

## Influence of Acibenzolar-S-methylon on the Expression of Phenylpropanoid Biosynthetic Genes and the Accumulation of Phenylpropanoids in *Agastache rugosa*

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*Agastacherugosa*, (Korean mint), contains sesquiterpenes, essential oils, diterpenes, flavonoids, triterpenes, and carotenoids that are used for the treatment of cancer. Medicinal plants can activate defensive mechanisms upon exposure to pathogens, various chemicals, or physical stress. The present study aimed to determine the expression levels of phenylpropanoid pathway genes and accumulation of phenylpropanoids in *A. rugosa* plantlets in response to acibenzolar-S-methyl (ASM) treatment. ASM treatment stimulated the expression of phenylpropanoid biosynthetic genes such as *PAL*, *C4H*, *CHS*, *CHI*, *HPPR*, *TAT*, and *RAS* after 1, 3, 5, and 7 days of cultivation. The expression pattern of the upstream and downstream phenylpropanoid biosynthetic genes was directly proportional to the ASM exposure times. In particular, the expression level of the *RAS* gene was 1.59-, 2.88-, 1.36-, and 1.41-fold higher at 1, 3, 5, and 7 days after ASM treatment, when compared to respective controls. The levels of rosmarinic acid, tilianin, and acacetin accumulation were comparatively 2.28-, 1.88-, and 1.61-fold higher than those of the control after 7 days of ASM treatment. Among the phenylpropanoids examined, rosmarinic acid was highest (5 mg/g dry weight) in the control and ASM-treated plantlets. Our results indicated that ASM enhances the expression of genes related to phenylpropanoids and accumulation of phenylpropanoids during the development of *A. rugosa* plantlets.

**Key words:** *Agastacherugosa*, Acibenzolar-S-methyl,  
Phenylpropanoid genes, Rosmarinic acid, Tilianin.

Microbial pathogens such as bacteria, fungi, and viruses present in the soil and environments continuously attack plants irrespective of the plant family. Following a microbial attack, the defense mechanisms of

plants, such as cell wall lignifications, papilla formation, and rapid changes in specific gene expression levels and subsequent synthesis of defensive proteins, are stimulated<sup>1</sup>. The proteins produced after infection have specific surface markers for systemic acquired resistance (SAR)<sup>2</sup>, which is similar to the inborn immune system found in animals. This resistance is shown both at the site of pathogen attack and in uninfected parts

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of the plant. SAR is beneficial for plants not only in providing resistance to disease but also for recovery from disease once it has developed<sup>3</sup>. SAR can be caused by a wide range of pathogens and the resistance developed following the induction of SAR is effectual against a wide range of pathogens<sup>4</sup>. SAR has been reported in a wide range of flowering plants, including both dicotyledons and monocotyledons<sup>5,6</sup>.

Various organic and inorganic compounds, such as 2,6-dichloroisonicotinic acid (INA) acibenzolar-*S*-methyl (ASM), and benzothiadiazole (BTH) have been employed as SAR inducers. Among these, acibenzolar-*S*-methyl (ASM) is a synthetic molecule manufactured by Novartis (Switzerland), and its role as a plant defense activator has been demonstrated in a number of annual plants, including *Arabidopsis*<sup>7</sup>, tobacco<sup>8</sup>, maize<sup>9</sup>, wheat<sup>10</sup>, and cucumber<sup>11</sup>. It is commercially developed as a plant health enhancer of annual crops under the name of Actigard<sup>®</sup> (Syngenta, Switzerland), and it has been reported that pre-treatment of cucumber plants with ASM increases *PAL* expression in plants treated with 100 $\mu$ M ASM or greater concentrations (500 $\mu$ M)<sup>12</sup>. Therefore, the present study aimed to investigate the effect of ASM on the enhancement of rosmarinic acid in *Agastache rugosa*. The present study also aimed to determine whether supplementation with ASM plays a role in the expression of phenylpropanoid pathway genes in *A. rugosa*.

