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Transcriptional Repressor Protein based Macrolide Biosensor Development with Improved Sensitivity

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Introduction

Macrolides, antibiotics class ot are biosynthesized via "giant assembly line polyketide synthases(PKS) which could be modified by Combinatorial biosynthetic methods. However, it is challenging due to the size and complexity of PKSs. To overcome this, directed evolution can be used where a large libraries of enzyme variants need to be screened. It is important to develop high screening methods to identify the throughput variants which can produce novel enzymatic MphR is a macrolide macrolides. sensing transcriptional repressor protein which regulates a gene cassette where GFP is expressed upon binding of the macrolide ligand to MphR. This research is an insight of improving the sensitivity of MphR biosensor. Developing this system can address the need of novel macrolide antibiotic derivatives in the case of drug discovery.

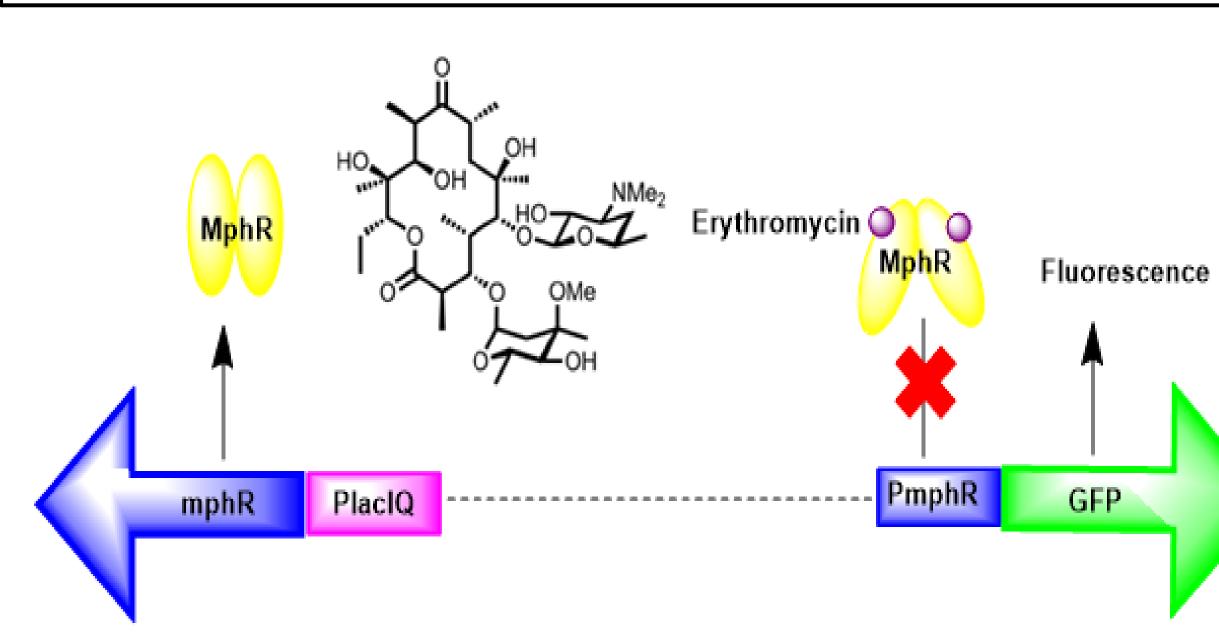


Figure 1. Schematic illustrating the role of MphR protein regulating the gene cassette containing GFP

Experimental Design and Results

Gene knockouts is a method of disrupting and inactivating chromosomal genes so the respective This proteins are longer expressed. no high phenomenon has been used to obtain sensitivity of the MphR biosensor.

Transcriptional Repressor Protein based macrolide biosensor development with improved sensitivity Jayani A. Christopher, Ashton Cropp* Department of Chemistry, Virginia Commonwealth University, Richmond, VA 23284

TolC is a member in AcrAB-TolC multidrug efflux pump which can exclude the drugs from the cell. Knocking out genes expressing TolC from the bacterial the chromosome can retain more antibiotic in the cell to be detected by the biosensor.

BamB is a lipoprotein in the β barrel assembly machinery (BAM) which is involved in folding and insertion of outer membrane β barrel proteins. Knocking out bamB gene can reduce the membrane integrity leading to increased permeability for macrolides.

