

## GENE ASSEMBLY IN AGROBACTERIUM VIA NUCLEIC ACID TRANSFER USING RECOMBINASE TECHNOLOGY (GAANTRY)

*Tashkent State Technical University named after Islam Karimov*  
**Hamidullayev F. L**  
*hamidullayevfatxulla@gmail.com*  
*National University of Uzbekistan named after Mirzo Ulug`bek*  
*Military training reading center*  
*p/p-k Kurbonov G.A.*  
*m-r Axatov.S.A*

**Abstract** Plant biotechnology provides a means for the rapid genetic improvement of crops including the enhancement of complex traits like yield and nutritional quality through the introduction and coordinated expression of multiple genes. GAANTRY (gene assembly in Agrobacterium by nucleic acid transfer using recombinase technology) is a flexible and effective system for stably stacking multiple genes within an Agrobacterium virulence plasmid transfer DNA (T-DNA) region. The system provides a simple and efficient method for assembling and stably maintaining large stacked constructs within the GAANTRY ArPORT1 Agrobacterium rhizogenes strain. The assembly process utilizes unidirectional site-specific recombinases in vivo and an alternating bacterial selection scheme to sequentially assemble multiple genes into a single transformation construct. A detailed description of the procedures used for bacterial transformation, selection, counter selection, and genomic PCR validation with the GAANTRY system are presented. The methods described facilitate the efficient assembly and validation of large GAANTRY T-DNA constructs. This powerful, yet simple to use, technology will be a convenient tool for transgene stacking and plant genetic engineering of rice and other crop plants.

**Key words** Plant biotechnology, Transformation, Agrobacterium rhizogenes, Transfer DNA (T-DNA), Transgene assembly, Site-specific recombination, Gene stacking, Virulence plasmid, Genetic engineering

**Introduction** Plant research has utilized Agrobacterium-mediated plant transformation as a means of plant genetic engineering for more than 30 years. In most

instances one or a few genes are introduced into the plant genome, but recently the assembly of large transformation constructs that carry multiple genes has been desired. Unfortunately, it is typically challenging to construct and efficiently transform plants with large constructs carrying five or more genes. Since the *in vitro* manipulation of large constructs can be difficult and/or inefficient to perform using traditional cloning techniques, a variety of alternative approaches have been developed for stacking multiple genes together. Strategies employing rare-cutting homing endonucleases, commercial cloning systems (i.e., multisite Gateway), Gibson assembly, type IIS restriction enzymes, homologous recombination in yeast, the Cre site-specific recombinase, as well as combinations of these methods have been developed. Although these efforts have been shown to successfully produce large and complex constructs, these systems all utilize either a binary vector plasmid or a binary bacterial artificial chromosome plasmid vector as the transformation construct and have frequently exhibited inefficient assembly processes and/or instability problems in *E. coli* or *Agrobacterium*. Also, relatively few of these approaches have been shown to develop large stacked constructs that efficiently generate low copy, high-quality stable transgenic plants with all of the expected functional phenotypes. Recently, we designed and constructed the gene assembly in *Agrobacterium* via nucleic acid transfer using recombinase technology (GAENTRY) system and demonstrated its capacity to sequentially stacking ten cargo sequences within the virulence plasmid T-DNA of the *Agrobacterium rhizogenes* strain ArPORT1 (Fig. 1) [14]. The GAENTRY assembly process utilizes three unidirectional site-specific recombinases *in vivo* and an alternating bacterial selection scheme to iteratively build multiple genes into a transfer DNA (T-DNA). Below we provide a detailed description for a simplified protocol for GAENTRY assembly and strain validation. This powerful, yet simple to use, transgene stacking technology will be a valuable tool for plant genetic engineering of rice and other crop plants.

