News Letter

NO.3

2015. 6. 15 Today's Topic

SHOW OUR PROJECTS

Welcome to our newsletter.

· Amoy · Paris_Bettencourt · Pasteur_Paris ·

T O D A Y ' S T O P I C

SHOW OUR PROJECTS

Dear All,
Here comes the third issue.

We hope to receive more suggestions on
how to make the Newsletter server for iGEM!

Thanks so much to Stockholm for their suggestions on issuu.com;
We want your advice!

Project Part(12):
(in alphabetical order)
BIT, CAU_China, ETH-Zürich, IONIS_Paris, Missouri_Rolla,
NCTU_Formosa, OUC-China,
Paris_Bettencourt, Slovenia_HS, Stockholm,
Toulouse and Valencia_UPV,

Thanks to all of you for your devotion!

Any questions or suggestions?
We can always find us at igemxmu@gmail.com

All the best! Cheer for the summer!

iGEM Amoy
2015-6-15

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Project

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By: Twelve iGEM Teams
Show you our projects

iGEM 2015 team

BIT

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We sincerely hope our project can play a role in the future. With more communications and teamwork, we believe that help from outside team can push us together onto a higher level!

Team BIT_China

Our team, BIT-china, is a fresh and creative team founded in 2012 and now is guided by Prof Chun Li , Prof Shuyuan Guo and Aso.Prof Jun Li. BIT_CHINA had some experience in synthetic biology, especially in biochemical industry aspect. In 2013 iGEM competition, our work on helping fermentation industry was rewarded with a gold medal. In 2014 BIT_CHINA designed a genetic lock, E.co-Lock, to keep important strains safe from ecological threatening or commercial loss even when they are accidentally leaked out or intentionally stolen. With more new members joining in us from different majors and grades, we believe that our ideas and products can bring more surprises to iGEM.

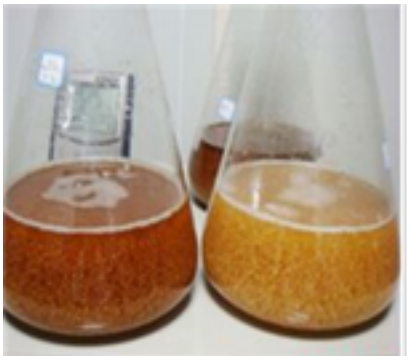
BIT-China

Our 2015 project: pH-balance machine

This year BIT_CHINA wants to design a pH-balance machine. There is worldwide concern related to the issue of fermentation. Scientists have to precisely control the pH in a narrow range because fluctuation of pH level can tremendously influence the strains' performance. Therefore, a pH balance machine is needed to solve these problems.

Our pH-balance machine contains two sub-systems, one is the resistance system and the other is the regulation system. The resistance system can make bacteria survive in an expanded range of pH. The regulation system is used to adjust the microenvironment pH. The two sub-systems working together allows for lowered cost and energy of artificial pH regulation, because the host with our machine can maintain the high fermentation efficiency when the environmental pH is not optimal.

Since our machine is now under construction, if you want to get more information about this project, please continue to pay attention to our team. You may come across some surprises!



Here are the team members of 2015 BIT_CHINA.

iGEM 2015 team

CAU_China

About our project of this year

Email: igemcau@gmail.com

Our project is to create 4 kinds of transgenic plants, each of which has a resistant gene synthesized by us. The 4 resistant genes are BAG, GAB, BT and TB. We use a section of polypeptide called 2A which has 20 amino acids to linage the glyphosate resistant gene and the glufosinate resistant gene. And then we synthesize the BAG and GAB genes. The only difference between them is the order of the glyphosate resistant gene and the glufosinate resistant gene. Similarly, the BT and TB genes both have the glyphosate and the 2, 4-Dichlorophenoxyacetic acid resistance. And the order is the only difference.

