Review

T-DNA direct repeat, vector backbone and gene trap counter selection by a new vector (pNU435) for high throughput functional genomics

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The nature of T-DNA/Ds insertion decides the utility of launch pad lines for iAc/Ds based insertional mutagenesis. Direct or inverted T-DNA/Ds repeats and insertions with vector backbone lead to poor recovery of flanking sequences; whereas T-DNA/Ds insertion leading to gene trap would limit the use of such launch pad lines. A new Ds tagging/trapping vector, pNU435 containing two copies of intron-interrupted barnase was used in tomato to counter select such T-DAN/Ds insertions. T₁ and T₂ plants generated in this study were devoid of direct repeats, vector backbone and gene traps as evidenced by the lack of barnase expression. Further evidence based on the LB flanking sequence recovered through TAIL-PCR did not show any vector backbone or direct repeats. But two out of six plants showed inverted repeats. Genome search with LB flanking sequence indicated that the insertions were not in genic region, and hence not led to gene traps. pNU435 with features for counter selecting undesirable T-DNA/Ds insertions can be employed for high throughput functional genomics.

Key words: pNU435 vector, T-DNA/*Ds* insertion, *barnase*, tomato, flanking sequence, functional genomics.

INTRODUCTION

Functional genomics aims at assigning function to genes and their regulatory elements of a genome by various approaches (Hirochika et al., 2004; Krishnan et al., 2009) such as comparative genomics, transcriptome analysis, mutagenesis, gene silencing and FOX (full length cDNA over-Expression) hunting (Nakamura et al., 2007), etc. Mutagenesis is a direct way of discovering novel genes and regulatory elements involved in various biological processes. High throughput functional genomics using maize Ac/Ds system has been widely employed for insertional tagging in various crops (Bancroft et al., 1992: Enoki et al., 1999). Insertional inactivation with Ds requires large scale production of launch pad lines harbouring T-DNA/Ds. Further, mobilization of Ds is brought about by crossing with iAc lines. Launch pad line with a single copy, clean T-DNA/Ds insertion [without vector backbone (VB) and repeats] and insertion not being

a gene trap is considered as most useful in insertional inactivation. Earlier efforts have observed that about 30-60% of launch pad lines contain T-DNA repeats (direct and inverted) and vector backbones, and such plants are prone to post-integration rearrangements and gross deletions (Jeon et al., 2000; Upadhyaya et al., 2002; Kim et al., 2003; Eamens et al., 2004; Sallaud et al., 2004). Also rescuing the sequence flanking T-DNA is very difficult or in some cases impossible in such lines.

Since T-DNA has preferential insertion in gene-rich regions when compared with repetitive DNA, significantly large number of launch pad lines can be expected to be gene traps (Jeon et al., 2000; Upadhyaya et al., 2002; Kim et al., 2003; Eamens et al., 2004; Sallaud et al., 2004). In rice, ~23% of launch pad lines were gene traps (Eamens et al., 2004). T-DNA/Ds gene traps might result in untagged mutations in the stable mutant derived from such launch pad lines. Though the copy number is not under control, recovering clean integration of T-DNA/Ds without any gene traps could be manipulated by improvising the vectors used for developing launch pad

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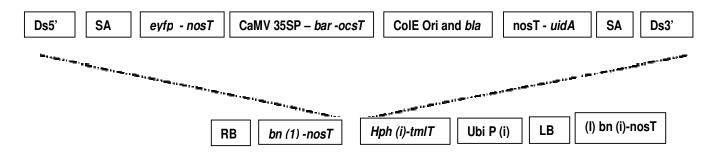


Figure 1. T-DNA/*Ds* of pNU435. 1. A promoterless intron interrupted *barnase-nos*T cassette placed next to RB to serve as T-DNA/*Ds* direct repeat (RB–LB–RB and LB) counter selector and T-DNA/*Ds* gene trap counter selector; 2: maize ubiquitin promoter-first exon-modified intron (with LB repeat sequences incorporated)-intron interrupted *barnase* [bn (i)]-*nos*T, to serve as vector backbone counter selector.

lines. Bidirectional gene trap constructs (Eamens, et al. 2004) utilizing an intron-interrupted *barnase* gene as a VB counter selector outside the T-DNA region of pEU334AN or pEU334BN could reduce the VB containing T-DNA/Ds lines (Hanson et al., 1999). However, ~27% lines still contained direct or inverted repeats of T-DNA. Therefore, Upadhyaya et al. (2006) constructed a *Ds* vector, pNU435 (Gen Bank Acc. No. DQ225750) by incorporating features that can counter select lines with T-DNA/Ds direct repeat, insertion with VB, and insertion in genic region (gene trap).

