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Microbial factories under control
Auto-regulatory control through engineered stress-induced feedback

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Severely stressed, with their resources depleted, and their cellular machinery working beyond capacity, the host cells that are used for heterologous protein production have no option but to activate their stress response pathways in order to mitigate the accumulating effects of expressing a foreign, possibly toxic, protein at vast quantities. The result is lower protein yield and quality, with many products being misfolded or part of inclusion bodies that need further processing. Recently, new techniques aim to shift the control of protein production from humans to cells and empower the latter to regulate the production process, thus leading to increased protein quality. Herein we provide a perspective on the way integrative synthetic biology can be applied to traditional biotechnological applications with potentially transformative results.

From early on, the production of recombinant proteins in microbial cells has revolutionized our ability to produce industrial and medical products in vast quantities. Human insulin, human growth hormone (HGH), α/β/γ interferons are some examples of the mass-produced products in the multi-billion dollar recombinant protein production industry. Several organisms, such as bacteria, yeasts, plants, insect and mammalian cells, currently serve as production systems for heterologous proteins. Several organisms, such as bacteria, yeasts, plants, insect and mammalian cells, currently serve as production systems for heterologous proteins. E. coli is arguably one of the most widely used hosts for recombinant protein production since it can achieve high yields, it is fast and inexpensive to grow and it can be easily modified. Remarkably, E. coli can accumulate up to 80% of its dry weight in recombinant proteins, and thus has the potential for very high protein yields that is desired in an industrial scale process. Unfortunately, recombinant protein expression can be detrimental for cells, as it constitutes a metabolic burden through the depletion of precursor metabolites. Additionally, high levels of expression lead to cellular stress that involves the induction of chaperones, foldases and proteases. With the cellular machinery over its capacity, recombinant proteins form inclusion bodies, which represent insoluble protein aggregates and necessitate downstream processing with expensive and time-consuming denaturation methods. Finding the optimal balance between protein yield and quality is always a challenge, as these two variables tend to have opposing dynamics during protein production.

To this end, several of the available expression platforms depend on the constitutive expression or manual fine-tuning of target and auxiliary protein expression in order to achieve the desired balance. For example, since high protein expression leads to lower protein quality and to highly stressed cells, molecular chaperones and foldases are usually co-expressed from accessory plasmids with no further control. Too much or too little expression of these proteins results in drastically decreased recombinant protein quality and yield. This leads to time-consuming fine-tuning, that is not robust to process modifications (e.g., a change in temperature, medium or target protein) that may shift the optimal operating point. In addition, control of the protein production...
systems can be achieved through inducible promoters that drive the recombinant protein expression, although this necessitates the use of expensive chemicals that can interfere with the process.\textsuperscript{6}

In our recent effort to empower the host with control of the protein production process, we introduced a synthetic feedback loop that decreases the production of the recombinant protein, once cellular stress is detected.\textsuperscript{7} As shown in Figure 2, the expression of the recombinant protein, which was GFP in our case, induced a stress response that activated expression of the downstream gene from a stress-inducible promoter. We selected the promoter of the icsA operon, as it encodes inclusion binding proteins that are upregulated during the expression of recombinant products. The downstream gene is a repressor (TerR here) that binds to the recombinant protein promoter and significantly decreases its expression.

To engineer a system with the characteristics mentioned above, we used a synthetic biology approach: First, we created a model of the proposed circuit topology to gain an insight on its dynamics and obtain the operation point for the different combinations of the key circuit components. Then we used the Registry of Standard Biological Parts to acquire the basic building blocks for each of the circuit elements and to build biobrick-compatible constructs. To fine-tune the circuit behavior we altered the ribosomal binding site affinity and stress promoter strength through random mutagenesis and subsequent screening. Cells were able to modulate their protein production and achieved much higher soluble protein fractions relative to those lacking the self-regulatory control (80% vs. 55% soluble fraction) and the system operated without modifications in different media and temperature ranges. In our proof-of-concept, “flight-to-quality,” system, this increase in the solubility was at the expense of protein yield (in some cases more than 50% reduction) and further experimentation is needed to bring the proposed method to a production scale. Despite this shortcoming, these promising results argue that the complex bioreactor environment will also increase protein yield, as this will lower the metabolic burden of their other-wise constant expression.

Finally, integration of all these concepts in a single protein production system is particularly challenging problem as the system complexity increases exponentially with each additional component that we introduce. Here is where the structured synthetic biology approach of model abstractness, standardization and automation is of paramount importance. Well-characterized and standardized parts will allow us to create computational models of dynamic circuit behavior with high predictive capacity, although efficiently capturing the dynamics in the complex bioreactor environment will always be a challenge. Despite the recent advances in computational tools for
This is a very exciting time for synthetic biologists, computational scientists and biotechnology professionals since synergistic interactions among researchers in these disciplines are likely to result in transformative advances in the field.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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