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Fungal endophytes attune withanolide biosynthesis in Withania somnifera, prime to enhanced withanolide A content in leaves and roots.

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Abstract

Endophytes have been reported from all plant species from different parts of tissue including root, stem and leaves. Here we report, three fungal endophytes, Aspergillus terreus strain 2aWF (2aWF), Penicillium oxalicum strain 5aWF (5aWF), and Sarocladium kiliense strain 10aWF (10aWF) from Withania somnifera, which could enhance withanolides content in leaf and root. Upon treatment with the above endophytes to 4 weeks old plants in field conditions, W. somnifera elicited withanolide A content (97 to 100%) in leaves without considerable changes in withaferin A content. Furthermore, withanolide A content in roots of 5aWF and 10aWF endophyte treated W. somnifera plants increased up to 52% and 65% respectively. Incidentally, expression profile of withanolide and sterol biosynthetic pathway genes HMGR, DXR, FPPS, SQS, SQE, CAS, SMT1, STE1 and CYP710A1 were significantly upregulated in 2aWF, 5aWF and 10aWF fungal endophyte treated plants. Besides, modulation of withanolide biosynthetic pathway genes, fungal endophytes also induce a host resistant related gene, NPR1 resulting in 2, 4 and 16 fold expression levels in 2aWF, 10aWF and 5aWF endophyte treatments respectively, compared to control plants. Overall, our results illustrate that application of native-fungal endophytes 2aWF (96.60%), 5aWF (95%) and 10aWF (147%) enhances plant biomass in addition to withanolide content.

KEYWORDS: Aspergillus terreus; Endophytes; Penicillium oxalicum; Sarocladium kiliense; Withaferin A and Withanolide A; Withania somnifera

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