Multi-input CRISPR/Cas genetic circuits that interface host regulatory networks

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Abstract

Genetic circuits require many regulatory parts in order to implement signal processing or execute algorithms in cells. A potentially scalable approach is to use dCas9, which employs small guide RNAs (sgRNAs) to repress genetic loci via the programmability of RNA:DNA base pairing. To this end, we use dCas9 and designed sgRNAs to build transcriptional logic gates and connect them to perform computation in living cells. We constructed a set of NOT gates by designing five synthetic Escherichia coli σ70 promoters that are repressed by corresponding sgRNAs, and these interactions do not exhibit crosstalk between each other. These sgRNAs exhibit high on-target repression (56- to 440-fold) and negligible off-target interactions (<1.3-fold). These gates were connected to build larger circuits, including the Boolean-complete NOR gate and a 3-gate circuit consisting of four layered sgRNAs. The synthetic circuits were connected to the native E. coli regulatory network by designing output sgRNAs to target an E. coli transcription factor (malT). This converts the output of a synthetic circuit to a switch in cellular phenotype (sugar utilization, chemotaxis, phage resistance).

Keywords CRISPR; genetic compiler; synthetic biology; TALE; TetR homologue

Subject Categories Synthetic Biology & Biotechnology; Methods & Resources

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Introduction

Genome editing has been revolutionized by the RNA-guided endonuclease Cas9 from Streptococcus pyogenes due to its ability to target DNA sequences adjacent to “NGG” motifs using a guide RNA (Cong et al., 2013; Esvelt et al., 2013; Jiang et al., 2013; Shalem et al., 2013; Wang et al., 2013; Zhou et al., 2014). This programmability has been harnessed for gene regulation using a Cas9 double mutant that eliminates nuclease activity (dCas9) so that guide RNAs cause it to bind tightly to the corresponding DNA sequence without cleaving it (Jinek et al., 2012). This complex can serve as a repressor by blocking RNAP binding to a promoter or by terminating transcription (Bikard et al., 2013; Esvelt et al., 2013; Qi et al., 2013). A chimeric small guide RNA (sgRNA) is sufficient to drive Cas9 to a target (Jinek et al., 2012), and it comprises a complementary domain that binds to the DNA followed by a “handle” that is bound by Cas9. Considering the programmability of DNA:RNA interactions and the existence of a “seed” region at the 3′-end of the sgRNA’s complementary region, this system could yield ~10^7 orthogonal sgRNA:DNA pairs. This is a potentially versatile platform for building genetic circuits, which have been limited in size and sophistication by the number of available orthogonal transcription factors.

Extensible circuits, whose inputs and outputs are of an identical form, can be connected in different ways in order to perform user-defined computational operations (Nielsen et al. 2013). For genetic circuits, the simplest way to achieve this is to design gates with inputs and outputs that are both promoters (Tamsir et al., 2011; Moon et al., 2012; Stanton et al., 2014). In this formalism, the common signal carrier is RNAP flux and gates are connected by having the output of one serve as the input to the next. The majority of transcriptional gates have been built using DNA-binding proteins. The challenge has been to obtain large sets of orthogonal proteins that do not cross-react with each other’s binding sites. These sets can be obtained either by part mining, where bioinformatics is applied to search databases for classes of regulators that are synthesized and screened (Moon et al., 2012; Rhodius et al., 2013; Stanton et al., 2014), or by building variants of modular DNA-binding proteins whose domains can be engineered to target different operators [e.g. ZFPs (Beerli & Barbas, 2002; Miller et al., 2007) and TALEs (Morbitzer et al., 2010; Miller et al., 2011)]. For both approaches, cross-reactions are prevalent and many variations have to be screened to obtain an orthogonal core set. Another challenge is that within a regulator class, some can be non-toxic whereas others exhibit extreme toxicity (Kimelman et al., 2012; Stanton et al., 2014). Collectively, restrictions on function, orthogonality, and toxicity reduce the size of the libraries dramatically; for example, an initial set of 73 TetR homologues was reduced to 16 repressors (Stanton et al., 2014).

