

Abstracts

1 **1. Gomez-Polo et al., 2017, An exceptional family: Ophiocordyceps-allied fungus domi-**
2 **nates the microbiome of soft scale insects (Hemiptera Sternorrhyncha: Coccidae).**

3 Ribosomal genes from seven soft scale (Coccidae) species showed high prevalence of an *Ophiocordyceps*-
4 allied fungal symbiont, which is from an lineage widely known as entomopathogenic. The *Ophiocordy-*
5 *ceps*-allied fungus from soft scales is closely related to fungi described from other hemipterans, and they
6 appear to be monophyletic, although the phylogenies of the *Ophiocordyceps*-allied fungi and their hosts
7 do not appear to be congruent. Microscopic observations show that the fungal cells are lemon-shaped,
8 are distributed throughout the hosts body and are present in the eggs, suggesting vertical transmission.

9 **2. Deng et al., 2021, The ubiquity and development-related abundance dynamics of**
10 **Ophiocordyceps fungi in soft scale insects.**

11 Nuclear ribosomal internal transcribed spacer (ITS) gene fragment was used to analyze the diversity of
12 fungal communities in 28 soft scale (Coccidae) species. Coccidae-associated *Ophiocordyceps* fungi (COF)
13 were prevalent in all 28 tested species with high relative abundance. Meanwhile, the first and second
14 instars of *C. japonicus* had high relative abundance of COF, while the relative abundances in other stages
15 were low, ranging from 0.68% to 2.07%. The result of fluorescent in situ hybridization showed that the
16 COF were widely present in **hemolymph** and vertically transmitted from mother to offspring.