NEWSLETTER

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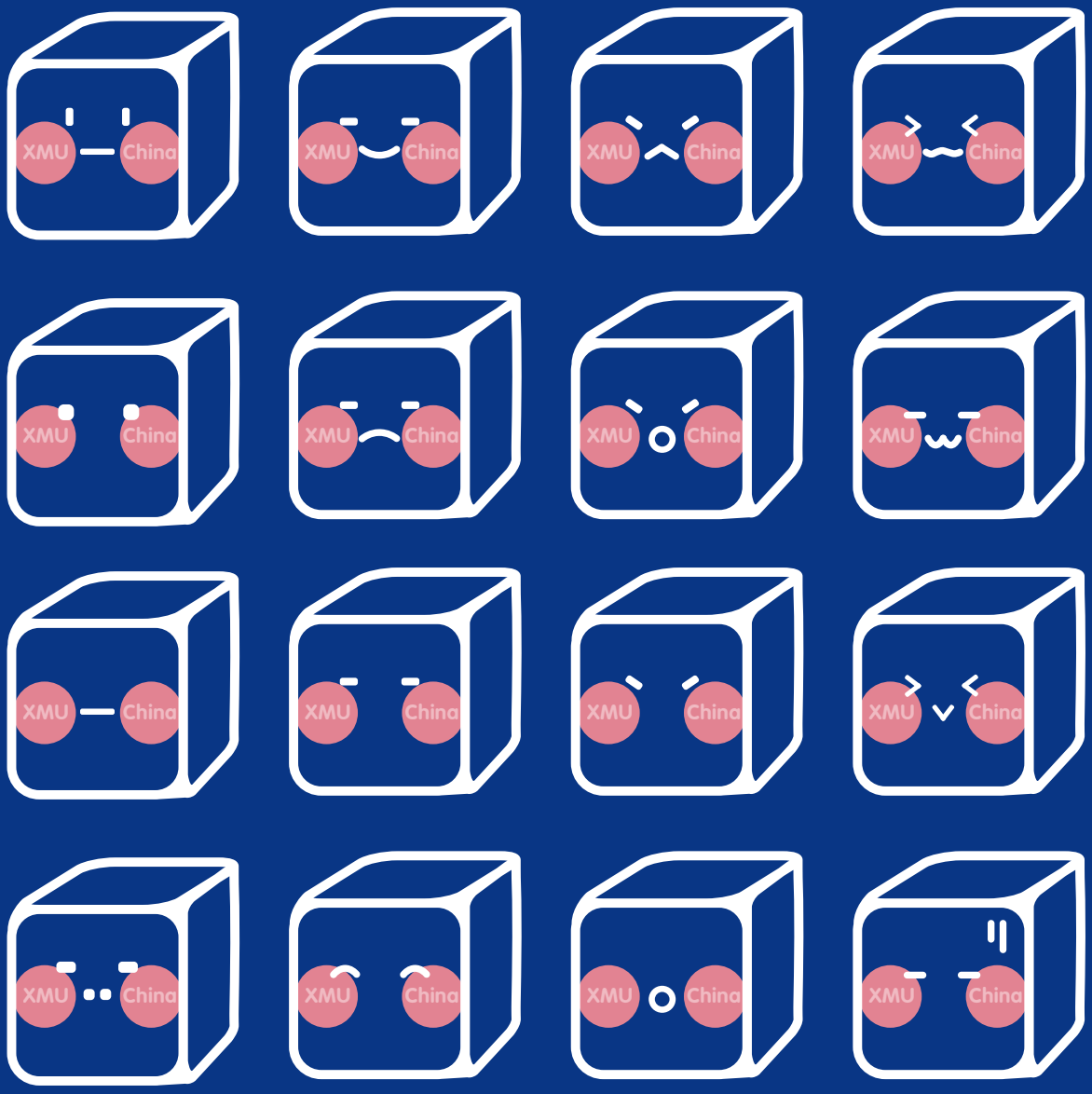

