

Transcriptomic and Metabolomic Analyses Reveals That Exogenous Methyl Jasmonate Regulates Galanthamine Biosynthesis in *Lycoris longituba* Seedlings

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Abstract: The Amaryllidaceae alkaloid galanthamine (Gal) in *Lycoris longituba* is a secondary metabolite that has been used to treat Alzheimer's disease. Plant secondary metabolism is affected by methyl jasmonate (MeJA) exposure, although the regulatory mechanisms of MeJA on *L. longituba* seedlings remains largely unknown. In the present study, 75, 150, and 300 μ M MeJA were used as treatments on *L. longituba* seedlings for 7, 14, 21, and 28 days, while 0 μ M MeJA was used as the control (MJ-0). The effect of exogenous MeJA on Gal synthesis in *L. longituba* was then investigated using transcriptomic sequencing and metabolite profiling via GC-MS and LC-MS analysis. Galanthamine (Gal), lycorine (Lyc), and lycoramine (Lycm) abundances were 2.71-, 2.01-, and 2.85-fold higher in 75 μ M MeJA (MJ-75) treatment plants compared to MJ-0 treatment plants after 7 days of cultivation. Transcriptomic analysis further showed that MJ-75 treatment significantly induced the expression of norbelladine synthase (NBS) and norbelladine 4'-O-methyltransferase (OMT), which are involved in the Gal biosynthesis pathway. In addition, increased expression was observed in MJ-75 treatment plants for genes in the JA synthesis and JA signaling pathways including those of allene oxide cyclase (AOC), 12-oxo-phytodienoic acid reductase (OPR), jasmonic acid amino acid synthase (JAR), and transcription factor MYC. The *L. longituba* tyrosine decarboxylase (LITYDC) enzyme was identified and proposed to be involved in the Gal biosynthetic pathway. Metabolomics results demonstrated that the accumulation of Amaryllidaceae alkaloids, and especially alkaloids in the Gal biosynthesis pathway, could be induced by MJ-75 treatment. Interestingly, metabolites in the JA synthesis pathway were also affected by MeJA treatment. Overall, this multi-omics study suggests that both the JA synthesis/JA signaling and Gal biosynthesis pathways were affected by exogenous MeJA treatment. This comprehensive study of gene expression and metabolite contents can help us better understand the molecular mechanisms underlying MeJA-mediated Gal biosynthesis in *L. longituba*.