The pGinger family of expression plasmids

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Abstract

The pGinger suite of expression plasmids comprises 43 plasmids that will enable precise constitutive and inducible gene expression in a wide range of gram-negative bacterial species. Constitutive vectors are composed of 16 synthetic constitutive promoters upstream of RFP, with a broad host range BBR1 origin and a kanamycin resistance marker. The family also has seven inducible systems (Jungle Express, Psal/NahR, Pm/XylS, Prha/RhaS, LacO1/LacI, LacUV5/LacI, and Ptet/TetR) controlling RFP expression on BBR1/kanamycin plasmid backbones. For four of these inducible systems (Jungle Express, Psal/NahR, LacO1/LacI, and Ptet/TetR), we created variants that utilize the RK2 origin and spectinomycin or gentamicin selection. Relevant RFP expression and growth data have been collected in the model bacterium

Escherichia coli as well as *Pseudomonas putida*. All pGinger vectors are available via the Joint BioEnergy Institute (JBEI) Public Registry.

Introduction

Precise and reliable control over gene expression is one of the most fundamental requirements of synthetic and molecular biology (1). Consequently, there has been considerable effort towards identifying myriad genetic elements that enable researchers to regulate the strength and timing of transcription across all domains of life (2–4). The end result of these efforts are often consolidated families of plasmid vectors that facilitate advanced genetic engineering, such as the BglBrick family of plasmids for *E. coli (5, 6)* and the jStack vectors used in multiple plant species (7). However, as the field of synthetic biology moves beyond traditional model organisms, families of expression vectors must be tailored to meet the specific requirements of particular hosts. Advances in non-model organisms often come in the form of species or genus specific toolkits (8–10), though more recently comprehensive plasmid toolkits have been developed and validated for a wide range of gram-negative organisms (11). Resources such as the Standard European Vector Architecture (SEVA) platform provide repositories of standardized sequences and constructs (12, 13). Still, given that many bacteria require very particular combinations of promoters, origins, and selectable markers to enable controlled gene expression, there remains a need for vectors that will allow rapid prototyping of genetic circuits in understudied bacteria.

To facilitate the exploration of non-model hosts, we have developed a small suite of plasmids that permit both constitutive and inducible expression from the broad host-range origin of replication BBR1 using a kanamycin selection marker. For a subset of the inducible systems that are known to work across multiple hosts, we have assembled combinatorial variants that

utilize the compatible broad host-range origin RK2 (14) as well as both spectinomycin and gentamicin selection markers. This family of plasmids, which we have named the pGinger suite, requires no assembly of these parts, can be easily cloned into via standard Gibson assembly techniques, and has both digital sequences and physical samples that can be publicly accessed through the Joint BioEnergy Institute (JBEI) registry (15).

Results

Design and Architecture of pGinger Plasmids

All pGinger vectors express RFP with a consensus ribosomal binding site (RBS - TTTAAGAAGGAGATATACAT) derived from the BglBrick plasmid library. The overall conserved plasmid architecture and naming convention of the pGinger suite are shown in **Figure 1**.

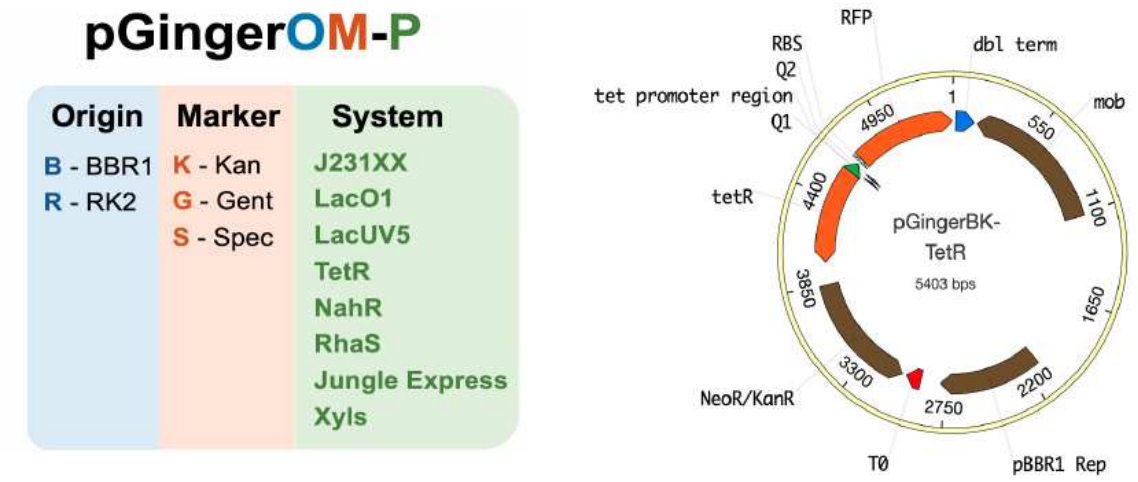

Figure 1: **Plasmids architecture of the pGinger suite**: The pGinger plasmids share a common naming convention where the first two letters after pGinger correspond to the origin and resistance marker respectively, followed by the expression system. All plasmids share the same architecture as the above map of pGingerBK-TetR, whereby a

conserved RBS-RFP is downstream of the promoter followed by a strong terminator. All selectable markers are upstream of the promoter, with the origin between the marker and the RFP cassette.