BostonU
EXYUST
FJNU-China
Jiangnan
NPU-China
TU Delft
TUST-China
XMU-China

iGEM 2018

BostonU

Twitter @BostonUiGEM2018
Email bu.igemwl2018@gmail.com

Team BostonU is super excited to be participating in iGEM this year! A small team of three, BostonU includes Kevin Lorch, a senior studying Biomedical Engineering, Cass Leach, a junior studying Biomedical Engineering, and Linda Luo, a sophomore studying Computer Engineering! We love bonding over Pokemon, cloning struggles, and old Vines. We are incredibly grateful to our wonderful mentors Rachel Petherbridge and Meghan Bragdon, as well as our mentee Alicia Lau.

Project BostonU 2018 is characterizing and optimizing a pair of light–inducible promoters, LOV2 & PhiReX, in S. cerevisiae for use in eukaryotic transcriptional control and in industrial fermentation. Light–inducible promoters lend synthetic biologists greater spatiotemporal control over transcription than small molecule–inducible promoters, and represent an expansion of tools for transcriptional control. Further, LOV2 is activated by blue light and PhiReX by red, allowing for multiple layers of control. We are characterizing these light–inducible promoter systems using the eVOLVER, a novel cell culturing platform developed by Brandon Wong at Boston University's Khalil Lab. The eVOLVER allows us to fully characterize our systems across an expansive parameter space, as well as multiplex across strains while retaining control of individual cultures. Using the eVOLVER, we will be able to rapidly gather data on the optimal conditions under which PhiReX and LOV2 operate, which will allow us to improve light–inducible tools for transcriptional control. Optimizing light–inducible transcriptional control can be applied to multiplexed control of gene expression, as well as to the finely–tuned expression required for effective biofuel production. By improving light–inducible control of eukaryotic transcription, BostonU 2018 will make a significant contribution to the range of tools available to synthetic biologists.

FJNU–China

Twitter @FJNU iGEM 2018
Email igem2018fjnu@gmail.com
Wechat 福师大 iGEM

Team As the team that participated in the iGEM competition for the first time in our school,it was very difficult to construct our team which is consisted of only eight girls. However, because of the small number of people, our team is closer and more united. We know each other very well and make the most of each person's strengths in the work.

Project 2–PLEAsant

According to statistics, the microbes we touched each day are about 3 times more than the human cells. The infection with some specific microbes can cause infectious diseases and give unpleasant smell. Bacteria can infect any area of the body and cause different diseases: pneumonia, meningitis, food poisoning, etc.

Our project focuses on inhibition of the infectious microbes in a more efficient, environmentally friendly way. Based on the principles of metabolic engineering, we engineered an E.coli strain producing phenyllaclic acid that has broad–spectrum antibacterial effects, and the rose–like aroma compound 2–phenylethanol. We incorporated the common components of temperature and salt control in the synthesis system, which applied phenyllaclic acid and 2–phenylethanol to the natural environments. In addition, we designed the toxic protein mazF as a suicide switch to ensure biosafety. In the future research, we plan to promote the system into various types of fields and solve more environmental problems.

ECUST

Email ecustigem@yeah.net
Wechat ESUSTLab

Team

Team ECUST consists of 14 students, who mainly major in Bioengineering, but we also have members majoring in Art Design and Computer Science. As a united team, we often do experiments together, have meals together, and hold meetings together. Sometimes we may have disagreements over some issues, but we can always solve the problems after discussion in detail. We are all proud of being a part of ECUST iGEM and we hope ECUST iGEM will also be proud of us!

