number of styles, calix size, anthophore length, calix endumentum) and to a large morphological intraspecific diversity that sometimes led to the splitting of locally adapted populations into different species. The use of molecular markers in a phylogenetic frame helped disentangling the taxonomy at a large scale since it is well recognised now that the genus comprises two subgenera, namely subgenus *Behen* (Dumort.) Rohrb. and subgenus *Silene* (Rohrbach, 1868) but at lower levels, uncertainties remain.

Within subgenus *Silene*, we are interested in the composition and delimitation of section *Siphonomorpha* Otth. This section was first described by Otth (in De Candolle, 1824) and included 66 species that display paniculate-like inflorescence and tubulate calyx. Recent taxonomic revisions have considerably modified the circumscription of this section. Here, we aim at confronting the classical morphological classifications with the one obtained using molecular markers, and more specifically ITS. We therefore used the *Sileneae* database (Oxelman et al. 2013) and completed it with many accessions from the groups under study. More specifically we want to assess whether the *Siphonomorpha* section (sensu lato) is monophyletic and whether the different groups that were described within the section are supported.

Tribe Caryophylleae (fam. Caryophyllaceae, subfam. Caryophylloideae) in the Southern Transcaucasus and Adjacent Regions.

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Investigations are based on the herbarium materials of B, ERE, G, G-DC, G-BOIS, K, LE, TBI, TGM, W, WU including type material as well as on field observations.

Tribe *Caryophylleae* is represented in the region by the genera *Acanthophyllum* C. A. Mey. (7 species from 2 sections), *Allochrusa* Bunge (3 species), *Dianthus* L. (45 species, 7 sections), *Gypsophila* L. (27 species, 4 subgenera, 8 sections), *Kohlrauschia* Kunth (2 species), *Petrorhagia* (DC.) Link (3 species), *Saponaria* L. (6 species, 3 subgenera, 4 sections), *Vaccaria* Wolf (1 species) and *Velezia* L. (1 species).

Allochrusa bungei Boiss., *A. takhtajanii* Gabrieljan & Dittrich, *Dianthus atschurensis* Sosn., *D. canescens* K. Koch, *D. gabrielianae* Nersesian, *D. grossheimii* Schischk., *D. martuniensis* M. Kuzmina, *D. juseptchukii* M. Kuzmina, *D. sessiliflorus*, *D. takhtajanii* Nersesian, *D. zangezuristicus* Nersesian, *Gypsophila szovitsiana* Lazkov, *G. iranica* Barkoudah, *G. wilhelminae* Rech.f., *G. bazorganica* Rech.f., *G. robusta* Grossh., *G. lipskyi* Schischk., *G. takhtadzhanii* Schischk. are endemics of the investigated region. According to the first results of the ongoing molecular studies on Caucasian *Dianthus* species (A. Nersesyan, N. Korotkova, unpublished data), *Dianthus orientalis* seems to be a non-monophyletic species. Considering the morphological features and results of molecular studies (S. Fior et al., 2006; D. T. Harbaugh et al. 2010), the closest relatives of the genus *Dianthus* are the genera *Velezia*, *Petrorhagia* and *Kohlrauschia*. The genus *Acanthophyllum* is close to the genus *Allochrusa*. The genus *Gypsophila* is closely related to the genera *Vaccaria* and *Saponaria*.

Molecular phylogenetics and classification of *Cactaceae*: insights from exploring GenBank and applying a supermatrix approach

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Molecular phylogenetic studies of the past two decades have greatly increased our knowledge on the evolution and classification of *Cactaceae*. Meanwhile, more than 10'200 sequences of the family *Cactaceae* are hosted by GenBank. This large dataset is explored for information on species and exemplar coverage, molecular markers, and voucher specimens for identity verification. In total, some 1'300 species from all currently recognized genera represented. The plastid molecular markers *rbcl*, *trnK/matK*, *rpl16*, *trnL-trnF*, *trnS-trnG*, *psbA-trnH*, *atpB-rbcL*, and *trnT-trnL* are most prominently represented.