The BBR1 origin and kanamycin cassette of relevant pGinger vectors were both derived from plasmid pBADTrfp (16). To develop a family of constitutive expression plasmids, the AraC coding sequence and promoter of pBADTrfp were replaced with 16 different synthetic promoters from the Anderson Promoter Library (http://parts.igem.org/Promoters/Catalog/Anderson). For the inducible vectors, the AraC coding sequence and promoter of pBADTrfp were replaced with the following seven inducible systems: Jungle Express - derived from pTR_sJExD-rfp (17); Psal/NahR - derived from pPS43 (18); Prha/RhaS - derived from pCV203 (18); Ptet/TetR - derived from pBbE2a-RFP (6); Pm/XylS - derived from pPS66 (18); LacO1/LacI - derived from pBbE6a-RFP (6); LacUV5/LacI - derived from pBbE5a-RFP (6). Three of these inducible systems, Pm/XylS, Psal/NahR, Prha/RhaS, utilize an activator or bifunctional transcription factor; the other systems feature transcriptional repressors. These BBR1 vectors contain the *mob* element that facilitates conjugal transfer. For four of the inducible systems (Jungle Express, Psal/NahR, LacO1/LacI, and Ptet/TetR), additional vectors were constructed that varied both the origin and antibiotic marker. All RK2 origins were derived from pBb(RK2)1k-GFPuv (8), while the gentamicin resistance cassette was derived from pMQ30 (19), and the spectinomycin cassette was derived from pSR43.6 (20). The RK2 vectors do not contain the *mob* element. A full description of each pGinger vector can be found in **Table 1**.

Name	Origin	Marker	Promoter Class	System	Inducer	JBEI ICE No.
pGingerBK-J23100	BBR1	Kanamycin	Constitutive	J23100	NA	JPUB_020797

pGingerBK-J23101	BBR1	Kanamycin	Constitutive	J23101	NA	JPUB_020799
pGingerBK-J23102	BBR1	Kanamycin	Constitutive	J23102	NA	JPUB_020815
pGingerBK-J23103	BBR1	Kanamycin	Constitutive	J23103	NA	JPUB_020801
pGingerBK-J23104	BBR1	Kanamycin	Constitutive	J23104	NA	JPUB_020803
pGingerBK-J23105	BBR1	Kanamycin	Constitutive	J23105	NA	JPUB_020817
pGingerBK-J23106	BBR1	Kanamycin	Constitutive	J23106	NA	JPUB_020793
pGingerBK-J23107	BBR1	Kanamycin	Constitutive	J23107	NA	JPUB_020819
pGingerBK-J23108	BBR1	Kanamycin	Constitutive	J23108	NA	JPUB_020821
pGingerBK-J23110	BBR1	Kanamycin	Constitutive	J23110	NA	JPUB_020805
pGingerBK-J23111	BBR1	Kanamycin	Constitutive	J23111	NA	JPUB_020807
pGingerBK-J23113	BBR1	Kanamycin	Constitutive	J23113	NA	JPUB_020809
pGingerBK-J23114	BBR1	Kanamycin	Constitutive	J13114	NA	JPUB_020811
pGingerBK-J23117	BBR1	Kanamycin	Constitutive	J13117	NA	JPUB_020795
pGingerBK-J23118	BBR1	Kanamycin	Constitutive	J23118	NA	JPUB_020823
pGingerBK-J23119	BBR1	Kanamycin	Constitutive	J23119	NA	JPUB_020813
pGingerBK-JE	BBR1	Kanamycin	Inducible	Jungle Express	Crystal Violet	JPUB_020825
pGingerBK-NahR	BBR1	Kanamycin	Inducible	Psal/NahR	Salicylic acid	JPUB_020831
pGingerBK-RhaS	BBR1	Kanamycin	Inducible	Prha/RhaS	Rhamnose	JPUB_020829
pGingerBK-TetR	BBR1	Kanamycin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020835
pGingerBK-XylS	BBR1	Kanamycin	Inducible	Pm/XylS	Benzoate	JPUB_020827
pGingerBK-Lac	BBR1	Kanamycin	Inducible	LacO1/LacI	IPTG	JPUB_020833
pGingerBK-LacUV5	BBR1	Kanamycin	Inducible	LacUV5/LacI	IPTG	JPUB_020837
pGingerBG-JE	BBR1	Gentamicin	Inducible	Jungle Express	Crystal Violet	JPUB_020847
pGingerBS-JE	BBR1	Spectinomycin	Inducible	Jungle Express	Crystal Violet	JPUB_020855
pGingerRK-JE	RK2	Kanamycin	Inducible	Jungle Express	Crystal Violet	JPUB_020871
pGingerRG-JE	RK2	Gentamicin	Inducible	Jungle Express	Crystal Violet	JPUB_020881
pGingerRS-JE	RK2	Spectinomycin	Inducible	Jungle Express	Crystal Violet	JPUB_020863
pGingerBG-NahR	BBR1	Gentamicin	Inducible	Psal/NahR	Salicylic acid	JPUB_020845
pGingerBS-NahR	BBR1	Spectinomycin	Inducible	Psal/NahR	Salicylic acid	JPUB_020853
pGingerRK-NahR	RK2	Kanamycin	Inducible	Psal/NahR	Salicylic acid	JPUB_020869
pGingerRG-NahR	RK2	Gentamicin	Inducible	Psal/NahR	Salicylic acid	JPUB_020879

pGingerRS-NahR	RK2	Spectinomycin	Inducible	Psal/NahR	Salicylic acid	JPUB_020859
pGingerBG-TetR	BBR1	Gentamicin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020843
pGingerBS-TetR	BBR1	Spectinomycin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020851
pGingerRK-TetR	RK2	Kanamycin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020865
pGingerRG-TetR	RK2	Gentamicin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020877
pGingerRS-TetR	RK2	Spectinomycin	Inducible	Ptet/TetR	Oxytetracycline	JPUB_020861
pGingerBG-LacO1	BBR1	Gentamicin	Inducible	LacO1/LacI	IPTG	JPUB_020841
pGingerBS-Lac	BBR1	Spectinomycin	Inducible	LacO1/LacI	IPTG	JPUB_020849
pGingerRK-LacO1	RK2	Kanamycin	Inducible	LacO1/LacI	IPTG	JPUB_020867
pGingerRG-LacO1	RK2	Gentamicin	Inducible	LacO1/LacI	IPTG	JPUB_020875
pGingerRS-LacO1	RK2	Spectinomycin	Inducible	LacO1/LacI	IPTG	JPUB_020857

