Pogostick: A New Versatile piggyBac Vector for Inducible Gene Over-Expression and Down-Regulation in Emerging Model Systems

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Abstract

Background: Non-traditional model systems need new tools that will enable them to enter the field of functional genetics. These tools should enable the exploration of gene function, via knock-downs of endogenous genes, as well as over-expression and ectopic expression of transgenes.

Methodology: We constructed a new vector called Pogostick that can be used to over-express or down-regulate genes in organisms amenable to germ line transformation by the piggyBac transposable element. Pogostick can be found at www.addgene.org, a non-profit plasmid repository. The vector currently uses the heat-shock promoter Hsp70 from Drosophila to drive transgene expression and, as such, will have immediate applicability to organisms that can correctly interpret this promoter sequence. We detail how to clone candidate genes into this vector and test its functionality in Drosophila by targeting a gene coding for the fluorescent protein DsRed. By cloning a single DsRed copy into the vector, and generating transgenic lines, we show that DsRed mRNA and protein levels are elevated following heat-shock. When cloning a second copy of DsRed in reverse orientation into a flanking site, and transforming flies constitutively expressing DsRed in the eyes, we show that endogenous mRNA and protein levels drop following heat-shock. We then test the over-expression vector, containing the complete cDNA of Ultrabithorax (Ubx) gene, in an emerging model system, Bicyclus anynana. We produce a transgenic line and show that levels of Ubx mRNA expression rise significantly following a heat-shock. Finally, we show how to obtain genomic sequence adjacent to the Pogostick insertion site and to estimate transgene copy number in genomes of transformed individuals.

Significance: This new vector will allow emerging model systems to enter the field of functional genetics with few hurdles.

Introduction

With the completion of a number of genome projects, probing the function of individual genes has become a main challenge. Non-traditional model systems, in particular, need new tools that will enable them to enter the field of functional genetics. These tools should enable the exploration of gene function, via knock-downs of endogenous genes, as well as over-expression and ectopic expression of transgenes.

The most popular development in the field has been the use of dsRNA to knock-down homologous genes via RNA interference (reviewed in [1]). RNAi was first discovered in plants as a mechanism for post-transcriptional gene silencing [2] and is now known to exist also in fungi and animals [3,4,5]. RNAi depends on the successful delivery of dsRNA into the cytoplasm of target cells and current delivery methods include viral transformation, lipofection, electroporation, direct injection, biolistics, soaking, and feeding [6,7]. Once inside a cell, the ability of RNAi to spread to other cells to produce systemic effects varies across species and tissues and it is still unclear which spreading mechanisms are used outside of C. elegans [8,9,10]. So, while successful systemic RNAi knock-downs have been achieved in hemipterans [11] and various beetles [10,12,13], systemic spreading does not readily happen in Drosophila, Anopheles, or Aedes [10], and appears to work in limited tissues in the Lepidoptera [14,15,16,17]. A way to overcome the limitation of systemic spreading is to induce the RNAi mechanism directly inside the cells, using transgenesis [18].
In addition to RNAi-mediated knock-downs, ectopic expression and over-expression of genes are also informative regarding gene function. Ectopic expression can be useful to test gene sufficiency in the development of a trait, and over-expression can test whether reverse phenotypes, relative to those observed from the knock-down experiments, are produced. For these experiments, transgenesis is usually required. Heritable over-expression and knock-downs mediated by transgenesis have been successfully applied for determining gene function in various organisms, e.g. the former in tobacco [19], mosquito [20] and mouse [21], and the latter in nematode [22], Drosophila [23], and mouse [24].

The development of new transgenic systems for emerging model systems depends, to a large extent, on the availability of transformation vectors of wide applicability across taxa. It also depends on the versatility of these vectors, i.e., being designed for use in a variety of gene function assays. The transposable element piggyBac is arguably one of the most promiscuous transposons discovered to date. Transposons related to piggyBac have been found in the genomes of almost all eukaryotes [25], and Drosophila, nematode [22], tobacco [19], mosquito [20] and mouse [21], and the latter in vertebrate and invertebrate species [26,27,28,29,30,31,32].