Here, we present a set of transcriptional gates based on sgRNA-guided repression of synthetic Escherichia coli σ70 promoters (Fig 1A). The input to an sgRNA NOT gate is a promoter that contains a precise transcription start site (+1) so that additional nucleotides are not added to the 5′-end of the sgRNA, which has
been shown to reduce activity (Larson et al., 2013). The sgRNA includes a guide region that targets dCas9 to the cognate bacterial promoter. A strong terminator (Chen et al., 2013; Qi et al., 2013) is placed after the sgRNA to stop transcription. The output of the gate is an E. coli constitutive promoter (BBa_J23101) that has been modified to include both forward and reverse “NGG” PAMs (for targeting either the template or non-template strands of the promoter), and a unique 13 bp “operator” region between the −35 and −10 sigma factor binding sites. When the dCas9 handle of the sgRNA (dark green) complexes with dCas9 (blue), the sgRNA binds the operator (light green) and a sigma factor binding site (gray), causing steric repression of transcription initiation at the output promoter.

**Figure 1.** Schematics of dCas9 logic circuit design and construction.

- **A** CRISPR/Cas-based NOT gates comprise a catalytically dead dCas9 protein, an input promoter that transcribes a small guide RNA (sgRNA), and a synthetic output promoter with an sgRNA operator between the −35 and −10 sigma factor binding sites. When the dCas9 handle of the sgRNA (dark green) complexes with dCas9 (blue), the sgRNA binds the operator (light green) and a sigma factor binding site (gray), causing steric repression of transcription initiation at the output promoter.

- **B** CRISPR/Cas genetic circuits are easily constructed from pairs of ssDNA oligonucleotides ≤200 nt long that encode the necessary genetic parts (promoter, sgRNA, terminator, assembly scars, and restriction enzyme recognition sites). These oligos are annealed to each other at the dCas9 handle and extended. The resulting dsDNA modules are assembled in a one-pot Golden Gate assembly reaction. (Colored diamonds are assembly scars.)

- **C** Genetic circuits that respond to chemical input signals can be constructed from simple NOT and NOR gate motifs. In these circuits, dCas9 (blue) mediates repression of synthetic promoters by programmable sgRNAs (visualized as solid colored rectangles from here on). Both heterologous and endogenous genes can be regulated at circuit outputs by expressing sgRNAs tailored to target transcription initiation or elongation.

Multi-input NOR and NAND gates are “Boolean-complete” and are each sufficient to build any user-defined digital computational operation (Katz & Boriello, 2004). Transcription factor-based NOR gates have previously been built by placing two input promoters in series upstream from a repressor gene (Tamsir et al., 2011; Stanton et al., 2014). Without additional RNA processing, this design does not work for sgRNA circuits because of the detrimental influence of 5′-mismatches and the “roadblocking” effect of CRISPRi, which is small for template-targeting sgRNAs and substantial for non-template-targeting sgRNAs (Qi et al., 2013). Hammerhead ribozymes and endoRNase cleavage of 5′-mismatches have both been shown to effectively remove extraneous 5′-RNA from sgRNAs (Gao & Zhao, 2014; Nissim et al., 2014) and could be employed in multi-input dCas9 circuits. Instead, our design is based on two transcription units per NOR gate, each of which contains a different input promoter. When either promoter is active, the sgRNA is transcribed and represses the output promoter. This design allows larger circuits to be constructed simply by changing the pattern of input and output promoters around the sgRNAs. This approach requires that the sgRNAs be able to be layered into a cascade, which has been shown to work in mammalian cells (Kiani et al., 2014; Nissim et al., 2014).

