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TITLE:

Plant Growth and Agrobacterium Mediated Floral-dip Transformation of the Extremophyte *Schrenkiella parvula*

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SUMMARY:

Agrobacterium-mediated transformation using a floral-dip method can be successfully employed to create stable transgenic lines of the extremophyte model *Schrenkiella parvula*. We present a protocol modified from that for *Arabidopsis thaliana*, considering different growth habits and physiological characteristics of the extremophyte.

ABSTRACT

Schrenkiella parvula is an extremophyte adapted to various abiotic stresses, including multiple ion toxicity stresses. Despite high-quality genomic resources available to study how plants adapt to environmental stresses, its value as a functional genomics model and tool has been limited by the lack of a feasible transformation system. In this protocol, we report how to generate stable transgenic *S. parvula* lines using an *Agrobacterium*-mediated floral-dip method. We modified the transformation protocol used for *A. thaliana* to account for unique traits of *S. parvula*, such as an indeterminate flowering habit and a high epicuticular wax content on leaves. Briefly, *S. parvula* seeds were stratified at 4 °C for five days before planting. Plants were grown at a photoperiod of a 14-hour light and 10-hour dark and a 130 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light intensity, at 22 °C to 24 °C. Eight to nine week-old plants with multiple inflorescences were selected for transformation. These inflorescences were dipped in an infiltration solution of *Agrobacterium tumefaciens* GV3101 carrying the *pMP90RK* plasmid. We performed two rounds of flower dipping with an interval of three to four weeks to increase the transformation efficiency. The T1 seeds were collected and dried for four weeks in a container with desiccants before germination to screen for candidate

transformed lines. Resistance to BASTA was used to screen T1 plants. We sprayed the BASTA solution three times with an interval of three days starting at two week-old plants to reduce false positives. A BASTA drop test was performed on surviving individual plants to identify true positive transformants. The transformation efficiency was 0.033%, yielding 3-4 transgenic plants per 10,000 T1 seeds propagated.

INTRODUCTION

In this protocol, we describe the growth and establishment of stable transgenic lines for the extremophyte model *Schrenkiella parvula*. The availability of an efficient transformation system is a hallmark of any versatile genetic model. Plants that thrive in extreme environments, referred to as extremophytes, provide a critical resource for understanding plant adaptations to environmental stresses. *Schrenkiella parvula* (formerly *Thellungiella parvula* and *Eutrema parvulum*) is one such extremophyte model, with expanding genomic resources¹⁻⁵. However, transformation protocols have not yet been reported for *S. parvula* in published studies.

The genome of *S. parvula* is the first published extremophyte genome in Brassicaceae (mustard-cabbage family) and shows an extensive overall genome synteny with the non-extremophyte model, *Arabidopsis thaliana*¹. Thus, comparative studies between *A. thaliana* and *S. parvula* could benefit from the wealth of genetic studies performed on *A. thaliana* to make informative hypotheses on how the *S. parvula* genome has evolved and regulated differently to cope with extreme environmental stresses⁵⁻⁷. *S. parvula* is one of the most salt-tolerant species (based on soil NaCl LD50) among known wild relatives of *A. thaliana*⁸. In addition to the NaCl tolerance, *S. parvula* survives and completes its life cycle in the presence of multiple salt ions at high concentrations toxic to most plants⁷. In response to the abiotic stresses prevalent in its natural habitat, it has evolved various traits, among which several have been studied at the biochemical or physiological level⁸⁻¹¹.

Since 2010, there have been over 400 peer-reviewed publications that used *S. parvula* as a target species or used it in a comparison with other plant genomes. However, a clear bottleneck could be identified with a closer look of what type of studies have been conducted. The majority of these reports discuss the potential use of *S. parvula* in future studies or use it in comparative genomic or phylogenomic studies. Due to the lack of a proof-of-concept transformation protocol established for *S. parvula*, it has not been used in functional genomic studies, despite having one of the highest quality plant genomes available to date (>5 Mb contig N50) assembled and annotated into chromosome-level pseudomolecules¹.

The Agrobacterium-mediated floral-dip transformation method has become the most broadly used method to create transgenic lines in *A. thaliana*, and the development of a reproducible system of transformation was a critical factor in its success as a genetic model^{12,13}. However, not all Brassicaceae species have been shown to be successfully transformed using the floral-dip method developed for *A. thaliana*. Specially, the Brassicaceae Lineage II species that include *S. parvula* has been recalcitrant to floral-dip based transformation methods^{14,15}.

The indeterminate flowering growth habit of *S. parvula*, combined with its narrow leaf

morphology has made it challenging to adopt the standard *Agrobacterium*-mediated floral-dip transformation method. In this study, we report the modified protocol we have developed for reproducible transformation of *S. parvula*.

PROTOCOL

1. Plant Growth

1.1. Seed sterilization (optional)

1.1.1. Prepare 50% bleach in double-distilled water (ddH₂O) with 1 or 2 drops of a non-ionic detergent (see **Table of Materials**) in a 50 mL tube. Invert the tube several times to mix the solution.

Note: It is preferable to conduct seed sterilization in a laminar flow cabinet with a UV sterilized surface for 15 minutes.

1.1.2. Add the bleach solution to ~100-200 *S. parvula* seeds in a 1.5 mL tube. Mix thoroughly and let the tube sit for 5 minutes.

1.1.3. Remove the bleach from the tube and add 70% ethanol. Wash the seeds by pipetting several times and then remove the ethanol solution immediately.

1.1.4. Wash the seeds in sterilized water to remove excess bleach and ethanol, then remove the water. Repeat this step 5 to 6 times.

1.2. Seed stratification

1.2.1. Immerse the seeds in sterilized water, and store for 5 to 7 days at 4 °C. Alternatively, sow dried unsterilized seeds directly on wet soil, and place the soil tray for 5 to 7 days at 4 °C.