Given these qualities we chose it as the vehicle around which we of vertebrate and invertebrate species [26,27,28,29,30,31,32]. We document here the new versatile piggyBac vector, Pogostick, which can be used both to over-express transgenes, as well as down-regulate endogenous genes, in a controlled temporal fashion, by means of a heat-shock. We note that piggyBac vectors that can either over-express or down-regulate genes in Bombyx have been previously described [33,34], but these vectors were not specifically designed to serve both functions, nor were they designed to function with multiple genes, and described in sufficient detail to be of general use to the emerging model system community.

After a brief description on how Pogostick was constructed, we detail its main features and how candidate genes can be inserted into it for use in either over-expression or down-regulation experiments. We subsequently test Pogostick in functional genetic experiments with Drosophila. In particular, we document 1) the over-expression of the fluorescent protein DsRed at the larval and pupal stages of development, after a heat-shock is administered, and 2) the down-regulation of DsRed in a line constitutively expressing this gene in the eyes, also following a heat-shock. We document DsRed regulation both by directly monitoring DsRed mRNA levels using q-PCR and by monitoring fluorescent levels of the protein using fluorescent microscopy. We then test Pogostick in an emerging model system, the butterfly Bicyclus anynana. We construct a vector containing the previously cloned complete coding sequence of Ultrabithorax (Ubx) from another butterfly, Junonia coenia, produce a new transgenic line, and describe the transcriptional profile of Ubx mRNA following a single heat-shock in B. anynana larvae. Finally, we show how to obtain sequences-flanking Pogostick genomic insertions, how to determine insertion number in transformed individuals, and how to set-up homozygous lines.

Materials and Methods

Pogostick vector construction

The new versatile piggyBac vector, Pogostick (7572 bp; Fig. 1), was constructed with three steps. Firstly, the EGFP fragment (700 bp) in the plasmid pBac[3xP3-DsRed, HS-white intron 2] [35] was replaced with the 74 bp White intron 2 (X02974) of Drosophila melanogaster and flanking MCSs (PstI, AscI, AflII, AatI and NdeI in 5’ end, SpeI, BspEI, AfeI and SfuI in 3’ end) as a spacer/linker, cut and inserted with the flanking Hpal and NotI (Fig. 1B). Then, the 600 bp fragment containing D. melanogaster Hsp70 promoter/white intron 2/Hsp70 polyA, from the newly-built pBac[3xP3-DsRed, HS-white intron 2], was cloned into the transposon piggyBac-based vector pBac[3xP3-EGFPafm] [36], cut and inserted both with the unique AfeI. The Hsp70 promoter directs transcription from piggyBacL to SV40 polyA in the new pBac[3xP3-EGFPafm, HS-white intron 2] (Fig. 1A). Finally, the 2435 bp containing the plasmid origin of replication (pUC ori) and ampicillin resistant gene [PAP] in the pBac[3xP3-EGFPafm, HS-white intron 2] was moved from between piggyBacR and piggyBacL to between piggyBacL and the Hsp70 promoter. Unique restriction enzyme (RE) sites, PsiI, BclII, and SphI, were inserted between piggyBacR and pUC ori and a different set of unique sites, FnuI, AscI, BstXI, and BsuNI, were inserted between the Hsp70 promoter and the ampicillin resistant gene (Fig. 1A).

Using Pogostick to make new vectors for candidate gene over-expression and down-regulation: an example with DsRed and Ubx

DsRed cDNA. The 681 bp of DsRed complete cDNA (AY609780.1) was amplified with PCR from pBac[3xP3-DsRed] [36] using forward primer AGGCCTCTCAATGUTGGCGCGCTCTGAAAGACCTCAT and reverse primer TCTGACGGATCCCCGACACCA. The length for this PCR fragment was first digested with XbaI and purified with QIAprep Miniprep Kit (Qiagen), before being inserted into Pogostick at different positions.

