

## 배 검은별무늬병 감염과 저항성 방어반응 연관 전사체 프로파일

신일섭<sup>1\*</sup>, 천재안<sup>2</sup>, 김세희<sup>3</sup>, 조강희<sup>4</sup>, 원경호<sup>5</sup>, 정해원<sup>6</sup>, 김금선<sup>7</sup>

<sup>1</sup>농촌진흥청 국립원예특작과학원 배연구소, 연구관, <sup>2</sup>중앙과수묘목관리센터, 연구원,  
<sup>3</sup>농촌진흥청 국립원예특작과학원 과수과, 연구사, <sup>4</sup>농촌진흥청 국립원예특작과학원 과수과, 연구관,  
<sup>5,6</sup>농촌진흥청 국립원예특작과학원 배연구소, 연구사, <sup>7</sup>농촌진흥청 국립원예특작과학원 배연구소, 전문연구원

### Transcriptomic Profile in Pear Leaf with Resistance Against *Venturia nashicola* Infection

Il Sheob Shin<sup>1\*</sup>, Jaean Chun<sup>2</sup>, Sehee Kim<sup>3</sup>, Kanghee Cho<sup>4</sup>, Kyungho Won<sup>5</sup>,  
Haewon Jung<sup>6</sup> and Keumsun Kim<sup>7</sup>

<sup>1</sup>Senior Researcher, Pear Research Institute, NIHHS, RDA, Korea

<sup>2</sup>Researcher, Korea Fruit Agricultural Co. Federation, Korea

<sup>3</sup>Researcher, Fruit Research Division, NIHHS, RDA, Korea

<sup>4</sup>Senior Researcher, Fruit Research Division, NIHHS, RDA, Korea

<sup>5,6</sup>Researcher, Pear Research Institute, NIHHS, RDA, Korea

<sup>7</sup>Postdoc., Pear Research Institute, NIHHS, RDA, Korea

The molecular understanding of resistance and susceptibility of host plants to scab, a most threatful disease to pome fruit production worldwide, is very limited. Comparing resistant line '93-3-98' to susceptible one 'Sweet Skin' at seven time points of 0, 0.5, 1, 2, 3, 4, 8 days post inoculation, RNA-sequencing data derived from infected and mock-inoculated young leaves were analyzed to evaluate the tolerant response and to mine candidate genes of pear to the scab pathogen *Venturia nashicola*. Analysis of the mapped reads showed that the infection of *V. nashicola* led to significant differential expression of 17,827 transcripts with more than 3-fold change in the seven pairs of libraries, of which 9,672 (54%) are up- and 8,155(46%) are down-regulated. These included mainly receptor (NB-ARC domains-containing, CC-NBS-LRR, TIR-NBS-LRR, seven transmembrane MLO family protein) and transcription factor (ethylene responsive element binding, WRKY DNA-binding protein) related gene. An arsenal of defense response of highly resistant pear accessions derived from European pear was probably supposed no sooner had *V. nashicola* infected its host than host genes related to disease suppression like Polyketide cyclase/dehydrase and lipid transport protein, WRKY family transcription factor, lectin protein kinase, cystein-rich RLK, calcium-dependent phospholipid-binding copine protein were greatly boosted and eradicated cascade reaction induced by pathogen within 24 hours. To identify transcripts specifically expressed in response to *V. nashicola*, RT-PCRs were conducted and compare to the expression patterns of seven cultivars with a range of highly resistant to highly susceptible symptom. A DEG belonging to the PR protein family genes that were higher expressed in response to *V. nashicola* suggesting extraordinary role in the resistance response were led to the identification. This study provides the first transcriptional profile by RNA-seq of the host plant during scab disease and insights into the response of tolerant pear plants to *V. nashicola*.

[본 연구는 농촌진흥청 시험연구사업(과제명: 배 검은별무늬병 저항성 형질도입을 위한 육종기술 개발, 세부과제번호: PJ00659502)의 지원에 의해 이루어진 결과로 이에 감사드립니다.]

\*(Corresponding author) shinis3@korea.kr, Tel: +82-61-330-1540