I present a pipeline implemented in the programming language Python for the semi-automated but assisted compilation of aligned matrices for the iterative combining into supermatrices for subsequent Bayesian and likelihood analyses. Fast-evolving sequences are grouped into subsets based on insights from the analysis of slow-evolving markers and profiling based on reference sequences. Preliminary analyses are visually inspected and problematic taxa are identified and excluded.

The largest cactus phylogeny presented includes 960 species and 8 plastid markers in a supermatrix with some 70% of missing data. More conservative variants with fewer fast-evolving markers provide fewer resolved clades but often higher clade support values. These highly inclusive phylogenies of *Cactaceae* are used for calculating phylograms and chronograms for subsequent comparative evolutionary investigations. Furthermore, the results confirm the relationships among the major cactus clades and are congruent to the most recent infrafamilial phylogenetic classification system.

Cladistics using morphology and its impact on ontology and diagnosis

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Soon after the cladistic method became the paradigm for the postulation of phylogenetic hypotheses, molecular data quickly took over morphology for those purposes. Morphological data in phylogenetic analyses in most cases are analyzed *a posteriori*, mapping the characters onto phylogenetic trees constructed exclusively with molecular data. This practice reduces efforts to understand morphological homology, as only characters that are *a priori* considered to be important are coded to be mapped onto the trees. The original methodological basis of cladistics, which was the postulation of individual morphological homology hypotheses to be corroborated or refuted, testing simultaneously all information using parsimony as the preferred test, is currently seldom used. At the same time, there is an increasing interest to standardize terminology (ontology) and to produce global taxonomic treatments, highlighting the need to deeply understand morphology, which is ideally done through the postulation of homology hypotheses. Arguments have been provided against the incorporation of morphological characters in the reconstruction of phylogenetic hypotheses. None of them have been sufficiently strong to abandon their use in phylogenetics. Even more, making efforts to postulate homology hypotheses for morphological characters to be incorporated into phylogenetic analyses helps clarifying ontology and provides a common understanding for communication in global taxonomic treatments. Matrices with characters that are postulated as homology hypotheses can also be used for diagnostic purposes either as synapomorphies or as combination of features.

Diversity and distribution of *Coccoloba* (*Polygonaceae*, *Eriogonoideae*, *Coccolobeae*) in Mesoamerica

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Coccoloba is the most species-rich genus of the subfamily *Eriogonoideae* including about 150 species mainly distributed in the Caribbean and Amazon basin. Mesoamerica is to be considered as the third

major center of species diversity of the genus and as such we would expect a great deal of morphologic diversity as well. From the morphological point of view, *Coccoloba* can be identified by its simple and alternate leaves, well defined ochreae, its achenes surrounded by an accrescent hypanthium and perianth lobes. It is well known that useful characteristics to identify and classify the species of this genus are few so species recognition is difficult. As a part of the Flora Mesoamericana project we carried out an extensive specimen examination of BM, F, MEXU y MO herbaria to update the taxonomic knowledge of the region. Distributional maps were generated based on specimen localities. As a result in Mesoamerica the genus is represented by 44 species, including 16 endemics. The most useful characters to differentiate species are the shape of leaf blades, inflorescences and fruits. Detailed examination of this last structure shows different shapes, sizes, and degrees of fusion, so that it is critical that to be observed when it is mature. Three main patterns of geographic distribution of the *Coccoloba* species were found: 1) Neotropical (11 species); 2) Mesoamerican (31 species); 3) Mesoamerican-Antillean (2 species). A list of the Mesoamerican species, along with ecological data and conservation status is presented.