Over-expression DsRed vectors. Two DsRed over-expression vectors were constructed by cloning DsRed cDNA into each of the two MCSs of Pogostick: One between the Hsp70 promoter and the white intron and the other between the white intron and Hsp70 polyA tail (Fig. 2). For the first vector, Pogostick-up-1, previously digested DsRed cDNA was cloned into the Ndel restriction site in Pogostick. A phosphatase [Apex TM Heat-Labile Alkaline Phosphatase, Epicentre] was used for dephosphorylation of the cut vector ends prior to cloning to prevent recircularization. Competent cells (JM109, Promega) were transformed with the plasmid and grown on ampicillin selective medium. Clones were picked and confirmed to contain the insert via PCR amplification and sequencing with primers HSPI-1 (TCAACTGCAACT-TACTGAAATCTGCCA) and HSPI-1 (ACACAGATCAGG CGACTGCGGAA: intron-analyzed). The length for this amplicon was 833 bp. For the second vector, Pogostick-up-2, DsRed was cloned into SpeI of Pogostick and PCR amplification and sequencing of (picking clones) was done with primers HSP2-F (TCCGAGTCCGGTCTGATCGT; intron-analyzed) and HSP2-R (TGCAGGGATCCCGACACCA). The length for this amplicon was 845 bp. Both plasmids, Pogostick-up-1 and Pogostick-up-2 were 8,259 bp long.

Over-expression Ubx vector. We obtained a plasmid with the complete coding sequence (762 bp) of Junonia coenia cDNA (gi|18353619) from Sean Carroll’s lab. Using primer sets Ubx-Junonia-FW: AGGCCTCTAGAATGCAATCCTATTACTCCA AGCA and Ubx-Junonia-RV: GTCCATCTAGATTAGTG CTCGGGTTGGCCT we PCR-amplified the complete Ubx sequence while adding Ndel restriction sites (bold) at both ends of the amplicon. Then we followed the cloning steps detailed above in order to insert Ubx into the MCS of Pogostick immediately following the Hsp70 promoter. We used primers Clone-RV: AAGCAGTACTGCTTCGTT and Ubx-Junonia-RV to pick up positive clones for sequence conformation.

Down-regulation DsRed vectors. Two down-regulation vectors were constructed based on Pogostick-up-1 and Pogostick-up-
For the first vector, using Pogostick-up-1, DsRed cDNA was cloned into SpeI in reverse direction to produce Pogostick-down-FR, whose correct ligation was confirmed by the size (845 bp) and the sequence of the amplicon using primers HSP2-F and HSP2-R (Fig. 3A). Similarly, using Pogostick-up-2 as the starting plasmid, DsRed was cloned into NheI in reverse direction to produce Pogostick-down-RF, whose correct ligation was confirmed by the size (833 bp) and sequence of the PCR amplicon using primers HSP1-F and HSP1-R (Fig. 3C). Both copies of DsRed cDNA were in a reverse orientation inside each vector, but each vector had a different general orientation of the sequences (compare Figs. 3A and 3C).

**Drosophila transformation and bioassays**

**Drosophila transformation.** We tested three over-expression constructs, Pogostick (control vector), Pogostick-up-1 and Pogostick-up-2, and two down-regulation constructs, Pogostick-down-FR and Pogostick-down-RF, by injecting each separately into wild-type white-D. melanogaster together with the piggyBac helper plasmid, pbac-pBac [37]. Stable lines were produced by using balancer chromosomes. Pogostick-down-FR and Pogostick-down-RF lines were then separately crossed with a pbac[3×P3-DsRed]/ line that constitutively expresses DsRed in the eyes and central nervous system [38], to produce transheterozygous situations. Germ line transformation and rearing of D. melanogaster were conducted with the methods described in [39].
Over-expression bioassays. About 50 2nd instar larvae were separately collected from *Pogostick* (control), *Pogostick-up-1* and *Pogostick-up-2* lines and placed in a Petri dish on some food. Five larvae from each line were randomly picked, photographed under a fluorescent microscope (Nikon SMZ1500) and fixed in RNAlater (Ambion). The other larvae were subject to 1.5 hours of heat-shock at 39°C in an incubator and then returned back to room temperature (20°C). Groups of five larvae were randomly picked at 2 hr, 6 hr, 12 hr, 24 hr, 36 hr and 48 hrs after the heat shock, respectively, photographed and then fixed in RNAlater. The same treatment was applied to young pupae, but the heat shock period was 3 hr.