1.3. Growing plants in preparation of transformation

1.3.1. Fill the soil mix (see **Table of Materials**) into 7 x 6 cm² pots, soak the pots in water, and spray water from the top to ensure a uniformly wet growth medium. Add 5-6 fertilizer beads (see **Table of Materials**) on the soil surface of each pot.

Note: As far as we have experienced, *S. parvula* grows well on any soil mix where *A. thaliana* can grow.

1.3.2. Using a wet toothpick, transfer 20~25 seeds per pot on the soil surface.

Note: A convenient practice is to put a batch of 4-5 seeds in the four corners and the center of the pot (**Figure 1**, Day 15, left panel).

1.3.3. Cover the pot tray with a clear dome to keep the seeds under high humidity during germination.

1.3.4. Keep the plant trays in a growth chamber with a light intensity set at $130 \mu\text{mol m}^{-2} \text{s}^{-1}$ light, 22 – 24 °C temperature, and 14-h-day/10-h-night cycle. Remove the domes after 7 – 10 days following germination. Add water from the bottom of the tray to keep soil moistened uniformly at a desirable level.

1.3.5. Weed out extra seedlings and leave only 4-5 healthy seedlings per pot well separated from each other (**Figure 1**, Day 15, right panel).

1.3.6. Gently water the plants every two days and fertilize with 0.2x Hoagland's solution¹⁶ once every two weeks.

Note: Keeping the soil moisture at a uniform level is key to growing *S. parvula* consistently and healthily.

1.3.7. Continue to grow the plants for 8-10 weeks until multiple inflorescences produce 100-150 floral buds per plant (**Figure 1**, Day 60-80). On the day planned for the floral-dip based transformation (step 4.5), remove all mature and developing siliques from the plants.

2. Cloning the Gene/Genomic Element of Interest into a Vector for Plant Transformation

2.1. Amplify the target DNA fragment using polymerase chain reaction (PCR)¹⁷ and isolate the PCR product using a gel extraction kit (see **Table of Materials**) according to the kit protocol or any other appropriate method to purify DNA using agarose gel electrophoresis^{17,18}. Verify the sequence of the isolated PCR product through Sanger sequencing¹⁹.

2.2. Clone the desired PCR product into the cloning vector and transform the cloned construct into the competent *E. coli* cells using a topoisomerase-based cloning kit (see **Table of Materials**) following manufacturer's guidelines.

2.3. Spread 50 μL of transformed products on Luria-Bertani²⁰ (LB) agar bacterial growth media (**Table 1**) with appropriate antibiotics, e.g., 50 $\mu\text{g/ mL}$ Spectinomycin (see **Table of Materials**), and incubate at 37 °C overnight.

2.4. The following day, select 5-10 single colonies, inoculate into liquid LB medium with appropriate antibiotics, and incubate with gentle shaking at 37 °C overnight.

2.5. Isolate plasmids using a plasmid isolation kit (see **Table of Materials**) and verify through Sanger sequencing¹⁹ whether the target sequence amplified in 2.1 is properly cloned.

2.6. Transfer the cloned and verified PCR product to a destination vector for plant transformation

compatible with recombination-based cloning (see **Table of Materials**), using a recombinase enzyme mix kit (see **Table of Materials**), following the kit manufacturer's instruction. Repeat from step 2.3 to step 2.5 to isolate and verify clones harboring proper plasmid constructs.

3. Transforming the Vector Construct for Plant Transformation into *Agrobacterium tumefaciens*

3.1. Transform the plasmid of the vector construct from 2.6 into the *A. tumefaciens* strain GV3101:pMP90RK²¹, which harbors a Rifampicin resistance gene for chromosomal background selection. Use appropriate antibiotics, *e.g.* Gentamycin or Kanamycin (see **Table of Materials**), for the selection of plant transformation construct (Ti plasmid). A brief protocol for *A. tumefaciens* transformation via electroporation is included in section 3.2.

3.2. *A. tumefaciens* transformation by electroporation

3.2.1. Thaw the *A. tumefaciens* competent cells²² on ice. Mix 0.1 – 1 µg of the plasmid prepared from 2.6, dissolved in 1-2 µL of ddH₂O, with competent cells on ice. Transfer the mixture into an electroporation cuvette (see **Table of Materials**).

3.2.2. Perform electroporation on the mixture of plasmids and competent cells from 3.2.1, using an electroporator (see **Table of Materials**) following the manufacturer's guidelines.

Note: Clean the surface of the cuvette before starting the electroporation.

3.2.3. Transfer the reaction mixture from the cuvette to a microcentrifuge tube that contains 1.5 mL of liquid LB and mix well with pipetting and incubate for 1 hour at 28 °C with gentle shaking.

3.3. Inoculate the transformed *A. tumefaciens* from section 3.2 on LB plates containing appropriate selection antibiotics (*e.g.* Kanamycin 25 µg/ mL, Spectinomycin 50 µg/ mL, Gentamycin 25 µg/ mL, and Rifampicin 50 µg/ mL) and incubate at 28 °C for 3 days.

4. *Agrobacterium*-mediated Transformation of *S. parvula*

4.1. Inoculate the single transformed colonies from plates into 10 mL of LB liquid media containing antibiotics (the same as in 3.3) in a sterile 50 mL conical tube (see **Table of Materials**). Incubate for 24 hours in a shaking incubator (see **Table of Materials**) at 250 r.p.m. at 28 °C.

4.2. Transfer the bacterial solution from 3.4.1 to a sterile 250 mL flask, add 40 mL of LB liquid media with appropriate antibiotics, and incubate 12-36 h until the optical density at 600 nm wavelength (OD₆₀₀) reaches around 2.0.