Table 1: **Plasmids in the pGinger suite**: Relevant characteristics of pGinger plasmids including origin of replication, antibiotic selection, promoter characteristics, and if applicable inducing molecule. JBEI public registry numbers are also included for digital accessibility.

Evaluation of Constitutive Expression pGinger Plasmids

To evaluate the relative strength of constitutive Anderson promoters in the context of the pGinger vectors, plasmids were introduced into both *P. putida* and *E. coli*. Fluorescence was measured after growth in LB medium after 24 hours. When fluorescence was normalized to cell density, expression from Anderson promoters showed significant correlation (Spearman's ρ = 0.49, p = 0.045) between *P. putida* and *E. coli* (**Figure 2**). Promoters J23103 and J23113 were significantly stronger in *E. coli* than in *P. putida*, while promoter J23111 was significantly stronger in *P. putida*. Promoter sequences and mean expression values in both *E. coli* and *P. putida* are listed in **Table 2**.

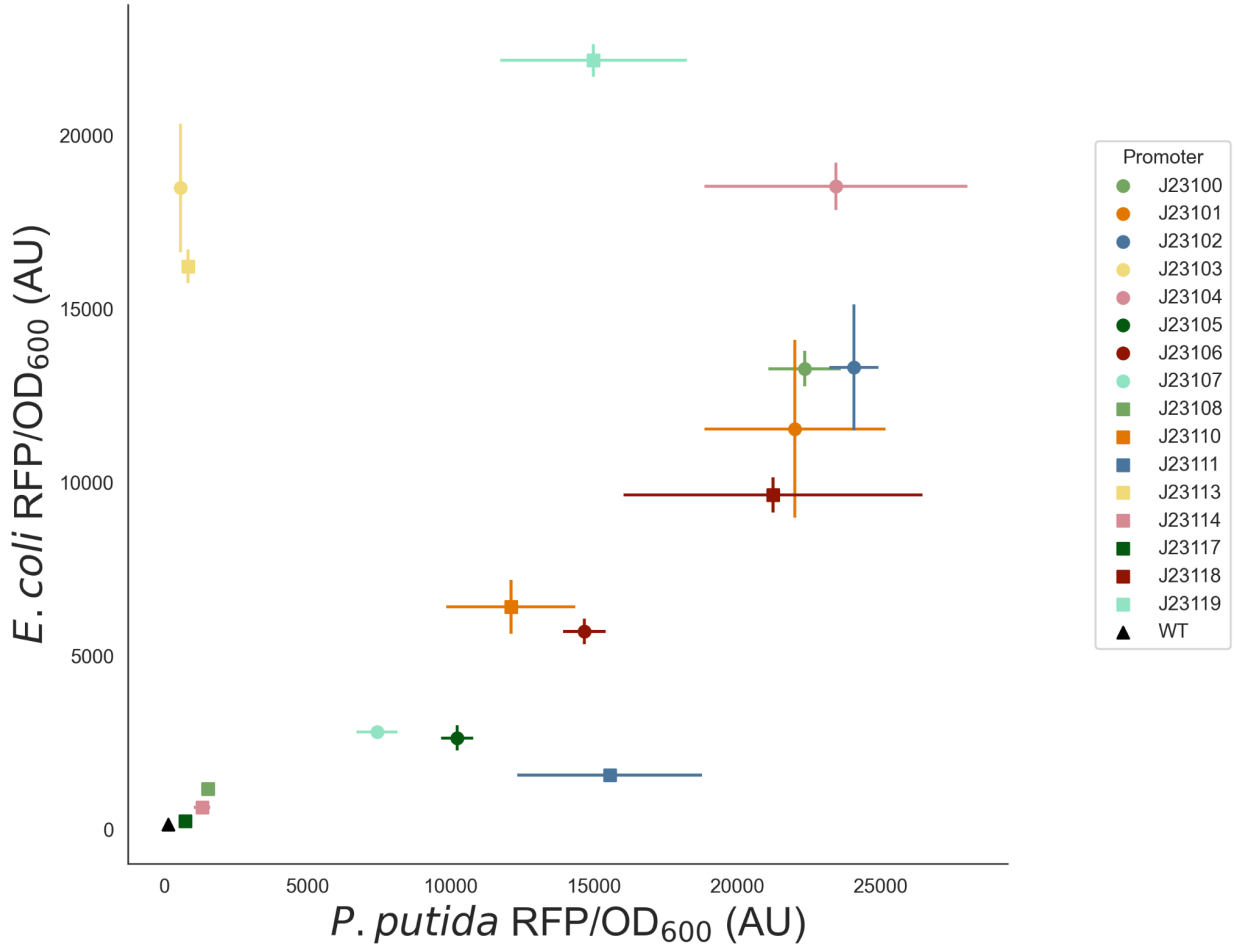

Figure 2: Activity of Constitutive Promoters in *E. coli* and *P. putida*. RFP expression normalized to cell density from Anderson promoters within either *E. coli* (y-axis) or *P. putida* (x-axis) are shown with standard deviations (n=3). The background fluorescence of the two bacteria is indicated by WT (wild-type). Optical density measurements are shown in Figure S1.