Down-regulation bioassays. Larvae and pupae from three lines: Homozygous pBac[3×P3–DsRedaf] (control), transheterozygous *Pogostick–down2FR* × pBac[3×P3–DsRedaf] and *Pogostick–down2RF* × pBac[3×P3–DsRedaf] were collected and treated as described above for the over-expression lines.

Bicyclus transformation and bioassays

**Bicyclus transformation.** A total of 3035 eggs were injected with 25 ul of *pogostick-Ubx-up1* (1.2 ug/ul) mixed in with 25 ul of the helper plasmid (800 ng/ul). We obtained 431 hatchings (14% hatching rate). From these larvae, 145 (34%) survived to the adult stage. We crossed males and females in two separate mating cages. One cage (#1) had 43 females crossed to 30 males. The other cage (#2) had 43 females crossed with 29 males. While screening the offspring of these two mating cages we picked a single male from cage #2 with extremely bright eyes (when viewed under a fluorescent scope with a EGFP filter) and mated him with 12 virgin females. This male and two of his offspring, all with bright green eyes, were later confirmed as positive for *EGFP*. Roughly half the F2 offspring of this male (127) displayed bright stemmata (larval eyes) whereas the other half looked wild type, suggesting that the insertion was at a single locus. Several (around 30) bright-eyed heterozygous F2 individuals were crossed with each other to produce a F3 generation. All F3 individuals were photographed under the fluorescent scope. They segregated according to Mendelian ratios. From 77 females, 16 had a wild-type phenotype (expected frequency = 19), and the other females had very bright or immediately bright eyes in approximately the predicted ratios for homozygous and heterozygous classes. Eight females and six males with the brightest eyes were selected for parents of a F4 generation in order to produce an homozygous line. We subsequently performed the qPCR experiments using offspring from this line.

**Over-expression bioassays.** Fifth instar Ubx transgenic larva were put into plastic cups and heat-shocked for 3 hrs at 39°C. Immediately after the heat-shock, 3 larvae were collected (0 hrs) whereas the rest were moved (still inside cups) to the normal rearing temp of 27°C. Three additional larvae were collected at 5, 10, 15, and 20 hours after the end of the heat shock. Three control non-heat-shocked larvae were also collected. Immediately after collection larva were decapitated and gutted. About 25 mg of tissue was then cut off and set aside for RNA extraction. These samples were kept frozen at −80°C until RNA extraction.

**Real-time q-PCR**

Total RNA isolation from larvae and pupae kept in RNAlater (*Drosophila*) or kept at −80°C (*Bicyclus*) was performed using an RNeasy Mini kit (Qiagen). RNA was treated with RNase-free

Figure 2. Alternative locations where a candidate gene can be inserted for over-expression experiments. Top: the gene is inserted just before the white intron. Bottom: the target gene is inserted just after the intron. Insertions at both positions are also possible.

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**Figure 3. Secondary structures of alternative hairpin-loops in RNAi constructs.** A and C correspond to structures before the intron is spliced and B and D correspond to structures after splicing, both when the transgene fragment is inserted into *NheI* and *SpeI* restriction enzyme sites. Red and green denote complementary sequences of the fragment with the arrows indicating 5’ to 3’ sequence orientation.