Sileneae.info: A continuously updated taxonomic revision of *Sileneae*, based on species tree phylogenies and morphological data

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The tribe *Sileneae* receives considerable interest not only from taxonomists, but also from ecologists, geneticists, conservationists, and other evolutionary biologists. Generic delimitations have been controversial, but is starting to settle in light of recent trestles from gene phylogenies. Still, however, the infrageneric classification is in need of formal revision. At the species level, several new species are being described annually. In addition to the unpublished information that has already been generated, it is likely that we will see an increase in the pace at which new information regarding phylogenetic relationships and species delimitations is generated. I will present some recent results from our group where genome-scale data are used to elucidate such aspects. For future taxonomic and applied research on *Sileneae*, it is important that results are communicated efficiently. I therefore propose an international, multi-disciplinary project, aiming at sharing and publicly presenting taxonomic, phylogenetic, morphological and other trait, molecular, and chorological information through the World Wide Web.

Pleiomery and meiomery in *Montiaceae*: mechanical pressure as driver of floral diversification

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Montiaceae and most *Portulacineae* are characterized by the presence of two median bracts enclosing the flowers and functioning as a calyx. The original perianth consists of petaloid sepals. We investigated the floral development of several members of *Montiaceae* to understand how mechanical forces affect the number and position of floral organs. Median bracteoles have a strong influence on growth, arrangement, and number of petaloids and stamens. Lateral petaloids always arise first, where there is minimal pressure from the bracteoles. Median petaloids are variously

delayed, depending on the pressure of the bracteoles, often arising after the stamens. In *Lewisia*, *Calandrinia*, and *Montiopsis*, pressure of the bracteoles leads to a multiplication of median petaloids and stamens. In *Montia* and *Claytonia* petaloids become absorbed in stamen tissue and arise centrifugally from the base of the stamens.

The gynoeceum also exercises pressure on the stamens, influencing their arrangement and number. Inner stamens or stamen groups always alternate with carpels. A concerted pressure of carpels and bracteoles may lead to a stamen reduction to 1-3 stamens (*Montia* sp.), while a carpel number increase is generally accompanied by greater stamen numbers.

The evidence presented in *Montiaceae* is discussed in the wider context of *Portulacinae*. Mechanical pressures exercised by bracteoles and carpels are important factors influencing the shape and development of flowers, leading to increases and reductions of petaloid numbers and stamens. Our data demonstrate that epigenetic forces are important players in the floral diversification of the former *Portulacaceae*, especially in *Montiaceae*.

What's inside? - Four anatomical leaf types in the *Amaranthaceae* s.str.

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The *Amaranthaceae* s.str. comprise 78 genera and approximately 840 species distributed mainly in tropical and subtropical regions of America, Eastern and Southern Africa and Australia. Most *Amaranthaceae* grow in semi-arid or seasonally dry, warm areas but they also occur in various other habitats. Growth forms present in the family include annual or perennial herbs, subshrubs, shrubs, lianas and trees. C4 photosynthesis evolved at least five times in the family and occurs in about 10 genera with 250 species (Sage et al. 2007). In previous concepts of leaf anatomical types *Amaranthaceae* receive comparatively little attention, probably because of their relatively simple leaf morphology. Therefore a general overview of leaf anatomy in *Amaranthaceae* is missing.

We examined the anatomy of cotyledons and adult leaves of 19 species representing 12 genera of *Amaranthaceae* s.str. Based on previous work and this study, a total of four anatomical leaf types for *Amaranthaceae* s.str. can be discerned: I. Axyroid-C3-type, a dorsiventrally organized, amphistomatous C3-leaf, II. Axyroid-BS-C3-type, includes leaves with conspicuous bundle sheath cells, III. Axyroid-C4-type, dorsiventrally organized, amphistomatous C4-leaf with complete wreath of bundle sheath cells and IV. Amaranthus-type, C4-leaf with isobilateral leaf symmetry, complete wreath of bundle sheath cells and pronounced, parenchymatous ribs on ab- and adaxial site of the vascular bundles (mainly the central bundle). On the background of the existing molecular phylogeny this study shows that the Axyroid-C4-type repeatedly evolved in *Amaranthaceae* s.str. while the Amaranthus-type is restricted to *Amaranthus*.

Floral evolution and development in subfamily *Gomphrenoideae* (*Amaranthaceae* s.str.)