However, till date pNU435 has not been tested and validated for its aforesaid activities in any of the systems. In the present study, an effort was made to check T-DNA/Ds direct repeat, vector backbone and gene trap counter selection activity of *Ds* vector, pNU435 in tomato. pNU435 (kindly donated by Dr. Narayana Upadhyaya, CSIRO Plant Industry, Canberra, Australia) contained two copies of intron-interrupted barnase; one in the VB immediately after ubiquitin promoter-LB sequence and the other immediately after the RB sequence (Figure 1) to counter-select transformants with either VB or direct repeat of T-DNA/Ds. barnase placed next to RB would also counter select regenerants with T-DNA/Ds integration in genic region (gene trap). Seeds of Pusa Ruby cultivar of tomato were sown in vitro on half strength MS media (Murashige and Skoog, 1962). Seven-day old cotyledonary leaves were used for cocultivation by following the standard protocol of Agrobacterium-mediated transformation (McCormick, 1991). Co-cultivated cotyledonary leaves were transferred to regeneration medium (MS with 3% sucrose, 2 mg/l zeatin, 0.1 mg l⁻¹ IAA, 200 μg ml⁻¹ cephotaxime). Shoots were transferred to MS basal medium supplemented with 0.05 mg/l of IBA for rooting. Transgenic plants were confirmed by gus-specific PCR (RB59 GUS F 5' TCACCGAAGTTCATGCCAGTCC 3' and RB59 GUS R2 5' ACGCTCACACCGATACCATCAG 3') (Figure 2).

Barnase is a bacterial protein with 110 amino acids possesses ribonuclease activity (Hartley, 1988). It is lethal to

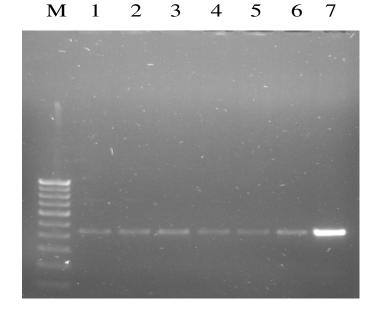


Figure 2. Agarose gel electrophoresis of products amplified by *gus*-specific PCR. Lane M, 100 bp DNA ladder; lanes 1-6, promoter trap lines (PT1, PT2, PT3, PT4, PT5 and PT6); lane 7, Pnu 435 (positive control).

the cell when expressed without its inhibitor barstar. T-DNA/Ds integration in genic region leading to either promoter or gene trap would express barnase resulting in cell death. Also in any T-DNA insertion with direct repeat (RB-LB-RB and LB) or with vector backbone (LB-VB), ubiquitin promoter would drive barnase gene. But in this study, transgenic plants were normal (without cell/tissue death) and did not show barnase expression upon RT-PCR (data not shown) indicating that T-DNA/Ds insertion was neither a gene trap, nor associated with direct repeat or vector backbone. Further confirmation that T-DNA/Ds insertion was not in geneic region came from right border flanking sequence tag (FST) of T-DNA/Ds as recovered by TAIL-PCR (Liu et al., 1995) in randomly selected two plants (PT4 and PT5). These FSTs showed homology to



Figure 3. T₂ plants resistant to Basta. A, Parent (Pusa Ruby); B, Progenies of PT4.