4.3. Centrifuge the *A. tumefaciens* culture at 3100 x g for 10 min. Remove the supernatant and re-suspend the bacterial culture in 40 mL of *A. tumefaciens* infiltration solution (**Table 1**).

221 4.4. Dilute the resuspended *A. tumefaciens* with infiltration solution to a final OD₆₀₀ of 0.8. Add
222 25 µL of surfactant solution (**Table 1**) to 50 mL of diluted *A. tumefaciens* solution and mix by
223 inverting several times.

224
225 4.5. Dip the inflorescence of the plants in the *A. tumefaciens* solution prepared in the section 4.4
226 for 20 seconds. Use a fresh bacterial solution after dipping inflorescence from six pots. Make sure
227 all flowers are in contact with the solution. Pipet bacterial solutions directly onto flowers located
228 in the lower part of the inflorescence if they cannot be dipped into the solution.

229
230 Note: For the first-round transformation, make sure to remove all mature and developing siliques
231 using a sharp scalpel or small scissors. Do not remove siliques if performing transformation for
232 the second time.

233 234 **5. Post-transformation Plant Care and the Second Transformation**

235
236 5.1. Place the floral-dipped plants horizontally in clean trays with domes to cover the plants and
237 place in a dark growth room for 1-2 days.

238
239 Note: Keeping the flowers under high-humidity is important at this stage (**Figure 1**, Plants after
240 transformation).

241
242 5.2. Return the plants to an upright position and transfer the plants to a growth room with a 14-
243 h-day/ 10-h-night cycle, 130 µmol m⁻² s⁻¹ light intensity and 22 to 24 °C temperature.

244
245 5.3. Monitor the dipped inflorescences in the following week. If a significant number of flowers
246 abort (**Figure 2**), repeat the floral dip (step 4) after about 4 weeks or after a large number of
247 flowers have newly developed.

248
249 Note: Unlike the preparation step for the first transformation (step 1.3.7), do not remove pre-
250 existing or developing siliques (**Figure 2**) before the second round of transformation.

251
252 5.4. Grow the plants until seeds mature and harvest seeds at ~21 weeks.

253
254 5.5. Dry seeds for 2-3 weeks at room temperature in an airtight container with filled with
255 desiccants (see **Table of Materials**).

256 257 **6. Selection of Positive Transformants**

258
259 6.1. Plant the T1 seeds as described for wild type seeds in steps 1.2 to 1.3.

260
261 6.2. Grow the plants until the first 2-3 true leaves develop, approximately 10 - 14 days after
262 germination.

263
264 6.3. Perform the first selection for herbicide resistance (**Figure 3A and 3B**) as detailed below.

265
266 6.3.1. Dilute the glufosinate-ammonium (11.3%) herbicide (or BASTA) (**Table 1**) to 1:1000 (v/v).
267 Spray diluted BASTA solution on the seedlings and cover the plants with domes overnight.

268
269 6.3.2. Repeat BASTA spraying 2-3 times every 5-7 days.

270
271 6.4. Perform the second selection using a BASTA-drop test as detailed below.

272
273 6.4.1. Identify plants that survive after being sprayed 3-4 times with BASTA solution. Grow the
274 plants for another 2-3 weeks until 3-5 leaves develop a relatively large surface area.

275
276 6.4.2. Select the largest mature leaf per plant, rub the surface of the leaf gently with a finger to
277 remove the wax layer, and place a drop of the diluted BASTA solution (from step 6.3.1).

278
279 Note: Mark the location of the leaf applied with the BASTA drop by placing a paper tape on the
280 nearest stem.

281
282 6.4.3. Monitor the leaves applied with the BASTA drop for signs of wilting for up to one week.
283 Select the plants with leaves unaffected by the BASTA drops.

284
285 Note: Leaves from most false-positive plants start to wilt within two days, while leaves from true-
286 positives are intact even after the drop of BASTA solution dries up (**Figure 3C**).

287
288 6.5. Confirm positive transformants using genomic PCR.

289
290 6.5.1. Collect 2-3 leaves from the surviving plants at step 6.4.5.

291
292 6.5.2. Extract genomic DNA from the leaves using the CTAB method²³ or any other appropriate
293 DNA extraction method.

294
295 6.5.3. Perform PCR using extracted genomic DNA samples from target plants, wild-type plants
296 (as negative controls), and the plasmid construct from the step 3.1 (as a positive control). Use an
297 appropriate pair of PCR primers specific to the selective marker gene, *e.g.*, for BASTA-resistant
298 gene (*bar*), TCAGCAGGTGGGTGTAGA (forward) and GTCAACCACTACATCGAGACAA (reverse).

299
300 6.5.3.1. For the example PCR primers targeting the *bar* gene, use the following PCR conditions:
301 the initial denaturation step at 98 °C for 30 seconds; followed by 30 cycles of denaturing at 98 °C
302 for 30 seconds, annealing at 59 °C for 30 seconds, and extending at 72 °C for 30 seconds; and the
303 final extension at 72 °C for 5 minutes.

304
305 Note: To ensure the insertion of the entire T-DNA, we recommend also performing genomic PCR
306 using a PCR primer from the selective marker gene and another PCR primer specific to the target
307 sequence cloned to the plant transformation vector at the step
308

6.5.4. Confirm the presence of the expected size of the amplified *bar* PCR product by agarose gel electrophoresis¹⁷ for the target samples (**Figure 4A**) as well as by sequencing the isolated PCR product¹⁹ using the same procedure as in step 2.1.

