Inducible reporter/driver lines for the Arabidopsis root with intrinsic reporting of activity state

DR PETER DOERNER (Orcid ID : 0000-0001-7218-8469)

Article type : Technical Advance

Inducible reporter/driver lines for the Arabidopsis root with intrinsic reporting of activity state

Frank Qasim Machin[1], Malin Beckers[1], Xin Tian[1], Alice Fairnie[1], Teri Cheng[1], Wolf-Rüdiger Scheible[2] and Peter Doerner[1,2,3]

[1] Institute for Molecular Plant Science; University of Edinburgh; [2] Max-Planck Institute of Molecular Plant Physiology, Science Park Golm; [3] Laboratoire de Physiologie Cellulaire & Végétale, Univ. Grenoble Alpes, CNRS, CEA, INRA, BIG-LPCV, 38000 Grenoble, France.

Corresponding Author, Peter Doerner, Daniel Rutherford Building, King's Buildings, Mayfield Road, Edinburgh, EH9 3BF

Current address:

XT, Department of Biological Sciences and NUS Centre for BioImaging Sciences, National University of Singapore, Singapore 117543, Singapore. W-RS, Noble Research Institute, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA.

Summary: Inducible expression system for comparable and reproducible characterisation of gene function.

Running title: Tissue and cell type-specific reporters

Keywords: tissue- and cell-type specific reporter, Estradiol-inducible, Reference lines, PRODUCTION OF ANTHOCYANIN PIGMENT 1 (PAP1), Arabidopsis thaliana

This article has been accepted for publication and undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process, which may lead to differences between this version and the Version of Record. Please cite this article as doi: 10.1111/tpj.14192

Abstract

Cell-, tissue- or organ-specific inducible expression systems are powerful tools for functional analysis of changes to the pattern, level or timing of gene expression. However, plant researchers lack standardised reagents that promote reproducibility across the community. Here, we report the development and functional testing of a Gateway-based system for quantitatively, spatially and temporally controlling inducible gene expression in Arabidopsis which overcomes several drawbacks of legacy systems. We used this modular driver/effector system with intrinsic reporting of spatio-temporal promoter activity to generate 18 well-characterised homozygous transformed lines showing the expected expression patterns specific for the major cell types of the Arabidopsis root; seed and plasmid vectors are available through the Arabidopsis stock centre. The system's tight regulation was validated by assessing the effects of diphtheria toxin A chain (DTA) expression. We assessed the utility of Production of Anthocyanin Pigment 1 (PAP1) as an encoded effector mediating cell-autonomous marks. With this shared resource of characterised reference driver lines, which can be expanded with additional promoters and the use of other fluorescent proteins, we aim to contribute towards enhancing reproducibility of qualitative and quantitative analyses.

Introduction

Inducible gene expression systems are commonly used molecular tools to examine gene function, which remains an important challenge in the post-genomic era. These systems are used to conditionally knock-down or induce gene expression, and to investigate the short- or long-term effects of specific transgene expression when its precise control is essential for the experimental design. Many variations of such systems exist that allow for spatial and or temporal control of gene expression. Inducible systems are frequently used in developmental studies (Brand *et al.,* 2006, Haseloff 1999, Marques-Bueno *et al.,* 2016, Siligato *et al.,* 2016). However, existing systems have a number of drawbacks: enhancer-trap or promoter-trap lines are in a background now rarely used for genetic studies (*e.g.* C24, (Goddijn *et al.,* 1993, Haseloff 1999)), thus resulting in plants with a mixed-accession lineage when introduced into commonly used mutants in the Col or L*er* backgrounds which can cause undesired side-effects (Haseloff 1999, Laplaze *et al.,* 2005). Some systems are not restricted to specific cell types or developmental domains (Haseloff 1999), are not inducible (Haseloff 1999), or use the dexamethasone-inducible system GVG which is known to have side-effects and does not show a differentiated dose-response (Kang *et al.,* 1999, Marques-Bueno *et al.,* 2016, Schurholz *et al.,* 2018, Zuo *et al.,* 2000). Some systems do not necessarily or intrinsically report successful induction as the inclusion of a fluorescent reporter is not a mandatory feature (Siligato *et al.,* 2016), others offer few or no options for fluorescent reporters (Brand *et al.,* 2006, Marques-Bueno *et al.,* 2016), utilize a more involved three-fragment recombination system (Marques-Bueno *et al.,* 2016, Siligato *et al.,* 2016), or do not provide freely accessible, specific and well-characterised transgenic lines as reference and basis for comparative studies in different laboratories (Siligato *et al.,* 2016). While the widespread use of existing expression systems attests to their utility in many situations, we identified a need for a system of standard parts that can be used for accurate and reproducible, qualitative *and* quantitative, comparison of gene expression, for example when present in different mutant backgrounds or when utilised in different laboratories. The community-wide use of such well-defined reference resources has recently been facilitated by the optimisation

of CRISPR/Cas9-based methods, which make it easier to re-generate desired single or multiple hypomorphic alleles in such a standard reporter line than to introgress such alleles over several generations (Ordon *et al.,* 2017).