## MATERIAL AND METHODS

### Seed sterilization and germination

Seeds of *A. rugosa* were purchased from Aram Seed Company (Seoul, Korea). The collected seeds were washed with sterile distilled water and then surface-sterilized with 70% (v/v) ethanol for 1 min, followed by a 4% (v/v) sodium hypochlorite solution containing a few drops of Tween 20 for 10 min, and finally rinsed three times with sterilized distilled water. Single seeds were planted in plastic pots containing nursery box soil and germinated at 25°C under standard cool white fluorescent tubes using a 16-h photoperiod. After 1 month of germination, plantlets showing ordinary growth rate were used for ASM treatment.

### ASM treatment

For ASM treatment, Actigard<sup>®</sup> (Syngenta,

Switzerland), which stimulates SAR in a number of annual plants, was dissolved in distilled water (200 mg/l). Immediately after preparation, ASM solutions were sprayed on the leaves of 1-month-old *A. rugosa*. To examine time effects, ASM-treated leaves were randomly collected at 0, 1, 3, 5, and 7 days after the treatment. The collected leaves were immediately frozen in liquid nitrogen, and stored at -80°C until used.

### Total RNA extraction and cDNA preparation

Total RNA was extracted from collected samples using a modified Trizol method. Harvested plantlet samples were finely ground in liquid nitrogen using a mortar and pestle. One hundred grams of the ground sample was dissolved in 1 ml of Trizol, to which 200  $\mu$ l of chloroform was added for phase separation. The aqueous phase was collected and centrifuged at 13,000 rpm using a micro-high-speed centrifuge (Micro 17TR, Hanil Science Medical, Korea) for 15 min at 4°C to pellet RNA. The supernatant containing RNA was carefully collected and washed with 70% ethanol and the pellet was resuspended in DEPC water. The integrity of the RNA was determined using a NanoVue<sup>™</sup> Plus Spectrophotometer (GE Healthcare, UK) and electrophoresis with formaldehyde RNA agarose gels.

### Quantitative real-time PCR for gene expression analysis

First-strand DNA of the fragment was synthesized using 1  $\mu$ g of total RNA by following kit instructions (ReverTra ace, Toyobo, Japan). The reverse-transcribed cDNA products were used as templates for gene expression analysis using gene-specific primers (Table 1). The expression level of each gene was presented as a relative expression, i.e., the Ct value of each gene was compared to that of a housekeeping gene (*Actin*). Quantitative real-time PCR (qRT-PCR) was performed using a CFX96 real-time system (BIO-RAD Laboratories, USA) with the 2 $\times$  Real-Time PCR Smart mix (Bio FACT, Korea) under the following conditions: 95°C for 15 min, followed by 40 cycles of 95°C for 15 s, annealing for 15 s at 55°C, and elongation for 20 s at 72°C. Transcript levels were normalized relative to the *Actin* housekeeping gene. Three replications of each sample were used for real-time PCR analysis and significant differences between treatments were evaluated by standard deviation.

### Analysis of phenylpropanoids by HPLC

Phenylpropanoids were quantified using high-performance liquid chromatography (HPLC). For the analysis, the samples were freeze-dried in a vacuum dryer for at least 48 h, ground into a fine powder using mortar and pestle, and then 100-mg samples were vortexed with 5 ml of 100% methanol for 1 h at 60°C. Phenylpropanoids, namely rosmarinic acid and tilianin, were extracted using methanol. After centrifugation, the supernatant was filtered through a 0.45- $\mu$ m PVDF filter (Whatman, GE Healthcare, UK) and the extracts were analyzed using an HPLC system (NS-4000, Futecs, Korea) and monitored using a UV detector at 340 nm and reverse-phase column (C18, 250 mm  $\times$  4.6 mm, 5 $\mu$ m) (Prontosil, Bischoff, Germany) at 30°C. The mobile phase was a gradient mixture of absolute methanol and 0.1% (v/v) acetic acid in water. The flow rate was maintained at 1.0 ml/min and the sample injection volume was 20  $\mu$ l. The concentration of phenylpropanoids in samples was calculated using a standard curve. Standard compounds were purchased from Sigma-Aldrich Corporation (USA). Mean values were obtained from three independent replicates.