REPRESENTATIVE RESULTS

We developed a transformation protocol that enables harvesting of T₀ seeds within 150 days, using a floral-dip method modified from that for *A. thaliana*. **Figure 1** shows a summary of the timeline and *S. parvula* plants that represent the optimal stage for executing the transformation through floral-dip. We selected *S. parvula* plants with 70 – 80 flowers in multiple inflorescences at 60 – 80 days after germination as the target stage for transformation. A small number of pre-existing open or fertilized flowers and siliques at this stage were removed before the infiltration of *A. tumefaciens* by the floral-dip method. Infection with *A. tumefaciens* resulted in abortion of some flowers (**Figure 2**, bracket (a)). Siliques fully developed after the floral-dip are likely to contain transformed seeds (**Figure 2**, bracket (b)). Even after transformation, *S. parvula* continued to develop new inflorescences and flowers as long as the plants were kept healthy (**Figure 2**, white arrows). Due to this indeterminate flowering habit, a second round of transformation can be performed if the plant does not show signs of stress or senescence. **Figure 2A** and **2B** show examples of *S. parvula* plants after the first and second round of transformation, respectively, 25 days apart from each other. In the second transformation, existing siliques should not be removed because they may contain transgenic seeds. Also, the *A. tumefaciens* can be applied by pipetting the infiltration solution (**Table 1**) onto newly emerging flower clusters, instead of dipping the entire shoot into the solution, to minimize the damage to siliques from the first transformation.

The transformation efficiency is 0.033%, yielding 3-4 transgenic plants per 10,000 T₁ seeds propagated using the current protocol. This estimate is based on ~50,000 T₁ seeds tested during ten independent transformation attempts. While the efficiency is lower than that of the *Arabidopsis thaliana*, it is comparable to the transformation of another extremophyte plant *Eutrema salsugenum*²⁴ and some of the *Arabidopsis thaliana* ecotypes²⁵. The transformation efficiency may be further optimized by using alternative *Agrobacterium* strains and modifications of surfactant and infiltration solutions. The multiple BASTA spray and drop tests (steps 6.3 and 6.4) will be critical to identify true positive transformants and reduce the number of samples tested using the PCR confirmation in step 6.5 (**Figure 4A**). Further confirmation of transformation can be checked with a reporter gene expression, if the cloned sequence includes a reporter gene (**Figure 4B**).

FIGURE AND TABLE LEGENDS

Figure 1: Timeline of *S. parvula* transformation.

Figure 2: *S. parvula* plants after transformation by floral-dip. Plants were photographed 10 days after the first floral-dip at Day 60 (**A**) and 25 days after the second round of floral-dip at Day 85 (**B**). Infiltration with *Agrobacterium* may abort silique development of flowers as shown in brackets a. Siliques fully developed after floral-dip are likely to contain transformed seeds

(brackets **b**). White arrows indicate flowers and inflorescences newly emerged after each transformation.

Figure 3: Selection of *S. parvula* transformants based on BASTA resistance. (A) T1 seedlings before the BASTA spray. (B) Red circle indicates a candidate transformant surviving the first-round selection by the BASTA spray. (C) The second-round selection by BASTA drop test. An example of false positives (top panel) and true transgenic plants (lower panel) are shown.

Figure 4: Confirmation of *S. parvula* transformation. (A) PCR amplification of *bar* gene from genomic DNAs extracted from *S. parvula* plants. Lane 1 and 13: size markers; Lane 2: negative control; Lane 3-5: wild-type *S. parvula* ; Lane 6-10: transgenic *S. parvula* candidates; Lane 11, 12: vector control. Lanes 7, 8, and 9 exemplify positive transformants. (B) Example of *GUS* reporter gene expression in a positive *S. parvula* transformant.

Table 1. Composition of bacterial growth media and *Agrobacterium* infiltration solution.

DISCUSSION

The physiological state of the plant significantly influences the efficiency of transformation²⁵. The use of healthy and vigorous plants for transformation is a key requirement for successful transformation in *S. parvula*. Water or light stressed plants will have fewer flowers compared to the healthy plants ideal for transformation (**Figure 1**, center panel). *S. parvula* can grow at a light intensity less than $130 \mu\text{mol m}^{-2} \text{s}^{-1}$, but the plants tend to be frailer; such plants would lead to more aborted flowers following floral-dip. *S. parvula* tends to abort *Agrobacterium*-dipped flowers at a higher rate than *A. thaliana*. Therefore, every step taken to minimize aborted flowers when dipped in the *A. tumefaciens* infiltration solution contributes to a higher transformation efficiency. We recommend a light period no longer than 14 hours per day. Often, transformation of *A. thaliana* is performed on plants grown in a long-day condition (*e.g.* 18-hour light and 6-hour dark) or even under continuous light. However, we found such practices result in less resilient *S. parvula* plants and lead to a low transformation efficiency.

Flower buds are continuously produced on the inflorescence axes of *S. parvula* (**Figure 2**, white arrows). Therefore, allowing transformation of new flowers would significantly increase the chance of getting positive transformants. A second floral-dip (step 5.3) is not essential, but strongly suggested. However, this step is relatively time consuming compared to *A. thaliana* floral dipping, because *S. parvula* produces multiple inflorescence axes.

Wild-type *S. parvula* is sensitive to BASTA, although the initial screen for positive transformants with BASTA spray (step 6.3) will leave 5-8 surviving plants out of 100 seeds germinated (**Figure 3A and 3B**). Most of this (>80%) will be false positives. This is largely due to the narrow leaf shape and the leaf angle of *S. parvula*, which do not provide sufficient leaf surface in an appropriate orientation to retain the BASTA solution for a sufficient duration to observe a phenotype. Additionally, due to the high wax content of the adaxial leaf surface of *S. parvula*¹⁰, it tends to create a more impervious surface for BASTA. Therefore, the second screening for positive transformants using a BASTA drop on individual leaves (step 6.4, **Figure 3C**) is an essential step

to avoid PCR testing on hundreds of false positives (step 6.5).