Several inducible systems are based on the synthetic XVE transcription factor (Brand *et al.,* 2006, Siligato *et al.,* 2016, Zuo *et al.,* 2000). The XVE factor is constructed from three modules, the bacterial transcriptional repressor *LexA* as a DNA binding domain, the transcription activating domain of the herpes simplex virus transcription factor VP16, and the regulatory region of the human estrogen receptor (Zuo *et al.,* 2000). This sensitive system has negligible or no background expression in Arabidopsis and is not known to cause XVE-independent gene expression in Arabidopsis (Brand *et al.,* 2006, Siligato *et al.,* 2016, Zuo *et al.,* 2000). Plants grown in tissue culture are easy to induce with small molecules, and every part of the plant can easily be exposed to estradiol, which does not move readily over long distances in the plant (Brand *et al.,* 2006). Moreover, the XVE system is dose-responsive allowing induction can be tuned quantitatively (Zuo *et al.,* 2000). Therefore, by placement of XVE under control of tissue-, cell type-, or developmental phase-specific promoters, exquisite quantitative fine-tuning of spatial and temporal gene expression can be achieved.

In the presence of estradiol, the XVE factor enters the nucleus and binds to LexA operator sequences (LexAop) placed upstream of a minimal promoter, allowing transcription of the gene of interest. Activation of gene expression mediated by XVE is not restricted to a single target, the introduction of one or more genes under control of LexAop sequences enables expression of multiple genes in parallel within the same domain.

We exploited the properties of the XVE/LexAop system to develop a set of binary vectors that permit the introduction, with Gateway® technology, of a promoter of choice to express XVE. The desired promoter or secondary effector gene must be flanked with attL1/attL2 sequences, for which established collections exist (Xiao *et al.,* 2010). These vectors carry, in *cis*, LexAop sequences located upstream of alternatively, H2B-GFP, H2B-YFP, H2B-mKusabira Orange or H2B-mCherry fluorescent fusion proteins which function as primary effector genes to report successful induction by estradiol (Karasawa *et al.,* 2004, Nagai *et al.,* 2002, Shaner *et al.,* 2004, Tsien 1998). Secondary effector genes are then introduced into the driver lines by crossing or by transformation. The use of a specific effector line introduced by crossing across different driver–effector line combinations provides better comparability in functional studies. To facilitate the use of common reagents and increase reproducibility across the community, we generated robustly characterised cell type-specific driver lines for most cell types in the Arabidopsis root, which can be used as standard, modular components for gene expression and synthetic biology studies. Each of these primary lines need only be made once, and then is used as a standard part into which secondary genes are transformed. These lines have been donated to the Nottingham Arabidopsis Stock Centre.

Results

A pXVE system with fluorescent reporters for modular control of localised gene expression.

We developed an inducible expression system that uses two different plasmid constructs, one that acts as a Driver, which directs estradiol-inducible gene expression of a nuclear-localised fluorescent

protein used to indicate successful induction and appropriate localisation in *cis*. The second plasmid construct is the Effector, that allows the expression of one or more additional genes under the control of the promoter used in the Driver line in *trans, e.g.* pMDC160 or pMDC221 (Brand *et al.,* 2006)(Fig. 1A, Fig. S1, Fig. S16).

Four different Driver plasmid constructs were made, each carrying either eGFP (pXVG), Venus (pXVV), mKO2 (pXVK) or mCherry (pXVC), respectively (Fig. S2). This facilitates their use in genetic backgrounds with pre-existing fluorescent markers or other fluorescent dyes. We tested these vectors by recombining each one with the 1947 bp promoter for AQC1 (Zhou *et al.,* 2010), which directs expression in the QC, columella stem cells and their immediate progeny (Fig. 1A-D). These lines are listed in Supplemental Table 2.

Reporter lines marking the major tissue types of the *Arabidopsis* root

The *Arabidopsis* primary root comprises distinct cell types, including the root cap, epidermis, cortex, endodermis, and vasculature. We generated reporter lines marking the individual cell types that comprise the radial pattern of the primary root (Supplemental Table 2).

The epidermis of the *Arabidopsis* primary root is divided into two types of cells, trichoblasts which elongate to form root hairs, and atrichoblasts which do not. The atrichoblast line is marked by a line (V101) making use of the GL2 (At1g79840) promoter. When induced by estradiol, this line shows H2B-Venus accumulation only in the atrichoblast file of the epidermis, beginning at the stem cells, and continuing into the mature root (Fig. 2A). The transverse section and view of the root surface shows that accumulation is present only in alternating cell files of the epidermis layer, and absent in the trichoblast file (Fig. 2B; Fig. S3A-D). The transverse section shows that this file is located above the cell walls of single cortex cells, a trait that is necessary to pattern the atrichoblast file (Fig. 2C).

Elongating trichoblast cells were marked using the SHV2 (At5g49270) promoter as this gene is required for the remodelling of the cell wall that occurs during elongation. Venus accumulation in this line (V111) is absent in the apical meristem (Fig. S4D) and becomes visible starting from the transition domain, where the root hairs begin to extend from the root surface (Fig. 2D; Fig. S4A, C, E). This continues into the mature root, where the labelled nuclei move into the basal region of the root hair (Fig. 2E; Fig. S4B, F). The transverse section image shows that the accumulation is complementary to that of the atrichoblast line and that the labelled cells are localised above the groove between two cortex cells (Fig. 2F).

We did not identify a promoter sequence that directs gene expression uniformly in the entire cortex file. Therefore, two lines were made: one that expresses in the meristem cortex cells, and one in the mature cortex cells. The CO2 (At1g62500) promoter sequence was used to develop a line (V251) expressing in the young cortex cells of the root apical meristem (Heidstra *et al.,* 2004). This line shows H2B-Venus accumulation in the cortical layer that begins at the stem cells and continues in the meristem region (Fig. 2G, I; Fig. S5B-D). The fluorescence stops before or at the transition domain and is not present in the mature root (Fig. 2H; Fig. S5A). The mature cortex line (V121), driven by the E49 (At3g05150) promoter (Lee *et al.,* 2006), shows H2B-Venus accumulation in only the cortical layer that begins in the transition domain and continues into the mature root (Fig. 2J, K; Fig. S6A-C). The fluorescence is restricted to the cortical layer, as can be seen in the transverse section (Fig. 2L).

