ABSTRACT BOOK II

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Posters and Abstracts

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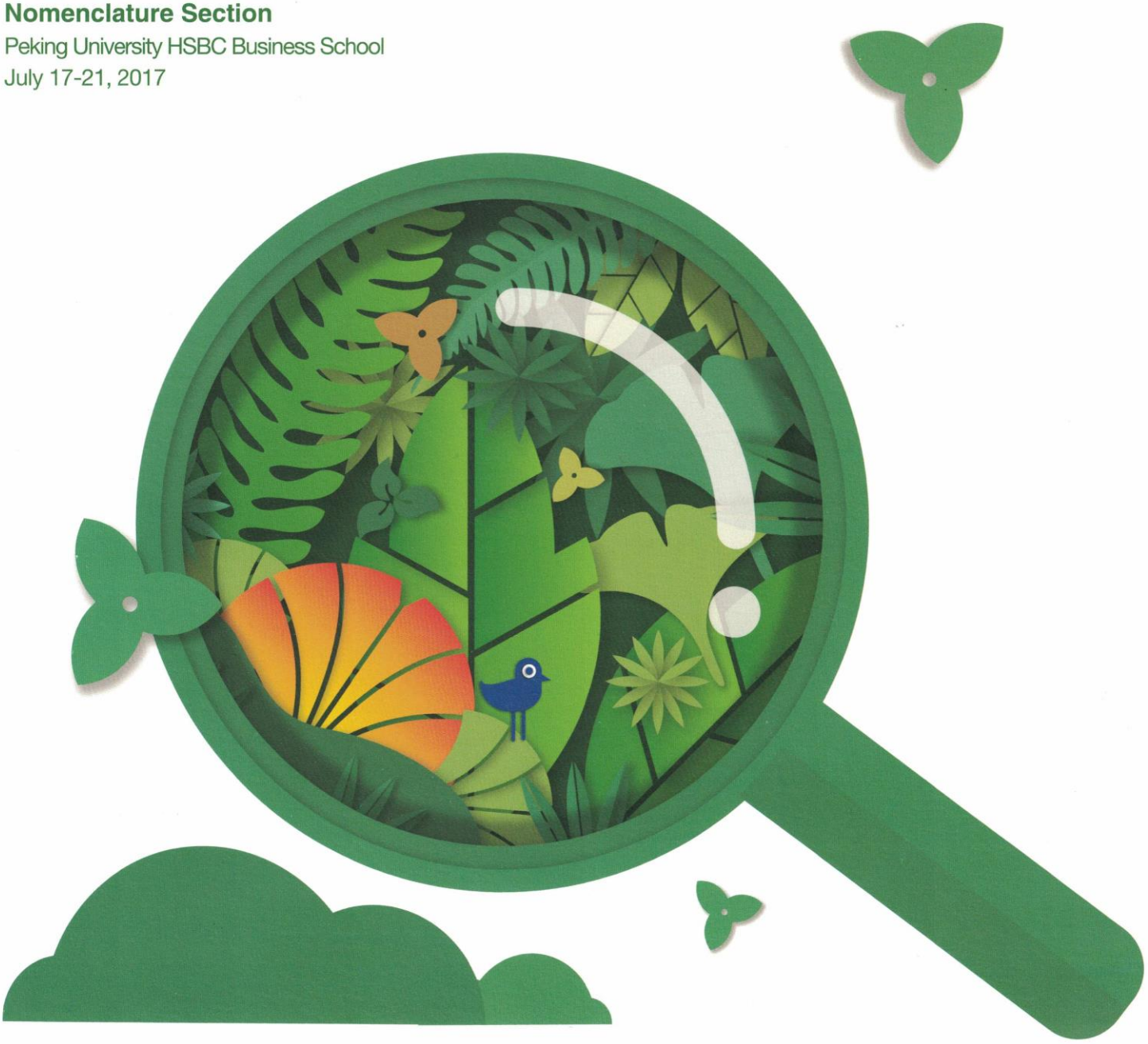

interaction matrices with floral functional units based on (pantrap) colours. Considering the robustness of plant-bee interactions in different habitats should vary depending on the availability of diverse floral functional groups, we tested in agroecosystems and forests of Doon Valley, (1) whether real mutualistic (bee-plant communities) interactions varied compared with three random-mut networks (using null models), and (2) how bee interactions with floral functional groups affect network attributes in different selected habitats. Network attributes viz. connectance, interaction evenness, linkage density and nestedness were selected to assess their patterns and ecological implications across agroecosystems and forests habitats in Doon Valley. Real plant-bee interactions varied from null models. Highest bee interactions were seen in the white floral functional groups (n = 236), and the least were in blue floral functional groups (n = 75). Bee families showed differential floral colour preferences in forests and agroecosystems. Plant-bee communities were more robust in forests than agroecosystmes. Network attributes such as weighted linkage density and weighted nestedness confirmed benefits of quantitative data over only presence-absence records for the conservation of mutualistic interaction. A detailed investigation into the types of forests revealed riverine habitats were robust to invasive species than Sal forests, indicating forest managers to take appropriate steps in vegetation management. Network interactions in agroecosystems indicated to agriculturists adopt a polyculture approach to cultivation to maintain robust mutualistic interactions for better productivity in crops. The study also highlighted that pantraps could be reliably used by numerous unskilled surveyors, in different areas simultaneously for long-term investigation and monitoring of plant-bee interactions.

