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Name & Surname of the presenting author: Pepe Cana-Quijada E-mail: <u>pepecana@uma.es</u> Session: Interacción plantas-otros organismos Communication (Oral or Poster): Oral

## NAHG INCREASES TRANSIENT TRANSFORMATION OF ARABIDOPSIS LEAVES BY AGROBACTERIUM

<u>Pepe Cana-Quijada<sup>1</sup></u>, Tábata Rosas-Díaz<sup>2</sup>, Vitor Amorim-Silva<sup>1</sup>, Miguel A Botella<sup>1</sup>, Rosa Lozano-Durán<sup>2</sup>, Eduardo R Bejarano<sup>1</sup>

<sup>1</sup>Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", (IHSM-UMA-CSIC), Universidad de Málaga, Málaga, Spain, <sup>2</sup>Shanghai Center for Plant Stress Biology/CAS Center for Excellence in Molecular Plant Science, Chinese Academy of Sciences, Shanghai, China

Corresponding author: Eduardo R Bejarano (edu\_rodri@uma.es)

*Agrobacterium tumefaciens*-mediated transient transformation has demonstrated to be an invaluable tool in plant molecular biology studies. However, low efficiency and inconsistency of this method in *Arabidopsis* has forced the implementation of *Nicotiana benthamiana* as a surrogate system, limiting applicability. One of the main reasons to underlie the recalcitrance of *Arabidopsis* to *Agrobacterium*-mediated transformation is the activation of plant immune responses upon perception of the bacteria. Perception of bacterial pathogen-associated molecular patterns (PAMPs), including EF-Tu, leads to activation of PAMP-triggered immunity (PTI). Activation of PTI ultimately induces salicylic acid (SA) accumulation, which in turn shuts down expression of the vir genes, potentially interfering with the transfer of the T-DNA, and therefore T-DNA gene expression (Yuan et al., 2007; Anand et al., 2008). However, previous results suggested that besides depletion of SA other hormone-mediated defence responses, including jasmonic acid (JA), might be responsible for the low efficiency of transient transformation in Arabidopsis (Tsuda et al., 2012).

In this work, we evaluate the efficiency of Agrobacterium-mediated transient transformation in Arabidopsis genotypes affected in JA perception or signalling (*coi1*, *jin1*), or with low SA or JA content (*sid2*, *NahG*, *aos*). The results show that impairment of JA signalling reduces or does not affect transient expression in mature leaves, but expression of the *NahG* transgene dramatically improves this process. We demonstrate that Arabidopsis *NahG* plants can be efficiently used for transient expression-based functional assays routinely performed in *N. benthamiana*, such as determination of subcellular localization of GFP-fused proteins or analysis of protein-protein interactions by Bimolecular Fluorescent Complementation, this

system can enormously facilitate research in this model plant species, allowing for an efficient use of the full potential of the numerous tools and resources currently available to

the community.

Anand, A et al. (2008). Plant Physiol. 146:703–715. Tsuda, K et al. (2012). Plant J. 69:713–719. Yuan, Z.C. et al. (2007). Proc. Natl. Acad. Sci. USA 104:11790–11795.

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