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Recently, there is a growing interest for the study of homologies in floral characters of the order *Caryophyllales* and mainly in the *Amaranthaceae* family and subfamilies that comprise it. Because homology assumptions are critical in studies of comparative biology and evolution, the following

work is based on proposing new hypotheses, while contrasting different hypotheses of homology of floral structures that have been important in the classification below family and generic in the *Amaranthaceae*.

The *Amaranthaceae* family is divided into two subfamilies: *Gomphrenoideae* (basically represented in America) and *Amaranthoideae* (mainly present in the Old World). The *Gomphrenoideae* subfamily (*Amaranthaceae* s.str.) includes a variety of 19 genera and 400 species distributed in the Neotropics. Traditional classifications recognized genera in the subfamily based primarily on the characteristics of the "pseudostaminodia" and gynoecium. While recently, there have been studies based on molecular data using *rbcl*, *trnL-F* and *rpl16* markers, the basic morphology of these structures is not well defined yet, although these structures are the most important in the taxonomy of the group. This study will be focused on some floral structures: tepals; "pseudostaminodia" (mainly for *Gomphrena* and *Pfaffia*); and gynoecium. This research will be conducted through comparative studies analyzing floral morphology using: a) SEM (Scanning Electron Microscope) observations and developmental-histological study, and b) the analysis of gene expression during floral development of some representatives of the subfamily *Gomphrenoideae*.

Biodiversity of *Tamarix* in Iran

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Iran with about 1.65 million square kilometer surface area has a rich flora in southwest Asia. Iran phytochoria is composed of Euro Siberian, Irano-Turanian and Saharo-Sindian elements and is influenced by the penetration of Somali – Masaei and Mediterranean Species. *Tamarix* with 54 species is native in the Old World, and one of its major centers of speciation is in the Pakistan, Afghanistan, Iran, Turkmenistan, Southern Kazakhstan and Western China region. Another center is located at the eastern parts of Mediterranean region. *Tamarix* with its complex taxonomy has been studied by different authors in the world. Previous studies revealed that there are still many problems in the taxonomy of this genus. Due to the hybridization and polyploidy the classification of this genus has been changed several times. In this study, different accessions of Semnan province has been gathered and studied and the biodiversity of *Tamarix* in the studied area is discussed.

Next-gen data for a next-gen problem: Resolving relationships and taxonomy of the tuberous, perennial *Claytonia* (*Montiaceae*).

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Recent efforts to revise hypotheses concerning relationships among tuberous, perennial *Claytonia* L. (*Montiaceae*) species have catalyzed further exploration into patterns of hybridization, ecological niche differentiation and speciation in the genus, yet a fully resolved phylogeny is still lacking. This paper addresses prior and future molecular phylogenetic studies of *Claytonia* using traditional and next generation sequencing methods, highlighting our examination of the *C. lanceolata* species

complex. Molecular phylogenetic study of *C. lanceolata* and relatives (i.e., tuberous, perennial *Claytonia*) indicates that numerous cryptic species complexes abound and that some species are widely paraphyletic as currently circumscribed. New phylogenetic information is used to evaluate the evolutionary significance of morphological characteristics that have been traditionally used to circumscribe sections in the genus *Claytonia*.

Exact delimitation of the morphologically similar but phylogenetically distant genera *Blitum* and *Oxybasis* (*Chenopodiaceae*–*Amaranthaceae*): a case study of several enigmatic taxa