Expression in the endodermis cell layer was controlled by the SCR (At3g54220) promoter. The line transformed with this construct (V141) shows H2B-Venus accumulation in the endodermis, beginning at the stem cell niche, endodermal/cortical stem cells and continuing into the mature root (Fig. 2M, N; Fig. S7A, B). This is consistent with previous observations (Helariutta *et al.,* 2000). Radially, H2B-Venus accumulation in V141 is confined to the endodermis layer, as seen in the digital cross-section (Fig. 2O).

The stele line (V181) shows H2B-Venus accumulation in multiple tissues of the vascular cylinder, under the control of the DAG1 (At3g61850) promoter (described as S2 in (Lee *et al.,* 2006)). Fluorescence begins at the stele stem cells (Fig. 2P; Fig. S8B, C) and continues into the mature root (Fig. 2Q; Fig. S8A) and includes H2B-Venus accumulation in the pericycle layer in the mature tissues (Fig. 2R).

The root cap is a major sensory and assimilatory tissue of the *Arabidopsis* root that perceives external conditions, assimilates nutrients and coordinates growth responses (Kanno *et al.,* 2016, Su *et al.,* 2017, Tsugeki and Fedoroff 1999). The APL4 (At2g21590) promoter was used to generate a line (V431) for root cap expression (Birnbaum *et al.,* 2003). H2B-Venus fluorescence was localised to the root cap (Fig. 2S) and was not seen in other parts of the primary root (Fig. 2T). Venus accumulation was seen in both the columella cells as well as the lateral root cap cells (Fig. 2S, U).

Reporter lines marking the pericycle

Pericycle cells comprise the outermost layer of the vasculature. They are functionally patterned by their position relative to the underlying phloem and xylem vessels and hence are referred to as phloem pole and xylem pole pericycle cells, respectively. These are important cell types in *Arabidopsis* growth and development as the phloem pole pericycle cells have been implicated in regulating efflux from the phloem (Ross-Elliott *et al.,* 2017), and the xylem pole pericycle cells are the site of lateral root initiation (Charlton 1991, Esau 1965, Parizot *et al.,* 2008, Steeves and Sussex 1989, van Tieghem and Douliot 1888). We made lines marking the pericycle layer as a whole (V151), using promoter sequences of At5g09760 (Brady *et al.,* 2007) and additional lines for the phloem pole pericycle cells (V161), using promoter sequences of At2g22850 (described as S17 in (Lee *et al.,* 2006)); and xylem pole pericycle cells (V171), using promoter sequences of At3g29635 (Brady *et al.,* 2007), respectively (Supplemental Table 1).

Fluorescent protein accumulation in the pericycle line (V151) can be seen from the beginning of the transition zone (Fig. 3A; Fig. S9B, C), where the vascular tissues begin to develop, at the same time as the polar pericycle cells are specified (Parizot *et al.,* 2008, Pyo *et al.,* 2004, Yamaguchi *et al.,* 2008), and persisting through the mature root (Fig. 3B; Fig. S9A,D). The transverse image shows fluorescent protein accumulate in all cells of the pericycle layer (Fig. 3C).

Fluorescent protein accumulation in phloem pole pericycle nuclei (V161), can be seen from the beginning of the transition zone (Fig. 3D) clustered around the developing phloem vessels, seen most clearly when the phloem is labelled with CTER (Fig. 3E), a phloem-mobile fluorescent dye (Knoblauch *et al.,* 2015). After loading cotyledons with CTER, it is translocated *via* the phloem to the primary root tip, staining only the phloem vessels with a bright fluorescent signal. This is necessary to distinguish the location of cells in the centre of the root, as propidium iodide is not able to diffuse past the intact

Casparian strip, which is present in differentiated endodermis cells. Loading the leaves with CTER results in the appearance of bright fluorescence in the phloem at the centre of the root (Fig. 3E). The phloem pole pericycle nuclei marked with H2B-Venus fluorescent protein are situated adjacent to the phloem vessels, as seen in the transverse section image of a root stained with CTER (Fig. 3F).

The H2B-Venus fluorescent marker protein reporting the activity of the xylem pole pericycle-specific promoter begins to accumulate in nuclei clustered around xylem vessels (V171), which fluoresce with propidium iodide staining in a characteristic pattern of rings, indicating maturing xylem vessels (Fig. 3H). This promoter is not yet active in the primary root apical meristem (Fig. 3G). Fluorescent protein accumulation can also be seen in the centre of the transverse section, with the fluorescent nuclei of the xylem pole pericycle cells positioned adjacent to the xylem vessels (Fig. 3H).

Reporter lines marking different vascular tissues

The vasculature of the *Arabidopsis* primary root is patterned both radially and longitudinally, with cells developing and differentiating in the longitudinal axis of the root, and during this developmental process, the opposing poles of the xylem and phloem are organised radially. Therefore, we made marker lines specific for the vascular cell types themselves, and also for their progenitor cells in the apical meristem (Supplemental Table 2).

Mature xylem vessels are dead, so it was not possible to generate a marker line. In its place, we made use of a promoter that is expressed in the developing xylem cells. The mature phloem tissues, in contrast, comprise living cells and so can be marked with a reporter line. Two separate lines were made for the phloem, one specific for the protophloem cells and another for the companion cells of the mature phloem.