The current protocol was tested with the *A. tumefaciens* strain GV3101 carrying the *pMP90RK* plasmid. The efficiency of transformation may be improved with other *A. tumefaciens* strains, including strains ABI, LMG20, and C58C1 Rif^r, with the *pMP90* virulence plasmid reported to increase transformation efficiency in *A. thaliana*²⁵. *Brassica* and *Eutrema* species are taxonomically more closely related to *S. parvula* compared to *A. thaliana*¹. Therefore, the *A. tumefaciens* strain LBA4404 that was successfully used to transform *Brassica napus* and the strain EHA105 that has been used successfully to transform *Eutrema salsugineum* may offer a higher transformation efficiency than the reported efficiency of the strain currently used^{26–28}.

Reducing the time and labor required by a transformation protocol is another significant factor in improving the transformation efficiency. Placing individual BASTA drops on leaves and monitoring the leaf for a week on multiple plants (step 6.4) are tedious. A future effort to increase the transformation efficiency could search for appropriate alternative selectable marker genes²⁹.

The availability of an established transformation protocol will greatly advance our ability to identify genes and novel mechanisms that allow extremophyte model plants to survive multiple abiotic stresses^{2,4}. Novel genetic variation in *S. parvula* will provide a broader pool of genetic variation that cannot be mined from the collective allelic variation identified as stress-responsive genes in the relatively stress-sensitive model, *A. thaliana* pan-genome^{5,6}. Therefore, our floral-dip based *A. tumefaciens* mediated transformation protocol developed for *S. parvula* will fill a gap for the need for such tools to perform functional genomic experiments in an extremophyte model closely related to *A. thaliana*.

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DISCLOSURES

The authors have nothing to disclose.

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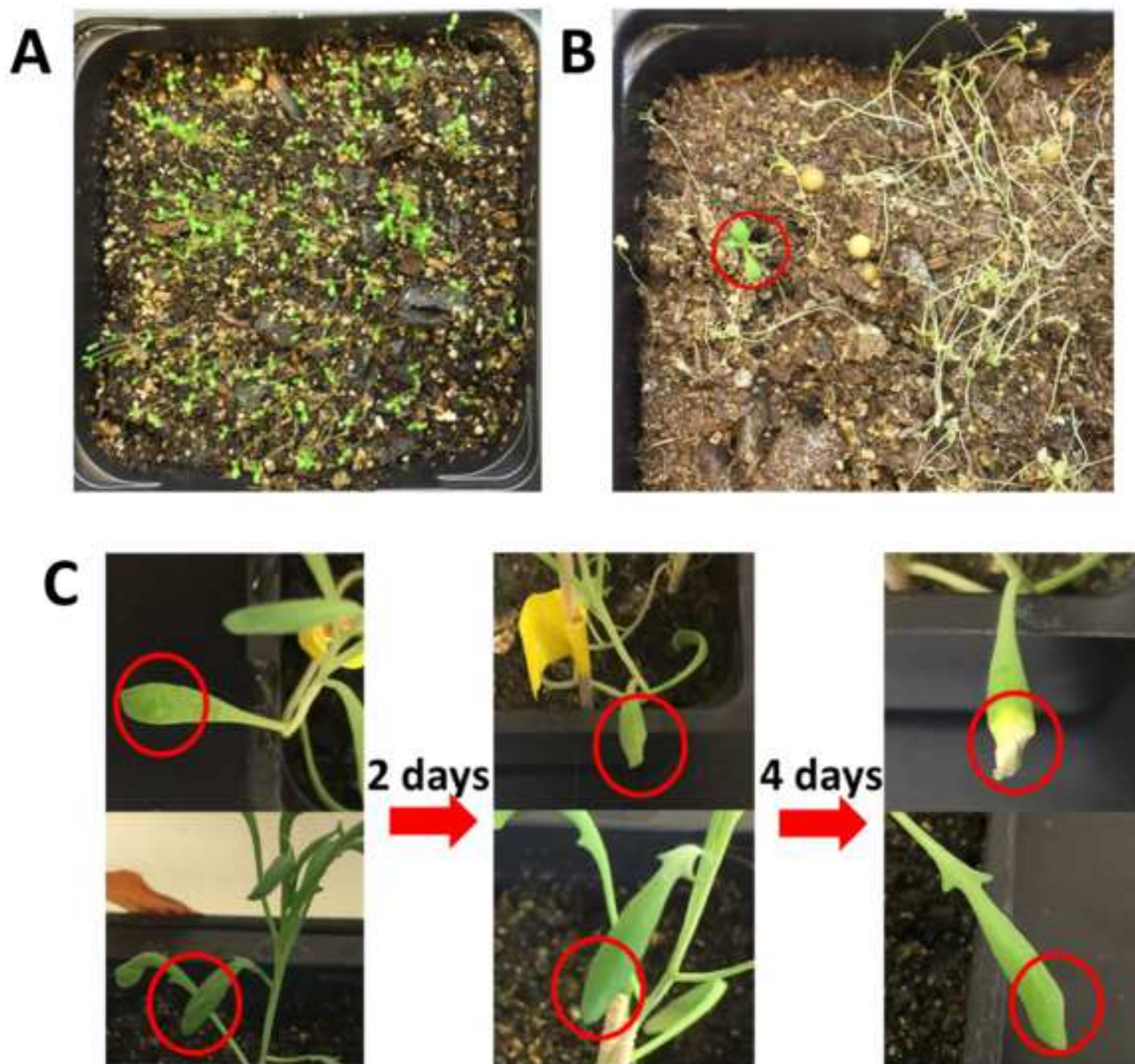
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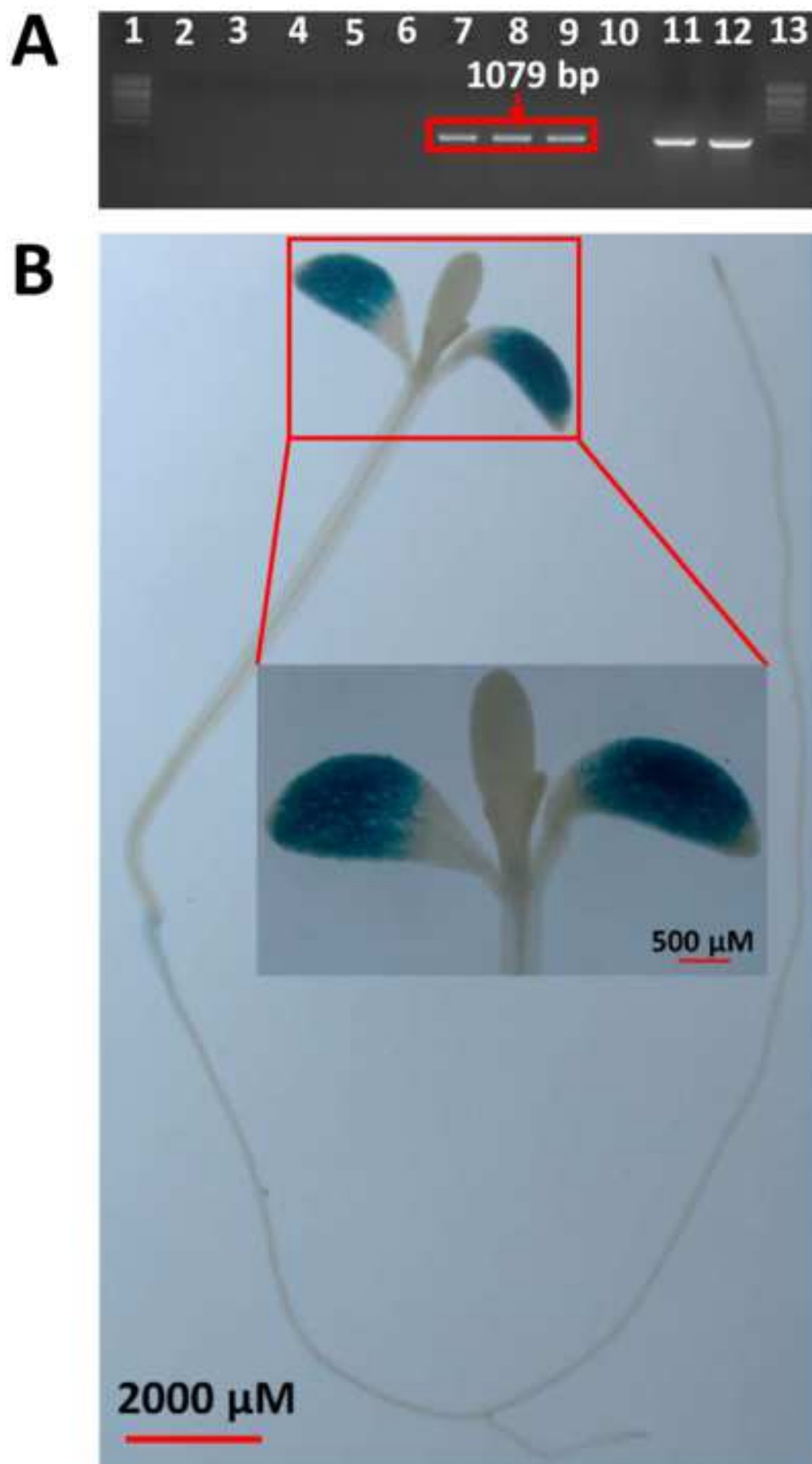