Project

Iron Guardian

Abstract The global cost of blocking and corrosion in cooling towers is estimated to be several billion dollars each year, which mainly results from the colonization of microbes. The microbes cause the formation of corroded objections and biofilm, directly leading to severe blocking. In this year, iGEM ECUST is trying to solve the problem by synthetic biology, presenting a totally new idea. By constructing engineered Escherichia coli, we design an integrated gene circuit which assembles sensing, cleaning rust, eliminating biofilm and killing iron bacteria. The microbes in pipelines will firstly be sensed through quorum sensing, then two key substances will be secreted to clear rust and biofilm respectively. When this method achieves the certain effect, the expression of antimicrobial peptides will be triggered to kill the bacteria without adhesion ability, basically preventing the pipelines from being blocked again.

Background The circulating cooling water system is a kind of heat sink being able to absorb and release heat through water, which is used extensively in oil refinery, petrochemical plants and power stations. According to the US Department of Energy, more than 100,000 cooling towers are located in America. Merely for one individual circulating cooling water system, the treatment fee caused by corrosion and water quality problem will hit 50,000 to 100,000 dollars. If suitable chemical reagents provided, the number will even reach 100,00 to 250,000 dollars. Adding chemical reagents is one of the most commonly–used methods for companies to solve this problem, but being intensely corrosive and oxidative, they will always bring severe damages to the environ–ment and human body.

The corrosion and blocking caused by bacteria is a complicated process with various kinds of microorganisms involved. Among them, Bacillus licheniformis can make pipelines oxidized and produce insoluble FeOOH. Over time, corroded objections will come into existence, which will reduce flow rate considerably and provide points of attachment for bacteria. At the same time, Bacillus licheniformis will form biofilm along with other bacteria to shield them, and the extracellular metabolites secreted by them comprise the microenvironment they live in, where the antimicrobial effects of added reagents will be significantly minimized. Therefore, before adding substances that kill germs, giving priority to destroying the microenvironment will solve the problem more efficiently.

The attempt we make can minimize the chemical reagents' effects on environment and human body and reduce the maintenance costs greatly, therefore, it'll bring considerable economic and environmental benefits.

Solve the problem by synthetic biology

Based on the principal of quorum sensing of, the first step of our solution is to make our engineered bacteria able to sense the existence of Bacillus licheniformis and express siderophore and glucosaminidase (the former to chelate ferrous ion and make rust dissolve, the latter to make biofilm degrade). After the destruction of microenvironment, the engineered bacteria will express cecropin to kill harmful organisms. Based on the above idea, here is the gene circuit we designed.

Based on Quorum Sensing–I, the transcription factor AfeR which can bind to AHL (a kind of self–inducible molecule of Bacillus licheniformis) is constitutively expressed in our engineered bacteria. After being activated by AHL, AfeR will trigger the expression of rust–removal and biofilm–removal substances by activating the synthesis of siderophore and glucosaminidase. When secreted to environment, siderophore will chelate ferrous ion, make rust dissolve and form siderophore–Fe3+ complex. And as a main component of biofilm, chitosan can be hydrolyzed to soluble aminoglucose by glucosaminidase. Wild type bacillus has natural systems which can absorb siderophore–Fe3+ complex and regulate downstream parts, therefore, we utilize the promoter of siderophore biosynthesis gene in Escherichia coli. By doing so, we can control the LacI reverse system to express cecropin AD, make holes in cell membrane of G– bacteria, and kill harmful bacteria.

Jiangnan

Twitter shidingchang
Email 1024579493@qq.com
Wechat 18861853281

Team This is the first year of Jiangnan to participate in iGEM, therefore, our team is constantly improving in every exploration. After the adjustment in the early stage, finally this young and energetic team has been built. Now we've worked together for almost 1 year, and have become a lovely family.

Project Vaccine is considered as one of the most cost-effective public health solution which would significantly prevented a large varieties of diseases. However, vaccine still has its limiting elements for the future development, such as the high cost, unstable quality, weak supervision, etc. This year, Jiangnan team is trying to make our own contribution to reduce the cost of vaccine production which would greatly reduce the economic burden of vaccination for the masses.