The protophloem cells are marked by using promoter sequences of At2g18380 (described as S32 in (Lee *et al.,* 2006)) in the V201 line. H2B-Venus accumulation in this line begins in the nuclei of the vascular initial cells and is strong in the meristem (Fig. 4A, B; Fig. S10A-D). The number of cells accumulating H2B-Venus is reduced in the transition domain as cells begin to expand and the phloem develops and then accumulates more strongly in phloem and phloem-associated cells of the mature root (Fig .4A, C; Fig. S11A, C).

The G235 line marking the companion cells of the phloem, driven by the SUC2 (At1g22710) promoter, shows H2B-GFP absent in the meristem (Fig. S12C) and beginning to accumulate at the transition domain where the phloem matures (Fig. 4D), and continues through the length of the phloem (Fig. 4E; Fig. S12B, D). A digital cross-section reveals expression confined to the companion cells (Fig. 4F). In CTER treated plants, the fluorescence is localised in the nuclei of cells next to the phloem sieve elements that transport CTER (Fig. S12A).

The developing xylem cells are marked by using promoter sequences of At3g25710 (described as S4 in (Lee *et al.,* 2006), line V261). Nuclei accumulating H2B-Venus are observed in the vascular stem cells and in the xylem vessels as they develop (Fig. 4G, H; Fig. S13A-D, Fig. S11B, D). Fluorescent nuclei can be clearly seen within cells that have entered into the process of lignification, as the characteristic rings of lignin can be seen as bands already surrounding this cell in Figure 4I.

Reporter lines marking developmental stages of the primary root

Cells in the primary root progress through a series of developmental identities, from stem cells to the transit amplifying cells of the meristem, and the post-mitotic, but endo-replicating cells of the differentiation zone. The processes that control the progressive reduction of proliferation and the transition to differentiation are still not well understood, so lines marking these developmental transitions are likely to be of high utility. We aimed to generate such orthogonal markers to report in all tissue types at any one developmental stage (Supplemental Table 2).

The AQC/TPST (At1g08030) promoter-driven stem cell line (V241) marks the stem cell niche and in most of the stem cells surrounding the stem cell niche (Fig. 1B-E). However, expression in the vascular stem cells is variable, with 50% of the selected lines lacking expression in the vascular stem cells (Fig. 1B, D). H2B-Venus fluorescence is also seen in the 1-2 immediate progeny of the columella and lateral root cap stem cells, but no expression is seen outside of this region within the root apical meristem.

The V311 line uses the promoter from TCP7 (At5g23280) that marks all tissues in the mature root, outside of the meristem (Fig. S14A, B). The expression is not correlated with an increase in ploidy, as it is also expressed in the pericycle layer (Fig. S14B, C), in which the cells do not endoreplicate (Beeckman *et al.,* 2001).

Several lines were constructed to generate a line specific to the root apical meristem, or the root apical meristem and transition domain, including DEL1 (At3g48160), APC11 (At3g05871). However, we failed to identify a line that satisfied the requirement to be specific to the meristem: fluorescent protein accumulation was observed in the differentiation zone of the root. In addition, several promoter sequences were tested for the development of a stem cell niche-specific reporter line, including QC46 (ten Hove *et al.,* 2010) and mAGL42 (Nawy *et al.,* 2005) but none was found to result in expression that was specific to the QC cells beyond 4 d.a.g..

Reporter lines as tissue-specific drivers of secondary gene expression.

One or more additional Effector plasmid constructs containing a gene expressed under control of the LexAop sequence can be introduced into a Driver line, resulting in tissue-specific, estradiol-inducible gene expression. Effector constructs may be inserted into Driver lines by crossing, as was done with the Diphtheria Toxin chain A (DTA) Effector line or by direct transformation as was done with the PAP1 effector line (Fig. 5A-D).

The p35S line (C01) uses H2B-mCherry as a fluorescent reporter, and fluorescence is observed in every cell in the plant, including the root apical meristem (Fig. S15A, B). DTA functions as an extremely potent, cell-autonomous ADP-ribosylase of the EF2 translation initiation factor; and consequently, inhibits all protein translation, eventually leading to cell death (Collier 1975, Pappenheimer 1977, Yamaizumi *et al.,* 1978). Controlled delivery of DTA to ablate cells has been successfully used in plants for studies of pistil and anther development, lateral root development, regeneration and root cap sensing (Che *et al.,* 2007, Laplaze *et al.,* 2005, Tsugeki and Fedoroff 1999). We used DTA to evaluate the tightness of regulation of activation of the XVE system.

C01 was crossed with the DTA Effector line (see Fig. S16 for map of construct) containing the LexAop-DTA plasmid construct. F3 progeny were selected on hygromycin and kanamycin for the presence of at least one copy of the Driver (C01) and Effector (DTA) construct, and transferred to 0.5x MS plates with 5µM estradiol. All seedlings were bleached 7d after transfer (Fig. S17). Without estradiol, however, all plants grow to maturity after transplanting to soil with no observed growth defects, demonstrating that DTA is not being expressed and revealing the robust control of the estradiol induction in this system (Fig. S17).

DTA expression was also shown to function in a tissue specific manner by crossing the LexA:DTA construct into V101 to produce estradiol inducible DTA expression specific to the atrichoblast cells of the epidermis (Figure S19). Propidium iodide is used here as a live/dead stain so that cells with damaged membranes are heavily stained with propidium iodide. The cell death is restricted to the atrichoblast file of the epidermis and does not appear to cause damage to the other tissue layers of the root. This cell death phenotype was not clearly highlighted by propidium iodide in the root apical meristem, but the absence of H2B-Venus expression in the meristem suggests the onset of DTA-dependent translation inhibition.