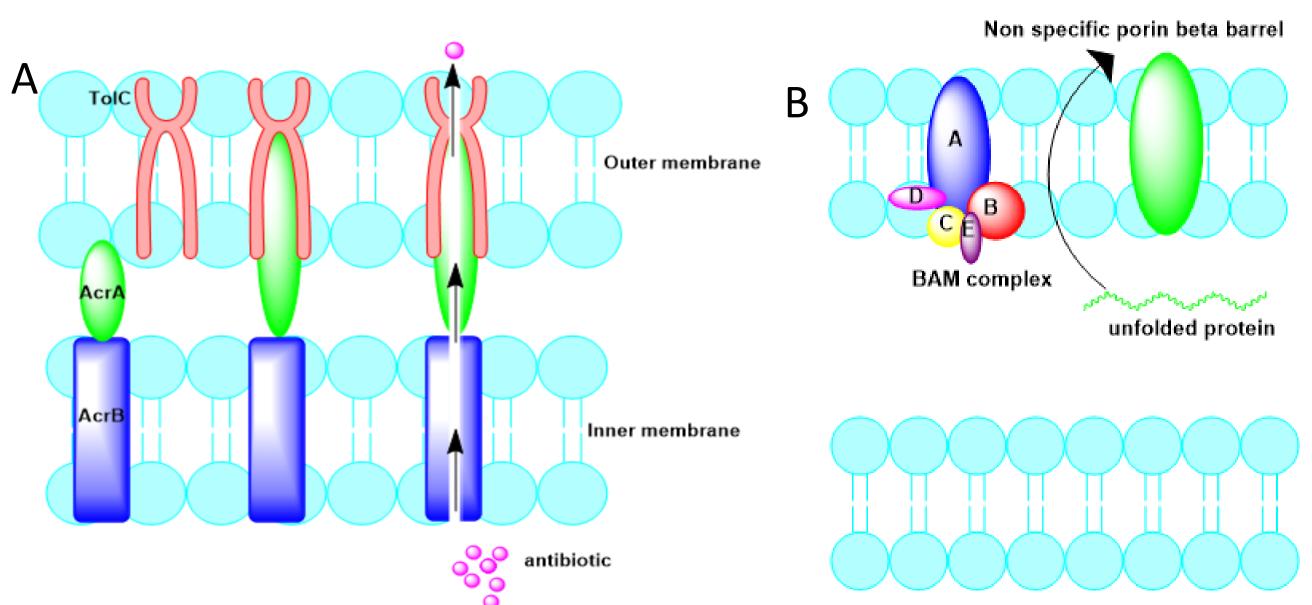
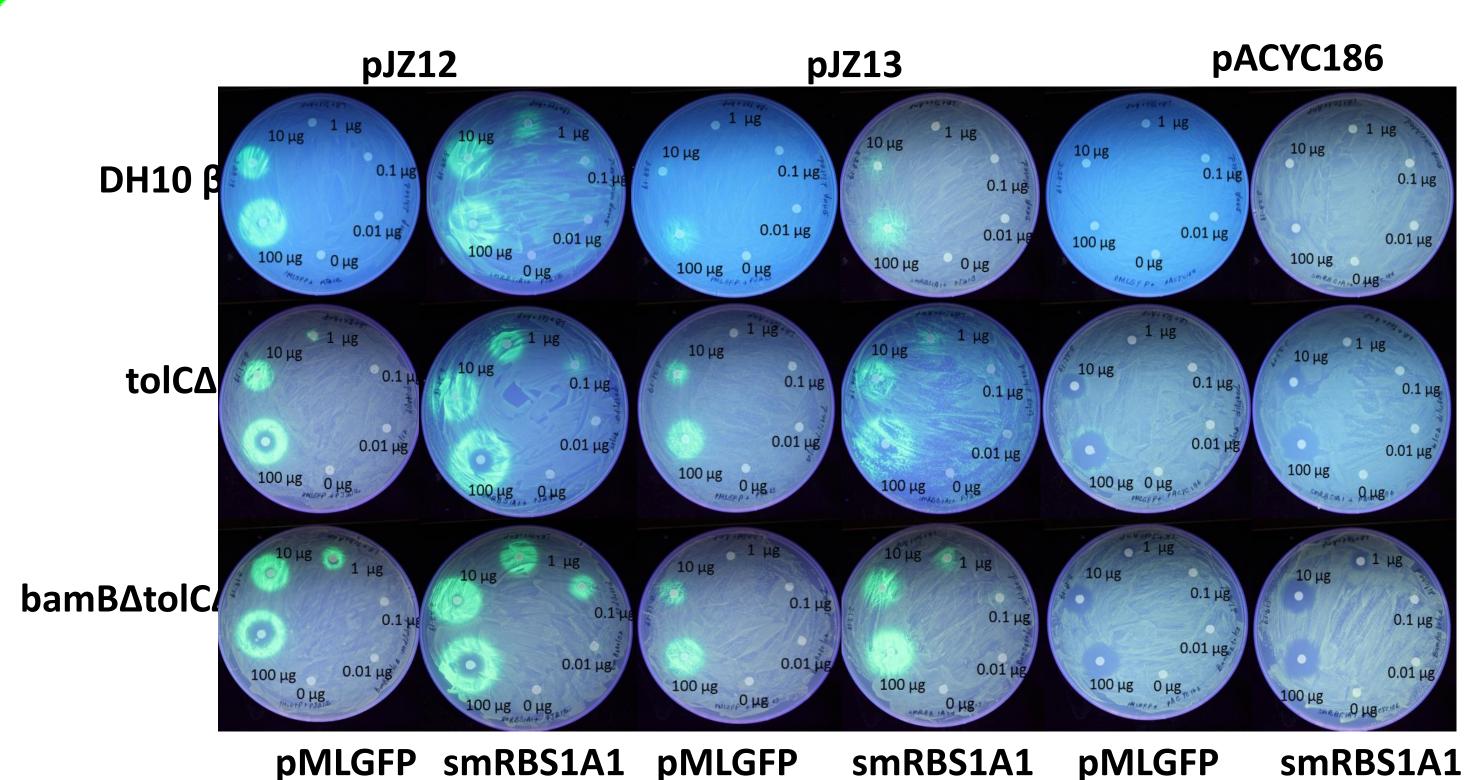


