

ABSTRACT BOOK II

Posters and Abstracts

XIX International Botanical Congress

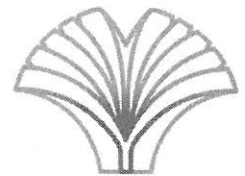
Shenzhen Convention & Exhibition Center

July 23-29, 2017

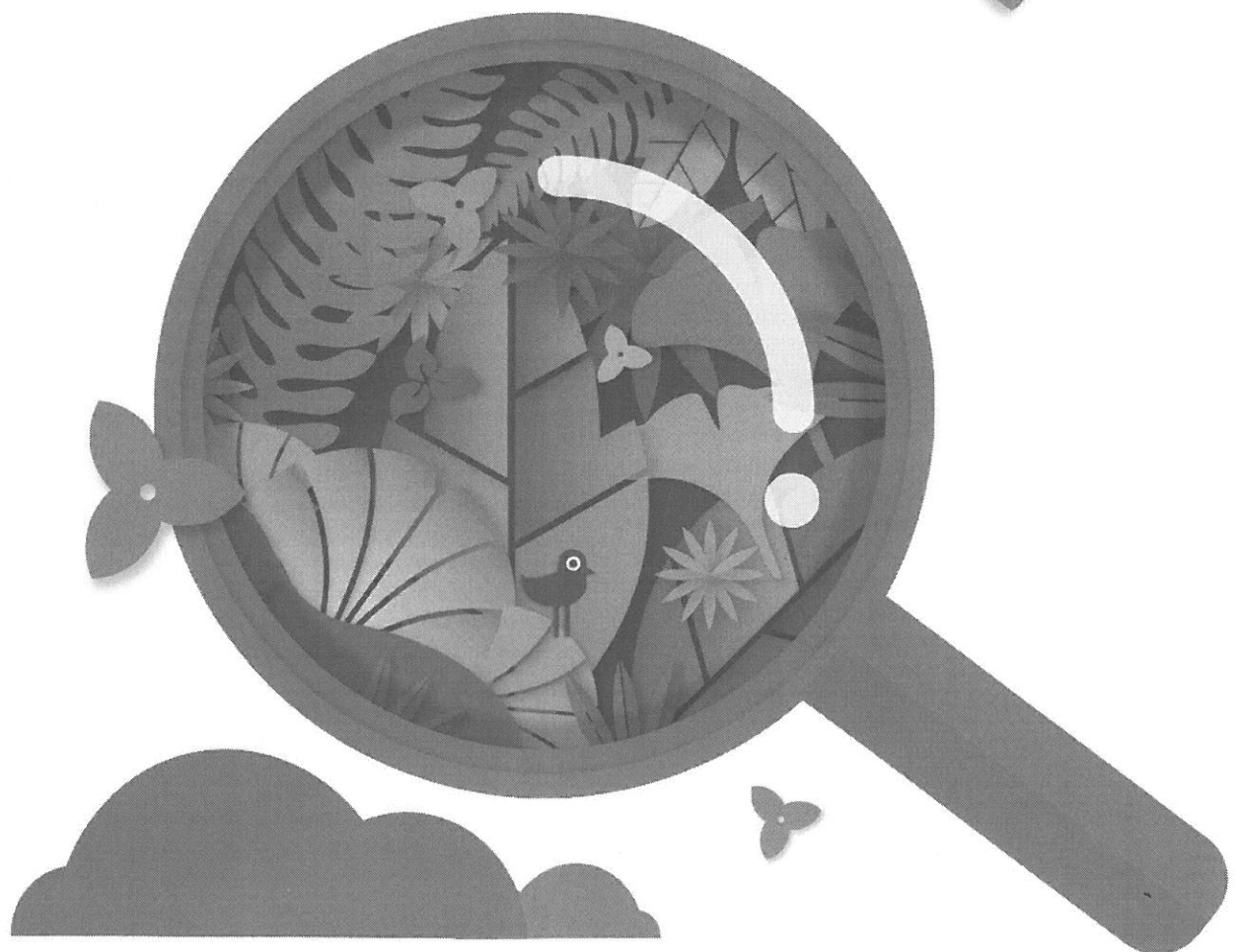
Nomenclature Section

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Juncus articulatus L. (Juncaceae) is a species of rush occurring in Eurasia, Canada and the United States of America. In 2013 symptoms of “witches’ brooms”, similar to those associated with phytoplasma infection in other plants, were observed on jointleaf rush plants in Lower Silesia, with some pests feeding on them. “Witches’ brooms” is a disease or deformity in a plant, where the natural structure of the plant is changed, i.e., a dense mass of shoots grows, usually from a single point, with the resulting structure resembling a broom. The direct causes of the enormous changes of the inflorescence have not been known to date, although they were related to the presence of the insect. *Livia junci* (Liviinae, Hemiptera), is a small plant-feeding sap-sucking insect that affects monocotyledonous plants. To confirm the presence of phytoplasma in fifteen examined plants, total DNA was extracted from 100 mg of inflorescence and leaf samples collected on July 2013, in Bogatynia, Poland, from six symptomatic and six asymptomatic plants. Additionally, three leaf samples from asymptomatic rush plants, collected from a location where the disease was not observed (Wrocław, Poland), as well as water blank samples were included as negative controls. Moreover, thirty-two insects were collected from symptomatic plants. DNA from *L. junci* specimens (the imago and the last larva stage) was extracted. Extracted nucleic acids were used as templates for PCR employing: a) phytoplasma universal rRNA primer pairs P1/P7 followed by R16F2n/R16R2 (1), b) primers rp1-rp2 followed by rp3-rp4 allowing amplification of fragments of ribosomal protein rpl22 and rps3 genes (2), and c) primers AYsecYF1/AYsecYR1 (3) for amplification of the secY gene. The phytoplasma was detected in insects and plant samples. No amplification products were detected in negative control samples from Wrocław or in water blanks. The fact that we detected the pathogen in some asymptomatic plants indicated that a low titre may have been prior to the development of disease symptoms. Amplicons representing three genetic loci were sequenced. To avoid sequencing errors, all DNA samples were sequenced twice in both directions. The obtained sequences were nearly identical, and representative sequences isolated from two plants and one insect, were deposited in GenBank. BLAST analysis of the sequenced 16S rDNA fragments revealed that tested strains shared more than 99% sequence identity to the sequences of phytoplasmas from the aster yellows group. The same analysis performed for