- 1 CAACGACTGA CTGTAGTATT AGGGGATTAG AGTGTCACGT TCCGACACAA TAAGAATAAA GAGAATGAAT
- A 71 CTGGAATTAT GTTAATATAC TCAATTTAAA GAACCTATTT CCCAAGTGAG TATGGTGTGG
 AGGCTTGAGT
 - 141 CCTCATAGGT GTGCTCGGTG TTGACGCCTA TCCTGAAAAA
- B 1 ACGAGCTGAC ATGTAGTATT AGGGGATTAG AGTGTCACGT TCCGACACAA TAAGACTAAA GAGAATGAAT
 - 71 CTGGAATTAT GTTAATATAC TCAATTTAAA GAACCTATTT CCCAAATGAG TATGGTGTGG
 AAGCTTGTGA
 - 141 CCCCTCATAG GTGTGCTCAA AGTTGACCCC CTATCCTGCA

Figure 4. Left border flanking sequence tag obtained from PT4 (A) and PT5 (B).

RB, indicating the possibility of inverted repeats (LB-RB-RB and LB). This was further tested among the progenies (T₂) of PT4 and PT5. T₂ plants were first confirmed for the presence of T-DNA/Ds by spraying BASTA. Majority of the plants could survive the selection (Figure 3). Left border FSTs (Figure 4) recovered using TAIL-PCR in T₂ progenies showed neither repeat nor vector backbone. PT4 and PT5 were therefore confirmed to contain LB-RB-RB and LB inverted repeats without any vector backbone.

Regeneration of such lines with inverted repeats is possible since pNU435 can counter select only direct repeats, but not inverted repeats. BLAST search of these FSTs against tomato genome showed that T-DNA/Ds insertion was in retrotransposons like Tork-1 and Jinling-2, but not in any genic region. Therefore, PT4 and PT5, like other plants tested in this study, were confirmed not to be gene traps. Launch pad line with already one of its genes insertionally-tagged/trapped with T-DNA/Ds, is not generally employed for generating Ds tagged mutants for functional genomics (Sallaud et al., 2004). Reason being,

such mutants might carry empty T-DNA (without *Ds*) and *Ds* tags in two different genes leading to untagged mutations. To the best of our knowledge, pNU435 is the only T-DNA/*Ds* vector available to counter select T-DNA/*Ds* direct repeat, vector backbone and gene trap. Majority of the cells upon transformation with pNU435 may not regenerate due to complex insertions, where barnase would express and kill the cell. This was reflected in this study by the relatively low regeneration frequency compared to that obtained with other constructs (data not shown). Thus pNU435 with features for counter selecting undesirable T-DNA insertions at cell level would save time and resources in checking the events for generating launch pad lines for high throughput functional genomics.

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REFERENCES

- An S, Park S, Jeong DH, Lee DY, Kang HG, Yu JH, Hur J, Kim SR, Kim YH, Lee M, Han S, Kim SJ, Yang J, Kim E, Wi SJ, Chung HS, Hong JP, Choe V, Lee HK, Choi JH, Nam J, Kim SR, Park PB, Park KY, Kim WT, Choe S, Lee CB, An G (2003). Generation and analysis of end sequence database for T-DNA tagging lines in rice. Plant Physiol., 133: 2040-2047.
- Bancroft I, Bhatt AM, Sjodin C, Scofield S, Jones JD, Dean C (1992). Development of an efficient two-element transposon tagging system in Arabidopsis thaliana. Mol. Gen. Genet., 233: 449-461.
- Chen S, Jin W, Wang M, Zhang F, Zhou J, Jia Q, Wu Y, Liu F, Wu P (2003). Distribution and characterization of over 1000 T-DNA tags in rice genome. Plant J., 36: 105-113.
- Eamens AL, Blanchard CL, Dennis ES, Upadhyaya NM (2004). A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice (*Oryza sativa* L.). Plant Biotechnol. J., 2: 367-380.
- Enoki H, Izawa T, Kawahara M, Komatsu M, Koh S, Kyozuka J, Shimamoto K (1999) Ac as a tool for the functional genomics of rice. Plant J, 19: 605-613
- Hanson B, Engler D, Moy Y, Newman B, Ralston E, Gutterson N (1999). A simple method to enrich an Agrobacterium-transformed population for plants containing only T-DNA sequences. Plant J., 19: 727-734
- Hartley RW (1988) Barnase and barstar. Expression of its cloned inhibitor permits expression of a cloned ribonuclease. J. Mol. Biol., 202: 913-915.
- Hirochika H, Guiderdoni E, An G, Hsing YI, Eun MY, Han CD, Upadhyaya N, Ramachandran S, Zhang Q, Pereira A, Sundaresan V, Leung H (2004). Rice mutant resources for gene discovery. Plant Mol. Biol., 54: 325-334.
- Hsing YI, Chern CG, Fan MJ, Lu PC, Chen KT, Lo SF, Sun PK, Ho SL, Lee KW, Wang YC (2007). A rice gene activation/knockout mutant resource for high throughput functional genomics. Plant Mol. Biol., 63: 351-364.
- Jeon JS, Lee S, Jung KH, Jun SH, Jeong DH, Lee J, Kim C, Jang S, Lee S, Yang K, Nam J, An K, Han MJ, Sung RJ, Choi HS, Yu JH, Choi JH, Cho SY, Cha SS, Kim SI, An G (2000). T-DNA insertional mutagenesis for functional genomics in rice. Plant J., 22: 561-570.
- Jeong DH, An S, Park S, Kang HG, Park GG, Kim SR, Sim J, Kim YO, Kim MK, Kim SR, Kim J, Shin M, Jung M, An G (2006). Generation of a flanking sequence-tag database for activation-tagging lines in japonica rice. Plant J., 45: 123-132.