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Plasmid: A New Versatile piggyBac Vector

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DNase I (Qiagen) to eliminate genomic DNA. cDNA was reverse-transcribed from total RNA using random primers and using a High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Real-time q-PCR was performed with TaqMan Universal PCR Master Mix and Custom TaqMan Gene Expression Assays in STANDARD mode using the Applied Biosystems 7500 Fast Real-Time PCR System. Eukaryotic 18 S rRNA was used as the endogenous control. Relative quantification in 2^{ΔΔCt} [40] was normalized to the 18 S rRNA to indicate levels of DsRed and Ub transcripts.

Obtaining flanking sequence to Pogostick genomic insertions

A plasmid-rescue technique was used to obtain flanking genomic sequences for each side of the Pogostick insertion in the Drosophila lines, via two separate experiments, using genomic DNA of the transformed individuals. Briefly, each experiment used a unique restriction enzyme that cuts at one of the known ends of the ampicillin resistant and pUC ori sequence block and at multiple unknown locations throughout the genome. Genomic fragments are then circularized into plasmids by ligation, inserted into competent bacterial cells and cells grown in ampicillin selective medium. Only cells containing a plasmid with the ampicillin resistant gene and origin of replication should survive. These plasmids also contain either right or left Pogostick flanking genomic sequences.

Genomic DNA of transformed Drosophila was extracted with a Qiagen DNeasy kit and digested with BsaNI in order to DNA target genomic sequences adjacent to the terminal inverted repeat (TIR) of piggyBacL. Other alternative unique vector RE sites are BsrHI, BamHl, AoeI or ForI. After a plasmid mini-prep, genomic sequences were obtained using the piggyBacL-anchored sequencing primer 5’-AACAAGCTCTGATCATCGTTT-3’. Genomic sequences adjacent to piggyBacR were obtained using RE BlclI (alternatively, Prel or SdaI can also be used) and the piggyBacR-anchored sequencing primer 5’-CATGAATGACGGGGAGATTT-3’. No restriction enzyme that cuts inside the transgenes should be used. The diversity of sequences obtained from multiple plasmids gives a lower estimate of Pogostick insertion copy number. A Southern blot (see [35]), on the other hand, will estimate total insertion numbers.

Results and Discussion

Pogostick main features

Pogostick was designed to facilitate cloning of candidate genes to produce either over-expression or down-regulation vectors. For the construction of over-expression vectors, the full-length cDNA of the target gene should be inserted into either the 5’-MCS, the 3’-MCS, or into both sites (Fig. 1B). For the construction of down-regulation vectors, a cDNA fragment of the target gene should be inserted into both MCS sites, in reverse orientation, to form inverted repeats (IR), hairpin RNA structures that can specifically silence gene expression via the mechanism of RNAi. Pogostick can be found at www.addgene.org, a non-profit plasmid repository.

The Multiple Cloning Sites. The design of the two multiple cloning sites of Pogostick (Fig. 1B), with carefully chosen RE recognition sequences, give the vector its versatility and ease of use for multiple candidate genes. Two of these sites, NheI (in the 5’ MCS) and SpeI (in the 3’ MCS), should be sufficient for most cloning strategies, but other sites were also included as back-up. The basic idea is to use one of a suite of four alternative REs, NheI (5’-GCTAGG-3’), SpeI (5’-ACTAGT-3’), Avrl (5’-CCTAGG-3’) and XbaI (5’-TCTAGA-3’), all producing the same sticky ends, 5’-CTAG-3’, to digest any candidate gene fragment before cloning it into Pogostick. Each gene fragment, in turn, has one of these sites added to its ends via the use of modified PCR primers (see specific example for DsRed below). In addition, the RE chosen for cloning each gene fragment into Pogostick should not cut the gene at any other site, aside from the artificially extended ends. For down-regulation vectors, the size of the cDNA fragment should be between 300-1000 bp in length, as this triggers stronger silencing than shorter fragments [41] and should preferably be a single complete exon from the target gene, since exons often contain sequences that facilitate the processing of transcripts [41]. Exons that are known to be alternatively spliced should be avoided, since these might contain silencing sequences that repress or restrict splicing [41].