In terms of biosafety issues, we would not conduct the experiments associated with the human viruses, therefore, what we focus on is the animal vaccine which will not pose any risks to the lab or environment. We construct a cell line(MDBK) with self-owned intellectual property and feasible for rapid production of a broad spectrum of viruses.

The goal of our project is to enable three features of our chassis cell, i.e., high titration, suspension cultivation, and broad spectrum to reduce the production cost and increase the yield of viruses for vaccine production. The chassis cell we used here is MDBK cells.

1) Board spectrum

Through text mining, we classified cell receptors according to the Baltimore subtyping of viruses and summarized the primary receptors mediating the entry of different types of viruses. After systematic analysis, we aim to express Nectin 4 and TFR on our chassis cells to make them susceptible to a broad spectrum of viruses.

2) Suspension cultivation

High throughput RNA sequencing was conducted upon normal adherent cells and suspension cells. We found a panel of genes responsible for the suspension feature of cells following network construction using computational approach. The top gene was functionally validated before applied to the chassis cell for genomic modulation.

3)High titer

Through bioinformatics analysis and mathematical modeling, we constructed the protein-protein interaction network involved in virus infection and replication. The top gene was selected, functionally validated in vitro and used for genomic modulation in the chassis cells to enable them the feature of high titer. On the other hand, we manufactured a cold atmospheric plasma generator that can ionize the Helium gas, which was used to treat the cell culture median. The plasma activated median (PAM) subsequently used for MDBK cell culturing displayed a significant ability in facilitating the infection of virus.

NPU-China

Email 510301271@qq.com

Team NPU-China, the participant team of iGEM on behalf of North-western Polytechnical University. Located in the historic city of Xi'an, cradle of Chinese civilization and terminus of the ancient Silk Road, NPU-China is the first team to partake in the competition in Shaanxi. With the support of NPU Ecological and Environmental Protection Research Center, the School of Life Science, International Cooperation Office of NPU and Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, we joined the family of iGEM in 2016. Our exploration has been always wide and vast, from the design of artificial biological carbon sequestration pathway in the first year and the construction of a new acrylic biosynthetic cell factory in 2017 to the design and synthesis of the minimalist S. cerevisiae mitochondrial genome this year. We have an edge on multi-genomic-based homologous evolution analysis, rational design and transformation of enzyme element, gene synthesis and editing technologies. Plus, we are also experienced in the commercialization of results. We are exceedingly looking forward to the collaboration and communication with other iGEM teams through this Newsletter event and further substantial coopera-tion.

Project Our project this year, which is called MitoCRAFT, pertains to the design and synthesis of minimalist S. cerevisiae mitochondrial genome. We hope to construct a model mitochondrial chassis by simplifying this genome, laying the foundation for further research and application. The mitochondrial genome of Saccharomyces cerevisiae is 85,779 bp in length and contains 35 functional genes, which control the function of the electron transport chain and the expression of relevant proteins. In the design process, we first carried out a conservative analysis of the entire genome and found that the functional genes on the mitochondrial genome are highly conserved, so we retained all of them and removed all non-conservative introns. At the same time, we deleted the redundant sequence among transcription units along with some non-functional oris, simplifying the 85K genome to 39K. In order to enhance the expression of this design, we designed a mitochondrial tailored to GFP for the mitochondrial-specific codon table to observe the replication of the mitochondrial genome.

In the subsequent research, we found that the current mitochondrial gene editing technology still has a lot of limitations, and that complexity of the operation, difficulty of screening can scarcely meet our needs. Hence, we chose the strategy of artificial synthe-sis in vitro. The remarkable complexity of the sequence of the mitochondrial genome itself, low content of GC and the existence of multitudes of local GC clusters and AT regions all lead to great trouble for our in vitro assembly. In order to solve this problem, we divided it into 21 regions with relatively uniform GC content distribution for the characteristics of this genome, allowing the relevant company to further explore and optimize the splicing methods and conditions after synthesis. We successfully assembled four 10K genomic fragments using the homologous recombination (TAR) system in yeast, but there was a problem of non-amplifi-cation after transfer into E. coli. We speculate that a large amount of fragment of high AT content in E. coli is toxic to cells, destroying the balance of four nucleotides in E. coli cells. Now we intend to construct two 20K large fragments employing the new vector pGF to complete the genome-wide construction. In the future, We shall use the gene gun method to transfer the designed genome into the S. cerevisiae rho0 cells that have lost the mitochondrial genome, verify their function, and collect the data to optimize our original design.