To demonstrate the tissue-specificity of secondary gene expression, we used a vital reporter of activity. PAP1 (At1g56650) is a master regulator for anthocyanin production and, when overexpressed, can produce visible anthocyanin staining (Borevitz *et al.,* 2000). The accumulating anthocyanins are visible by both fluorescence (Poustka *et al.,* 2007) and brightfield microscopy and thus PAP1 can also function as a new genetically-encoded visible reporter gene. The PAP1 plasmid construct was transformed directly into the homozygous Driver lines of V101, the atrichoblast marker line and V111, the trichoblast marker line and the resulting transformed plants screened by brightfield microscopy for visible pink colouration after estradiol induction. We deliberately screened for visible anthocyanin expression to identify high-level anthocyanin accumulation. Hence, we likely missed many low-expressing lines, as the sensitivity for brightfield detection of anthocyanins in this system is significantly lower than when detecting by fluorescence. For the transformation of V101, we analysed 42 independent transformants, of which 29 segregated 3:1, of which 7 showed the expected, correct pattern of high-level expression, none showed an unexpected pattern of expression. For the transformation of V111_25D, we analysed 42 independent transformants, of which 35 segregated 3:1, of which 2 showed the expected, pattern of high-level expression, none showed an unexpected pattern of expression. V101>>PAP1 and V111>>PAP1 demonstrate the tissue-specificity of the Effector gene expression system (Fig. 5A-D): Anthocyanin fluorescence is exclusively localised to the cells with yellow fluorescent nuclei.

Discussion

We developed and functionally tested a versatile system for quantitatively, spatially and temporally controlling inducible gene expression in Arabidopsis. All reagents are available from the Arabidopsis Stock Centre, to provide the basis for a well-characterised community resource that can be further expanded (Supplemental Table 2). Promoter activity is visualised by the accumulation of nuclear-localised fluorescent proteins. This system was used to generate and characterise plant lines with expression directed to all major cell types of the root, and three developmental domains of the root:

the distal meristem (V431; lateral root cap, columella; Fig. 2S-U), the stem cell niche and stem cells (G240, V241, K242, C243; Fig. 1B-E), and differentiating cells (V311, expanding and differentiating cells; Fig. S14). Experiments with DTA revealed very tight regulation of dependant protein accumulation after addition of estradiol to the specifically expressed synthetic transcription factor XVE (Fig. S17). Silencing of constructs was not observed over 4-5 generations. These results validate the utility and specificity of the system to provide an expandable community-wide resource for more reproducible and comparable data generation.

Design principles

We implemented several design principles to allow these lines to be shared with and efficiently used by other researchers. First, we embedded a nuclear-localized reporter that indicates activation by estradiol of the XVE transcription factor expressed under control of the desired promoter (Fig. S1) in *cis*, which together comprise the Driver construct. This will facilitate crosses of the Driver into the desired mutant or transgenic backgrounds. Second, all constructs were transformed into Col-0, as this is the most commonly used genetic background in *Arabidopsis* research, again to facilitate their use alongside existing mutants and transformed lines. As the XVE vectors and promoter-XVE constructs are available, new lines can be generated in any desired accession, or other species to expand the utility of the system for the community further. Third, there are four alternative plasmids for driver constructs, each made with a different fluorescent protein, (Green Fluorescent Protein, Venus, monomeric Kusabira Orange and monomeric Cherry). The variety of different fluorescent protein reporters enables the lines to be used alongside existing fluorescent reporter lines by selecting a complementary fluorescent protein that can be spectrally resolved from the pre-existing reporter in the desired plant background. Lastly, the decision was made to use nuclear-localised fluorescent proteins. This gives more clarity than cytosolic fluorescence when determining expression domains by microscopy, especially at low expression levels, and improves quantification of fluorescence from fluorescence image data.

Characterisation of expression patterns

Reporter constructs introduced into Arabidopsis by Agrobacterium-mediated transformation insert at semi-random positions, which can influence the pattern and magnitude of fluorescent reporter activity of individual transformation events (Marques-Bueno *et al.,* 2016, Peach and Velten 1991, Schubert *et al.,* 2004). To enhance the utility of the reporter lines, and promote efforts to increase reproducibility across different laboratories, we extensively characterised and documented the expression patterns in the lines we share as a resource with the community to provide a degree of experimental standardisation. We observed differences in accumulation of nuclear localised fluorescent reporters, with respect to intensity and pattern after standardised estradiol induction treatments between independently transformed lines. This is, to a minor extent, reflected in the subtle variations observed in the different lines transformed with AQC1 promoter-directed expression of GFP, Venus, mKO, and mCherry, respectively (Fig. 1). Such variation reinforces the need to utilise well-characterised and shared Driver lines across the community to enhance reproducibility. The community-wide use of such well-defined reference resources has recently been

facilitated by the optimisation of CRISPR/Cas9-based methods, which make it easier to re-generate desired single or multiple hypomorphic alleles in such a standard reporter line than to introgress such alleles over several generations (Ordon *et al.,* 2017).