The GAENTRY system requires only a recipient *Agrobacterium* strain and four plasmid vectors for construct assembly [14]. 1. The ArPORT1 bacterial strain is a

kanamycin-resistant *Agrobacterium rhizogenes* GAANTRY recipient strain. It is a disarmed strain (where the native T-DNA has been removed from the pRi virulence plasmid) and is *recA* making it deficient in homologous recombination. The *recA* gene was inactivated using a tetracycline resistance marker and homologous recombination. Although the strain is resistant to 5 mg/L tetracycline, the antibiotic is not typically used for selection. The strain contains a 320 base pair (bp) sequence of the left border region of *Agrobacterium tumefaciens* strain C58 (including the 25 bp LB direct repeat), the 56 bp A118 attP recognition site, the *nptIII* gene conferring bacterial kanamycin resistance, and the 106 bp ParA single multimer resolution site (MRS) in place of the native T-DNA.

The BandP “Donor” vectors carry attB (or attP) recombinase recognition sites respectively. In short, the A118 and TP901-1 recombinase recognition sites flank a cloning region in each plasmid where cargo sequence(s) of interest can be inserted. The cloning region includes a large number of unique restriction recognition sites for traditional restriction enzyme-based cloning of sequences of interest. The donor plasmids also contain a kanamycin or gentamicin bacterial resistance marker, respectively, as well as the *sacB* negative selection marker (conferring sucrose sensitivity) and a ParA MRS recognition sequence. Diagrams of the B and P Donor plasmids are shown in Fig. 2. The complete annotated plasmid sequences for the B Donor (MG687272) and P Donor (MG687284) plasmids are available from GenBank. Note, Donor vectors that enable Gateway or Golden Gate cloning of cargo sequences are also available [14]. (b) The B and P “Helper” plasmids confer ampicillin resistance in *E. coli* and carry an operon expressing either the A118 and ParA or the TP901-1 and ParA recombinase enzymes, respectively. The annotated plasmid sequences for the BandP Helper vectors are available from GenBank (MG687274, MG687275).

## 2.2 Growth Medium, Culture Conditions, and Equipment

1. Low-salt Luria-Bertani (LB) medium: 10 g/L Bacto Tryptone, 5 g/L yeast extract, and 5 g/L NaCl. Adjust pH to 7.5 with sodium hydroxide (NaOH) and sterilize by autoclaving. For LB solid medium add 10 g of Bacto agar prior to autoclaving.

Supplement LB medium with appropriate antibiotics for plasmid selection in *E. coli* and strain selection in *Agrobacterium* (see item 3).

2. LB solid medium with 5% (w/v) sucrose: LB medium (as described above) with 50 g/L sucrose added and the appropriate antibiotic.

3. Antibiotics gentamicin, kanamycin, and carbenicillin. For plasmid selection in *E. coli*, 10 mg/L gentamicin is used, while 100 mg/L gentamicin is for selecting GAENTRY *Agrobacterium* ArPORT1 strains. For both *E. coli* and *Agrobacterium*, 50 mg/L kanamycin is used for selection. Carbenicillin at 100 mg/L is the concentration used for selecting the helper plasmids in *E. coli*.

4. Incubator/shaker at 30 and 37 C.

5. Eppendorf ThermoMixer.

6. Microcentrifuge.

7. Electroporation cuvettes (2 mm gap).

8. Gene Pulser electroporation apparatus.

9. PCR thermocycler.

10. Agarose gel electrophoresis apparatus

### **Preparation of Donor and Helper Plasmids**

1. To insert cargo DNA sequences within the Donor plasmids, manipulate P and B Donor vectors using standard cloning and *E. coli* microbiological techniques.

2. To prepare the plasmids, streak desired clones for single colony selection from a 80 C glycerol stock onto LB plates with the appropriate antibiotic selection.

3. Transfer a single colony to 5 ml of LB liquid broth with appropriate selection in a 15 ml snap-cap tube and incubate overnight at 37 C under continuous shaking (250 rpm).