TU Delft

Twitter TUDelft_iGEM
Facebook iGEM TU Delft
Instagram igemtudelft
Linkedin igemtudelft
Email tudelft.igem@gmail.com
Phone +31 15 278 5394

Team

This year, the TU Delft iGEM team consists of 12 students with 6 different nationalities. Our educational background varies between nanobiology, chemical engineering, and life science and technology. Each member is taking up different roles in human practices, dry lab and wet lab with a common end goal of completing our project, ADOPE.

Figure 1: Team Group Photo. Up, left to right: Susan, Alex, Nicole, Janine, Lisbeth, Lisa. Down, left to right: Gemma, Monique, Timmy, Venda, Jard, Kavish.

Project

Our team aims to prevent the abuse of synthetic biology in sports by developing a method to detect genetic doping. Gene doping has been on the list of prohibited substances in sports since 2003, yet no method has been implemented to enforce this ban. Our project, Advanced Detection of Performance Enhancement (ADOPE), aims to provide the proof–of–concept for an efficient, secure and versatile detection method. We have modelled the doping detection window; implemented a suitable sample preparation method from blood; developed a valid pre–screen based on gold nanoparticle technology and developed a unique and cutting–edge targeted sequencing platform based on a novel dxCas9–Transposase fusion protein and nanopore sequencing technology. Finally, we have developed an algorithm that is able to group our sequencing outputs and indicates wheth–er the athlete used gene doping.

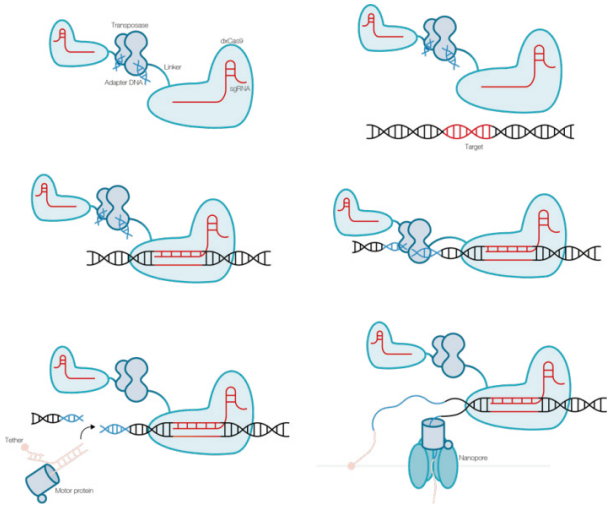

Figure 2: Working concept of our dxCas9–Transposase fusion protein for targeted sequencing.

TUST-China

Weibo iGEM_TUST
Facebook TUST iGEM
Email Tustigem2018@163.com

Team The second iGEM team from the Tianjin University of Science and Technology (TUST) consists of 15 highly motivated undergraduate students from very different fields of study: Biology Engineering, Biopharmaceutics and even Computer Science. Our senior, Wenxin Lin, who was a part of the team last year is our team leader. Especially, professor Cheng Zhong, advisor Tingyue Deng and instructror Longhui Huang provide us with excellent supports of lab equipment and academic consults. All members are from the College of Biology Technology in TUST. All of us are enthusiastic about participating in iGEM and exploring in synthetic biology field.