Figure 2. Schematic illustrating the mechanism of A)AcrAB-tolC efflux pump B) Bam complex

GFP bioassays

PMLGFP (MphR) +pJZ12 (MphA)/pJZ13 (MphA+mrX)/pACYC186 (No MphA or mrX) >smRBS1A1 (mutated pMLGFP)

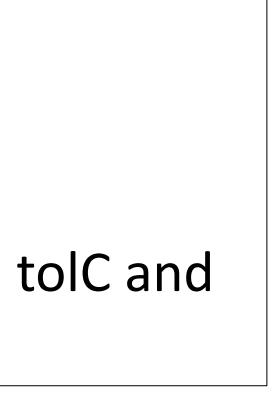
+pJZ12/pJZ13/pACYC186 are transformed in tolC and bamBtolC knockout strains.



pMLGFP smRBS1A1 pMLGFP smRBS1A1

Figure 3. Agar diffusion assay plates with 2 plasmid systems in wild type, single and double gene knockout *Ecoli*





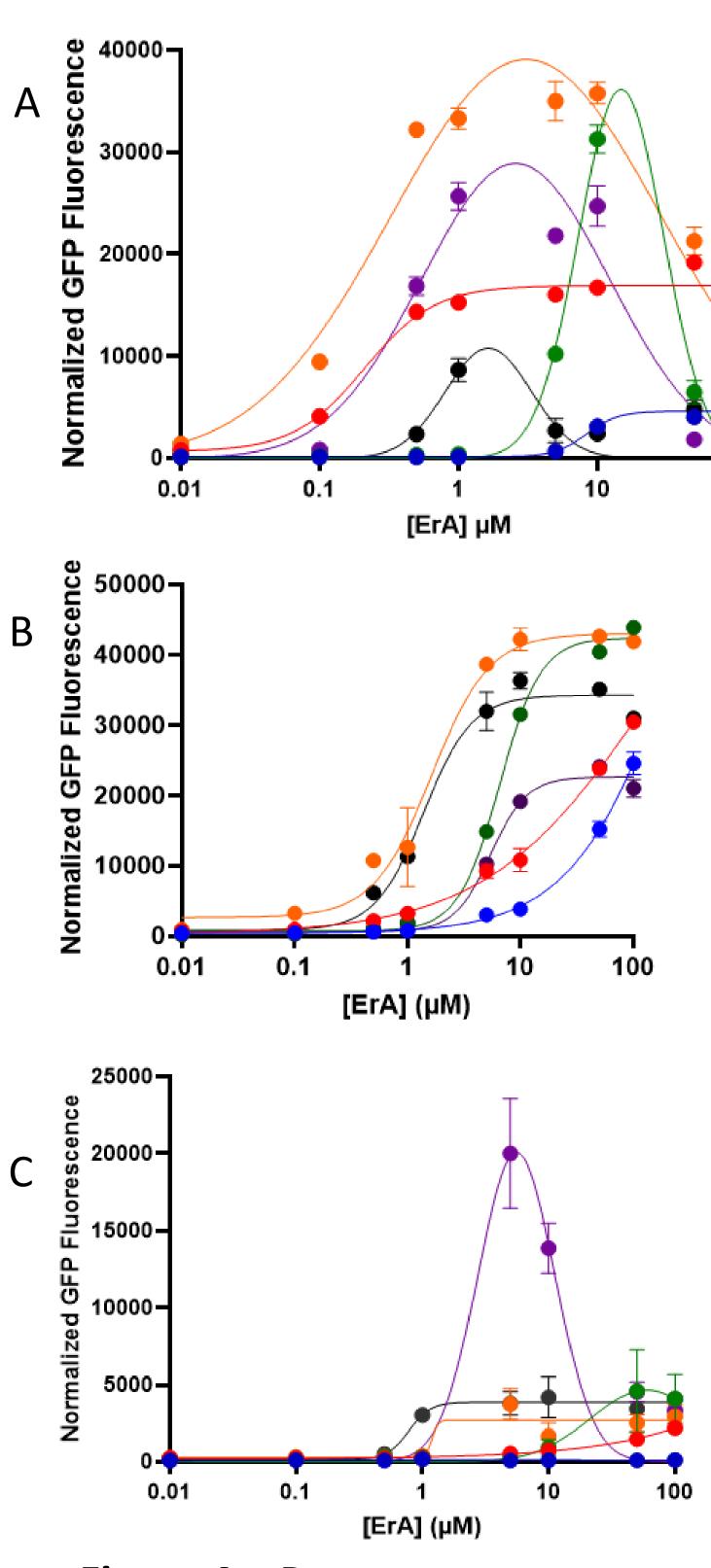


Figure 4. Dose response curves of A) pJZ12 strains B) pJZ13 strains) C)pACYC186 strains

Conclusions

- Gene knockouts improves the sensitivity of the biosensor and erythromycin can be detected down to 0.1 μ g with smRBS1A1 + pJZ12/ bamB Δ tolC Δ strain.
- Dynamic range is reduced with the double knockout strains due to cell death at high concentrations of erythromycin.

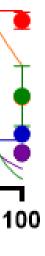
