

DAVIS EXPEDITION FUND

REPORT ON EXPEDITION/PROJECT

Expedition/Project Title: Gesneriaceae collections in China.....

Travel Dates: 28.8.2008 – 29 September 2008

Location: China; Yunnan, Sichuan, Guangxi, Guangdong, Hainan

Group Members: Michael Moeller

Aims: the main aims were to collect DNA samples, and herbarium voucher specimens of Gesneriaceae

OUTCOME (not less than 300 words):-

Background for Field Work:

The taxonomy of the family Gesneriaceae in China has always been weak, even at the generic level, and it has been B.L.Burt's opinion that too many small and monotypic genera exist. Our most recently accepted phylogenetic analysis included 46 out of 77 Asian genera of the Old World Gesneriaceae. The paper focussed on the incongruencies between our phylogeny and available tribal classifications of the family. DNA material for another 17 genera are present from previous collections, leaving 14 genera remaining to be included. Five of these occur in China and represent small (2-4 ssp.) or monotypic genera. They occur mainly in the provinces Sichuan, and Guangxi & neighbouring Guangdong & Hainan.

Fieldwork 2008:

During the collection trip, from 28 August to 29 September 2008 I was accompanied by Prof Wei YG in the field. We visited localities in Yunnan, Sichuan, Guangdong, Guangxi and the island of Hainan. We made 220 plant collections (herbarium voucher specimens, DNA samples, seeds, alcohol fixed material), including 76 Gesneriaceae accessions (and several of families Begoniaceae and Zingiberaceae). The Gesneriaceae samples included 41 species in 23 genera, two were from the small genera, *Didymostigma* (3 species) and *Bournea* (2 species), and the monotypic *Metapetrocosmea peltata* and *Cathayanthe biflora*. The monotypic genera were collected on the island of Hainan. *Cathayanthe* was collected for the first time since the mid 1970th.

The seed material has now been sown and will be incorporated into the Living Collection at RBGE. These new accessions will be analysed cytologically and the results incorporated into our studies on the genome evolution in Old World Gesneriaceae.

The collected DNA samples of Gesneriaceae will be analysed and incorporated into our next publication on generic relationships among Old World Gesneriaceae.

The kind donation towards our research on Gesneriaceae by the Davis Expedition Fund will appropriately be acknowledged in our publications on this subject.