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Genotyping of *Agaricus bisporus* Strains by PCR Fingerprints

KyongJin Min¹, YounLee Oh³, and HeeWan Kang^{1,2*}

¹Graduate School of Future Convergence Technology, Hankyong National University, Ansong 456-749, Korea

²JK BioTech. Co. Ltd., Ansong 456-749, Korea

³Mushroom Science Division, National Institute of Horticultural and Herbal Science, RDA, Eumseong 369-873, Korea

Agaricus bisporus, commonly known as the button mushroom, is the most widely cultivated species of edible fungi. Low frequency of recombination ratio and homokaryotic or monokaryotic spore on meiotic basidia form obstacles for breeding programs. Since the first hybrid varieties for white button mushrooms were released in Europe, new varieties released afterwards were either identical or very similar to these first hybrids on morphologies. Therefore, different DNA markers have been used to define unique varieties of *A. bisporus* strains. Aim of this study is to assess the genetic diversity of different *A. bisporus* strains in Korea. Twelve UFP (Universal fungal primer, JK BioTech. Ltd), 12 simple sequence repeat (ISSR) and 30 SSR primers were used to assess genetic diversity of monokaryotic and dikaryotic *Agaricus bisporus* strains including other 19 *Agaricus* spp. Of them, four UFP, four SSR primers, (GA)₈T, (AG)₈YC, (GA)₈C and (CTC)₆ and seven SSR markers produced PCR polymorphic bands between the *Agaricus* species or within *A. bisporus* strains. PCR polymorphic bands were inputted for UPGMA cluster analysis. Forty five strains of *A. bisporus* are genetically clustered into 6 groups, showing coefficient similarity from 0.75 to 0.9 among them. In addition, genetic variations of monokaryotic and dikaryotic *Agaricus bisporus* strains were partially detected by PCR technologies of this study. The varieties, Saea, saedo, Saejeong and Saeyeon that have recently been developed in Korea were involved in the same group with closely genetic relationship of coefficient similarity over 0.96, whereas, other strains were genetically related to *A. bisporus* strains that were introduced from USA, Europe and Chinese.

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