The inducible heat-shock promoter. The heat-shock promoter of Hsp70 of Drosophila and its polyA signal, shown to work across different insect species including mosquitoes, moths, sawflies and butterflies [34,35,42,43] were used as the inducible promoter and transcription termination signal in this vector (Fig. 1A). The temporal control of transgene over-expression and down-regulation via a heat-shock is especially important when the genes in question have multiple functions during development, allowing each of these functions to be investigated separately.

In case the Drosophila promoter does not work efficiently in a particular species, as demonstrated in Tribolium castaneum [44], it can be replaced using the following steps: The new promoter should be amplified with primers PromoterF (ATTACCTT-GAGTC + 10 bp of the most 5’ sequence of the new promoter) and PromoterR (TCGCTTAATATTAGT + the reverse complement sequence of the most 3’ 10 bp of the new promoter) from DNA containing the new promoter sequence. The amplified fragment and the Pogostick vector should then be digested with AoeI and PseI, and the digested promoter fragment inserted and ligated into the cut vector. The insertion should be confirmed through 5’ sequencing with primer TCGAGCTTAAGaGATCTGTCA (producing 57 bp of old vector + 5’ end of the new insertion) and/or 3’ sequencing with primer TGACAGATGTGTTAGCAG (producing 10 bp of old vector + 3’ end of the new insertion).

The 3xP3-EGFP marker for transgenesis. The 3xP3-EGFP cassette that mediates EGFP expression in all larval, pupal, and adult eyes of Diptera, Lepidoptera and Coleoptera tested so far [38,45,46] and predicted to work across metazoa with eyes, was used as the marker for transgenesis (Fig. 1A).

The white intron. An intron (the second intron of the white gene from D. melanogaster) positioned between the two MCSs (Fig. 1B) has multiple functions. First, it provides an anchor for primers when these are used to check the orientation of the inserted transgenes. Second, the intron stabilizes both the expression of the transgene [47] and the plasmid replication in E. coli [41]. Thirdly, having a spacer between the IRS is known to strongly enhance RNAi silencing activity in plants [48] and produce strong and uniform RNAi silencing in Drosophila [41]. Flanking the intron sequence we placed consensus sequences that code for short intron splicing throughout all organisms (GTAGCAGC at the 5’-end and GTAGTGT at the 3’-end [49]). These splice sites remove the white intron after the mRNA is transcribed (Figs. 1B, 3A, 3C).

In the event that this intron needs to be replaced, the new intron should be amplified with primers InteronF (TTAAGGTAGCAG + 10 bp of the most 5’ sequence of the new intron) and InteronR (CCCGAAGTGTAGC + the reverse complement sequence of the most 3’ 10 bp of the new intron) from donor DNA. The amplified fragment and the Pogostick vector should then be digested with NheI and SpeI, and the digested intron fragment inserted and ligated into the cut vector. The insertion should be confirmed through 5’
sequencing with primer CAAGCGCAGCTGAACAAGCTA (producing 187 bp of old vector + 3’ end of the new intron) and/or 3’ sequencing with primer AGAATGTAGAATGACGTGTA (producing 368 bp of the old vector + 3’ end of the new intron).

**Construction of DsRed specific vectors**

The cloning strategy outlined above, using only XbaI, NheI, SpeI or AvrII REs was successfully applied to construct DsRed and Ubx over-expression vectors using both of the Pogostick MCS (Pogostick-up-1, Pogostick-up-2) and DsRed down-regulation vectors (Pogostick-down-FR and Pogostick-down-RF). Subsequently, other over-expression and down-regulation vectors were also constructed using the same cloning strategy, suggesting its wide applicability for different genes. Over-expression vectors were made using the 1077 bp full-length Distal-less CD (AF404825) and the 1059 bp full-length engrailed CD (unpublished) of the butterfly Bicyclus anynana. And down-regulation vectors were constructed with CD fragments of wingless (459 bp, unpublished), decapentaplegic (437 bp, unpublished) and spalt (140 bp, unpublished) of B. anynana.

