

Comparative analysis of CRISPR/Cas9 delivery approaches for polyphenol oxidase 2 gene editing in potato

Abstract

- StPPO2 gene editing was analyzed by Agrobacteriumtransformation CR-PPO mediated with vector, ribonucleoprotein complexes (RNP-PPO) transfection to protoplasts, and CR-PPO transient expression in protoplasts, yielding efficiencies of 9.6%, 18.4%, and 31.9%, respectively.
- Transient expression of CR-PPO in protoplasts resulted in tetra-allelic edited lines, observed in 46% of total edited lines.
- On-target DNA insertions were found in lines from all three approaches.
- Loss of function of the StPPO2 protein was confirmed in a tetra-allelic edited line.

Introduction

Delivery of the CRISPR/Cas9 components to the plant cells, and further regeneration of edited lines, are key steps in the use of this technology. In potato, genomic integration of Cas9 and sgRNAs coding sequences via Agrobacterium tumefaciensmediated transformation is the most commonly used approach (Van Eck 2018). As an alternative, CRISPR/Cas9 components can be delivered to protoplasts (Nadakuduti et al. 2018). Such a strategy allows the delivery of the components encoded in DNA molecules but, also, assembled as ribonucleoprotein complexes (RNPs). The use of RNPs is of particular importance when using this technology to obtain improved commercial crops (Zhang et al. 2020). In this study, all three approaches were analyzed to direct the CRISPR/Cas9 components for StPPO2 gene editing. StPPO2 is the principal contributor to the polyphenol oxidase activity in the tuber, responsible for enzymatic browning in potato (González et al. 2020).

Methods and Materials

Components design: sgRNA1 and sgRNA2 (Figure 1A) were designed RGEN with Cas-Designer (<u>http://www.rgenome.net/cas-designer/</u>). CR-PPO vector was constructed (Figure 1B), and RNP-PPO (Figure 1C) were obtained with GeneArt Precision sgRNA Synthesis Kit (Thermo Fisher Scientific). Agrobacterium-mediated transformation: potato explants were transformed as described in Kumar (1995) (Figure 2). Protoplasts transfection and plant regeneration: Performed according to Nicolia et al. (2015), with the modifications described by Andersson et al. (2017) (Figure 2). Mutations screening: Performed by High Resolution Fragment Analysis (HRFA, Andersson et al. 2017) of the region spanning both sgRNAs target sites. Results were confirmed by Sanger sequencing. Phenotypic characterization: Tubers were analyzed for enzymatic browning and PPO activity, as previously described (González et al. 2020).

Contact

Matías N. González, Lic Laboratorio de Agrobiotecnología, IPADS Balcarce (INTA-CONICET) Ruta 226, Km 73.5, B7620 Balcarce, Argentina gonzalez.matiasn@inta.gob.ar Cell phone: +54 9 223 5129238

González M.N.^{1,2}, Massa G.A.^{1,2,3}, Andersson M.⁴, Décima Oneto C.A.^{1,3}, Turesson H.⁴, Storani L.^{1,2}, Olsson N.⁴, Fält A-S.⁴, Hofvander P.⁴, Feingold S.E¹. Laboratorio de Agrobiotecnología, IPADS Balcarce, ²Consejo Nacional de Investigaciones Científicas y Técnicas, ³ Facultad de Ciencias Agrarias, UNMDP, ⁴ Department of Plant Breeding, SLU.



Figure 2. CRISPR/Cas9 components delivery approaches. Agrobacterium-mediated transformation with CR-PPO (top) and protoplasts transfection and regeneration with CR-PPO and RNP-PPO (bottom)

Table 1. *StPPO2* gene editing in regenerated lines.

CRISPR/Cas9 system	Delivery method	Analyzed lines	StPPO2 genotype		Efficiency	Tetra-allelic
			WT	Edited (at least one allele)		euiteu iiies
CR-PPO	A. tumefaciens	93	84	9	9.6%	0% (0)
CR-PPO	Protoplasts	47	32	15	31.9%	46.6% (7)
RNP-PPO	Protoplasts	76	62	14	18.4%	0 % (0)

Table 2. On-target DNA insertions.