Linking the output(s) of a genetic circuit to regulate host genes provides control over cellular responses. For example, cells could be programmed to sense the cell density in a fermenter and respond by expressing enzymes to redirect flux through global metabolism (Nielsen et al., 2014). Similarly, the cell phenotype could be controlled, like the ability to swim or associate into biofilms. Various approaches have been taken to link synthetic circuits to endogenous genes. For example, MAGE has been used to insert T7 RNAP promoters upstream from genes participating in lycopene biosynthesis in order to upregulate production by expressing the polymerase.
as a circuit output (Wang et al., 2009). Natural and synthetic sRNAs have been used to knockdown endogenous genes involved in motility (Sharma et al., 2013), iron metabolism (Kang et al., 2012), acetone formation (Tummala et al., 2003), β-glucuronidase (Man et al., 2011), membrane porin and flagellin genes (Sharma et al., 2012), and to increase tyrosine and cadaverine production (Na et al., 2011).
Results

Orthogonal NOT gates based on dCas9 and sgRNAs

A three-plasmid system was built to measure sgRNA orthogonality and characterize their performance in the context of a NOT gate (Fig 2A). The first plasmid controls the expression of \( S. \) pyogenes dCas9 from an aTc-inducible \( \text{P}_{\text{Tet}} \) promoter. The sgRNA is carried on a high-copy plasmid and transcribed using a variant of the arabinose-inducible \( \text{P}_{\text{BAD}} \) promoter that is truncated to end at the transcription start site (+1). Finally, the output promoter repressed by the dCas9-sgRNA complex is transcriptionally fused to red fluorescent protein (RFP) and carried on a low-copy plasmid.

dCas9 can exhibit toxicity when overexpressed. To reduce background expression, we selected an aTc-inducible \( \text{P}_{\text{Tet}} \) variant that exhibits low leakiness and added the strong \( \text{L3S3P21} \) terminator (Chen et al, 2013) upstream to insulate from read-through transcription on the plasmid backbone. As the expression of dCas9 is increased, higher fold repression is observed, but this comes at the cost of reduced cell growth (Fig 2B). These effects are balanced at 0.625 ng/ml aTc, which elicits near-full repression with a growth impact of \(< 15\%\) (after 6 h, an OD\(_{600}\) of 0.44 versus 0.51). This induction level is used for all subsequent experiments.

A set of five synthetic promoters (\( P_{A1} - P_{A5} \)) were designed to be targeted by corresponding sgRNAs. An \( E. \) coli constitutive promoter (BBa_J23101) was chosen as a scaffold, and the operator that is recognized by the sgRNA was inserted between the −35 and −10 consensus sites where the housekeeping \( \sigma_{\text{70}} \) binds (Fig 2C). The region between these sites is 17 bp, the center of which contains a unique 13 bp sequence that is bound by the “seed” of the sgRNA complementary region, which is less tolerant of RNA:DNA mismatches (Jinek et al, 2012). This is flanked by forward and reverse “NGG” protospacer adjacent motifs (PAMs), which are required for dCas9 binding (Marraffini & Sontheimer, 2010). When dCas9 is directed to this region by a corresponding sgRNA, the promoter is repressed by dCas9 sterically blocking the binding of \( E. \) coli RNAP. The orthogonal sgRNAs (sgRNA-A1–sgRNA-A5) were designed by selecting distinct 13 bp seed sequences that have no matches to PAM-proximal sequences in the \( E. \) coli genome. Two variants of each sgRNA were built that target the non-template (−NT) and template (−T) strands of each promoter. Each of the sgRNAs strongly represses its target promoter (56- to 440-fold), with no preference for the non-template or template strand, as observed previously (Bikard et al, 2013). The orthogonality of the promoters and sgRNAs are near perfect, with essentially no off-target interactions (Fig 2D). In addition, we observe only a small amount of toxicity when the sgRNAs are highly expressed, and no growth differences between the sgRNA variants (Supplementary Figures S1, S2, S3 and S4 and Supplementary Tables S1 and S2).

The response function of a gate captures how the output changes as a function of input. This is critical in predicting how gates can be connected to form larger circuits. To characterize the gates, the \( \text{P}_{\text{Tet}} \) promoter serves as the input, which we characterized separately as a function of arabinose concentration. This is used to rescale the data to report it as a function of promoter activity, as opposed to inducer concentration (Fig 2E). The log-linear shape of this response curve is approximated well by a power law and is very different from those observed from similar gates based on transcription factors, which saturate as a Langmuir isotherm. This log-linearity is also evident when observing the relationship between the intermediate and output promoters of an sgRNA cascade (Fig 3B, right).