4. Harvest the cells by centrifugation at 10,000 g and follow a protocol of choice for mini plasmid preparation (e.g., the Zymo Research ZR Plasmid Miniprep protocol or a similar product from other vendors) (see Note 1). Prior to use, dilute the Donor and Helper plasmids in water to a 50 ng/ $\mu$ l concentration.

### **Preparation of the Electrocompetent ArPORT1 Recipient Strain**

To prepare the electrocompetent cells, streak GAENTRY A. rhizogenes ArPORT1 recipient strain on LB medium to produce individual isolated colonies. Antibiotic selection will depend on the desired recipient strain. For the original strain or strains carrying two or other even numbered stacks of cargo, the antibiotic selection will be 50 mg/L kanamycin. Alternatively, if the desired strain contains odd numbered stacks of cargo, the appropriate selection will be 100 mg/L gentamicin. 2. Transfer a single colony to 5 ml LB medium with suitable selection in a 15 ml snap-cap tube and incubate at 30 C under continuous shaking (250 rpm) for 16–18 h ( $OD_{600} > 1.5$ ). 3. Dilute the overnight culture by adding 150  $\mu$ l of culture to 1.35 ml of nonselective LB medium in a 1.5 ml microcentrifuge tube. Make four tubes per transformation. 4. Place tubes in an Eppendorf ThermoMixer at 30 C and 900 rpm for 3–4 h until the density reaches  $OD_{600} \approx 0.4$ –0.6 (see Note 3). 5. When the desired optical density is reached, centrifuge the cells at 1000 g for 5 min at room temperature. 6. Discard the supernatant and gently resuspend the cells in 100  $\mu$ l of sterile water. Combine the four tubes. The cultures are kept at room temperature and all the procedures are performed at room temperature (~22–24 C) from this point on. 7. Add 1 ml of sterile water to the combined cell suspension. 8. Centrifuge at 1000 g for 5 min, and then pour off the supernatant. 9. Wash the cells one more time by repeating steps 7 and 8. 10. Resuspend cells in 50  $\mu$ l of sterile water and use for immediate electroporation.

It is important to use freshly prepared plasmid DNA, especially when the cargo size is >10 kilobase pairs, since large Donor constructs recombine less efficiently. Transformation efficiency is also significantly reduced when old or poor-quality plasmid samples containing predominantly non-supercoiled plasmid DNA are used. 2. Multiple different methods for the generation of electrocompetent cells can successfully be used with GAENTRY assembly; however it is recommended that the room temperature method described by Tu and colleagues (see Subheading 3.2) be used for Donor plasmid constructs that are greater than 15 kilobases in size [16]. If electrocompetent cells are being premade for archiving at 80 C and later use with modestly sized donor vectors, then the method described by Collier and colleagues is

preferred. 3. The best transformation efficiency occurs when cells in log phase growth (OD<sub>600</sub>  $\frac{1}{4}$  0.4–0.6 which typically takes 3–4 h of growth at 30 C after starting from a saturated culture) are used. The transformation efficiency drops if the bacterial cells grow beyond an OD<sub>600</sub>  $\frac{1}{4}$  0.6.

For optimal results, the cells should be used immediately for electroporation. Tu and colleagues reported a 30% loss in transformation efficiency when the cells were stored at room temperature for 1 h, ~60% loss after 4 h, and ~80% loss after 24 h [16].

5. Proper transformation occurs when no arcing within the electroporation cuvette is observed and a time constant of 4–5 ms is obtained. If the sample arcs, there is likely too much salt in the bacterial mixture or the plasmid DNA. To avoid this problem, use water to elute the plasmid DNA from the purification column (not the elution buffer provided in the plasmid isolation kit). If arcing persists, and the DNA was eluted in water, it is possible that the competent cells were not washed thoroughly enough; therefore, add an additional washing step (see Subheading 3.2, steps 7 and 8) to remove residual salts. Samples that arc within the electroporation cuvette typically will not produce colonies on the selection plate.