Promoter	**Promoter Sequence**	***E. coli* expression**	***P. putida* expression**
J23100	ttgacggctagctcagtcctaggtacagtgctagc	13267 (+/- 517)	22343 (+/- 1262)
J23101	tttacagctagctcagtcctaggtattatgctagc	11530 (+/- 2565)	22010 (+/- 3162)
J23102	ttgacagctagctcagtcctaggtactgtgctagc	13300 (+/- 1815)	24067 (+/- 858)
J23103	ctgatagctagctcagtcctagggattatgctagc	18476 (+/- 1857)	565 (+/- 135)

J23104	ttgacagctagctcagtcctaggtattgtgctagc	18522 (+/- 682)	23440 (+/- 4588)
J23105	tttacggctagctcagtcctaggtactatgctagc	2622 (+/- 363)	10220 (+/- 558)
J23106	tttacggctagctcagtcctaggtatagtgctagc	5697 (+/- 369)	14659 (+/- 748)
J23107	tttacggctagctcagccctaggtattatgctagc	2798 (+/- 44)	7429 (+/- 716)
J23108	ctgacagctagctcagtcctaggtataatgctagc	1149 (+/- 84)	1523 (+/- 84)
J23110	tttacggctagctcagtcctaggtacaatgctagc	6402 (+/- 782)	12098 (+/- 2251)
J23111	ttgacggctagctcagtcctaggtatagtgctagc	1547 (+/- 106)	15548 (+/- 3229)
J23113	ctgatggctagctcagtcctagggattatgctagc	16220 (+/- 480)	826 (+/- 92)
J23114	tttatggctagctcagtcctaggtacaatgctagc	625 (+/- 48)	1325 (+/- 289)
J23117	ttgacagctagctcagtcctagggattgtgctagc	229 (+/- 25)	730 (+/- 28)
J23118	ttgacggctagctcagtcctaggtattgtgctagc	9628 (+/- 507)	21237 (+/- 5215)
J23119	ttgacagctagctcagtcctaggtataatgctagc	22157 (+/- 473)	14979 (+/- 3262)
WT	NA	124 (+/- 6)	141 (+/- 17)

Table 2: Expression of pGinger Anderson promoters: For each Anderson promoter the sequence is provided as well as the mean cell density normalized RFP fluorescence in both *E. coli* and *P. putida*. Standard deviations are provided in parentheses, n=3. The background fluorescence of E. coli is indicated by WT (wild-type).

Evaluation of Inducible pGinger Plasmids

The expression of the seven inducible systems within the pGinger suite was evaluated using the BBR1 origin and kanamycin marker (pGingerBK) against a titration of the inducer in both *E. coli* and *P. putida* (**Figure 3**). All systems showed inducibility in *E. coli*, and all but the rhamnose inducible system Prha/RhaS showed inducibility in *P. putida*. Relevant expression

characteristics of the inducible pGingerBK vectors in both tested bacteria are listed in **Table 3**. The strongest normalized expression from an inducible system in *E. coli* was the Ptet/TetR system, while both the strongest in *P. putida* were found to be Psal/NahR and Jungle Express inducible systems, which showed nearly identical maximal expression. In both bacteria, the Jungle Express system demonstrated the greatest level of induction relative to background expression.