Table 1

Media / Solution	Reagent	Amount
Luria-Bertani (LB) bacterial growth media	NaCl	10 g
	Tryptone	10 g
	Yeast Extract	5 g
	Agar (for plates)	20 g
	ddH2O	955 mL
Agrobacterium infiltration solution	MS salt (1/4x)	2.16 g
	B5 vitamins (1X)	1 mL
	Sucrose (5%w/v)	50 g
	MES	0.5 g
	N ⁶ -benzylaminopurine (BA)	10 µL
	Silwet L-77 (0.05%v/v)	500 µL
	pH	5.7

Name	Company	Catalog Number
Agar	VWR International, Radnor, PA	90000-762
B5 vitamins	Sigma-Aldrich, St. Louis, MO	G1019
Desiccant	W A Hammond Drierite, Xenia, OH	22005
Destination vector for plant transformation	TAIR	Vector:6531113857
Electroporation cuvette	USA Scientific	9104-5050
Electroporator	BIO-RAD Laboratories, Hercules, CA	1652100
Fertilizer beads	Osmocote Garden, Marysville, OH	N/A
Gel extraction kit	iNtRON Biotechnology, Boston, MA	17289
Gentamicin	Sigma-Aldrich, St. Louis, MO	G1914-5G
Glufosinate-ammonium (11.3%) herbicide (BASTA)	Bayer environmental science, Montvale, NJ	N/A
Kanamycin	VWR International, Radnor, PA	200004-444
MES	Bioworld, Dublin, OH	41320024-2
MS salt	MP Biomedicals, Santa Anna, CA	092621822
N6-benzylaminopurine (BA)	Sigma-Aldrich, St. Louis, MO	B3274
NaCl	Sigma-Alrich	S7653
Non-ionic detergent	Sigma-Aldrich, St. Louis, MO	9005-64-5
Plasmid isolation kit	Zymo Research, Irvine, CA	D4036
Recombinase enzyme mix kit	Life Technology	11791-020
Rifampicin	Sigma-Aldrich, St. Louis, MO	R3501-1G
Shaking incubator	ThermoFisher Scientific, Waltham, MA	SHKE4450
Soil mix	Sun Gro	SUN239223328CFLP
Spectinomycin	VWR International, Radnor, PA	IC15206705
Sterile 50ml conical tubes	USA Scientific, Ocala, FL	1500-1811
Sucrose	VWR International, Radnor, PA	57-50-1
Surfactant solution	Lehle seeds, Round Rock, TX	VIS-02
Topoisomerase-based cloning kit	Life Technologies, Carlsbad, CA	K240020
Tryptone	VWR International, Radnor, PA	90000-282
Yeast Extract	VWR International, Radnor, PA	90000-722