ribosomal proteins and secY genes confirmed the highest identity (99%) of analyzed sequences with those of ‘*Candidatus* Phytoplasma asteris’. Thus the mass occurrence of this insect can cause a decrease in the yields of different rush species which are usually common components of the meadow communities of various parts of Europe. Namely, in such situations the plants cannot flourish, so it is impossible to produce fruit and seeds to be spread.

T3

P0878

Current and future potential distribution of *Selinum alatum* – Plausibly another invasive Apiaceae in Europe

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Selinum alatum (M. Bieb.) Poir. is native to the Caucasus and the Armenian Highlands. Recently a few established populations of this plant have been found in the north-eastern part of the Carpathians. Currently the species is spreading particularly in Poland where it outcompetes native plants in several areas. In this study a potential climatic niche of the plant is described with the goal to also highlight future spreading of the species. Our results demonstrate that the extent of the favourable habitat of this plant is broader than currently known. This suggests that *S. alatum* may become a potential new component in some semi-natural or disturbed ecosystems associated with mountainous areas, especially in Central and Southern Europe. Future (2070) models mostly rendered similar suitability maps, but showed slight differences over particular areas and a contraction of suitable habitats, mainly in the northern part of the non-native range.

T3

P0879

The late holocene mangrove dynamics in the upper Gulf of Thailand

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The mangrove dynamics in Samut Songkhram along the upper Gulf of Thailand was reconstructed using pollen analysis from a 460-cm sediment core. The results show that initial colonization of the area was made by true mangroves dominated by *Rhizophora* sp. and back mangroves characterised by *Suaeda* sp. This indicates that this area has been influenced by sea water since at least AD 1,200 until AD 1,250. After that, *Rhizophora* sp. gradually declined and were replaced by grass, indicating lower in sea level allowing mangroves to retreat seaward until AD 1,800. An increase in cereal pollen is also present suggesting possible human activities occurring around this area from AD 1,250 to the present day. Mangroves dominated by *Avicennia* sp. re-colonised at the top of the core suggesting a shift of mangroves landward probably due to a sea level rise until the present day.

T3

P0880

Bryophyte preferences in bryophagous insects – What matters?

Petr Pyszko, Katerina Kuravova, Zuzana Skoupa, Michaela Drgova, Petr Kocarek, Vitezslav Plasek, Pavel Drozd
University of Ostrava

Which features predetermine moss to be consumed by insects?