Line ID	CRISPR/Cas9 system	Delivery method	Insertion length (target site)	Inse
4.2.3	CR-PPO	A. tumefaciens	21 bp (sgRNA2)	n/d
CR1053	CR-PPO	Protoplasts	380 bp (sgRNA2)	CR- and
RNP6173	RNP-PPO	Protoplasts	152 bp (sgRNA2)	DNA tran

n/d indicates "no determined"

References

- 1. Andersson et al. (2017). Plant Cell Rep. 36, 117-128. https://doi.org/10.1007/s00299-016-2062-3
- 2. Andersson et al. (2018). Physiol. Plant. 164, 378-384. https://doi.org/10.1111/ppl.12731
- 3. Arndell et al. (2019). BMC Biotechnol. 19, 1-12. https://doi.org/10.1186/s12896-019-0565-z 4. Banakar et al. (2019). Sci. Rep. 9, 1-13. https://doi.org/10.1038/s41598-019-55681-y
- 5. Gelvin (2017). Annu. Rev. Genet. 51, 195-217. https://doi.org/10.1146/annurev-genet-120215-035320
- 6. González et al. (2020). Front. Plant Sci. 10, 1-12. https://doi.org/10.3389/fpls.2019.01649
- 7. Kumar (1995). Agrobacterium Protocols. Springer New York, Totowa, NJ, pp. 121-128. https://doi.org/10.1385/0-89603-302-3:121

ert origin

PPO vector (fragments of NPTII gene OCS terminator) A template used for sgRNA1 in vitro nscription

- around 75 bp as expected for Cas9 inducing cuts at both target sites.



Transient expression of CR-PPO resulted in a higher *StPPO2* gene editing efficiency in comparison to the Agrobacterium-mediated transformation with the same system. Even though selection pressure was applied during the whole transformation process, we cannot disregard the possibility of transgene silencing (Gelvin 2017). For protoplasts transfection, *StPPO2* editing efficiency was higher with CR-PPO than RNP-PPO. This supports the concept that RNPs are rapidly subjected to degradation in the cell (Kumlehn et al. 2018). All three approaches resulted in on-target DNA insertions. Insertions of T-DNA into the target sites seem to occur at low frequencies in plants obtained via Agrobacterium-mediated transformation (Banakar et al. 2019). Here, the small length of the 21 bp insertion found in one of such a line made it complex to determine its origin. In concordance with our results, transient expression of DNA in protoplasts has been reported to produce on-target insertions in potato (Andersson et al. 2017, 2018; Tuncel et al. 2019; Veillet et al. 2019) and wheat (Arndell et al. 2019), and RNPs obtained by invitro transcription of sgRNAs has been reported to produce on-target DNA insertions in potato (Andersson et al. 2018; González et al. 2020).

Gene editing efficiency in potato is affected by the delivery approach of CRISPR/ Cas9 components. For potato breeding applications, RNPs transfection into protoplasts represents a promising approach, although a careful design of the CRISPR/Cas9 components must be performed to accomplish a high editing efficiency and avoid unwanted DNA insertions.

8. Kumlehn et al. (2018). J. Integr. Plant Biol. 60, 1127-1153. https://doi.org/10.1111/jipb.12734 Nadakuduti et al. (2018). Front. Plant Sci. 9, 1-11. https://doi.org/10.3389/fpls.2018.01607 10. Nicolia et al. (2015). J. Biotechnol. 204, 17-24. https://doi.org/10.1016/J.JBIOTEC.2015.03.021 11. Tuncel et al. (2019). Plant Biotechnol. J. 17, 2259-2271. https://doi.org/10.1111/pbi.13137 12. Van Eck (2018). Curr. Opin. Biotechnol. 49, 35-41. https://doi.org/10.1016/j.copbio.2017.07.012 13. Veillet et al. (2019). Plant Cell Rep. 38, 1065-1080. https://doi.org/10.1007/s00299-019-02426-w 14. Zhang et al. (2020). Plant Biotechnol. J. 18, 1651-1669. https://doi.org/https://doi.org/10.1111/pbi.13383

Funding

- calidad industrial y nutricional

Results

The CR-PPO transient expression in protoplasts resulted in higher editing efficiency and a high frequency of lines edited in all four *StPPO2* alleles (Table 1). Only two lines (obtained by CR-PPO transient expression) carried deletions of

On-target DNA insertions were observed in 1.1% (1 line), 8.5% (4 lines), and 3.9% (3 lines) of analyzed lines from Agrobacterium-mediated transformation, CR-PPO, and RNP-PPO transfections in protoplasts, respectively (Table 2).

The tetra-allelic edited line CR1037 displayed a reduced PPO activity and enzymatic browning in tubers when compared to that of the wild type (Figure 3).

Figure 3. Phenotypic characterization of full edited line CR1037. A and B. Error bars represent the standard error from three plants per line. Significant differences according to the t-test (p < 0.05) is denoted *. C. Appearance of representative tubers after cut and 48 h air exposure

Discussion

Conclusions

- Trees and Crops for the Future (TC4F) area of SLU, supported by the Swedish Government





⁻ INTA PNBIO1131024: Desarrollo de sistemas alternativos de generación y utilización de variabilidad genética y su aplicación al mejoramiento de los cultivos

⁻ INTA-Fondo de Valorización Tecnológica (FVT-63): Variedades de papa editadas con mayor

INTA PE-I115: Edición génica, transgénesis y mutagénesis como generadores de nueva variabilidad en especies de interés agropecuario