#### Statistical analysis

For qRT-PCR and HPLC statistical analysis, the data were analyzed using the statistical analysis software (SAS version 9.3, SAS Institute Inc., USA). All data are given as the average (mean) and standard deviation of triplicate experiments. The experimental data were subjected to an analysis of variance (ANOVA), and significant differences among the means were determined by Duncan's multiple-range test.

## RESULTS AND DISCUSSION

### Effect of ASM on phenylpropanoid biosynthetic pathway genes

The effect of ASM on *A. rugosa* plantlet phenylpropanoid biosynthetic pathway gene expression was determined by harvesting at 0, 1, 3, 5, 7 days after treatment. The expressions of genes (*PAL*, *C4H*, *CHS*, *CHI*, *HPPR*, *TAT*, and *RAS*) were determined in each treatment by using qRT-PCR (Fig. 1). Among the genes, *CHI* and *RAS* showed higher levels of expression in all the sampling periods. The results indicated that the transcript levels of *CHI* increased markedly with increasing time of exposure to ASM up to 3 days and then

started to decline: the expression level was 1.62-, 6.44-, 2.38-, and 1.19-fold higher at 1, 3, 5, and 7 days after treatment. The expression level of *RAS* and *TAT* was 2.81, 4.42, and 2.64 times higher and directly proportional to the exposure time to ASM for 1, 3, and 5 days and then showed a moderate decline. The higher level of expression compared to the control was maintained up to 5 days after ASM treatment, but thereafter the expression level was lower than that of respective controls. Although the level of *C4H* expression was lower at 1 and 3 days, it then increased very sharply up to 7 days after treatment. The level of *C4H* expression was 2.9 and 5.3 times higher at 5 and 7 days after ASM treatment, respectively, compared to the respective controls. The level of *CHS* expression was the highest at 1 day after ASM treatment and then started to decline. The higher expression level of *CHS* was maintained up to 3 days after ASM treatment, and then the expression level became considerably lower than that of the respective control. The expression level of *CHS* was 4.74 and 2.04 times higher at 1 and 3 days after ASM treatment. For *HPPR*, the level of expression increased from 3 days after ASM treatment, continued to increase up to 5 days after treatment, and then declined sharply. The level of expression of *HPPR* was 2.03 and 2.72 times higher at 3 and 5 days after ASM treatment, respectively, compared to the respective controls.

### Quantification of phenylpropanoids

The contents of phenylpropanoids, rosmarinic acid, tilianin, and acetin present in the plantlets of *A. rugosa* treated with ASM were determined by harvesting after 0, 1, 3, 5, and 7 days of incubation (Figs. 2, 3, and 4). The levels of rosmarinic acid, tilianin, and acetin increased both in plantlets treated with ASM and in the controls. However, the increasing rate was higher in cases of ASM treatment. The level of rosmarinic acid was 1.8-, 2.15-, 2.23-, and 2.28-fold higher at 1, 3, 5, and 7 days after ASM treatment. This increasing tendency was still apparent beyond 7 days after ASM. Similar to rosmarinic acid, the amount of tilianin accumulation was 1.62, 1.87, 1.82, and 1.88 times higher at 1, 3, 5, and 7 days after ASM treatment. The increasing levels of acetin were slightly lower than those of rosmarinic acid and tilianin. This result revealed that the increasing tendency of acetin production was observed for

up to 3 days after treatment, but then the accumulation tended to decline compared to the respective controls.

The results of this investigation showed that the production of rosmarinic acid, tilianin, and acetin in *A. rugosa* plantlets was stimulated by ASM treatments. The quantified phenylpropanoids were present at maximum concentrations after 3 to 5 days of ASM treatment, whereas control plantlets produced the highest

levels nearly 2 days later than those in the ASM treatment, indicating that the ASM treatment activated SAR, thereby stimulating accumulations of phenylpropanoids such as rosmarinic acid, tilianin, and acetin.

