

early diversifications in southern Africa, resulting in at least three near-endemic groups (the *Relhania* clade, the *Metalasia* clade, and the *Lasiopogon* clade). Analyses using ChromEvol suggests that the ancestral base chromosome number for the tribe is most likely seven, and that the three basal lineages have experienced several chromosome gain or loss events. Four well-supported lineages are recognized in the crown group (i.e., HAP, *Gnaphalium* s.s., FLAG, and the Australasian group); and each of the four lineages has a world-wide distribution or independent large radiations. The HAP clade has a South African and diploid origin, followed by a radiation in southern Africa and several migrations towards the north of the African continent, the Mediterranean basin and Asia. These expansions and diversifications have been accompanied by a large number of genome duplications, as shown by several independent events of tetraploidy, hexaploidy and octoploidy. The FLAG clade is inferred to have a European diversification with a southern African and diploid origin, supporting a single dispersal/migration event in the early Miocene associated with both numerous duplications and dysploidyizations. The Australasian group was likely founded by a single dispersal event from southern Africa that resulted in a radiation of more than 550 species, with numerous genome duplications as well as gain or loss events, as indicated by all chromosome base numbers presented in this group. Our data strongly suggested that Gnaphalieae originated in southern Africa during the Oligocene, followed by repeated migrations into the rest of Africa and the Mediterranean region, with subsequent entries into other continents during various periods starting in the Miocene. Expansions in the late Miocene to Pliocene appear to have been the driving force that shaped the global distribution of the tribe as forests were progressively broken up by the midcontinent aridification and savannas and grasslands expanded into the interior of the major continents. Both polyploidy and dysploidy are indicated as the most significant evolutionary trend in chromosome number within the tribe and may have partly or even mainly contributed to the recent colonizations and rapid radiations of the Gnaphalieae worldwide.

### T2-35-06

#### Island-like mountain radiations in Asia: The case study of the genera *Saussurea* and *Jurinea*

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Evolutionary radiations represent events in which many species or lineages evolved from a common ancestor in a short period of time. Many plant radiations have been triggered by island-like ecological opportunities following mountain uplift; the mountain ranges with the steepest and widest environmental gradients, such as the Andes, are home of exceptional regional species pools (and also exceptional endemism rates), mainly derived from evolutionary radiations. The Himalayan-Qinghai-Tibetan Plateau (HQTP) and the adjacent Hengduan Mountains (HM) are considered one of the main biodiversity hotspots of the world thanks to its richness in species and endemics. Both regions show extreme altitudinal ranges compressed in short distances as a consequence of the collision of the Indian and Eurasian plates, and thus constitute ideal evolutionary scenarios to study diversification processes in mountain regions. We have identified two possible cases of alpine

radiations in the *Saussurea-Jurinea* complex (Compositae-Cardueae), involving some 550 species in total. *Saussurea* shows an amazing number of species (more than 300) in the HQTP and Hengduan mountains, although a considerable number of species are also found on the west side of the mountains of Middle Asia (Tian Shan and Pamir-Alay). *Jurinea*, in contrast, has the highest number of species (150 sp.) in the Tian Shan and Pamir-Alay. Our general objectives are the following: a) To carry out an extensive sampling of *Saussurea* and *Jurinea*, especially centred in the two main radiation areas in the HQTP and Tian Shan mountains; b) To generate well-resolved phylogenies of both genera using a multi-loci approach through next-generation-sequencing (NGS) analyzed by Bayesian inference and parsimony, and explore coalescent-based species tree estimation with our NGS data set; c) On the basis of the new phylogenies, conduct phylogenetic comparative analyses and multi-model biogeographical inference to address the following questions: Do the alpine species of both genera in Asian mountains constitute clades with clearly higher rates of diversification than their lowland relatives? How many independent radiations took place in the complex? If several, did they occur at the same period, and are they comparable in terms of speciation rates? Which factors (intrinsic or extrinsic) shape species radiations, i.e., do the radiations follow a geographical model, an adaptive model, or a mixed model? Our results will be a major contribution to the study of alpine radiations especially in the HQTP, and will open a methodological pathway for the analysis of very large radiations in other genera.

### T2-35-07

#### Phylogenetics of *Baccharis* (Astereae), a mega-diverse genus of compositae

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*Baccharis* L. is the fourth largest genus in the Compositae and the most speciose within tribe Astereae. With species number estimates ranging from 350 up to 500, *Baccharis* is among the largest plant genera in the Neotropics, and has long been considered a taxonomic nightmare. A comprehensive phylogenetic hypothesis for this American genus is necessary to test its monophyly, clarify the infrageneric relationships and shed light on its evolutionary and biogeographical history. Given its great morphological diversity and wide geographic distribution, phylogenetic studies based on molecular data to test the monophyly of the genus and investigate the relationships of its infrageneric groups are required, allowing the recognition of clades with evolutionary and biogeographical significance. Therefore, we provide the hitherto most comprehensive phylogenetic hypothesis for *Baccharis*. We performed Bayesian phylogenetic analyses based on four molecular regions from the nuclear and plastid genomes (ETS, ITS, *trnH-psbA*, *trnL-F*; in total 5041 aligned nucleotides) and including 248 species of *Baccharis*, from all previously segregated genera and all subgenera previously recognized, and 44 outgroups belonging to tribe Astereae, totalizing 1080 new sequences. Our results confirm subtribe Baccharidinae to be a monogeneric group,