The dynamics of repression were also measured (Fig 2F). After induction, there is an initial delay of 1.5 h corresponding to the activation of \( \text{P}_{\text{Tet}}/\text{P}_{\text{BAD}} \) and the accumulation of dCas9/sgRNA. After this delay, there is a consistent exponential decline in RFP (\( t_{1/2} = 33 \) min) over 7 h, which is consistent with the dilution rate of the reporter expected from cell division.

Circuits based on layered sgRNA gates

The advantage of transcriptional gates is that they can be easily interconnected in order to build more complex circuit functions. Gates where repression is based on a non-coding RNA (ncRNA) can be challenging to connect in series for three reasons. First, they require more precision in the promoter start site or additional RNA processing due to sensitivities in the addition or removal of nucleotides at the 5′-end. Second, changing the ribosome binding site (RBS) has been an important lever for functionally connecting protein-based gates. The RBS is not relevant for an ncRNA-based gate, and matching gate responses by promoter tuning is more challenging. This is exacerbated by the shape of the response functions for the sgRNA-based gates, which do not plateau at high- or low-input promoter levels (Fig 2E); therefore, the input to any gate needs to have a very wide dynamic range in order to avoid signal degradation at each layer. However, despite these challenges, sgRNA-mediated repression has desirable properties that other ncRNA technologies do not possess, such as high dynamic range, specificity, and the ability to be composed into cascades (Qi & Arkin, 2014).

The layering of two NOT gates based on sgRNAs has been previously demonstrated in mammalian cells (Kiani et al, 2014; Nissim et al, 2014). We built a similar circuit architecture by connecting two of our sgRNA-based gates in series in \( E. \) coli (Fig 3A). These were connected simply by combining the parts from the sgRNA-A2NT and sgRNA-A4NT gates in the appropriate order with no additional tuning. dCas9 is induced from a low-leakage variant of \( \text{P}_{\text{Tet}} \), as was done for the characterization of individual gates. In the absence of dCas9, the background activity of the output promoter (\( P_{A4} \)) is 1,040 au (arbitrary units, Fig 3B, leftmost bar). When dCas9 is induced, this resulted in a 98-fold repression of the circuit output (\( P_{A4} \)) compared to no sgRNA production (Fig 3B, left). When the circuit’s input promoter is induced with DAPG, the output state recovers completely to the level of the dCas9 (−) control. By observing the middle promoter (\( P_{A3} \)) in the cascade in a separate
experiment, the trade-off between PA2 and PA4 expression can be seen at intermediate sgRNA induction levels (Fig 3B, right). The log-linear response curve spans almost three orders of magnitude.

In addition to layering, the construction of more complex circuits requires that gates be able to receive multiple inputs. So-called “Boolean-complete” logic gates—NOR and NAND functions—are particularly useful because they can be connected to build any computational operation. Genetic NOR gates have proven to be particularly easy to build using transcriptional regulation where two input promoters drive the expression of a repressor that turns off an output promoter. The capacity for the orthogonality of sgRNA:promoter interactions has the potential to enable a very large number of NOR gates, which could be used to realize large integrated circuits. However, to date, it has not been shown that sgRNA-based gates can be designed to respond to more than one input promoter.

To build a simple NOR gate, we connected two input promoters to the transcription of independent copies of sgRNA-2NT (Fig 3C), either of which will repress a single output promoter (PA4). These two input promoters are responsive to small molecule inducers: DAPG (PA2) and arabinose (PA4). In the presence of DCas9, but neither arabinose nor DAPG, the NOR gate output from promoter...
P_{A2} remains high at only 2.3-fold reduction compared to the dCas9 (—) control due to leaky sgRNA production. When both inducers are added, there is 100-fold repression of the output promoter (Fig 3D), which is on par with the best gates that use protein-based repressors. The OFF state is ~threefold higher when only arabinose is added, which is likely due to the lower maximum activity from the P_{BAD} promoter compared to P_{PBAD}. While this does not significantly degrade the function of the NOR gate alone, it is representative of the sensitivity of sgRNA-based gates to the dynamic range of the inputs and is potentially problematic when building longer cascades.