Previously reported that addition of yeast elicitor to plant cells enhanced the production of rosmarinic acid, whereas benzothiadiazole treatment stimulated the activation of SAR in plants. Benzothiadiazole can be used as a tool for

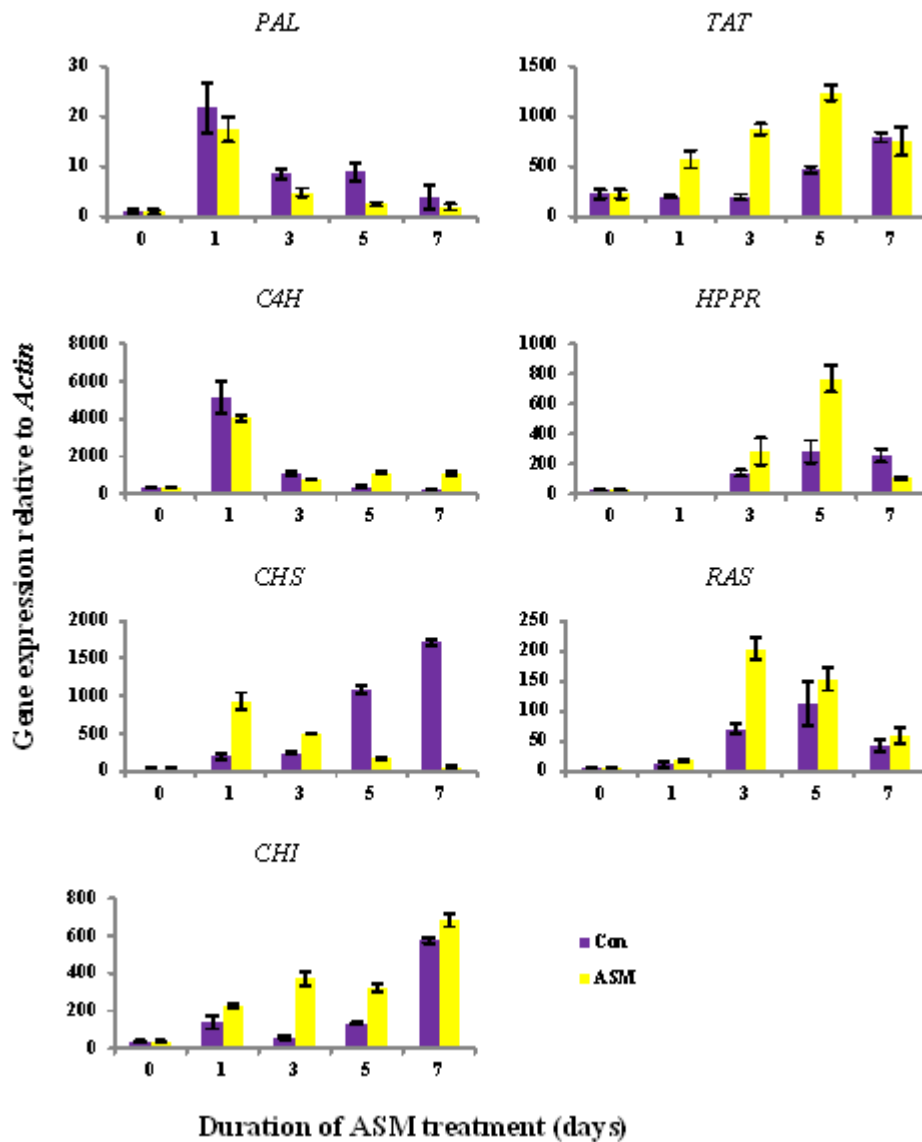
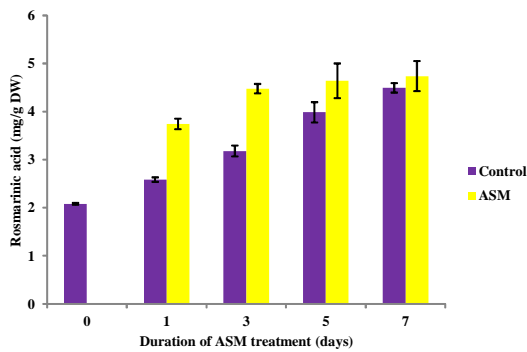
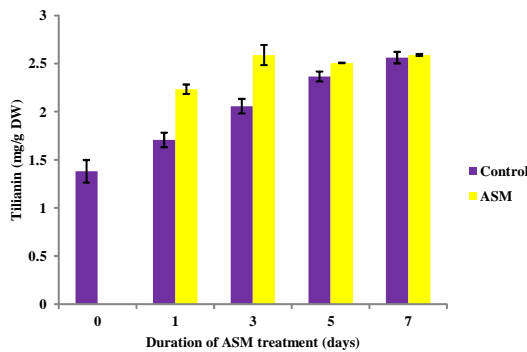