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Recent molecular investigations strongly suggest that the genus *Chenopodium* s.l. unites morphologically similar but phylogenetically distant taxa. The genera *Blitum* (tribe *Anserineae*) and *Oxybasis* (*Chenopodieae*) provide an example by virtue of homoplastic reduction in number of perianth segments. The exact definitions of these genera are still unclear, and the morphological characters do not play an important role in their diagnostics and delimitation. Some enigmatic taxa with pending taxonomy have not been included in the molecular analysis. Based on morphology, *Chenopodium antarcticum* has been recently transferred into *Oxybasis* (*O. antarctica*), and *Monolepis* is now considered to be a synonym of *Blitum*. We have investigated several species with pending taxonomy based on both molecular (using three markers: ITS, rbcL and trnH-psbA) and carpological methods. *Chenopodium antarcticum* (*Oxybasis antarctica*) does indeed belong to *Blitum* (*B. antarcticum*) as proposed by Hooker; the systematic placement of *Monolepis asiatica* or *M. nuttalliana* in the genus *Blitum* is confirmed. However, the third *Monolepis* species – *M. spathulata* transferred into *Blitum* (*B. spathulatum*) – is a sister group to all *Chenopodieae*. We note that all *Blitum* species in the re-defined genus have the seed-coat testa lacking “stalactites” in the cells, and the genus is distinguished by the easily visible protoplast; in contrast, all *Oxybasis* representatives and *Monolepis spathulata* possess vertical stalactites in the outer cell walls of the testa, and the protoplast is reduced to small strips (a feature of almost all *Chenopodieae*). This peculiarity in the seed-coat testa is a single useful trait separating *Blitum* and *Oxybasis* unambiguously.

Predictive Biogeography of Alpine *Caryophyllaceae* in the Context of Climate Change

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Recent climate change is rapidly altering the abundance and geographical distribution of species across the world. This ecological response is particularly important in alpine biotas. Studies have shown a latitudinal or altitudinal shift in species distributions, along with a reduction in their geographic range. Several species of *Caryophyllaceae*, and in particular, in the subfamily *Alsinoideae* are conspicuous elements of high-elevation ecosystems worldwide, thus offering a model to examine the biogeographic impact of climate change in these regions. Here we employ species distribution models based on a MaxEnt algorithm to analyze the potential impact of climate change

of 12 *Caryophyllaceae* species (four genera) in three geographical realms: *Pycnophyllum* and *Pycnophyllopsis* in the tropical Andes, and *Colobanthus* and *Scleranthus* in the alpine regions of New Zealand and Australia, including Tasmania. The analyses were performed under two climatic scenarios RCP 2.6 and RCP8.5. Our results show a marked decrease in the potential range based on the two future scenarios, the reduction rate ranging from 28.4% to 100% (mean 76.9%) under RCP 2.6 and from 48.9% to 100% (mean 88.1) under RCP 8.5. We also detected clear differences across the study area, being the Australian alpine habitat the most affected, with four out of six species showing a range reduction of 100% (RCP 8.5), including the endemics *Colobanthus nivicola* and *Colobanthus curtisiae*. Further modeling studies in other alpine *Caryophyllaceae* are proposed as well as in situ monitoring plans.

Molecular phylogeny of *Acantholimon*: a diverse Irano-Turanian genus of *Plumbaginaceae* (*Caryophyllales*)

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Acantholimon, with c. 200 thorn-cushion forming species, is one of the largest genera of Plumbaginaceae and among the most species-rich genera of the Irano-Turanian Region. However, it is represented poorly in previous molecular studies. Species of the genus are important components of the xerophytic vegetation of SW and C Asia and distributed mostly in dry and cold steppes of intermediate or high mountainous regions. Although the placement of *Acantholimon* in the subfamily *Limoniaioideae* has already been suggested, the monophyly of the genus and its relationship to other closely related genera have remained unresolved. In this study, sequence data of two plastid DNA regions, *trnL-F* and *petD*, and nuclear ribosomal internal transcribed spacer (ITS) of 185 samples of *Acantholimon*, considering the whole distribution area and all sections of the genus, and five samples representing four selected allied genera, were generated. Phylogenetic analyses were conducted using maximum parsimony, maximum likelihood and Bayesian methods. Trees obtained from cpDNA and nrDNA are largely congruent and strongly support two major clades (*Acantholimon* I and II) within *Acantholimon* besides the segregate genera *Cephalorhizum*, *Dictyolimon* and *Vassilczenkoa*. *Dictyolimon* is resolved as sister to clade II in the ITS tree with high confidence, whereas it appears in a polytomy with clades I and II and a *Cephalorhizum-Vassilczenkoa*-lineage in the plastid tree. The comparison of nrITS and cp topologies further reveals 18 cases of incongruence pointing to reticulate evolutionary events. However, these incongruences were specific to certain species or groups of species and occurred only within the two major clades but not among them. *A. collare*, for example, groups with a monophyletic core of dimorphic species of Sect. *Tragacanthina* in the plastid tree but appears in a different well-resolved subclade in the nuclear tree. On the other hand, *A. multiflorum*, *A. saxifragiforme* and *A. hohenackeri* constitute a strongly supported subclade (ACA C) in the nuclear tree while clustered with other species in plastid tree (ACA Vd). The currently used sectional classification of the genus, which is based on morphology, is found to be mostly inconsistent with the phylogenetic results.