Project Tetracycline, a kind of widely-used antibiotics, has been utilized on a massive scale in fishing industry since it was discovered in 1953. In recent years, some side effects caused by tetracycline are exposed and becoming increasingly acute and serious, which negatively influence public health and deteriorate our environment, like tetracycline tooth, and contamination resident in water and in soil. To alleviate these problems, we designed D&D system.

Double D system consists of tetracycline detecting system and degradation system. It is a comprehensive mechanism which can be used to measure tetracycline concentration in the environment, then discharge it from the cell, and finally degrade it with a high efficiency. In the first place, detecting device is responsible for measuring tetracycline concentration in the surroundings and indicating it by fluorescence intensity, simultaneously a transmembrane protein will be expressed to pump tetracycline complex out of the cell for avoiding engineered strain deterioration.

After a certain concentration tetracycline being detected, the second part is ready to work for degrade these toxins. We exerted ourselves to select an ideal combination of two peroxidase enzymes, which was validated can eliminate tetracycline with a much higher efficiency. Importantly, taking safety into consideration, we connected lacI sequence in the constructed plasmid to stop cell lysis. If no peroxidase enzyme is expressed, the bacteria will be killed duo to cell lysis. As a result, there is no engineered strain existed in the environment without tetracycline.

XMU-China

Twitter XMU_iGEM
Facebook IGEM XMU-China

Team

This is the eighth year of Xiamen University to participate in the iGEM competition. Since 2011, Xiamen University team has won 7 gold medals and 1 silver medal. Most teammates who have participated in iGEM competition will go to worldwide famous universities for further studies. The iGEM competition greatly broadens the international horizons of the teammates and our team shows specialties of Xiamen University on the international stage.

Project

Cell-free Systems for Disease Detection and Treatment

This year team XMU-China developed cell-free systems to detect and treat diseases. Protein detection is unique and significant in biology fields, especially for the detection of protein biomarkers which produced by diseased cells. In order to overcome the deficiencies of traditional detection methods, we have developed an Aptamer Based Cell-free Detection system (ABCD system) of protein. The core of the ABCD system is the specific binding of the aptamer and its target protein. After protein detection, we use outer-membrane vesicles (OMVs) to treat the diseased cells. We designed a system that has realized the efficient, customiz-able production of OMVs, which serves to encapsulate specific siRNA for disease treatment. To guarantee the practicability detection and treatment system, we also improved KaiABC system and TDPs system to regulate the expression rate of OMVs and store fragile chemicals or biological materials.

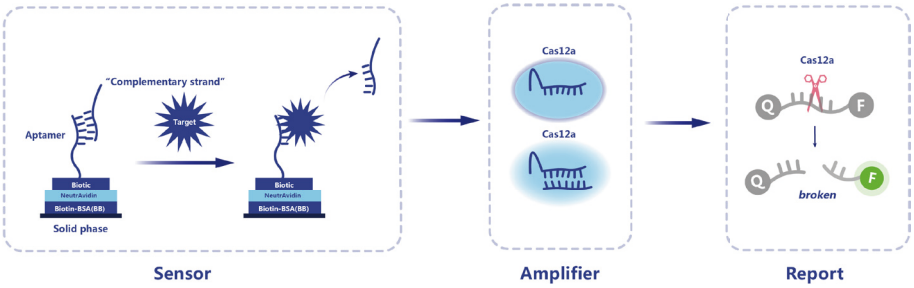

Figure 1: Detection of biomarkers of protein-type

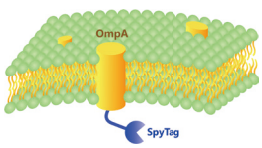

Figure 2: Fusing OmpA with SpyTag

Figure 3: The overall OMVs targeting for $KRAS^{G12D}$ in pancreatic cancer

XMU-China Credit

Chief Editor
Rengwei Liu

Correspondent
Qiupeng Wang, Junhong Chen

Art & Design
Hang Yu

Proof-readers
All teammates of XMU-China 2018