

Overexpression of *Panax ginseng* sesquiterpene synthase gene confers tolerance against *Pseudomonas syringae* pv. *tomato* in *Arabidopsis thaliana*

Sung-Joo Yoon¹ · Johan Sukweenadhi² · Altanzul Khorolragchaa¹ ·
Ramya Mathiyalagan² · Sathiyamoorthy Subramaniam¹ · Yeon-Ju Kim¹ ·
Ho-Bin Kim³ · Mi-Jung Kim³ · Yu-Jin Kim¹  · Deok-Chun Yang^{1,2}

Received: 20 July 2016 / Revised: 30 September 2016 / Accepted: 3 October 2016
© Prof. H.S. Srivastava Foundation for Science and Society 2016

Abstract Sesquiterpenes are an abundant group belonging to the terpenoid family, with a C15 structure comprise of three isoprene units. Many sesquiterpenes are volatile compounds and it act as chemical messenger in plant signalling, particularly in the defense mechanism against biotic and abiotic stresses. *Panax ginseng* Meyer is important medicinal herbs with various reported pharmacological efficacies in which its triterpenoid saponins, called ginsenosides, were mostly studied. However, there have been few studies on volatile sesquiterpenes compounds regulation on *P. ginseng*. As slow-growing perennial plant, *P. ginseng* received many kind of stresses during its cultivation. The pathogen attack is one of the most devastated perturbation for ginseng yield. Thus, we aimed to analyze *P. ginseng* STS gene (*PgSTS*) expressions in ginseng organs as well as mono-, sesquiterpenes contents from ginseng seedlings treated with elicitors. qRT-PCR and GC-MS analysis showed that two elicitors- salicylic acid (SA) and methyl jasmonate (MeJA) triggered *PgSTS* expression at different time points and significantly induced mono-, sesquiterpene yield. Overexpression of

PgSTS in *Arabidopsis* also induced high terpene content and conferred tolerance against *Pseudomonas syringae* pv. *tomato* infection. These results suggested that *PgSTS* transcripts are involved in terpenoid biosynthesis in response to environmental stress mediated by MeJA and SA elicitors; thus, generate tolerance against pathogen attack.

Keywords Gene expression · Ginseng · Methyl jasmonate · Salicylic acid · Terpene content · Sesquiterpene synthase

Introduction

Terpenoids are the most abundant group with over 30,000 known compounds among secondary metabolites (Degenhardt et al. 2009). Sesquiterpenes (C15), the most diversified group of the terpenoid family, plays a variety of ecological roles such as defense signalling (Schnee et al. 2006) and also as medicines (i.e. artemisinin for anti-malaria) (Kuhn and Wang 2008). All sesquiterpenes are produced either through mevalonic acid pathway (MVA) pathway or 1-deoxy-d-xylulose/2-C-methyl-d-erythritol-4-phosphate (DOXP/MEP) pathway (Hampel et al. 2005). Until now, at least 300 types of sesquiterpenes have been discovered and numerous sesquiterpenes are volatile compounds which usually are released from the leaves and flowers as a signal to attract pollinators or dispel predatory and parasitic insects. The synthesis and accumulation of volatile sesquiterpenes have also been demonstrated in rhizomes and roots (Arimura et al. 2008).

The synthesis of sesquiterpenes is catalyzed by sesquiterpene synthase (STS). STS frequently was revealed as rate-defining enzymes in the pathways they take part

Sung-Joo Yoon and Johan Sukweenadhi have contributed equally to this work.

✉ Yu-Jin Kim
yujinkim@khu.ac.kr

✉ Deok-Chun Yang
dcyang@khu.ac.kr

¹ Department of Oriental Medicinal Biotechnology, College of Life Science, Kyung Hee University, Yongin 449-701, Korea

² Graduate School of Biotechnology, College of Life Science, Kyung Hee University, Yongin 446-701, Korea

³ Woongjin Foods Co., Ltd., JEI-PLATZ, 186, Gasan Digital 1-ro, Room 201, Gemcheon-gu, Seoul 153-792, Korea