

6th Annual Conference on

MICROBIOLOGY

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Annual Conference on

MICROBES AND BENEFICIAL MICROBES

October 16-17, 2017 Baltimore, USA

Microbial modulation of bacoside: A biosynthetic pathway and systemic defense mechanism in *Bacopa monnieri* under *Meloidogyne incognita* stress**Rupali Gupta**

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Plant-associated beneficial microbes have been explored to fulfill the imperative function for plant health. However, their impact on the host secondary metabolite production and nematode disease management remains elusive. The present work has shown that chitinolytic microbes viz., *Chitinophilus* sp. MTN22 and *Streptomyces* sp. MTN14 singly as well as in combination, modulated the biosynthetic pathway of bacoside A and systemic defense mechanism against *Meloidogyne incognita* in *Bacopa monnieri*. Interestingly, expression of bacoside biosynthetic pathway genes (3-hydroxy-3-methylglutaryl coenzyme A reductase, mevalonate diphosphate decarboxylase and squalene synthase) were upregulated in plants treated with the microbial combination in the presence as well as in absence of *M. incognita* stress. These microbes not only augmented bacoside A production but also strengthened host resistance via enhancement in chlorophyll a, defense enzymes and phenolic compounds like gallic acid, syringic acid, ferulic acid and cinnamic acid. Furthermore, elevated lignification and callose deposition in the microbial combination treated plants corroborate well with the above findings. Overall, the results provide novel insights into the underlying mechanisms of priming by beneficial microbes and underscore their capacity to trigger bacoside A production in *B. monnieri* under biotic stress.

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