

## Central European Journal of Biology

## Candidate plant gene homologues in grapevine involved in *Agrobacterium* transformation

Research Article

Tamás Deák¹, Tünde Kupi¹, Róbert Oláh², Lóránt Lakatos³, Lajos Kemény³, György D. Bisztray¹,\*, Ernő Szegedi⁴,#

<sup>1</sup>Corvinus University of Budapest, Institute for Viticulture and Enology, Department of Viticulture, 1118 Budapest, Hungary

<sup>2</sup>Corvinus University of Budapest, Faculty of Horticultural Sciences, Department of Genetics and Plant Breeding, 1118 Budapest, Hungary

<sup>3</sup>University of Szeged, Department of Dermatology and Allergology, 6720 Szeged, Hungary

<sup>4</sup>Corvinus University of Budapest, Institute for Viticulture and Enology, Experimental Station of Kecskemét, 6000 Kecskemét-Katonatelep, Hungary

## Received 29 January 2013; Accepted 23 April 2013

Abstract: The grapevine (Vitis vinifera) genome was analyzed in silico for homologues of plant genes involved in Agrobacterium transformation in Arabidopsis thaliana and Nicotiana spp. Grapevine homologues of the glucomannan 4-betamannosyltransferase 9 gene Cs/A-09 involved in bacterial attachment to the cell wall, homologues of reticulon-like proteins BTI1, 2, 3 and RAB8 GTPases, both involved in T-DNA transfer to the host cell, homologues of VirE2 interacting protein VIP1 that contributes to the targeting of T-DNA into the nucleus and to its integration, and homologues of the histone protein H2A, which promotes the expression of T-DNA encoded genes, were selected. Sequences homologous to the arabinogalactan-protein AtAGP17 were not found in the grape genome. Seventeen selected candidates were tested by semiquantitative RT-PCR analysis for changes in their expression levels upon inoculation with Agrobacterium tumefaciens C58. Of the tested homologues, the expression of VvRab8a, VvVip1a and two histone genes (VvHta2 and VvHta10) increased significantly, therefore we hypothesize that these might be involved in Agrobacterium transformation of V. vinifera.

Keywords: Vitis vinifera • Crown gall disease • Pathogen-induced gene expression • Semiquantitative PCR

© Versita Sp. z o.o.

## 1. Introduction

Crown gall caused by the pathogenic *Agrobacterium* species is a serious disease affecting several crop plants including fruit trees, berries, ornamental plants and grapevines. However, genetic transformation of crop plants by non-tumorigenic ("disarmed") *Agrobacterium tumefaciens* strains has became a widely used method to introduce foreign genes into plants to improve agronomical traits [1,2].

Tumorigenic agrobacteria harbour a large plasmid called tumor inducing plasmid (pTi) that carries the genes which are essential for crown gall tumor induction. During the transformation process a region of this

plasmid, the transferred DNA (T-DNA) is transported into the host cell and it becomes stably integrated into the chromosomal DNA. The T-DNA transport through a type IV secretion system [3] from the prokaryotic bacterium into the eukaryotic plant cell is determined by the virulence (*vir*) genes located also on the pTi, but outside the T-DNA. The T-DNA is transported in a single-stranded form (T-strand), and this process is directed by the VirD2 protein that covalently binds to the 5' end of the T-strand [2]. Additionally, for T-DNA import the VirE2 protein forms an anion selective channel on the plasma membrane of the plant cells [4] and binds to the VirD2/T-DNA during the transport process. The VirD2/VirE2/T-strand called T-complex is targeted to the nucleus of

