were detected by PCR-RFLP analyses in these species. A group of 2x- and 4x-taxa of herbaceous perennial Achillea (Asteraceae) in E Asia has been studied by DNA-analyses (sequencing, AFLP, cpDNA and trnL-F) and closely related multidisciplinary methods. A. acuminata-2x belongs to A. sect. Ptilmica. A. asiatica-2x is an eastern member of the A. milletiifolium aggregate in sect. Achillea. A. alpina-4x and A. wilsoniana-4x form a nearly continuous morphological, ecological, and geographical link between the two very different diploids. A NJ genetic distance analysis of AFLP data clearly demonstrates an intermediate position of the 4x- between the two 2x-taxa. 5 plastid haplotypes obtained using Quantitative Feulgen photocytometry. Furthermore, the hybrids are either homoploid or allopolyploid. Such data will be used for a more detailed study at population level.

A. wilsoniana, A. asiatica. A. acuminata-2x is an eastern member of the A. milletiifolium aggregate in sect. Achillea. A. alpina-4x and A. wilsoniana-4x form a nearly continuous morphological, ecological, and geographical link between the two very different diploids. A NJ genetic distance analysis of AFLP data clearly demonstrates an intermediate position of the 4x- between the two 2x-taxa. 5 plastid haplotypes obtained using Quantitative Feulgen photocytometry. Furthermore, the hybrids are either homoploid or allopolyploid. Such data will be used for a more detailed study at population level.

P1634. Investigating ancient homoploly hybridisation patterns within the genus Diphasiastrum

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Several defined species within the genus Diphasiastrum are considered to be of hybrid origin. These assumptions are primarily based on observations of populations with intermediate morphology and high rates of spore abortion in both Europe and North-America. Cytological and molecular support for these theories is, however, lacking. The main goal of this project is to investigate and estimate the frequency of speciation through hybridisation within this genus. This primarily implies investigating congruence between cpDNA - and nuclear single copy gene sequences (LEAFY, RNA polymerase and phosphoglucone isomerase, PGi) to identify parental lineages of the putative hybrid species. As Diphasiastrum is known as a genus with notoriously unidentifiable chromosomes, assessing ploidal level is crucial to define what kind of hybridisation events that have occurred, i.e. if the hybrids are either homoploly or allopolyploid. Such data will be obtained using Quantitative Feulgen photocytometry. Furthermore, microsatellite - and allozyme markers will be used for a more detailed study at population level.

P1635. Reproductive isolation in Mediterranean deceptive orchids

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The maintenance of species boundary among related sympatric species is clearly dependent on the strength of reproductive isolation. Orchid flowers are often highly specialised to attract and fit their pollinators, suggesting a prominent rule for pre-mating reproductive isolation in maintaining species boundaries. To investigate the presence and the strength of post-mating barriers in Mediterranean orchids we performed a large number of interspecific crossing experiments and analysed fruit set production and seed viability. Then we tested the relationship between reproductive isolation and genetic distance for post-mating pre-zygotic barriers and for post-zygotic barriers. Results clearly indicate that post-mating barriers (both pre-zygotic and post-zygotic), including the post-zygotic barriers, as hybrid sterility, largely contribute to prevent gene flow among co-flowering food deceptive orchids with a generalized pollination compared with other orchid groups with an highly specialised pollination biology like the sexually deceptive Ophrys.