Expression patterns of genes change throughout the development of an organism, and so only one developmental stage (7-12 d.a.g.) was used for the characterisation of the lines. While characterisation of expression patterns in very young (3-5 d.a.g.) seedlings is relatively common in the literature, we observed that these seedlings do not reflect the gene expression patterns of fully photoautotrophic, environmentally responsive plants. For example, although we observed fluorescent protein expression in several independent lines that had been transformed with the QC46 (ten Hove *et al.,* 2010) and mAGL42 (Nawy *et al.,* 2005) promoters directing XVE expression at 3-5 d.a.g. but by 7 d.a.g. this had been lost. Therefore, the characterisation of expression patterns of the reporter lines focused only on primary roots at 7-12 d.a.g. to indicate expression behaviour in photoautotrophic seedlings.

Fusion of H2B fragments with fluorescent proteins can have a stabilising effect that can broaden the expression domain. In the lines presented here, however, the expression domains appear identical to those in the studies from which the promoter sequences were taken. The V251 line driving expression in the meristem cortex cells (CO2 promoter) shows a rapid extinguishing of fluorescence that is consistent with the predicted pattern of meristem cortex cells.

Advantages of the new XVE system

Fluorescent reporter lines that mark individual tissues have been developed previously, initially the enhancer trap lines developed by the Haseloff (Haseloff 1999, Laplaze *et al.,* 2005) and the promoter trap lines developed by the Pelletier (Bechtold *et al.,* 1993) groups, which were generated in the C24 or Wassilevskija (Ws) accessions, respectively, which are currently not widely used for molecular-genetic work. By contrast, we generated lines in the broadly used Col-0 accession. Moreover, the lines presented here are fully characterised in terms of expression pattern in order to facilitate use by other researchers, and we encourage other users to add to the collection by making their lines public.

A distinct advantage of the XVE system is its rapid inducibility and good dose-responsivity (Zuo *et al.,* 2000, this work): We examined a time course of induction and observed half maximal induction between 3-6 h, and a good range of dose-responsivity after 24 (Figure S18).

There remains a distinct lack of available reporter lines and characterised promoters that are specific for different developmental stages in the *Arabidopsis* root and that are in the same genetic background. The *Arabidopsis* root is composed of tissues that have markedly different properties including proliferation rate, ploidy, and vacuolation, so it is highly desirable to be able to label, separate, and drive ectopic expression in these tissues very specifically and accurately. Previously, this functionality has been approximated by microdissection, as seen in reports by Birnbaum, Brady, and colleagues (Birnbaum *et al.,* 2003, Brady *et al.,* 2007), but this is tedious and lacks the accuracy and reproducibility of a well-characterised reporter line.

Effector gene constructs can be added into driver lines by either direct transformation or by crossing. Both methods require the same number of generations to produce experimental lines that are homozygous for both constructs, but preliminary characterisation can occur earlier in transformed lines due to the semi-dominant nature of the XVE transcription factor. It should be noted that the transformation of the secondary plasmids will also result in variations in insertion, which will result in variations in expression level. This system still maintains the distinct advantage of an unchanging expression domain, so that only the level and not the spatial pattern of secondary gene expression needs to be measured when selecting lines.

PAP1 as a new vital reporter

PAP1 has been previously used to effect anthocyanin accumulation in shoot tissues (Borevitz *et al.,* 2000). We examined here the utility of PAP1 in controlling anthocyanin accumulation in specific root cell types with a view to generate a cell-autonomous, encoded effector to mediate stable marking of cells. Anthocyanin accumulated specifically in cells in which PAP1 was expressed, although it took several days for strong visible pigmentation to develop. We used the wild type coding sequence for PAP1, but as PAP1 requires phosphorylation for stability and full activity, anthocyanin accumulation could be accelerated by use of phospho-mimic mutations (Li *et al.,* 2016).

In conclusion, we have generated a modular, validated and expandable system to direct gene expression in many tissues and cell types of the Arabidopsis root with utility for developmental, physiological and cellular studies. These lines have been donated to the Nottingham Arabidopsis Stock Centre (Supplemental Table 2).

Materials and Methods

Generation and cloning of vectors and promoter sequences

Generation of vectors is described in Supplemental Methods. Promoter sequences were amplified using the primers listed in Supplemental Table 1, Arabidopsis Col-0 genomic DNA and Q5 (NEB) enzyme, using the manufacturer's recommended conditions.

Seedling sterilisation and growth for microscopy

Arabidopsis seeds were placed in either 1.5 ml Eppendorf tubes or 15 ml Falcon tubes. Seeds were washed with a solution of 70% ethanol with 0.05% Tween for 15 minutes with shaking, which was then replaced with a solution of 95% ethanol for 3 minutes. The ethanol solution and the seeds were placed on a sterile filter paper in a laminar flow hood until dry. Seedlings for microscopy were sterilised as above and sown on 12-centimetre square plates containing 50 ml of 0.5x MS salts, 1% sucrose, with pH adjusted to 5.8 using KOH and solidified with 1% agar. Media was supplemented with 5 µM estradiol from a stock of 100 mM estradiol in ethanol. Two rows of 10 seeds were sown on each plate. The plates were stratified at 4°C for 2 days and then transferred to a growth room where they were placed vertically for 7-10 days.

Estradiol induction for DTA

25 F2 seeds from the cross of 35S:XVE>H2B-mCherry and 35S:XVE>> LexAop:DTA were each sown onto 9 cm Petri dishes containing 25 ml of 0.5x MS salts, 0.6% sucrose and solidified with 1% agar. pH was adjusted to 5.8 with KOH. The seeds were stratified for 2 days and then placed in a growth chamber. At 7 days, the plates were flooded with 20 ml of 0.5x MS salts, 0.6% sucrose and either 5 µM estradiol or a control of vehicle only. 5 days post-induction (dpi), the plates were photographed using a digital camera and a lightbox.

