

灰毡毛忍冬工厂化快繁生产体系的建立及再生苗遗传稳定性的分子鉴定

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Establishment of Rapid Propagation System and Molecular Identification of Genetic Stability on *Lonicera macranthoides*

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摘要 以灰毡毛忍冬 (*Lonicera macranthoides* Hand.-Mazz.) 腋芽为材料, 建立了一套适合工厂化生产的离体再生技术体系。该体系包括腋芽诱导培养基 $MB + 1.0 \text{ mg} \cdot L^{-1}$  6-BA +  $0.2 \text{ mg} \cdot L^{-1}$  NAA, 继代

增殖培养基 $MB + 1.0 \text{ mg} \cdot L^{-1}$  6-BA +  $0.5 \text{ mg} \cdot L^{-1}$  IAA 和 $MB + 1.5 \text{ mg} \cdot L^{-1}$  6-BA +  $0.8 \text{ mg} \cdot L^{-1}$  IAA 和生根

培养基 $1/2MB + 2.0 \text{ mg} \cdot L^{-1}$  IBA +  $0.2 \text{ mg} \cdot L^{-1}$  IAA。分别从继代12、24、36 个月的再生植株中随机抽取8

株进行SRAP 分析其遗传的变化。在检出的147 条SRAP 条带中, 继代12 个月的再生植株未发现变异,

继代24 个月的再生植株中有2 株发生变异, 继代36 个月的再生植株中有4 株发生变异。结果表明, 建立的腋芽再生培养体系在一定继代周期内是稳定可靠的, 适合灰毡毛忍冬的规模化生产。

关键词: 灰毡毛忍冬 快繁体系 遗传稳定性 分子鉴定

Abstract: An efficient mass propagation system of *Lonicera macranthoides* Hand.-Mazz. was established based on axillary bud-derived meristems. The optimal media of tissue culture involving in the bud-induction medium ('MB medium supplemented with  $1.0 \text{ mg} \cdot L^{-1}$  6-BA,  $0.2 \text{ mg} \cdot L^{-1}$  NAA), subculture medium ('MB medium supplemented with  $1.0 \text{ mg} \cdot L^{-1}$  6-BA,  $0.5 \text{ mg} \cdot L^{-1}$  IAA or  $1.5 \text{ mg} \cdot L^{-1}$  6-BA,  $0.8 \text{ mg} \cdot L^{-1}$  IAA) and root-induction medium (' $1/2MB$  medium supplemented with  $2.0 \text{ mg} \cdot L^{-1}$  IBA and  $0.2 \text{ mg} \cdot L^{-1}$  IAA) were selected. Thereafter, the genetic variation of 8 plants randomly sampled from regeneration plants cultured for 12, 24 and 36 months respectively was investigated by SRAP analysis and there were 0, 25% and 50% in variation rate found in regeneration lines respectively based on the 147 bands detected by SRAP markers. The results showed that regeneration culture system can maintain genetic stability during certain subculture cycles, indicating that it can be readily employed for large-scale propagation.

Keywords: *Lonicera macranthoides*, rapid propagation system, genetic stability, molecular identification

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