Next, we connected multiple NOR and NOT gates to build larger layered circuits. First, we built a simple circuit that inverts the output of the NOR gate to make an OR gate (Fig 3E). The P_{A2} output of the NOR gate is used to drive the transcription of sgRNA-A4NT, which in turn represses the P_{A4} output promoter. A challenge that emerged from building these circuits is transcriptional readthrough, which occurs because the output promoters are strong and the sgRNAs short. To mitigate this, strong unique terminators (Chen et al, 2013) are placed after each sgRNA, immediately downstream from the dCas9 handle region of the sgRNA (Qi et al, 2013). For the OR gate, the TrnB and L3S2P55 terminators [terminator strengths, T5 = 84 for TrnB and T5 = 260 for L3S2P55, respectively (Chen et al, 2013)] are placed after the two sgRNA-A2NT sequences, and L3S2P21 (T5 = 380) is placed after sgRNA-A4NT. The output of the OR gate is strongly repressed >100-fold in the absence of both inducers compared to all other states (Fig 3F).

We then built a larger circuit by connecting three gates based on four sgRNAs. A cascade with two branches is formed by the A2NT and A4NT sgRNAs, which invert the output of the arabinose- and DAPG-inducible systems, respectively (Fig 3G). The output promoters from these NOT gates then connect to a NOR gate by using each to drive a different copy of sgRNA-A1NT. The computing portion of the circuit requires 1,234 nt to encode. This circuit should produce an AND logic operation, and, indeed, there is a 107-fold difference between the OFF and ON states when both inducers are absent and present (Fig 3H). There is some leakiness when either input is induced alone, and these states show 2.6- to 5.0-fold activity above the OFF state observed in the absence of both inducers. Four versions of this circuit were designed with varied sgRNA positions and orientations. Other versions were slightly less functional, with higher OFF states and lower ON state; the best version is presented here. This circuit can be compared to a similar AND gate design built from TetR homologues. That circuit generated a ~fivefold response and required 2,577 nt to encode (Stanton et al, 2014).

Interfacing the synthetic circuit with a native Escherichia coli regulatory network

Guide RNAs can be designed to knock down genes encoded in the host genome (Qi et al, 2013). In this way, native cellular processes can be easily actuated as an output of an sgRNA-based circuit using the same biochemistry. To demonstrate this, we started with the OR circuit (Fig 3E) and substituted the sgRNA used for the NOT gate with one designed to target the malT gene in the E. coli genome (Fig 4A). MalT is a positive regulator of the maltose utilization operons. A knockdown would alter sugar utilization and has additional impacts on the cellular phenotype (Tchetina & Newman, 1995; Boos & Bühm, 2000). Notably, it decreases the production of LamB—the lambda phage receptor—resulting in decreased susceptibility of E. coli to lambda phage infection (Thirion & Hofnung, 1972). To target malT, we designed sgRNA-MalT-3NT to target the non-template strand of the protein coding sequence from the 110th to the 117th codon. By targeting the non-template strand, the roadblock formed by dCas9 would disrupt any transcription from upstream promoters (Bikard et al, 2013; Qi et al, 2013).

Cells harboring this circuit exhibit a 240-fold reduction in lambda plaque formation in the absence of both inducers (Fig 4C). When either or both inducers are present, the cells show near-wild-type phage infectivity. In addition, we can separately report the activity of an internal state of the circuit by using P_{A2}, which is the output of the NOR gate alone, to drive the transcription of RFP. This results in a NOR gate that is repressed 120-fold when either inducer is present (Fig 4B). These experiments demonstrate that a heterologous output (knockdown of RFP) and an endogenous response (knockdown of MalT) can be simultaneously co-regulated according to different logic operations using the same underlying circuit.