6. Plating the cells directly on medium with 5% w/v sucrose after transformation (skipping the initial selection on medium without sucrose) is not recommended. This will significantly decrease the number of colonies recovered and can lead to the recovery of clones that have not undergone complete GAENTRY-mediated integration and excision.

7. The GAENTRY stacking system relies on the iterative toggling between kanamycin and gentamicin resistance to insert additional sequences of interest; therefore, if a cargo sequence that expresses nptII in *Agrobacterium* is inserted into the T-DNA, it will block the ability to effectively use kanamycin selection for the insertion of additional cargo sequences. For example, inserting a CaMV35S promoter-nptII-nos terminator cargo sequence into ArPORT1 will confer kanamycin resistance, making the strain constitutively resistant to kanamycin. This will block the ability to use this strain for the insertion of additional cargo sequences carried in a P Donor plasmid. This phenomenon will be detected in the normal screening process by recovering colonies that are sucrose insensitive, but

perpetually retain resistance to kanamycin. There are at least three ways to avoid this problem: (1) use promoter sequences on nptII cargo that do not express in *Agrobacterium*; (2) place a plant intron within the nptII coding sequence, blocking bacterial translation of a functional kanamycin resistance protein; or (3) stack the nptII-containing cargo sequence into the gene assembly last (when no more additional cargo needs to be added). Note, a similar problem will exist if a cargo sequence conferring bacterial resistance to gentamicin is added to the ArPORT1 T-DNA.

Sample a colony using a 20 µl micropipette tip held vertically at a 90° angle relative to the petri plate. Touch the colony lightly to ensure that only a small number of cells are removed. Picking up too many bacteria can inhibit the PCR reaction or cause nonspecific amplification products to appear. 9. To allow the use of a single thermocycling program for screening with multiple PCR reactions, it is worthwhile to design primers with similar annealing temperatures and to make the amplicon sizes for each junction a unique size between 300 and 2000 base pairs. Choosing the size of the amplicon such that it is unique to each of the newly formed junctions enables the size of each amplicon to be diagnostic for a particular GAENTRY assembled sequence during agarose gel electrophoresis. In addition, it is also useful to design a pair of primers that can be used as a positive control for ArPORT1 strain genomic DNA. This primer pair can be used as a positive control PCR reaction from any ArPORT1 DNA sample. Since this simple genomic isolation procedure can fail by taking too many or too few bacterial cells (see Note 8), it is helpful to include a positive control PCR amplification reaction to validate that each genomic DNA sample is of sufficient quantity and quality for amplification. 10. The PCR extension time can vary depending on the type of polymerase that is used and the size of the expected amplicon. Typically, 1 min of extension at 68 °C is used per kilobase of amplicon for Taq polymerase but follow the polymerase manufacturer's instructions when designing the thermocycler amplification program.