**Over-expression assays in Drosophila**

DsRed mRNA was similarly over-expressed in both Drosophila transformed Pogostick-up-1 (Fig. 4A) and Pogostick-up-2 lines (not shown), induced by 1.5 hrs of heat-shock at 39°C for larvae and 3 hrs for pupae. mRNA levels were at their maximum at the 7.5 hrs (45 fold higher) and 9 hrs (30 fold higher) sampling points after the beginning of the heat-shock for larvae and pupae, respectively (Fig. 4A). Levels declined with time and returned back to pre-heat-shock levels at 49.5 hrs and 51 hrs for larvae and pupae, respectively. Protein levels were visibly elevated at 27 hrs after the beginning of the heat-shock for pupae, as detected by fluorescence microscopy (Fig. 5). Protein levels continued to visibly rise from 27 hrs to 51 hrs, indicating that DsRed protein was not readily degraded (Fig. 5). There appears to be an 18 hrs time lag for DsRed mRNA transcripts to produce a functional fluorescing protein. Larvae showed a similar protein expression pattern to the

![Graph A](image1.png)  ![Graph B](image2.png)

**Figure 4. Heat-shocks lead either to DsRed mRNA over-expression or down-regulation in Drosophila larvae and pupae.** Quantitative RT-PCR analysis of DsRed mRNA levels in D. melanogaster in an over-expression line Pogostick-up-1 (A) and down-regulation line (B; resulting from a cross between pBac[3×P3−DsRedaf] and Pogostick-down-RF homozygous parents). Relative quantification in 2^ΔΔC_T indicate the levels of DsRed transcript normalized to the internal standard 18S rRNA. Error bars indicate the range of minimum and maximum levels of four repeats. Larvae were heat-shocked for 1.5 hrs at 39°C, and pupae for 3 hrs at 39°C.

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pupae (not shown). Three hour heat-shocks (applied to pupae) did not appear to produce more extreme mRNA or protein expression levels as compared to 1.5 hrs heat-shocks applied to larvae. There was no change in levels of red fluorescence in either the Pogostick control vector lines or in wildtype flies (Fig. 5) with the heat-shock treatments. Pogostick control lines constitutively expressed the EGFP marker in the eyes (not shown).

**Down-regulation assays in Drosophila**

DsRed mRNA levels were significantly reduced 7.5 and 9 hrs after the beginning of the heat-shock for larvae and pupae, respectively (Fig. 4B). mRNA levels continued to gradually decline until 25.5 hrs or 27 hrs for larvae and pupae, but returned to pre-heat-shock levels at 37.5 hrs and 39 hrs for larvae and pupae, respectively. The slight increase in mRNA levels immediately following the heat-shock could represent detection of the hairpin-loop dsRNA structure before the RNAi mechanism takes effect (Fig. 4B). Protein levels declined slightly from 15 to 27 hrs and declined more abruptly from 27 to 39 hrs after the beginning of the heat-shock for pupae, as detected by fluorescent microscopy (Fig. 5). Levels remained low at 51 hrs after the heat-shock (Fig. 5).

There appears to be a delay of around 30 h from the moment low mRNA levels are detected (9 hrs) to visibly reduced protein levels (39 hrs). Larvae showed a similar protein expression pattern to the pupae (not shown). Three and 1.5 hrs heat-shocks produced similar results.

**Correct intron splicing**

The correct splicing of the White intron was verified by sequencing the mature mRNA transcripts of DsRed over-expression and down-regulation Drosophila transformed lines. The sequence was confirmed to be that shown in Figs 3B and 3D.

### Table 1. PiggyBac transposition in Drosophila germlines.

| Germline         | FGSL          | FGSR                  | Chromosome | Gene Name | Insertion Position |
|------------------|---------------|-----------------------|------------|-----------|--------------------|
| Pogostick        | AGGTTGCGGTTAA | TTAACCTCAGGTCT        | X          |           | intergenic         |
| Pogostick-up-2   | AGCATATATTAA  | TTAATTGCATTAT         | 2L         | CG7261-PA | intron             |
| Pogostick-down-RF| AATTATTATTTAA | TTAATTTTATCAT         | 3R         |           | intergenic         |
|                  | GTTCATGTAGTTAA| TTAACCTGTTTGT         | U          |           | intergenic         |

The flanking genomic sequences obtained with insertion site TTA at the piggyBacL and piggyBar are shown separately as FGSL and FGSR.