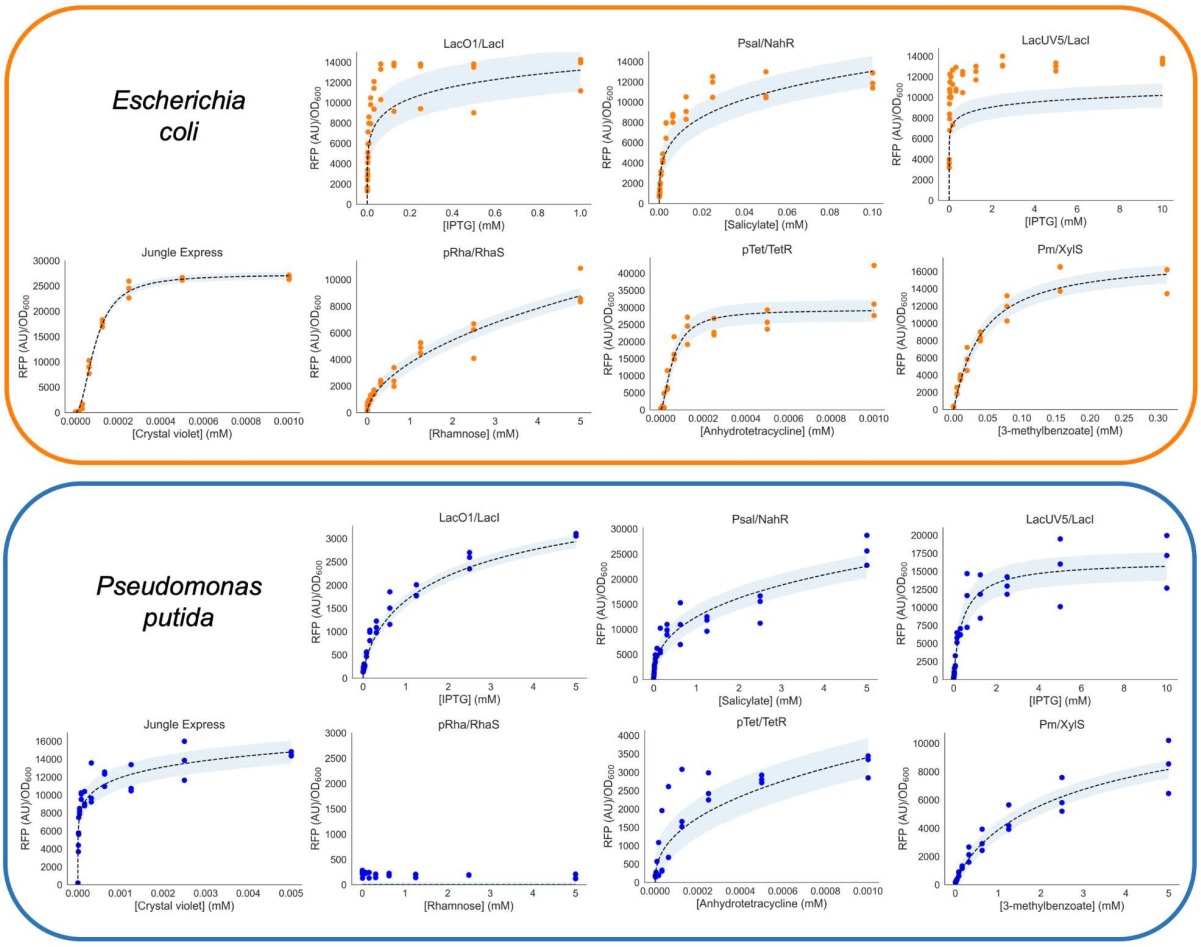

Figure 3: Activity of Inducible Systems in *E. coli* and *P. putida*. RFP expression normalized to cell density (y-axis) from inducible systems within either *E. coli* (top panel in orange) or *P. putida* (bottom panel in blue) as a function of inducer concentration in mM (x-axis). Fits to the Hill equation are shown as dashed lines and shaded to

show confidence intervals. Raw data points are overlaid (n=3). Corresponding optical density measurements are shown in Figure S2.

System	Organism	Background	Max Exp.	Max Conc.	Induction
LacO1/LacI	*E. coli*	1510 (+/- 186)	13127 (+/- 1693)	1 mM	9x
	P. putida	137 (+/- 5)	3074 (+/- 30)	5 mM	22x
Psal/NahR	*E. coli*	762 (+/- 130)	12051 (+/- 759)	100 uM	16x
	P. putida	237 (+/- 5)	25697 (+/- 2976)	5 mM	108x
LacUV5/LacI	*E. coli*	3577 (+/- 36)	10137 (+/- 855)	10 mM	4x
	P. putida	203 (+/- 53)	16622 (+/- 3671)	10 mM	82x
Jungle Express	*E. coli*	104 (+/- 7)	26717 (+/- 418)	1 uM	257x
	P. putida	176 (+/- 5)	14552 (+/- 145)	2.5 uM	83x
Prha/RhaS	*E. coli*	172 (+/- 42)	9251 (+/- 1389)	5 mM	54x
	P. putida	NA	NA	NA	NA
Ptet/TetR	*E. coli*	341 (+/- 10)	33631 (+/- 7692)	1 uM	98x
	P. putida	176 (+/- 9)	3214 (+/- 319)	1 uM	18x
Pm/XylS	*E. coli*	329 (+/- 57)	15280 (+/- 1590)	313 uM	46x
	P. putida	161 (+/- 7)	8401 (+/- 1877)	5 mM	52x

Table 3: Inducible Systems in *E. coli* and *P. putida*: For each inducible system on a BBR1 origin with a kanamycin marker, the experimentally observed background (uninduced) fluorescence and maximal fluorescence are given for both *E. coli* and *P. putida*. Standard deviations are provided in parentheses, n=3. Additionally, the inducer concentration used to achieve maximal expression and the relative induction levels are listed.

To evaluate the effect of varying origin and selectable markers on expression from inducible systems, all six variants of the Jungle Express, LacO1/LacI, Psal/NahR, and Ptet/TetR were investigated for their dose-response to their inducer molecules in *E. coli* (**Figure 4**). Relevant expression parameters are listed in **Table 4**. In general, BBR1 variants showed greater expression than RK2 origin plasmids, which is expected given the higher copy of BBR1 plasmids in *E. coli* (11). Amongst the pGinger Jungle Express vectors, both pGingerRS-JE and pGingerRK-JE showed dose-responses distinct from the other vectors (**Figure 4A**). Notably, all pGingerRS (RK2-Spectinomycin) plasmids showed the lowest expression across each system tested (**Table 4**).