Comment

Bacto Agar Solidifying Agent, BD Diagnostics

Gamborg's Vitamin Solution

Indicating DRIERITE 6 mesh

pKGWFS7

Electroporation cuvette, round cap, 0.2 cm gap

MicroPulser Electroporator

Osmocote Smart-Release Plant Food Flower & Vegetable

MEGAquick-spin Total fragment DNA purification kit

Gentamicin sulfate

FINALE herbicide

Kanamycin monosulfate

MES, Free Acid

Hoagland's modified basal salt mixture

6-Benzylaminopurine solution

Sodium chloride

TWEEN 20

Zyppy Plasmid Kits

Gateway LR Clonase II Enzyme mix

Rifampicin, powder, $\geq 97\%$ (HPLC)

MaxQ 4450 Benchtop Orbital Shakers

Sun Gro Metro-Mix 360 Grower Mix

50 ml conical screw cap tubes, copolymer, racks, sterile

Sucrose, ACS

Silwet L-77

pENTR/D-TOPO Cloning Kit, with One Shot TOP10 Chemically Competent E. coli

BD Bacto Tryptone, BD Biosciences

BD Bacto Yeast Extract, BD Biosciences

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Plant growth and Agrobacterium mediated floral-dip transformation of the extremophyte Schrenkiella parvula

Author(s):

Cuannan Wang, Pramod Pantha, Kieu-Nga Tran, Dong-Ha Oh, Maheshi Dassanayake

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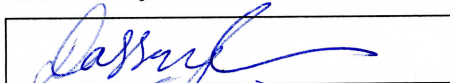
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Editorial comments:

Changes to be made by the Author(s):

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

[We proofread and revised the manuscript as instructed.](#)

2. Please upload each Figure individually to your Editorial Manager account as a .png, .tiff, .svg, .eps, .psd, or .ai file.

[We uploaded all figures as 300-dpi .png files as instructed.](#)

3. Please upload each Table individually to your Editorial Manager account as an .xls or .xlsx file.

[We converted Tables into separated .xlsx files and uploaded as instructed.](#)

4. Please remove the titles and Figure Legends from the uploaded figures. The information provided in the Figure Legends after the Representative Results is sufficient.

[We removed figure title and legends from uploaded figures.](#)

5. Please shorten the figure legends. The Discussion of the Figures should be placed in the Representative Results. Details of the methodology should not be in the Figure Legends, but rather the Protocol.

[We revised figure legends to be more concise, as instructed. If the figure is self-explanatory \(e.g., Figure 1\), we removed the legend entirely and instead added references in the appropriate places in the Protocol.](#)

6. The current Abstract is over the 150-300 word limit. Please shorten it.

[The Abstract in the original submission contained 292 words. We have further shortened it to 266 words in this revision.](#)

7. Please define all abbreviations before use.

[We spelled out all abbreviations at their first appearance in the revision.](#)

8. Please remove all commercial language from your manuscript and use generic terms instead. All commercial products should be sufficiently referenced in the Table of Materials and Reagents. For example: Osmocote, Scotts Miracle-Gro Co., MEGAquick-spin, iNtRON biotechnology, Gateway cloning technology, Invitrogen Co., Zymo Research, Gateway LR ClonaseII, USA Scientific, MicroPulser, BIO-RAD, Silwet L-77, etc.

[We replaced all commercial product names with generic terms as instructed. We added to the information on generic terms and their respective commercial products used in to the](#)

experiment, to the "List of Materials". Where the generic term of a commercial product was used in the revised text, we added references to the list of materials as [see Materials].

9. Please simplify the Protocol so that individual steps contain only 2-3 actions per step and a maximum of 4 sentences per step. Please revise 2.6, 4.1, etc. accordingly.

We revised the text as instructed.

10. 2.7: Please write the text in the imperative tense. Any text that cannot be written in the imperative tense may be added as a "Note."

We revised the text as instructed.

11. Please add more details to your protocol steps. Please ensure you answer the "how" question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action. Please revise 2.1, 6.5.3-6.5.5 accordingly.

We revised the text as instructed, by adding references or providing more details.

12. 2.1: Please provide more details or add a reference for gel extraction of PCR product.

We added the information on the gel extraction kit, as well as a couple references.

13. 6.5.3: Please list PCR conditions and primers.

We added PCR conditions and primer sequences for the amplification of the *bar* gene.

14. Please reference Figure 1 in the Protocol section.

We added references to Figure 1, as notes to the step 1.3.2 and 5.1.

15. Please reference Table 1 in the Protocol section for composition of growth media and infiltration solution.

We added references to Table 1 at steps 2.3 and 4.3.

16. There is a 2.75 page limit for filmable content. Please highlight 2.75 pages or less of the Protocol (including headings and spacing) that identifies the essential steps of the protocol for the video, i.e., the steps that should be visualized to tell the most cohesive story of the Protocol. Remember that non-highlighted Protocol steps will remain in the manuscript, and therefore will still be available to the reader.

We highlighted from the step 4 to step 6.4.3 by adding a gray shade to the text. We believe these steps are crucial because they contain the necessary modifications from conventional flower-dipping methods used for *Arabidopsis thaliana*.