Discussion

Extensible NOR and NOT gates are fundamental logic operations from which more complex circuitry can be built. Previously, these gates have been based on transcription factors that bind to DNA, such as phage repressors, LacI, and TetR homologues. Gates based on dCas9 and guide RNAs offer several advantages. The most significant is the ease by which new sgRNA:promoter pairs can be designed and the orthogonality that they exhibit with each other. While there has been much discussion regarding off-target Cas9 interactions and several efforts seeking to reduce it (Cradick et al, 2013; Fu et al, 2013, 2014; Hsu et al, 2013; Mali et al, 2013; Patanayak et al, 2013, 2014; Ran et al, 2013; Guilinger et al, 2014; Kucscu et al, 2014; Tsai et al, 2014; Wu et al, 2014), this is not as relevant for synthetic circuits because sgRNAs can be designed to be maximally different from each other and the host genome. Indeed, no designed sgRNAs had to be discarded from the orthogonal set that we built, either for activity, orthogonality, or growth defects. Further, one transcriptomic analysis of CRISPR interference revealed no off-target signatures (Qi et al, 2013). This is a major improvement over the protein-based gates, which have problems in all of these areas. The “operator” that is bound by the sgRNA seed region is also relatively small (13 bp) and can be easily inserted between the -10 and -35 region of a promoter (TetR homologue operators range from 20 to 50 bp). In addition, the gates are small and can be easily synthesized as oligos, including in pooled libraries (Kosuri et al, 2013). The gates also reliably produce >50-fold dynamic range. This is akin to the best protein-based gates, but those exhibit far more diversity in the leakiness, dynamic range, and shape of the response function.

Toxicity is observed from dCas9, where high levels reduce cell growth in Escherichia coli. While the mechanism of toxicity is still unclear, it has been reported to be more severe in other species. This may reduce the long-term evolutionary stability of dCas9 in engineered cells, as has been observed for other toxic genetic circuits (Sleight et al, 2010; Chen et al, 2013; Sleight & Sauro, 2013). However, we find that the toxicity can be managed by controlling the level of expression while still eliciting a substantial circuit response. Also, once dealt with, we do not observe substantial toxicity.
as more sgRNAs are transcribed. This is in contrast to protein-based gates, which may have less toxicity individually, but can be problematic if multiple repressors are used in a design because their growth defects often stack and become severe.

There are also some challenges in working with dCas9 that are unique compared to protein-based gates. The shape of the response function, where no saturation is observed at high or low levels, poses a problem when layering gates. Without nonlinearity, the signal is degraded at each layer. Indeed, we attempted to add another layer to the AND gate, and this yielded a non-responsive signal as more sgRNAs are transcribed. This is in contrast to protein-based gates, which may have less toxicity individually, but can be problematic if multiple repressors are used in a design because their growth defects often stack and become severe.

Figure 4. Interfacing logic circuits with host physiology.
A The wiring diagram and genetic schematic for a NOT[NOR(A,B)] gate are shown (i.e. an OR gate). The sgRNA-A2NT/P_{A2} pair is shown in orange, the sgRNA-A4NT/P_{A4} pair is shown in magenta, dCas9 is shown in blue, and both sgRNA-Malt-3NT and the malt gene are shown in yellow.
B The NOR gate digital RFP response is shown for the four input inducer states (with dCas9 induced by 0.625 ng/ml aTc), no input inducer, arabinose (2 mM), DAPG (25 µM), and arabinose and DAPG (2 mM and 25 µM). Also shown is the output without dCas9 induction (leftmost column). Gray columns are expected to be OFF, and black columns are expected to be ON. Error bars represent the standard deviation of three independent experiments on different days.
C The OR gate digital lambda phage infectivity response is shown for five input inducer states (as in B), where infectivity is measured by the number of lambda phage plaques formed on a bacterial lawn on an agar plate. Error bars represent the standard deviation of three independent experiments on different days.