## REFERENCES

1. Gelvin SB (2003) Agrobacterium-mediated plant transformation: the biology behind the “gene-jockeying” tool. *Microbiol Mol Biol Rev* 67(1):16–37
2. Vain P (2007) Thirty years of plant transformation technology development. *Plant Biotechnol J* 5(2):221–229. <https://doi.org/10.1111/j.1467-7652.2006.00225.x>
3. Dafny-Yelin M, Tzfira T (2007) Delivery of multiple transgenes to plant cells. *Plant Physiol* 145(4):1118–1128. <https://doi.org/10.1104/pp.107.106104>
4. Ma L, Dong J, Jin Y, Chen M, Shen X, Wang T (2011) RMDAP: a versatile, ready-to-use tool box for multigene genetic transformation. *PLoS One* 6(5):e19883. <https://doi.org/10.1371/journal.pone.0019883>
5. Weber E, Engler C, Gruetzner R, Werner S, Marillonnet S (2011) A modular cloning system for standardized assembly of multigene constructs. *PLoS One* 6(2):e16765. <https://doi.org/10.1371/journal.pone.0016765>
6. Untergasser A, Bijl GJM, Liu W, Bisseling T, Schaart JG, Geurts R (2012) One-step Agrobacterium mediated transformation of eight genes essential for Rhizobium symbiotic signaling using the novel binary vector system pHUGE. *PLoS One* 7(10):e47885. <https://doi.org/10.1371/journal.pone.0047885>
7. Zeevi V, Liang Z, Arieli U, Tzfira T (2012) Zinc finger nuclease and homing endonuclease-mediated assembly of multigene plant transformation vectors. *Plant Physiol* 158 (1):132–144. <https://doi.org/10.1104/pp.111.184374>
8. Buntru M, G€artner S, Staib L, Kreuzaler F, Schlaich N (2013) Delivery of multiple trans genes to plant cells by an improved version of GAANTRY Gene Stacking 17 MultiRound Gateway technology. *Transgenic Res* 22(1):153–167. <https://doi.org/10.1007/s11248-012-9640-0>
9. Binder A, Lambert J, Morbitzer R, Popp C, Ott T, Lahaye T, Parniske M (2014) A modular plasmid assembly kit for multigene expression, gene silencing and silencing rescue in plants. *PLoS One* 9(2):e88218. <https://doi.org/10.1371/journal.pone.0088218>
10. Shih PM, Vuu K, Mansoori N, Ayad L, Louie KB, Bowen BP, Northen TR, Loque D (2016) A robust gene-stacking method utilizing yeast assembly for plant synthetic biology. *Nat Commun* 7:13215. <https://doi.org/10.1038/ncomms13215>
11. Cermak T, Curtin SJ, Gil-Humanes J, Egan R, Kono TJY, Konecna E, Belanto JJ, Starker CG, Mathre JW, Greenstein RL, Voytas DF (2017) A multi-purpose toolkit to enable advanced genome engineering in plants. *Plant Cell*. <https://doi.org/10.1105/tpc.16.00922>
12. Zhang H-Y, Wang X-H, Dong L, Wang Z-P, Liu B, Lv J, Xing H-L, Han C-Y, Wang X-C, Chen Q-J (2017) MISSA 2.0: an updated synthetic biology toolbox for assembly of orthogonal CRISPR/Cas systems. *Sci Rep* 7:41993. <https://doi.org/10.1038/srep41993>



13. Zhu Q, Yu S, Zeng D, Liu H, Wang H, Yang Z, Xie X, Shen R, Tan J, Li H, Zhao X, Zhang Q, Chen Y, Guo J, Chen L, Liu Y-G (2017) Development of “purple endosperm rice” by engineering anthocyanin biosynthesis in the endosperm with a high-efficiency transgene stacking system. *Mol Plant* 10(7):918–929. <https://doi.org/10.1016/j.molp.2017.05.008>
14. Collier R, Thomson JG, Thilmony R (2018) A versatile and robust *Agrobacterium*-based gene stacking system generates high-quality transgenic *Arabidopsis* plants. *Plant J* 95 (4):573–583. <https://doi.org/10.1111/tbj.13992>
15. Green MR (2012) In: Green MR, Sambrook J (eds) *Molecular cloning : a laboratory manual*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. Volume accessed from <https://nla.gov.au/nla.cat-vn6039452>
16. Tu Q, Yin J, Fu J, Herrmann J, Li Y, Yin Y, Stewart AF, Muller R, Zhang Y (2016) Room temperature electrocompetent bacterial cells improve DNA transformation and recombination efficiency. *Sci Rep* 6:24648. <https://doi.org/10.1038/srep24648>
17. Sallaud C, Meynard D, van Boxtel J, Gay C, Bes M, Brizard JP, Larmande P, Ortega D, Raynal M, Portefaix M, Ouwerkerk PB, Rueb S, Delseny M, Guiderdoni E (2003) Highly efficient production and characterization of T-DNA plants for rice (*Oryza sativa* L.) functional genomics. *Theor Appl Genet* 106(8):1396–1408. <https://doi.org/10.1007/s00122-002-1184>