17. Please ensure that the highlighted steps form a cohesive narrative with a logical flow from one highlighted step to the next. Please highlight complete sentences (not parts of sentences). Please ensure that the highlighted part of the step includes at least one action that is written in imperative tense.

[Please see our response to the comment #16.](#)

18. Discussion: Please also discuss any limitations of the technique.

[The transformation efficiency lower than the most popular model plant *Arabidopsis thaliana* \(ecotype Col-0\) can be considered as a limitation. We added a more detailed discussion on this point.](#)

19. References: Please do not abbreviate journal titles.

[We revised the references as instructed.](#)

...

Reviewers' comments:

Reviewer #1:

Manuscript Summary:

This submission describes a plant transformation protocol that is suitable for use with *Schrenkiella parvula*, a highly stress tolerant extremophile relative of the far less stress tolerant genetic model plant, *Arabidopsis thaliana*. To fully exploit a species as a genetic model, it is essential to have a way of manipulating genes to validate their role(s) in generating a particular phenotypic response. An impediment to exploiting *S. parvula* has been the virtual absence of a transformation protocol. One commonly used approach that works well for *Arabidopsis* involved dipping flowers into a solution containing *Agrobacterium* carrying a cloned gene of interest. As the authors point out, not only has the conventional approach for transforming *S. parvula* been problematic, the plant continues to flower after the dipping is done and the screening for successfully transformed T0 plants is complicated by a screening strategy that leaves many false positives among very few true transformants. These are all deterrents to using *S. parvula* for finding genes associated with stress tolerance despite the extraordinary physiological stress tolerance features that this plant displays and the excellent genomic tools available for its study. The solutions to these concerns that this protocol provides make sense and are laid out clearly: multiple dipping treatments works well with a plant that is difficult to transform and has indeterminate flowering (and more chances to generate transgenic seeds) and considering the narrow leaves and wax as impediments to the penetration of a selection agent are factors that should be obvious...but no doubt also easily overlooked. The protocol will offer suggestions to those working with other extremophytes that suffer from poor transformation and/or

selection efficiencies and this should increase the research promise of other plants highly adapted to environmental stress.

The protocol is well written, the authors highlight steps that require extra precautions and they provide reasons why following the precautions yields better results. The title describes the contents of the manuscript well. It might be advantageous for the authors to include a former name in the keywords, for example, as changes in the taxonomy for several extremophytes has made for confusion in the literature. The illustrations are also clear and support the text well.

Thank you for the comments. Per reviewer's suggestion, we included two former names of the extremophyte, *Eutrema parvulum* and *Thellungiella parvula*, among the keywords.

Major Concerns:

No major concerns. The protocol is detailed and the results are described well. Although a recovery of 3 or 4 transformants from 10,000 seeds may seem problematic, this low recovery approximates the rates obtained for some *Arabidopsis* ecotypes that are also considered recalcitrant to transformation (eg. C24). It may well be that some of the floral features that make *S. parvula* resistant to transformation could be some of the same features that allows the plant to resist extreme stresses. However, that consideration cannot be addressed without having at least some means of generating transgenics in the first place. Finally, this submission also provides an important benchmark against which researchers can compare differences related to the use of other strains/plasmids/treatment conditions to devise an improved recovery of transformants in the future.

Minor Concerns:

There is a lot of good information and detail on how to propagate healthy plants. In that regard, it would be useful if the authors named the soil they used in the text as it only seems to be named in the list of supplies. Can any soil be used equally well or is the one given the only suitable substrate?

We appreciate the reviewer's comment. However, we were advised not to use commercial names in the main text, hence the reference to the exact soil mix was only in the list of supplies. In our experience, any soil mix where *Arabidopsis thaliana* can grow will also work for *S. parvula*. We added this information as a note to the step 1.3.1

...

Reviewer #2:

Manuscript Summary:

The manuscript by Dassanayake et al. focuses on a transformation protocol for *Schrenkiella*

parvula, a halophytic relative of Arabidopsis thaliana. Along with the related Eutrema salsugineum, S. parvula has been developed as a powerful tool for comparative physiological, biochemical and molecular analysis of adaptive mechanisms that allow plants to cope highly saline conditions. Such are the importance of these two halophytes, that they have been declared as new model organisms (Zhu et al., 2015, The next top models. Cell 163: 18-20). The development of functional genomics tools and protocols is essential to further the development of these model halophytes, and therefore this manuscript is not just another transformation protocol for an extra plant species but a critical platform to further our understanding of salt tolerance mechanisms in halophytes.

Overall the protocol described in the manuscript can be clearly followed and the figures nicely augment the written protocol to provide an excellent visual aid as well as confirming transformation.

Major Concerns:

None.

Minor Concerns:

1. My only question is whether PCR of the Bar gene alone is sufficient to prevent false positives, as plants can sometime be transformed with the selective marker but not with the target gene (or the target gene can suffer deletions/insertion etc). Would it not be wise to add that PCR with target gene-specific primers should be performed on the plants exhibiting the presence of the Bar gene?

We appreciate the reviewer's comment. We have also confirmed our transformants using one primer from the Bar gene and another from the target sequences. We added this as a recommendation in the note to the step 6.5.3 in the revised manuscript.

2. There are numerous English grammatical mistakes and erroneous use of terminology. While I understand that the manuscript will be copy-edited, I want to point out the terminological errors:

(a) Lines 140, 181 and 190: Bacteria are not "poured" onto plates or "dissolved" in liquid media. The plates or liquid are "inoculated" with bacteria.

(b) Lines 197-198: Bacterial pellets are not "dissolved" in a solution. They are "re-suspended".

We thank the reviewer for pointing out these. We have revised those two points as well as the entire procedures to replace casual languages to more appropriate scientific terms.