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**Figure 5. DsRed fluorescence following a heat-shock in Drosophila pupae.** Heat-shocks lead either to increased (A) or decreased (B) DsRed protein levels. Pupal phenotypes of wild-type, over-expression (Pogostick-up-1), and down-regulation (resulting from a cross between pBac[3×3–DsRedf] and Pogostick-down-RF homozygous parents) lines targeting the DsRed gene in transgenic Drosophila, before and after a heat-shock (HS). Fluorescence in wild-type lines remained constant, whereas DsRed levels visibly increased or decreased 27 hrs and 39 hrs after the beginning of the HS, respectively.

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Flanking sequences to Pogostick insertions

Five independent genomic sequences adjacent to piggyBacL TIR were recovered from Pogostick, Pogostick-up-2 and Pogostick-down-RF lines, using the unique RE site BstSNI. All of these sequences contained genomic DNA flanking the TIR, with the signature TTAA sequence at the integration site (Table 1). Corresponding genomic sequences adjacent to piggyBacR and confirmation of TTAA duplications were also obtained using the unique RE site BstCI (Table 1). The detection of piggyBacL adjacent sequences was more effective than the detection of piggyBacR adjacent sequences, as the produced plasmids were relatively smaller. Therefore, the detection of piggyBacL-adjacent genomic sequence with BstSNI is recommended.

Producing homozygous lines

In the current manuscript we used Drosophila genetic tools (balancer chromosomes) and levels of eye fluorescence in Bicyclus to produce homozygous transgenic lines. In the event that levels of eye fluorescence are difficult to distinguish between homozygous and heterozygous individuals, it is still possible to generate a homozygous line using the identified genomic flanking sequence

Over-expression assays in Bicyclus

Ubx mRNA levels were at their maximum immediately after the end of the heat-shock (3 hrs) (80 fold higher relative to non-heat-shocked controls) (Fig. 6). Levels declined with time and returned to close to pre-heat-shock levels at 23 hrs after the beginning of the heat-shock. The accelerated production of Ubx mRNA in Bicyclus relative to DsRed mRNA in Drosophila may have to do with the higher rearing temperature used for Bicyclus (27 °C relative to 20 °C for Drosophila). This may also explain why the degradation of the mRNA for Bicyclus also happened at about twice the speed as that observed for Drosophila.

In conclusion, the new piggyBac vector Pogostick has the following traits: 1) it can be used to induce the over-expression and down-regulation of candidate genes in a temporally controlled fashion by means of a heat-shock and; 2) it allows for the easy characterization of the genomic insertion site and copy number. The vector is available to anyone wanting to test it in different organisms. Future improvements to this vector may include addition of insulator elements to the ends of the piggyBac TIRs that may insulate the expression of the vector from position effects [51] and/or the addition of a attP site that will later allow the very efficient phiC31 integrase-mediated recombination to modify, replace or stabilize transgenes at the same genomic location [52,53].

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Author Contributions

Conceived and designed the experiments: BC AM. Performed the experiments: BC SH OP JBS AM. Analyzed the data: BC OP AM. Wrote the paper: BC AM. Critically revised manuscript and approved it for publication: BC SH JBS OP EAW AP AM.

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Figure 6. Levels of Ubx mRNA in transgenic Bicyclus anynana larvae before and after a heat-shock. A single 3 hr heat-shock lead to nearly a 80 fold increase in Ubx levels in Bicyclus larvae. Note that pre heat-shock levels are near zero because the levels we are measuring correspond to Junonia Ubx (the transgene used), rather than Bicyclus Ubx.

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