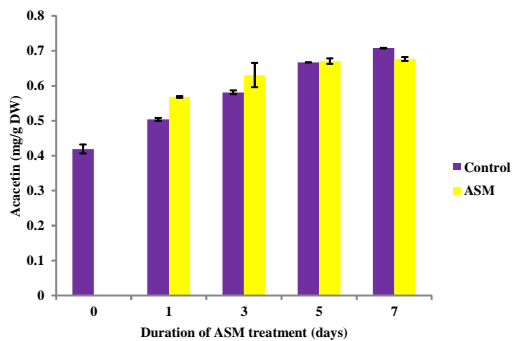
Fig. 1. Expression levels of phenylpropanoid biosynthetic genes in ASM-treated *Agastacherugosa* plantlets. Transcript levels from each of the three experimental groups were analyzed relative to that of *actin*. Error bars show standard deviation values



**Fig. 2.** Content of rosmarinic acid in ASM-treated *Agastacherugosa* plantlets. The level of accumulated rosmarinic acid in each of the three experimental groups was analyzed by HPLC. Error bars show standard deviation values. DW, dry weight.



**Fig. 3.** Content of tiliandin in ASM-treated *Agastacherugosa* plantlets. The level of accumulated tiliandin in each of the three individual experimental groups was analyzed by HPLC. Error bars show standard deviation values. DW, dry weight



**Fig. 4.** Content of acacetin in ASM-treated *Agastacherugosa* plantlets. The level of accumulated acacetin in each of the three individual experimental groups was analyzed by HPLC. Error bars show standard deviation values. DW, dry weight

improving secondary metabolite accumulation in cell cultures, particularly that of phenylpropanoids<sup>13</sup>. Addition of methyl jasmonate (MeJa) also increases rosmarinic acid accumulation in suspension cell cultures of *Coleus blumei*<sup>14</sup> and *Lithospermumerythrorhizon*<sup>15</sup>. MeJa treatment might also be an efficient natural strategy to protect grapevine berries in vineyards<sup>16</sup>. Recently,<sup>17</sup> claimed that MeJa induced the production anthocyanin and glucosinolates in radish.

Exogenous salicylic acid treatment not only protects plants against stress but also enhances their growth and productivity<sup>18</sup>. Salicylic acid treatment leads to increased activities of PAL and soluble peroxidases, whereas cell wall-bound peroxidases were down-regulated in a concentration-dependent manner by salicylic acid<sup>18</sup>. These results provide evidence that the differences in phenylpropanoid metabolism induced by salicylic acid could provide as a defense system contributing to a reduction in oxidative cellular damage, as suggested by the high anti-lipid oxidation activity in *Cistus* extracts<sup>18</sup>.

The high transcription levels of *PAL*, *C4H*, *CHS*, and *CHI* in ASM-treated *A. rugosa* may explain the high levels of acacetin and its derivative tiliandin observed in the present study. Similarly, the low expression levels of *ArPAL*, *ArC4H*, and *Ar4CL* may be correlated with the trace amounts of tiliandin and acacetin detected in roots<sup>19</sup>. The expression of *PAL*, *C4H*, and *4CL* has previously been correlated with flavonoid contents in various plants<sup>20,21</sup>.

## CONCLUSION

In conclusion, the application of ASM enhances the expression levels of the upstream and downstream genes of phenylpropanoid biosynthetic pathways. The quantification of the individual compounds confirmed that ASM treatment stimulated greater production of these compounds during the development of *A. rugosa* plantlets.

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