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GENETIC DIVERSITY OF *LENTINULA EDODES* COLLECTED FROM HUBEI PROVINCE, CHINA

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China is the leading country for production, consumption and export of the edible mushroom *Lentinula edodes* which itself holds second or third position in the popularity list of cultivated mushroom species in the world. This mushroom grows wild in China and the wild germplasm is under threat from the potential escape of commercial cultivars because outdoor cultivation on wood logs is commonly practised in scattered mountain farms. In this study we assess the genetic diversity of this natural resource in the wild and its potential value in strain improvement programmes. Genetic diversity was measured in terms of colony morphology, biochemical properties (oxidative enzymes), physiological properties (somatic incompatibility, tolerance to bacterial and fungal pathogens), genetic properties including the classical marker of mating type and the molecular markers DNA fingerprints by arbitrarily-primed polymerase chain reaction, nucleotide sequence at the internally transcribed spacer regions (ITS) and restriction polymorphism of the mitochondrial ribosomal gene. Two populations of isolates collected from two wild life reserves in Hubei Province, China were examined. Mating type polymorphism and somatic incompatibility were the most differentiating markers among all those used. A strain can be typed by amplification polymorphism using a panel of different arbitrary primers. The nucleotide sequence in the ITS region did not show great variation among the isolates examined and they showed great similarity to one another, implying a potential phylogenetic relationship. The sequences suggest they belong to the rDNA lineage group 1 of Hibbett et al. (1998) rather than their lineage group 5. Nevertheless, cluster analysis of these isolates indicates a highly heterogeneous population in the wild and the diversity promises potential for the wild germplasm to contribute to strain improvement programmes.