Confocal microscopy

Slides were prepared by placing primary roots onto the slide in a solution of 0.5x MS containing 5 µg/ml propidium iodide. Slides were used immediately for microscopy. An Olympus confocal FV300 on an IX70 inverted microscope with an Argon laser and a Helium-Neon laser (Ex, 488nm, 543nm, respectively) was used for all confocal imaging. Images were taken using either a 20x, 40x or 60x water immersion lens.

H2B-eGFP/Venus and propidium iodide fluorescence were visualised using both 488 nm and 543 nm excitation, a 510 nm long-pass filter (BA510IF), a 530 nm short-pass filter (BA530RIF) and a 585/640 nm band-pass filter (BA585-640). mKO fluorescence was visualised using 543 nm excitation and a 585/640 nm band-pass filter (BA585-640). mCherry fluorescence was visualised using 543 nm excitation and a 585/640 nm band-pass filter (BA585-640). The transmitted light channel was used to provide a spatial reference. Venus and anthocyanin fluorescence were visualised using both 488 nm and 543 nm excitation, a 510 nm long-pass filter (BA510IF), a 530 nm short-pass filter (BA530RIF) and a 585/640 nm band-pass filter (BA585-640), as described (Poustka *et al.,* 2007). The transmitted light channel was used to provide a spatial reference.

Images were converted to single-channel RGB colour images using FIJI. Digital cross sections were made in FIJI, using Z-stacks generated with 3 µm intervals.

Dye loading of CTER

Carboxytetraethylrhodamine (CTER, CAS, 37299-86-8; Acros) (Knoblauch *et al.,* 2015) was loaded into the cotyledons of seedlings 30 min prior to the start of microscopy. CTER was loaded as follows, cotyledons were first gently damaged by compression with a pair of ridged forceps, and then 1 µl of 0.8 mM CTER solution was added to the wounded cotyledon. Seedlings were kept in a closed petri dish for 30 minutes to maintain a humid environment and then seedlings were imaged by confocal microscopy.

Acknowledgements

We thank Vladimir Brukhin for contributions at an early stage of the project; Kirsten Knox for supplying us with CTER. MB thanks ERASMUS+ for support. We thank The Leverhulme Trust for the award of a Research Fellowship to PD (0437) and a Research Grant F/00 158/CR award to PD; the ANR for grant 10-CHEX-000-00 GENOTOX to PD, BBSRC Industrial CASE studentship (BB/L502637/1) to FQM. The authors declare no conflicts of interest.

Author contributions

XT and PD performed cloning of promoters and vectors, FQM and MB performed confocal imaging, FQM performed DTA experiments. MB, AF, and TC performed confocal imaging of anthocyanin fluorescence. FQM and PD wrote the paper. W-RS provided space and resources to PD during part of this work.

Frank Qasim Machin, 0000-0002-7607-8360, f.q.machin@gmail.com

Malin Beckers, 0000-0001-8267-433X, malin-beckers@web.de

Alice Fairnie, 0000-0001-6223-6957, almf2@cam.ac.uk

Teri Cheng, 0000-0002-8781-0203, teri.cheng@outlook.com

Xin Tian, 0000-0003-4705-3719, eric09711@gmail.com

Wolf-Rüdiger Scheible, 0000-0003-4363-4196, wrscheible@noble.org

Peter Doerner, 0000-0001-7218-8469, peter.doerner@ed.ac.uk

Short supporting legends

Supplemental Methods. Construction of pXVE-FP vectors.

Supplemental Table 1. Primers used for promoter amplification.

Supplemental Table 2. List of lines donated to Stock Centre

Figure S1. Map of pXVG vector

Figure S2. Maps of XVE>H2B-FP vector series

Figure S3. Images of pGL2>H2B-Venus (**V101**_15B).

Figure S4. Images of pSHV2>H2B-Venus (**V111**_25D).

Figure S5. Images of pCO2>H2B-Venus (**V251**_6G).

Figure S6. Images of pE49>H2B-Venus (**V121**_6B).

Figure S7. Images of pSCR>H2B-Venus (**V141**_21E).

Figure S8. Images of pDAG1>H2B-Venus (**V181**_23D).

Figure S9. Images of At5g09760>H2B-Venus (**V151**_27A).

Figure S10. Images of pAt2g18380>H2B-Venus (**V201**_18A).

Figure S11. Images of pAt2g18380>H2B-Venus (**V201**_18A) and pAt3g25710>H2B-Venus (**V261**_1F).

Figure S12. Images of pSUC2>H2B-eGFP (**G235**_32A).

Figure S13. Images of pAt3g25710>H2B-Venus (**V261**_1F).

Figure S14. Images of pTCP7>H2B-Venus (**V311**_1N).

Figure S15. Images of p35S>H2B-mCHERRY (**C01**_17B).

Figure S16. Map of the DT-A gene in the pMDC221 vector.

Figure S17. Images of the progeny of the cross of C01 (Driver) and DTA in pMDC221 (Effector).

Figure S18. Time course and dose-response of estradiol induction.

Figure S19. Tissue-specific cell ablation in V101>>DTA.