and support a wide circumscription of *Baccharis* as monophyletic, including the genera previously segregated from it (*Baccharidistrum*, *Baccharidiopsis*, *Heterothalamulopsis*, *Heterothalamus* and *Launogothamnus*). Seven main lineages are recognized and treated as subgenera, all of which re-circumscribed as monophyletic lineages. *Baccharis* subgen. *Baccharis*, *B.* subgen. *Molina* and *B.* subgen. *Tarchonanthoides* roughly match previous subgeneric concepts, while *B.* subgen. *Pteronioides* and *B.* subgen. *Stephananthus* are synonyms. Two previously segregated genera (*Heterothalamulopsis* and *Heterothalamus*) and two formerly existing sections (*Coridifoliae* and *Oblongifoliae*) are placed at subgeneric rank with new circumscriptions. Four new sections are recognized, and three new statuses at the rank of section are proposed to accommodate taxa not corresponding to any previously described section, while 22 sections are reduced to synonymy. In total, we propose that *Baccharis* should comprise 433 species classified into 7 subgenera and 47 sections. This study represents a major advance in elucidating the relationships among species in such a large predominantly Neotropical plant genus, and thus constitutes the basis for further exploration of the evolutionary processes that have allowed the group to attain its wide geographic distribution, morphological variation, varied sexual reproductive strategies, and complex chemical contents.

### T2-35-08

#### Analysis of genetic diversity and marker-trait associations in the medicinal non-model plant Chamomile (*Matricaria recutita* L.) using genome-wide snp-markers

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*Matricaria recutita* L. (syn. *Chamomilla recutita* (L.) Rauschert, commonly known as German chamomile, is a traditional medicinal plant already mentioned by Hippocrates, whose works can be considered as the basis of modern medicine, in the 5th century BC. In the last decades, rather limited research has been done on chamomile, often focusing on biochemical pathways analyses for medicinally-active compounds like alpha-bisabolol. NGS approaches are frequently used to exploit genetic resources and to improve breeding in major crops. Here, we applied genotyping-by-sequencing (GBS) to unravel the genetic structure of cultivated medicinal chamomile and create a first genomic resource for future applications to improve and facilitate breeding. A high number of SNP-markers were mined to characterize the genetic diversity in the panel of 91 plants from 33 predominantly cultivated varieties, populations and accessions, including diploids and artificially generated tetraploids, and from different geographic regions. 18 compounds (terpenoids) were measured by GC-MS from flower heads. Analyses of flowering time demonstrated that diploids generally flowered earlier than tetraploids. As revealed by STRUCTURE, PCoA and neighbor-joining analysis using 6495 high-quality SNPs, the outgroup *M. discoidea* was clearly distinct from *M. recutita*. The STRUCTURE analysis further showed that

tetraploids tend to display lower genetic diversity than diploids, potentially reflecting their origin by artificial polyploidisation from only a part of the chamomile genetic background. No connection between geographic origin and genetic structure was found, but varieties with genotypes possessing high alpha-bisabolol content (e.g. 'Manzana') could be genetically discriminated. GWAS enabled us to resolve a number of SNPs significantly associated with flowering time and high alpha-bisabolol content. Four sequences characterized by these alpha-bisabolol-associated SNPs are involved in plant biotic and abiotic stress response in different plants species, whereas six of these sequences are described to play a role in universal metabolic pathways. One sequence associated with flowering time is described to be involved with self-pollination in *Arabidopsis thaliana*. Further research could lead to the development of reliable and cost-effective markers applicable for marker assisted selection in chamomile breeding.

### T2-35-09

#### High altitude conservation biogeography: richness, turnover, endemism and regional hotspots of Andean Compositae

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The Andes is the largest, widest and highest mountain range in the world. It covers all possible climatic ranges, from the driest to the humid, and from the warmest to the coldest. From the biological point of view, it includes the Tropical Andes Biodiversity hotspot, considered the world's most biodiverse hotspot. It has been estimated that along the Andes there are about 50,000 plant species (~50% endemic). However, the patterns that shape Andean biodiversity show differences between plant groups and are still not well understood. Being the most diverse South American angiosperm family, and showing high levels of endemism, the Compositae is an excellent model for the study of Andean biogeography. There are some 3,000-3,500 Andean species of the family, with both ancestral and recent origins. This work aims to understand the patterns of richness, species turnover and endemism of the Compositae family throughout the Andes, to help understand the mechanisms that have facilitated its radiation in these high-altitude environments, and to identify regional areas of importance for conservation (regional Compositae hotspots). As a first step in this long-term study program, all georeferenced Asteraceae records are being compiled and analyzed in the different databases of biological collections, and analyses are being carried out on the basis of richness estimators, diversity indexes, Beta-diversity models and sampling efforts. The results show three to four richness centres mainly in the northern and Central Andes of Colombia, Ecuador and Bolivia. The southern Andes show comparatively reduced collection efforts, but levels of endemism appear remarkable. These results disaggregated at the tribe level, allow to test hypothesis regarding the radiation of the different lineages within the family, identifying areas with sampling gaps, and regional priority areas for conservation efforts, eventually related to the ancestral uses of the species.