T2

P0658

Pollination of two sympatric species of *Balanophora*: *B. fungosa* and *B. harlandii*.

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Balanophora is a genus of holoparasitic plants, which inhabit mainly in tropical regions of Asia. The genus divided to two subgenera (subgen. *Balanophora* and subgen. *Balania*) by merism of male flowers, while its female flowers are simplified to filiform structures. Species of the both subgenera inhabit the same territory (sympatric). In addition to morphological, ecological differences between the sympatric species are expectable, e.g. different system of pollination. Pollination biology of some species from subgen. *Balanophora* was investigated earlier. It was showed that *B. abbreviata* is pollinated by bees. Pyralid moths were recognized as pollinators of *B. kuroiwai*. Data on pollination of species from subgen. *Balania* are poor: ants and cockroaches were noted as visitors of *B. tobiracola*. The present research is dedicated to flowering biology of two species of *Balanophora* from different subgenera. *Balanophora fungosa* (subgen. *Balanophora*) and *B. harlandii* (subgen. *Balania*) were investigated in the same season and habitat in northern Vietnam. Inflorescences of the both species open acropetally. Within an inflorescence of *B. harlandii*, 9–16 flowers can be anthetic simultaneously; each flower remains anthetic for 1 day. Within an inflorescence of *B. fungosa*, 10–20 flowers can be anthetic simultaneously; each flower remains anthetic for 2–5 days. Inflorescences of both species were visited in daytime by flies (Calliphoridae, Drosophilidae, Syrphidae), wasps (*Vespa sp.*), ants (Formicidae, Mirmicidae), harvestmen (Phalangidae) and others. Drosophilid flies were the most frequent visitors of *B. fungosa*, while *B. harlandii* was visited predominantly by the wasps. Pollen grains of *Balanophora* were found at the bodies of the drosophilid flies and the wasps. On average, 102 pollen grains of *Balanophora* were found on the body of each wasp, while only 2 pollen grains were found on the body of each fly. Drosophilid flies visit male inflorescences of *B. fungosa* on average 433 times per day and visit female inflorescences 144 times per day. Wasps visit male inflorescences of *B. harlandii* on average 62 times per day and visit female inflorescences 18 times per day. It can be concluded, that drosophilid flies are the main pollinators of *B. fungosa* and wasps are the main pollinators of *B. harlandii*. However drosophilid flies can take minor part in pollination of *B. harlandii* as well as wasps can pollinate *B. fungosa*. The flies carry far less pollen than the wasps, but higher frequency of visits offsets this difference. As a result, sufficient effectiveness of pollination is ensured for the both species. Mechanism of plant-pollinator interaction is somewhat similar for *B. fungosa* and *B. harlandii*: sweet smell attracts insects and they feed on nectar as a reward. Probably, some differences in chemical composition of volatiles led to situation, when flies prefer one species but wasps prefer another one. Chemical change of volatiles and followed change of pollinators range can served as factors of divergence of this species during sympatric evolution. This study was funded by the Russian Foundation for Basic Research (project 16-34-00330).

T2

P0659

Dynamic evolutionary history of the East Asian Tertiary relict *Platycarya* (Juglandaceae) based on species distribution models and genetic data

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Subtropical East Asia harbours a large plant diversity and was an important glacial refugia for plant species throughout Quaternary glacial-interglacial cycles. However, the impact of past climate change on the dynamics of tree species in this region remains poorly understood. Here we use observations of *Platycarya*, a widespread subtropical Asian tree genus currently treated as monotypic (although two species have been formerly described), to explore the consequences of past climate change on species' evolutionary and population demographic history in subtropical China. We relied on species distribution models (SDMs) and genetic data (two cpDNA intergenic spacers, nuclear internal transcribed spacer regions and random genomic single nucleotide polymorphisms). By compiling distribution data and performing SDMs, we found that the two putative species, *P. strobilacea* and *P. longipes*, are sympatric over part of southern China and have similar climatic envelopes. Their past distributions as inferred by mapping their climatic envelopes at the Last Glacial Maximum