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Legends

Figure 1: Driver plasmids encode tissue-specific, estradiol-inducible fluorescent reporters. A, Schematic representation of the inducible activator/effector XVE system. Promoter of choice, recombined with vector of choice (Fig. S1, Fig. S2) by Gateway reaction is positioned upstream of the XVE synthetic transcription factor. XVE protein (hexagon) accumulation is determined by the activity domain of the promoter. Upon treatment with estradiol, the XVE protein enters the nucleus and binds to the LexAop, thus activating expression of the specific reporter and, if desired, of additional effector genes. The activity reporter (here: H2B-Venus) is localised to the nucleus, additional effectors may, but do not have to be nuclear-localised. B-E, Confocal images of plant lines transformed with constructs generated by recombining the AQC1 promoter upstream of the XVE transcription factor using GFP (B), VENUS (C), mKusabira Orange (D) or mCherry (E) in the pXVG, pXVV, pXVK, pXVC vectors (Fig. S2), respectively. B, Primary root meristem of the G240 line carrying proAQC1:XVE in pXVG. C, Primary root meristem of V241 line carrying proAQC1:XVE in pXVV. C, Primary root meristem of K242 line carrying proAQC1:XVE in pXVK. D, Primary root meristem of C243 line carrying proAQC1:XVE in pXVC. Scale bar for B is 50 µm and scale bars for C, D and E are 100 µm.

Figure 2. Driver lines for tissue-specific expression in major tissue layers of the primary root. Unless

otherwise stated, the green channel is H2B-Venus fluorescence and the magenta channel is propidium iodide (PI) staining. A-C: expression in the atrichoblast cells of the epidermis. A, Line V101 focused on the primary root meristem. Scale bar = 50µm. B, Transition zone of the upper epidermis of the primary root meristem of line V101. Scale bar = 100µm. C, Digital cross-section of the mature root of V101. Scale bar = 10µm. D-F: expression in the trichoblast cells of the epidermis. D, Line V111 focused on the transition zone. Scale bar = 100µm. E, Mature root of V111, not stained with PI. Scale bar = 100µm. F, Digital cross-section of the mature root of V111. Scale bar = 20µm. G-I: expression in the meristematic cortex cells. G, Primary root tip of V251. Scale bar = 100µm. H, Mature root of V251. Scale bar = 100µm. I, Primary root meristem of V251. Scale bar = 100µm. J-L: expression in the post-meristematic cortex cells. J, Primary root tip of V121. Scale bar = 100µm. K, Mature root of V121. Scale bar = 100µm. L, Digital cross-section of mature root of V121. Scale bar = 10µm. M-O: expression in the endodermis and stem cell niche. M, Primary root tip of V141. Scale bar = 100µm. N, Primary root meristem of V141. Scale bar = 100µm. O, Digital cross-section of mature root of V141. Scale bar = 10µm. P-R: expression in the stele. P, Primary root meristem of V181. Scale bar = 100µm. Q, Mature root of V181, Scale bar = 100µm. R, Digital cross-section of mature root of V181. Scale bar = 10µm. S-U: expression in the root cap. S, Primary root tip of V431. Not stained with PI. Scale bar = 100µm. T, Mature root of V431. Not stained with PI. Scale bar = 100µm. U, Maximum intensity projection of a Z-stack image of primary root meristem of V431. Scale bar = 100µm.

Figure 3: Driver lines for tissue-specific expression in the pericycle tissues of the primary root. Unless otherwise stated, the green channel is H2B-Venus fluorescence and magenta is propidium iodide (PI) staining. A-C: expression in pericycle cells. A, Primary root tip of V151. Scale bar = 100µm. B, Mature root of V151. Not stained with PI. Scale bar = 100µm. C, Digital cross-section of mature root of V151. Scale bar = 50µm. D-F: expression in phloem pole pericycle cells. D, Primary root tip of V161. Scale bar = 100µm. Arrowheads indicate the boundary of the transition domain, the arrow indicates the first phloem pole pericycle cell with visible accumulation of fluorescent H2B-Venus. E, Mature root of V161 stained with PI and CTER. CTER staining of the phloem is highlighted by the white dashed lines. Scale bar = 100µm. F: Digital cross-section of mature root of V161 stained with CTER. CTER staining of the phloem is highlighted by the white dashed lines. Scale bar = 50µm. G-I: expression in xylem pole pericycle cells. G, Primary root tip of V171. Scale bar = 100µm. H, Mature root of V171. Scale bar = 100µm. I, Digital cross-section of mature root of V171. Scale bar = 10µm.

Figure 4: Driver lines for tissue-specific expression in the vascular tissues of the primary root. Unless otherwise stated, the green channel is H2B-Venus fluorescence and magenta is propidium iodide (PI) staining. A-C: expression in protophloem cells. A, Primary root tip of V201. Scale bar = 100µm. B, Primary root meristem of V201. Scale bar = 100µm. C, Digital cross-section of mature root of V201. Scale bar = 50µm. D-F: expression in companion cells. D, Transition zone of primary root of G235. Green fluorescence is H2B-GFP, the arrow marks a fluorescent nucleus. Scale bar = 100µm. E, Mature root of G235. Green fluorescence is H2B-GFP. Scale bar = 50µm. F, Digital cross-section of mature root of G235. Green fluorescence is H2B-GFP. Scale bar = 25µm. G-I: expression in protoxylem cells. G, Primary root tip of V261. Scale bar = 100µm. H, Primary root meristem of V261. Scale bar = 50µm. I, Digital cross-section of mature root of V261. Scale bar = 25µm.

Figure 5: PAP1-expressing lines demonstrate tissue-specificity of gene expression. White indicates H2B-Venus fluorescence and magenta indicates fluorescence caused by anthocyanin accumulation. A & B, Mature root of V101>>PAP1, with anthocyanin accumulating in the atrichoblast cells. C & D, Mature root of V111>>PAP1, anthocyanin accumulates in the trichoblast cells. Scale bar = 100μm.