Materials and Methods

Materials and Methods

Escherichia coli DH10b (F- mcrA Δ(mrr-hsdRMS-mcrBC) 980lacZΔM15 ΔlacX74 recA1 endA1 araD139 Δ(ara leu) 7697galU galKρpsLnapG k–) (Durfee et al., 2008) was used for cloning (New
Fluorescent protein production was measured using the LSRII Fortess flow cytometer analysis for measurement experiments. Ampicillin (100 μg/ml), kanamycin (50 μg/ml), and spectinomycin sulfate (50 μg/ml) were used to maintain plasmids. Arabinoise (Sigma Aldrich, MO, A3256), 2,4-diacetylphloroglucinol (Santa Cruz Biotechnology, TX, CAS 2161-86-6), and anhydrotetracycline (aTc) (Sigma Aldrich, MO, 37919) were used as chemical inducers. The fluorescent protein reporters YFP (Cormack et al, 1996) and mRFP1 (Campbell et al, 2002) were measured with cytometry to determine gene expression.

Flow cytometry analysis

Fluorescent protein production was measured using the LSRII Fortessa flow cytometer (BD Biosciences, San Jose, CA). Between 10⁶ and 10⁸ events were collected for subsequent analysis with the software tool FlowJo v10 (TreeStar, Inc., Ashland, OR). From the resulting fluorescence histograms for YFP and RFP, we calculated the geometric means of each sample and then corrected for cellular autofluorescence by subtracting the geometric mean of a strain harboring only pAN-P₆₃₉-dCas9 that was grown in an identical manner.

Computational design of sgRNA-promoter pairs

DNA sequences of 13 nucleotides in length were generated using the Random DNA Sequence Generator (http://www.faculty.ucr.edu/~mmaduro/random.htm), with a GC content probability parameter of 0.5. The resulting sequences were flanked by forward and reverse PAMs and the −35 and −10 sigma factor binding sites to generate sgRNA-repressible promoters. If the forward sequence for the promoter contained any stretches with more than three guanine nucleotides, the promoter design was discarded due to the difficulty in synthesizing oligos with G-quadruplexes (Burge et al, 2006). Next, the 12 nucleotides adjacent to either the forward or reverse PAM were searched for in the genome of E. coli strain K-12 substrain MG1655 (taxid: 511145) using Standard Nucleotide BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn) (Altschul et al, 1990) to search for similar sequences (blastn). The following parameters were used: Short queries were enabled; expect threshold = 10; word size = 11; match/mismatch scores = 2–3; gap costs = existence: 5, extension: 2; and low complexity regions unmasked. Of the ten sgRNAs designed, no 12 nt seed regions had complete homology to a PAM-adjacent locus in the E. coli genome. If the resulting 20 nucleotide sgRNAs had GC content < 35% or > 80%, the sequence was discarded and redesigned.

Induction endpoint assays

Escherichia coli MG1655* cells were transformed with three plasmids encoding: (i) inducible dCas9, (ii) one or more sgRNAs, and (iii) a fluorescent reporter. Cells were plated on LB agar plates with appropriate antibiotics. Transformed colonies were inoculated into MOPS EZ RichDefined Medium with 0.4% glycerol and appropriate antibiotics and were then grown overnight in V-bottom 96-well plates (Nunc, Roskilde, Denmark, 249952) in an ELM Digital Thermostat Microplates shaker incubator (Elmi Ltd, Riga, Latvia) at 1,000 rpm and 37°C. The next day, cultures were diluted 180-fold into EZ Rich Defined Medium with antibiotics and grown with the same shaking incubator parameters for 3 h. At 3 h, cells were diluted 700-fold into EZ Rich Medium with antibiotics and inducers. The cells were grown using the same shaking incubator parameters for 6 h. For cytometry measurements, 40 μl of the cell culture was added to 160 μl of phosphate-buffered saline with 0.5 mg/ml kanamycin to arrest cell growth. The cells were placed in a 4°C refrigerator for 1 h to allow the fluorophores to mature prior to cytometry analysis.