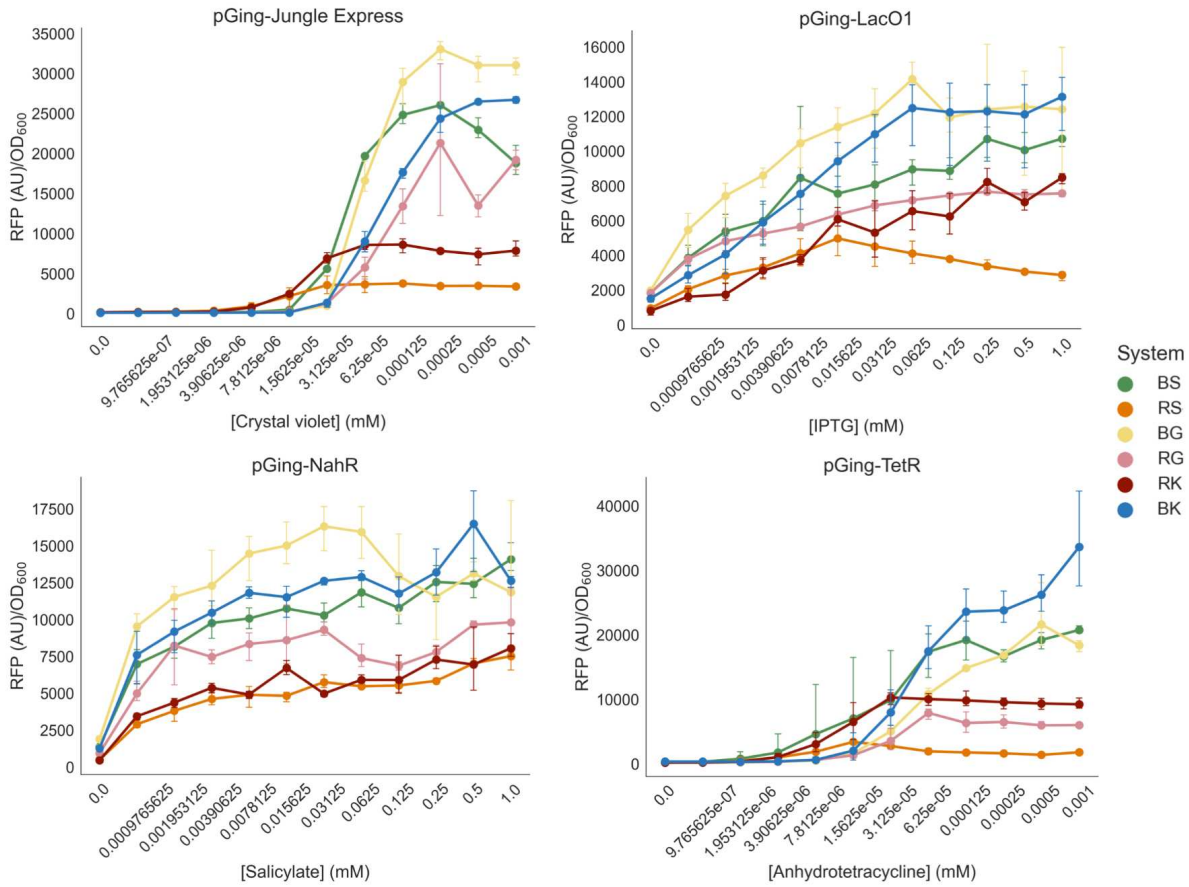

Figure 4: Activity of Inducible pGinger variants in *E. coli*. For origin and selection marker pGinger variants of

Jungle Express (A), LacO1/LacI (B), Psal/NahR (C), and pTet/TetR (D), dose-response curves of normalized RFP expression are shown as a function of mM inducer. Error bars represent standard deviations (n=3). Note that the x-axis is non-linear. Corresponding optical density measurements are shown in Figure S3. Kinetic experiments for these systems are shown in Figure S4-S7.

System	Origin	Marker	Background	Max Exp.	Max Conc.	Induction
LacO1/LacI	BBR1	Kan	1510 (+/- 186)	13127 (+/- 1693)	1 mM	9x
LacO1/LacI	BBR1	Gent	1976 (+/- 70)	14143 (+/- 1608)	63 uM	7x
LacO1/LacI	BBR1	Spec	1830 (+/- 320)	10694 (+/- 943)	250 uM	6x
LacO1/LacI	RK2	Kan	803 (+/- 216)	8213 (+/- 721)	250 uM	10x
LacO1/LacI	RK2	Gent	1823 (+/- 78)	7654 (+/- 230)	250 uM	4x
LacO1/LacI	RK2	Spec	950 (+/- 46)	4967 (+/- 895)	16 uM	5x
Psal/NahR	BBR1	Kan	1260 (+/- 57)	16484 (+/- 1693)	500 uM	9x
Psal/NahR	BBR1	Gent	1877 (+/- 334)	16317 (+/- 1534)	31 uM	9x
Psal/NahR	BBR1	Spec	1372 (+/- 84)	14083 (+/- 984)	1 mM	10x
Psal/NahR	RK2	Kan	445 (+/- 39)	8048 (+/- 859)	1 mM	18x
Psal/NahR	RK2	Gent	934 (+/- 56)	9299 (+/- 460)	1 mM	10x
Psal/NahR	RK2	Spec	482 (+/- 69)	7510 (+/- 817)	1 mM	16x
Jungle Express	BBR1	Kan	104 (+/- 6)	267175 (+/- 418)	1 uM	257x
Jungle Express	BBR1	Gent	136 (+/- 19)	33060(+/- 1185)	250 nM	243x
Jungle Express	BBR1	Spec	152 (+/- 5)	26039 (+/- 355)	250 nM	171x
Jungle Express	RK2	Kan	163 (+/- 27)	8616 (+/- 902)	125 nM	52x
Jungle Express	RK2	Gent	138 (+/- 51)	21314 (+/- 9517)	250 nM	155x
Jungle Express	RK2	Spec	168 (+/- 5)	3763 (+/- 204)	125 nM	22x

Ptet/TetR	BBR1	Kan	341 (+/- 10)	33631 (+/- 7692)	1 uM	98x
Ptet/TetR	BBR1	Gent	351 (+/- 32)	21646 (+/- 5579)	500 nM	62x
Ptet/TetR	BBR1	Spec	232 (+/- 43)	19224 (+/- 3027)	125 nM	83x
Ptet/TetR	RK2	Kan	184 (+/- 5)	10281 (+/- 967)	31 nM	56x
Ptet/TetR	RK2	Gent	232 (+/- 39)	7883 (+/- 865)	63 nM	34x
Ptet/TetR	RK2	Spec	197 (+/- 5)	3399 (+/- 143)	16 nM	17x

Table 4: Inducible pGinger variants in *E. coli*: For pGinger variants of LacO1/LacI, Psal/NahR, Jungle Express, and Ptet/TetR inducible systems, the experimentally observed background (uninduced) fluorescence and maximal fluorescence in *E. coli* are provided. Standard deviations are provided in parentheses, n=3. Additionally, the inducer concentration used to achieve maximal expression and the relative induction levels are listed.