References

1. Kasey et.al. Development of Transcription Factor-Based Designer Macrolide Biosensors for Metabolic Engineering and Synthetic Biology. 2018..

2. Wang et.al. An Allosteric Transport Mechanism for the AcrAB-TolC Multidrug Efflux Pump. **2017**, 1–19.

3. Jiang et.al. From Evolution to Pathogenesis : The Link Between 6 -Barrel Assembly Machineries in the Outer Membrane of Mitochondria and Gram-Negative Bacteria. 2012, 8038–8050.

- → pMLGFP + pACYC 186/ toICΔ ● smRBS1A1 + pACYC 186/ toIC∆ → pMLGFP +pACYC186/ bamB∆tolC∆ → smRBS1A1 + pACYC 186/ bamBtolC∆
- pMLGFP + pACYC 186/ DH10β smRBS1A1 + pACYC 186/ DH10β
- pMLGFP +pJZ13/ DH10β - smRBS1A1 +pJZ13/ DH10β → pMLGFP +pJZ13/ toICA smRBS1A1 +pJZ13/ toIC∆ → pMLGFP +pJZ13/ bamB∆tolC∆ - → smRBS1A1 +pJZ13/ bamB∆tolC∆



- pMLGFP + pJZ12/ DH10β - smRBS1A1 + pJZ12/ DH10β → pMLGFP + pJZ12/ toIC∆ smRBS1A1 + pJZ12/ tolC∆ pMLGFP + pJZ12/ bamBΔtoICΔ smRBS1A1 + pJZ12/ bamBΔtoICΔ