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GENETIC DIVERSITY IN A NATURAL POPULATION OF LENTINULA EDODES IN CHINA

Siu Wai Chiu, M. L. Yip, T. M. Leung, Z. W. Wang, F. C. Lin¹, F. C. & David Moore²

¹Chinese University of Hong Kong, Hong Kong SAR, China, ¹Huazhong Agricultural

²University, Wuhan, China, and ²The University of Manchester, Manchester, U.K.

China is the major producer and exporter of shiitake (*Lentinula edodes*), but the fungus is also native to China, the country being home to two of the seven lineages identified on the basis of rDNA sequences. Cultivation and natural occurrence in the same geographical region carries the risk of contamination of the wild population with the (probably narrower) genetic complement of commercial cultivars. We are therefore surveying the genetic diversity in wild Chinese shiitake using molecular and conventional tools. Collections have been made in Hubei Province (central China), where high summer temperatures limit shiitake cultivation to the autumn and winter and the landscape features deep river valleys and high mountains. Climatic extremes and geographic isolation are likely to minimise the spread of cultivated strains and their contamination of the native diversity. Field isolates had diverse colony morphologies and among 30 strains collected, 50 A and 55 B mating type specificities were identified. On the basis of somatic incompatibility grouping, all the strains collected were distinct individuals. Tests of fruiting ability of fifteen strains revealed that three made fruit bodies within six weeks, which would categorise them as fast fruiterers. One of the strains produced many primordia too and has potential for commercial exploitation. Ribosomal (especially ITS) DNA sequences and AP PCR DNA fingerprints are being compared. Analysis of the aligned ITS sequences of the rDNA repeats will establish whether the strains collected in Hubei Province fall into one single homogeneous lineage.