Toxicity measurements

For dCas9 toxicity measurements, cells were grown identically to the induction endpoint assays until the second dilution after the 3-h growth. From here, the cultures were diluted 360-fold into EZ Rich Defined Medium with 0.4% glycerol and antibiotics in 2 ml 96-deep well plates (USA Scientific, FL, 1896-2000) and were grown for 6 h in a Multitron Pro shaker incubator (In Vitro Technologies, VIC, Australia) at 37°C and 1,000 rpm. At this point, cultures were transferred to 1-cm optical cuvettes, and the cultures were grown using the same shaking incubator parameters for 6 h. For cytometry measurements, 40 μl of the cell culture was added to 160 μl of phosphate-buffered saline with 0.5 mg/ml kanamycin to arrest cell growth. The cells were placed in a 4°C refrigerator for 1 h to allow the fluorophores to mature prior to cytometry analysis.

Induction timecourse assays

Timecourse experiments were performed identically to endpoint assays, with the exception that cells were grown in 14-ml round-bottom polystyrene culture tubes (VWR, PA, 60819-524). After the second dilution into inducers, culture samples were taken every 30 min for 7 h and were added to phosphate-buffered saline with 0.5 mg/ml kanamycin for subsequent cytometry analysis.

Inducer concentrations

For dCas9 toxicity measurements, arabinose was added to 2 mM, and aTc was added to the following final concentrations (ng/ml): 0.0391, 0.313, 0.625, 1.25, 5, and 10. For sgRNA response curve experiments, aTc was added to 0.625 ng/ml and arabinose was added to the following final concentrations (mM): 0, 0.03125, 0.0625, 0.125, 0.25, and 0.5. For timecourse and orthogonality experiments, aTc was added to 0.625 ng/ml and arabinose was added to 2 mM. For digital genetic circuit measurements and lambda phage infection experiments, inducers were either absent or added to the following final concentrations: 0.625 ng/ml aTc, 2 mM arabinose, and 25 μM 2,4-diacyethylphloroglucinol. For the intermediate genetic circuit measurements, aTc was added to 0.625 ng/ml; arabinose was added to the following final concentrations (mM): 0, 0.00391, 0.00781, 0.0156, 0.0313, 0.0625, 0.125, 0.25, 0.5, 1, and 2; 2,4-diacyethylphloroglucinol was added to the following final concentrations (μM): 0, 0.0244, 0.0488, 0.0977, 0.391, 0.781, 1.56, 3.13, 6.25, 12.5, and 25.
Lambda phage infection assay

*Escherichia coli* MG1655* strains were grown from colonies overnight in EZ Rich Defined Media with antibiotics. The next day, cultures were diluted 180-fold into EZ Rich Medium with 0.4% glycerol and antibiotics and grown at 37°C shaking at 250 rpm in culture tubes for 3 h. Next, cells were diluted 180-fold once again into five different tubes of 4 ml of EZ Rich Medium with antibiotics and containing the five different inducer conditions. These cells were grown for 6 h using the same shaking incubator conditions in culture tubes. After 6 h, each culture was pelleted at 4,000 g and then resuspended in 100 μl of 10 mM MgSO4. Half of each resuspension (50 μl) was diluted into 950 μl of 10 mM MgSO4, and the optical density at 600 nm was measured. The remaining 50 μl of each cell resuspension was diluted to an OD600 of 3.0 in 10 mM MgSO4. Next, 1 μl of lambda phage was added to 100 μl of each cell resuspension, vortexed lightly, and then allowed to incubate at 37°C for 1 h. Finally, all 100 μl of cells were plated onto 1.5% agar LB Miller plate and allowed to grow overnight at 37°C. The next day, phage plaques were counted on each plate.

Supplementary information for this article is available online: [http://msb.embopress.org](http://msb.embopress.org)

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Author contributions

CAV and AAKN conceived of the study and designed the experiments. AAKN performed the experiments and analyzed the data. CAV and AAKN wrote the manuscript. CAV managed the project.

Conflict of interest

The authors declare that they have no conflict of interest.

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