Systematics and biogeography of *Stellaria* L. (*Caryophyllaceae*) of the Asian Russia and Mongolia

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The genus *Stellaria* L., s.l. (*Caryophyllaceae*, *Alsineae*) contains about 200 species (Lazkov, 2006), distributed in the cold and temperate regions. Most of the species occur in China (Cheng Shelong et al., 2001), 45 species in Siberia, the Russian Far East and Mongolia, in the steppe, forest and arctic regions. Herbaceous plants are annual, or perennial; flowers terminal, in cymes or solitary, petals (4) 5, 2-cleft nearly to base, or absent; styles 3 (4); capsule opening usually by 6 valves. The most recent infrageneric classification was proposed by Tzvelev (2000a, 2000b): he subdivided the *Stellaria* of Eastern Europe into three subgenera - *Alsine*, *Hylebya*, *Stellaria* - and several sections and subsections. Our study adds to this classification (Vlasova, 2012): the accepted section *Ruscifoliae* (3 species from the Far East), subsection *Discolores* (1 subendemic from the Far East). The section *Jacuticae* (1 endemic from Yakutia) is placed into the subgenus *Adenonema*. Recent analysis of molecular data supports this division only partially (Greenberg, Donoghue, 2011). The genera *Mesostemma* (styles 2, capsule opening by 4 valves) and *Fimbripetalum* (petals 5-7-cleft, seeds scrobiculate) are considered as separate genera (Ikonnikov, 1976, 1977).

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Evolution of C4 photosynthesis in *Caryophyllales*: the role of C3-C4 intermediate species

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In terrestrial plants, including grasses, sedges and dicots, different variants of C4-Kranz anatomy and biochemistry have evolved independently from C3 plants at least 66 times. There are 37 families in the eudicot order *Caryophyllales* (APG III system, 2009), which includes 23 C4 eudicot lines. C4 species acquired a C4 cycle and leaf structure with enlarged chlorophyllous bundle sheath cells surrounded by palisade cells (Kranz anatomy). Stepwise evolution is proposed from C3 to C3-C4 intermediates to C4 plants. Currently, only ~50 species have been identified as intermediates (based on structure, biochemistry, function) with properties intermediate to C3 and C4 (structural, biochemical and functional); 18 intermediate species are in *Caryophyllales*. Aridization is considered one of the main driving forces in C4 evolution. Two general paths are proposed for evolution of Kranz anatomy from C3 ancestors having planar versus succulent leaves. For species with planar leaves, increased vein density is the best supported preconditioning to date, leading to multiple Kranz units surrounding individual veins. There has been less focus on the evolutionary path from C3 to C4 in succulent plants. There are many succulent species in *Chenopodiaceae* and *Portulacaceae* which develop water-storage tissue in leaves, with 7 structural types where formation of Kranz anatomy is not linked to vein density. We have identified structural and biochemical diversity in *Salsola* which provides a model for the path of evolution from C3 to C4 in succulent species.

Phylogenetic analysis of the path to C4 in different lineages is limited by identification of C3-C4 intermediates.

The development from underlying intercalary meristems of the calyx and androecial tube in *Amaranthaceae* s. l.

