

DNA-free editing to improve stress resilience of wine grape genotypes recalcitrantto-regeneration

Giorgio Gambino¹, Floriana Nuzzo¹, Amedeo Moine¹, Walter Chitarra^{1,2}, Chiara Pagliarani¹, Annalisa Petrelli³, Paolo Boccacci¹, Andrea Delliri¹, Riccardo Velasco², Luca Nerva^{1,2}, <u>Irene Perrone^{1*}</u>

¹ Institute for Sustainable Plant Protection, National Research Council (IPSP-CNR), Strada delle Cacce 73, 10135 Torino (Italy)

² Research Centre for Viticulture and Enology, Council for Agricultural Research and Economics (CREA-VE), Via XXVIII Aprile 26, 31015 Conegliano (Italy)

³ Open Lab - Department of Veterinary Sciences, University of Turin (DSV-UNITO), Largo Paolo Braccini 2, 10095 Grugliasco, Italy

*Corresponding author: irene.perrone@ipsp.cnr.it

Abstract (250 words)

Wine viticulture, being firmly linked to the vine-terroir relationship, has always encountered significant bottlenecks to genetic innovation. Nonetheless, the development of new breeding strategies leading to the selection of stress resilient genotypes is urgent, especially in viticulture, where it would allow reducing the use of chemical treatments adopted to control fungal diseases. Genome editing represents an extremely promising breeding technique. Unfortunately, the wellknown recalcitrance of several wine grape cultivars to in vitro regeneration strongly limits the exploitation of this approach, which to our knowledge has so far been developed on table grape genotypes with high regeneration potential. By targeting the phytoene desaturase gene as visual editing proof, we developed a genome editing and regeneration protocol to produce transgene-free plants exploiting the lipofectamine-mediated delivery of CRISPR–Cas9 grapevine ribonucleoproteins into protoplasts. We regenerated edited grapevines of Vitis vinifera 'Nebbiolo', a cultivar extremely recalcitrant to *in vitro* regeneration and at the basis of outstanding quality wines, such as 'Barolo' and 'Barbaresco'. Successful editing was confirmed by a combination of approaches: HRM, Sanger and amplicon deep sequencing, phenotype visualization. We then exploited the method to silence two micro(mi)RNAs involved in biotic stress responses: vv-miR482, which is conserved in different species, and the grapevine-specific vv-miR3623. Since NBS-LRR disease-resistance genes are the targets of those miRNAs, the objective is to regenerate vines with a broad-spectrum level of plant tolerance/resistance to different pathogens. The developed strategy could be extended to other important wine grape varieties and recalcitrant woody species.

Keywords: genome editing, protoplast regeneration, lipofectamines, microRNAs, biotic stress