

GENETIC TRANSFORMATION OF *VITIS* SPP. AS A TOOL FOR THE DEVELOPMENT AND EVALUATION OF NEW TECHNICAL PLATFORMS

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ABSTRACT

Since 2002 a grapevine genetic transformation program has been carried out at La Platina Research Station of the National Agriculture Institute (INIA, Santiago de Chile) by development of a high throughput *Agrobacterium tumefaciens*-mediated transformation system using 'Thompson Seedless' somatic embryos (Reyes *et al.*, 2005). Formerly focused on *Botrytis* control, the more advanced lines from this program were developed using the *chi42* and *nag70* genes from *Trichoderma harzianum* P1, and the *chi33* gene from a local isolate of *T. virens*. About 3,000 candidate transgenic lines have been successfully established at greenhouse level (Hinrichsen *et al.*, 2005), from which 103 lines represented by 568 GM plants were released into a biosafety field in September 2004. Results allowed the generation of a fungus tolerant population (20 top lines) based on a discriminant multivariate analysis of *B. cinerea* and *E. necator* tolerances after three seasons of assays. Scaling up of the somatic embryogenesis (SE) technology was conducted by design of a bioreactor assisted SE platform (Tapia *et al.*, 2009), useful in the genetic transformation work flow of rootstock germplasms. Generation of Grapevine Fanleaf Virus resistant lines have been then started together to different approaches evaluating gene silencing in grapevines and the use of ds hairpin inducing DNA strategy. Several GM rootstock lines have been already generated and current evaluation procedures include micro-grafting assays on a population of GFLV infected Saint George plants. Lately, additional gene silencing studies are being developed as a proof of concept using undescribed *Vitis vinifera* inducible promoters conducting the expression of artificial microRNA based vectors in these species. Results and strategies will be shown in order to analyze and discuss the generation of new knowledge for grape biotechnology by networking with different research groups.

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