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In *Caryophyllales*, including *Amaranthaceae* s.l., there is consensus that the perianth is uniseriate and that the corolla is lost. The calyx consists of five (sometimes two) sepals originating from individual primordia.

Several species of *Amaranthaceae* have flowers with a so-called 'androecial cup' or 'staminal ring' or stamens becoming 'connate at their bases'. Moreover, often so-called 'pseudo-staminodia' occur on the rim of the androecial tube. Using SEM, we investigated the development of calyx and androecium and related structures aiming to determine their origin in *Alternanthera*, *Atriplex*, *Beta*, *Chenopodium* + *C. bonus-henricus*, *Dysphania*, *Iresine* and *Tidestromia*.

In all species studied, the sepals are congenitally fused. In *Dysphania*, the perianth originates from an annular primordium. Five individual stamen primordia originate opposite the sepals. In *Alternanthera*, *Iresine* and *Tidestromia*, the androecium is raised by the formation of a floral cup below the stamens, becoming nectariferous at later developmental stages. We call this the androecial tube. Moreover, alternating with the stamens, androecial tube appendages (pseudo-staminodia) are formed from meristematic bulges. In *Beta*, the androecial tube remains rudimentary. In *Atriplex* and *Chenopodium*, at later developmental stages, the bases of the stamens are fused. Although in the past postgenital fusion of the bases of the stamens was suggested, we now interpret the 'fused' part as homologous to the androecial tubes as observed in the other species; hence originating from an underlying annular intercalary meristem.

Conclusions: underlying intercalary meristems are responsible for the formation of respectively calyx tubes and androecial tubes. There is no evidence for postgenital fusion.

Biodiversity and Systematics in the *Silene* (*Caryophyllaceae*) species occur in Turkey

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Comprising about 700 species, *Silene* L. is one of the largest and most widely distributed genera. Adapting to various environmental conditions, most of the species are found in the temperate and alpine area of the Northern hemisphere. Turkey is one of the richest *Silene* species hosting areas. Currently occurrence of 171 taxa which about 43% of them are endemic, are recorded in the Flora of Turkey and East Aegean Islands plus recent publications.

In this study, the *Silene* species occurs in Turkey were investigated from morphological, geographical, and taxonomical aspects. Specimens collected from field trips in addition to the ones present in the main herbaria in Turkey and Europe were examined. Their conservation status, phytogeographical regions, and distributions in Turkey were evaluated.

Our work showed that 30 of the Turkish *Silene* have limited distributions. Despite the high number of the Iranian-Turanian species, Mediterranean *Silene* species are dominated over the other phytogeographical elements. Regarding the conservation status, about 74 endemic taxa which 20 of them are in Critically (CR), and 21 are in Endangered (EN) categories, are defined in the threatened category. In addition to these findings, morphological evidence indicate that taxonomic status of some *Silene* taxa, especially several of those among the recent records, are in great need to be checked.

Seed, pollen and chromosome morphology of the *Silene* (Caryophyllaceae) in Turkey

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In this study, I have investigated macro, and micromorphology of the seeds and pollen grains of the 140 *Silene* taxa occurring in Turkey, using the stereo and scanning electron microscopes. I have also checked the chromosome morphology of the 107 *Silene* taxa belonging to 34 sections of the genus, via a light microscope. 55 of the studied taxa are endemic to Turkey. Seeds are generally reniform and tubercles obtuse rounded. Testa cell boundaries (suture outline) are serrate, and sometimes sinuous. On the other hand, the hylar zone looks like recessed type. The shape of pollen grains of all studied *Silene* taxa is spheroidal and ornamentation mostly scabrate, microechinate-microperforate or perforate. Pollen structure is mostly tectate or semitectate. Somatic chromosome analysis were performed using aseto-orcein squash method. In karyological studies, somatic chromosome number is generally $2n=24$ and basic chromosome number is determined as $x=12$. Morphology of seeds, pollen grains and chromosomes can be especially used to discuss or distinguish the problematic taxa.