- Kim SR, Lee J, Jun SH, Park S, Kang HG, Kwon S, An G (2003). Transgene structures in T-DNA-inserted rice plants. Plant Mol. Biol., 52: 761-773.
- Krishnan A, Guiderdoni E, An G, Hsing YC, Han C, Lee MC, Yu SM, Upadhyaya N, Ramachandran S, Zhang Q (2009). Mutant Resources in Rice for Functional Genomics of the Grasses. Plant Physiol., 149: 165.
- Liu YG, Mitsukawa N, Oosumi T, Whittier RF (1995). Efficient isolation and mapping of Arabidopsis thaliana T-DNA insert junctions by thermal asymmetric interlaced PCR. Plant J., 8: 457-463.
- McCormick S (1991). Transformation of tomato with Agrobacterium tumefaciens. Plant Tiss. Cult. Manual., 6: 1-9.
- Murashige T, Skoog F (1962). A revised medium for rapid growth and bioassay with tobacco tissue cultures. Physiol. Plant., 15: 473-497.
- Nakamura H, Hakata M, Amano K, Miyao A, Toki N, Kajikawa M, Pang J, Higashi N, Ando S, Toki S, Fujita M, Enju A, Seki M, Nakazawa M, Ichikawa T, Shinozaki K, Matsui M, Nagamura Y, Hirochika H, Ichikawa H (2007). A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. Plant Mol. Biol., 65: 357-371.
- Sallaud C, Gay C, Larmande P, Bes M, Piffanelli P, Piegu B, Droc G, Regad F, Bourgeois E, Meynard D, Perin C, Sabau X, Ghesquiere A, Glaszmann JC, Delseny M, Guiderdoni E (2004). High throughput T-
- DNA insertion mutagenesis in rice: a first step towards in silico reverse genetics. Plant J., 39: 450-464.
- Upadhyaya NM, Zhou XR, Zhu QH, Ramm K, Wu L, Eamens AL, Sivakumar R, Kato T, Yun DW, Santhoshkumar C, Narayanan KK, Peacock JW, Dennis ES (2002). An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. Funct. Plant Biol., 29: 547-559.
- Upadhyaya NM, Zhu QH, Zhou XR, Eamens AL, Hoque MS, Ramm K, Shivakkumar R, Smith KF, Pan ST, Li S, Peng K, Kim SJ, Dennis ES (2006). Dissociation (Ds) constructs, mapped Ds launch pads and a transiently-expressed transposase system suitable for localized insertional mutagenesis in rice. Theor. Appl. Genet., 112: 1326-1341.