**MODIFICATION AND FUNCTIONAL ADAPTATION OF THE MBF1 GENE FAMILY IN THE LICHENIZED FUNGUS *Endocarpon pusillum* UNDER ENVIRONMENTAL STRESS**

Yanyan Wang1\*; Xinli Wei1; Jenpan Huang2; Jiangchun Wei1

1 State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences; 2 Science & Education, The Field Museum; \*E-mail: wangyan@im.ac.cn

The multiprotein-bridging factor 1 (MBF1) gene family is well known in archaea, non-lichenized fungi, plants, and animals, and contains stress tolerance-related genes. Here, we identified four unique *mbf1* genes in the lichenized fungi *Endocarpon* spp. A phylogenetic analysis based on protein sequences showed the translated MBF1 proteins of the newly isolated *mbf1* genes formed a monophyletic clade different from other lichen-forming fungi and Ascomycota groups in general, which may reflect the evolution of the biological functions of MBF1s. In contrast to the lack of function reported in yeast, we determined that lysine114 in the deduced *Endocarpon pusillum* MBF1 protein (EpMBF1) had a specific function that was triggered by environmental stress. Further, the *Endocarpon*-specific C-terminus of EpMBF1 was found to participate in stress tolerance. Epmbf1 was induced by a number of abiotic stresses in *E. pusillum* and transgenic yeast, and its stress-resistant ability was stronger than that of the yeast *mbf1*. These findings highlight the evolution and function of EpMBF1 and provide new insights into the co-evolution hypothesis of MBF1 and TATA-box-binding proteins.