Vegetative Growth and Genetic Diversity in Different Strains of Pink Oyster Mushroom Based on PCR Polymorphism

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Abstract

Pink oyster mushroom is known as Pleurotus salmoneostramineus. This experiment was undertaken to depict the favourable condition for mycelial growth, molecular identification and phylogenetic relationship of the selected strains of pink oyster mushroom. Suitable temperature and pH were obtained at 25°C and 6, respectively for the mycelial growth of pink oyster mushroom. Mushroom complete, glucose peptone and yeast malt extract culture media were the favorable, while Hennerberg and Hoppkins were unfavorable. Dextrin was the best and xylose was less effective carbon sources. Inorganic nitrogen sources were less effective for the mycelial growth of *P. salmoneostramineus*. The sequences of internal transcribed spacer (ITS) region of selected strains revealed that the total length ranged from 614 to 663 bp. The size of the ITS1 and ITS2 regions varied among the strains. Sequence analysis showed that 5.8S of rDNA sequences were identical. Phylogenetic tree of the ITS region sequences indicated that strains of *P. salmoneostramineus* belongs to a same cluster. The reciprocal homologies of the ITS region sequences ranged from 98 to 100%. The strains of *P. salmoneostramineus* were also analyzed by random amplification of polymorphic DNA (RAPD) with 20 arbitrary primers. RAPD results suggested that tested strains of *P. salmoneostramineus* were genetically similar with some variations.

Keywords: ITS sequence, Molecular identification, *Pleurotus salmoneostramineus*, RAPD, Vegetative growth

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