Discussion

The pGinger suite of plasmids offers researchers an array of small, pre-assembled vectors that will permit rapid identification of useful genetic elements in diverse gram-negative bacteria due to the use of broad host-range origins (RK2) and selectable markers known to work across many species (kanamycin, spectinomycin, gentamicin). The compatibility of RK2 and BBR1 origins may also permit researchers to introduce multiple pGinger vectors into a single strain simultaneously (14). In combination with other recent plasmid suites that have been publicly released, the pGinger plasmids have the potential to facilitate more advanced synthetic biology and metabolic engineering efforts in bacterial species that have been traditionally understudied.

Materials & Methods

Strains and Media

Cultures were grown in lysogeny broth (LB) Miller medium (BD Biosciences, USA) at 37 °C for *E. coli* XL1-Blue (QB3 Macrolab, USA) and 30 °C for *P. putida* KT2440 (ATCC 47054). The medium was supplemented with kanamycin (50 mg/L, Sigma Aldrich, USA), gentamicin (30 mg/L, Fisher Scientific, USA), or spectinomycin (100mg/L, Sigma Aldrich, USA), when indicated. All other compounds were purchased through Sigma Aldrich (Sigma Aldrich, USA).

Plasmid Design and Construction

All plasmids were designed using Device Editor and Vector Editor software, while all primers used for the construction of plasmids were designed using j5 software (15, 21, 22). Plasmids were assembled via Gibson Assembly using standard protocols (23). Plasmids were routinely isolated using the Qiaprep Spin Miniprep kit (Qiagen, USA), and all primers were purchased from Integrated DNA Technologies (IDT, Coralville, IA). The fluorescent protein used in all plasmids was mRFP1 (24).

Plasmid and Sequence Availability

All strains and plasmid sequences from Table 1 can be found via the following link to the JBEI Public Registry: https://public-registry.jbei.org/folders/771. Users can request strains via a MTA.

Characterization assays

To characterize RFP expression from these vectors, we measured optical density and fluorescence after growth in 96 well plates for 24 hours. First, overnight cultures were inoculated into 5 mL of LB medium from single colonies and grown at 30 °C or 37 °C. These cultures were

then diluted 1:100 into 500 µL of LB medium with the appropriate antibiotic in 96 square v-bottom deep well plates (Biotix™ DP22009CVS). For characterization of the inducible systems, inducer was added to wells in the first column of the plate at the maximum concentration tested and diluted two-fold across the plate until the last column, which was left as the zero-inducer control. Plates were sealed with a gas-permeable microplate adhesive film (Axygen™ BF400S) and grown for 24 hours at either 30 °C or 37 °C with shaking at 200 rpm. Optical density was measured at 600 nm, and fluorescence was measured at an excitation wavelength of 535 nm and an emission wavelength of 620 nm. All data was analyzed and visualized using custom Python scripts using the SciPy (25), NumPy (26), Pandas, Matplotlib, and Seaborn libraries. Fits to the Hill equation were done as previously described (27).

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Contributions

Conceptualization; A.N.P., M.G.T.; Methodology; A.N.P., M.G.T..; Investigation, A.N.P., M.G.T., L.D.K., C.H., K.M.V., L.M.W.; Writing – Original Draft, A.N.P., M.G.T..; Writing – Review and Editing, All authors.; Resources and supervision; P.M.S, J.D.K.

Competing Interests

J.D.K. has financial interests in Amyris, Ansa Biotechnologies, Apertor Pharma, Berkeley Yeast, Demetrix, Lygos, Napigen, ResVita Bio, and Zero Acre Farms.

References

Bibliography

1. Khalil AS, Collins JJ. 2010. Synthetic biology: applications come of age. Nat Rev Genet 11:367–379.

2. Nielsen AAK, Segall-Shapiro TH, Voigt CA. 2013. Advances in genetic circuit design: novel biochemistries, deep part mining, and precision gene expression. Curr Opin Chem Biol 17:878–892.

3. Zhang Y, Ding W, Wang Z, Zhao H, Shi S. 2021. Development of Host-Orthogonal Genetic Systems for Synthetic Biology. Advanced Biology 5:e2000252.

4. Johns NI, Gomes ALC, Yim SS, Yang A, Blazejewski T, Smillie CS, Smith MB, Alm EJ, Kosuri S, Wang HH. 2018. Metagenomic mining of regulatory elements enables programmable species-selective gene expression. Nat Methods 15:323–329.

5. Anderson JC, Dueber JE, Leguia M, Wu GC, Goler JA, Arkin AP, Keasling JD. 2010. BglBricks: A flexible standard for biological part assembly. J Biol Eng 4:1.

6. Lee TS, Krupa RA, Zhang F, Hajimorad M, Holtz WJ, Prasad N, Lee SK, Keasling JD. 2011. BglBrick vectors and datasheets: A synthetic biology platform for gene expression. J Biol Eng 5:12.

