the subfamily. The genus is distributed in South and Central America except for *Pitcairnia feliciana* that is a local endemic on a mountain range in West Africa. No extensive molecular systematic analyses have yet been undertaken in *Pitcairnia*, and infrageneric relationships remain largely unknown. Here we present a first

assembled for 181 accessions from 128 species, resulting in an alignment of 4,989 bp. A total of 540 characters turned out to be parsimony informative. The data set was subjected to Bayesian, maximum likelihood and maximum parsimony analyses. In the resulting trees, *Pitcairnia* is monophyletic and sister to the remainder of the subfamily. A deep basal split divides *Pitcairnia* into two large lineages. *Pitcairnia feliciana* takes a relatively early branching position in one of the two lineages. Its closest relatives are found in Venezuela. Some clades reflect the distributional pattern of the underlying species (e.g. a Brazilian clade and a Carribean clade), but no overall general geographical patterns could be discerned.

17:15

Flower color evolution within the Cichorieae (Asteraceae) – the Flavonoid-3'5'-Hydroxylase

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The blue flower color within the Cichorieae (Asteraceae) is thought to be determined by the presence of anthocyanins.The anthocyanin biosynthetic pathway is quite well studied. Two enzymes, flavonoid 3' hydroxylase and flavonoid 3', 5' hydroxylase, determine the hydroxylation pattern of the anthocyaninswhich exhibit three classes: cyanidins (mainly in charge of redish/pink flowers), delphinidins (in charge of bluish flowers), and pelargonidins (one possibility to exhibit orange flower color).

We here investigate flower color evolution in two closely related species of two different genera of the Cichorieae featuring yellow (*Catananchelutea* L.; *Lactucaserriola* L.) and bluish (*CatananchecaeruleaL.*, *Lactucaperennis* L.) flowers.Whereas, the yellow flowering species *C. lutea* and *L. serriola*did notexpress *F3'5'H* it was possible to partially sequence the *F3'5'H* mRNA in *C. caerulea* and *L. perennis*. The q-RT PCR expression pattern revealed *F3'5'H*to be expressed in different levels at differ-

ent times and developmental stages during flower development of *C. caerulea* and *L. perennis*.The expression is preceding the petal coloration in the flowers. A phylogenetic analysis revealed high similarity of the bluish CichorieaeF3'5'Hwith other AsteraceaeF3'Hs and F3'5'H pinpointing to a neofunctionalization of this enzyme, to enable the Asteraceae to produce delphinidins again. In addition, the flavonoid composition was analyzed via LC-MS and HPLC. All four species contain caffeic acid, *p*-coumaric acid and 3' hydroxylated flavonoids like quercetin derivatives.Delphinidin, Pelargonidin and Cyanidin were found in *C. caerulea*, while *L. perennis* only featured Pelargonidin and Cyanidin which was also found in much lower concentrations in *L. serriola*. Missing anthocyaninsin *C. lutea* might be indicative for an inactivation of the DFRenzyme(dihydroflavonol 4-reductase) in this species which might be yellow flowered due to carotinoids. Investigating enzyme activities will be the next step to reveal flower color evolution within the Cichorieae.

Systematics of Pelliaceae (Marchantiophyta, Jungermanniopsida) and the new genus *Apopellia* stat. nov.

17:30

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Recent molecular phylogenies and classifications reveal the Pelliales to be the earliest diverging lineage within the simple thalloid liverworts (Crandall-Stotler et al. 2009). The order comprises two families: Pelliaceae with eight species of *Pellia* Raddi, and Noteroclad aceae with the monotypic genus *Noteroclada* Taylor ex Hook.f. & Taylor. We conducted DNA sequence analyses of the plastid loci *rps*4 and *trn*L-F of all Pelliaceae species at hand and morphological studies of selected characters.

Within *Pellia*, a considerable split into two main clades was observed: one comprising *Pellia endiviifolia* and *P. megaspora*, the other including *P. neesiana, P. appalachiana* and *P. epiphylla*. We found several morphological characters, which supported this split: e.g. smooth calyptra vs. two-celled hairs on surface, erect vs. horizontal posture of archegonia, pluricellular vs. two-celled slimehairs. Due to the conspicuous distinctness of these two clades concerning molecular as well as morphological data, we established two different genera. The former subgenus *Apopellia* Grolle (Grolle 1983), which exhibited the single species *Pellia endiviifolia*, is now classified as genus and includes *Apopellia endiviifolia* and *A. megaspora*.

Our genetic data confirmed the distinctness of the species *Apopellia endiviifolia*, *A. megaspora*, *Pellia. neesiana* and *P. epiphylla* with high statistical support.