7. Shih PM, Vuu K, Mansoori N, Ayad L, Louie KB, Bowen BP, Northen TR, Loqué D. 2016. A robust gene-stacking method utilizing yeast assembly for plant synthetic biology. Nat Commun 7:13215.

8. Cook TB, Rand JM, Nurani W, Courtney DK, Liu SA, Pfleger BF. 2018. Genetic tools for reliable gene expression and recombineering in Pseudomonas putida. J Ind Microbiol Biotechnol 45:517–527.

9. Phelan RM, Sachs D, Petkiewicz SJ, Barajas JF, Blake-Hedges JM, Thompson MG, Reider Apel A, Rasor BJ, Katz L, Keasling JD. 2017. Development of Next Generation Synthetic Biology Tools for Use in Streptomyces venezuelae. ACS Synth Biol 6:159–166.

10. Calero P, Nikel PI. 2019. Chasing bacterial chassis for metabolic engineering: a perspective review from classical to non-traditional microorganisms. Microb Biotechnol 12:98–124.

11. Schuster LA, Reisch CR. 2021. A plasmid toolbox for controlled gene expression across the Proteobacteria. Nucleic Acids Res 49:7189–7202.

12. Martínez-García E, Fraile S, Algar E, Aparicio T, Velázquez E, Calles B, Tas H, Blázquez B, Martín B, Prieto C, Sánchez-Sampedro L, Nørholm MHH, Volke DC, Wirth NT, Dvořák P, Alejaldre L, Grozinger L, Crowther M, Goñi-Moreno A, Nikel PI, de Lorenzo V. 2023. SEVA 4.0: an update of the Standard European Vector Architecture database for advanced analysis and programming of bacterial phenotypes. Nucleic Acids Res 51:D1558–D1567.

13. Martínez-García E, de Lorenzo V. 2017. Molecular tools and emerging strategies for deep genetic/genomic refactoring of Pseudomonas. Curr Opin Biotechnol 47:120–132.

14. Pasin F, Bedoya LC, Bernabé-Orts JM, Gallo A, Simón-Mateo C, Orzaez D, García JA. 2017. Multiple T-DNA Delivery to Plants Using Novel Mini Binary Vectors with Compatible Replication Origins. ACS Synth Biol 6:1962–1968.

15. Ham TS, Dmytriv Z, Plahar H, Chen J, Hillson NJ, Keasling JD. 2012. Design, implementation and practice of JBEI-ICE: an open source biological part registry platform and tools. Nucleic Acids Res 40:e141.

16. Bi C, Su P, Müller J, Yeh Y-C, Chhabra SR, Beller HR, Singer SW, Hillson NJ. 2013. Development of a broad-host synthetic biology toolbox for Ralstonia eutropha and its application to engineering hydrocarbon biofuel production. Microb Cell Fact 12:107.

17. Ruegg TL, Pereira JH, Chen JC, DeGiovanni A, Novichkov P, Mutalik VK, Tomaleri GP, Singer SW, Hillson NJ, Simmons BA, Adams PD, Thelen MP. 2018. Jungle Express is a versatile repressor system for tight transcriptional control. Nat Commun 9:3617.

18. Calero P, Jensen SI, Nielsen AT. 2016. Broad-Host-Range ProUSER Vectors Enable Fast Characterization of Inducible Promoters and Optimization of p-Coumaric Acid Production in Pseudomonas putida KT2440. ACS Synth Biol 5:741–753.

19. Shanks RMQ, Kadouri DE, MacEachran DP, O'Toole GA. 2009. New yeast recombineering tools for bacteria. Plasmid 62:88–97.

20. Schmidl SR, Sheth RU, Wu A, Tabor JJ. 2014. Refactoring and optimization of light-switchable Escherichia coli two-component systems. ACS Synth Biol 3:820–831.

21. Chen J, Densmore D, Ham TS, Keasling JD, Hillson NJ. 2012. DeviceEditor visual biological CAD canvas. J Biol Eng 6:1.

22. Hillson NJ, Rosengarten RD, Keasling JD. 2012. j5 DNA assembly design automation software. ACS Synth Biol 1:14–21.

23. Gibson DG, Young L, Chuang R-Y, Venter JC, Hutchison CA, Smith HO. 2009. Enzymatic assembly of DNA molecules up to several hundred kilobases. Nat Methods 6:343–345.

24. Campbell RE, Tour O, Palmer AE, Steinbach PA, Baird GS, Zacharias DA, Tsien RY. 2002. A monomeric red fluorescent protein. Proc Natl Acad Sci USA 99:7877–7882.

25. Virtanen P, Gommers R, Oliphant TE, Haberland M, Reddy T, Cournapeau D, Burovski E, Peterson P, Weckesser W, Bright J, van der Walt SJ, Brett M, Wilson J, Millman KJ, Mayorov N, Nelson ARJ, Jones E, Kern R, Larson E, Carey CJ, SciPy 1.0 Contributors. 2020. SciPy 1.0: fundamental algorithms for scientific computing in Python. Nat Methods 17:261–272.

26. van der Walt S, Colbert SC, Varoquaux G. 2011. The NumPy Array: A Structure for

Efficient Numerical Computation. Comput Sci Eng 13:22–30.

27. Thompson MG, Costello Z, Hummel NFC, Cruz-Morales P, Blake-Hedges JM, Krishna RN, Skyrud W, Pearson AN, Incha MR, Shih PM, Garcia-Martin H, Keasling JD. 2019. Robust Characterization of Two Distinct Glutarate Sensing Transcription Factors of *Pseudomonas putida* l -Lysine Metabolism. ACS Synth Biol 8:2385–2396.