As the four genes are created, we put them into the plasmid pHSE-A. Then we construct four different plasmids. They are pHSE-BT/TB/BAG/GAB. Afterwards we transform the four kinds of plasmids into Agrobacterium tumefaciens（GV3101）. We use the Agrobacterium tumefaciens to infect the wild type Arabidopsis thaliana. After we get the To generation seeds, we use the three herbicides to filter. At last, we get the 4 kinds of transgenic plants.

Our Team

iGEM 2015 team

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CIA Coli (CTC identifying agent)

During the development of malignant tumours, cancer cells acquire new properties and mutations in their signal transduction pathways to adapt to changes in their environment, such as lack of oxygen or nutrient starvation, and evolve strategies to exploit endogenous signaling factors for excessive growth. Such changes are often triggered by the same circumstances for various kinds of cancerous tissues, which leads to the evolution of common markers for several types of cancers. These markers can then be used to detect cancerous cells and distinguish them from healthy cells.

Metastasis occurs when single tumor cells detach from their neighbouring cells, enter the bloodstream, and travel to distant locations, where they can invade foreign tissue and initiate the formation of a new tumor. These cells are referred to as Circulating Tumor Cells (CTCs) and are widely used as indicators of early stage metastasis in various clinical approaches. However, the methods currently employed make use of markers which are highly specific for certain types of cancer and thus can only be applied to a small subset of patients at a time. Moreover, these tests often rely on expensive detection methods such as Flow Cytometry or ELISA.

Our intention is the detection of several types of cancers in patient blood samples with one easy-to-use system. We propose a design for a CTC detection module that aims to use general cancer cell markers to make it applicable to a wider range of cancer types. The use of a microfluidic device, requiring only simple and well-established image analysis methods to process the data, is superior to previously described methods, which require specialized and expensive equipment for sample analysis.

Our system is designed to analyse clinical blood samples from patients. As a proof of principle, our initial experiments will be performed on samples prepared from a combination of mammalian cell lines representing healthy and cancerous cells in an artificial medium before we eventually test our system on mouse blood.

Our Team

iGEM 2015 team

IONIS_Paris

IGEM IONIS

The project

The main goal of IONIS Paris iGEM team is to make synthetic biology more accessible to people. Indeed, this field is not well understood especially in France and as every big innovation or scientific tool people are afraid and against it when it comes to public knowledge.

The team decided to break all the prejudices regarding synthetic biology by presenting it as an efficient scientific tool that can be controlled and that can be without any risk if well engineered.

The project is based on the popularization of synthetic biology using two approaches:

The first one is the design of a real synthetic biology game: our "Bio-console".

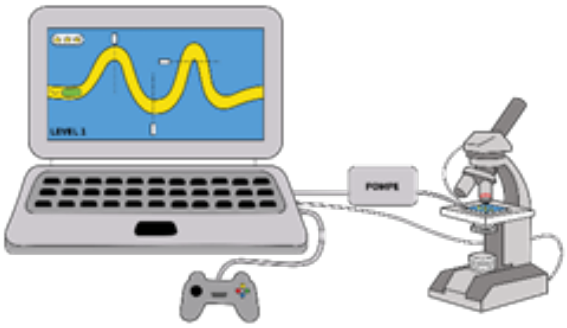
It is based on the control of engineered bacteria in a micro-fluidic chip connected to a computer interface.

Email

The game is dependent on optogenetic signals leading to either the fluorescence of our bacteria in order to visualize it or the death of our bacteria in order to control our system leading to an efficient kill switch.

The second one is the design of a mobile application game presenting several concepts of Biology, Synthetic Biology & safety.

The team wants to promote Synthetic Biology using an original point of view. The goal is to make this field accessible to everyone by using a playful & entertaining tool.



Key words: Synthetic Biology, Optogenetics, BioSafety, Kill Switch, Scientific vulgarization, Light, Game, Engineering, Micro

iGEM 2015 team

Missouri_Rolla

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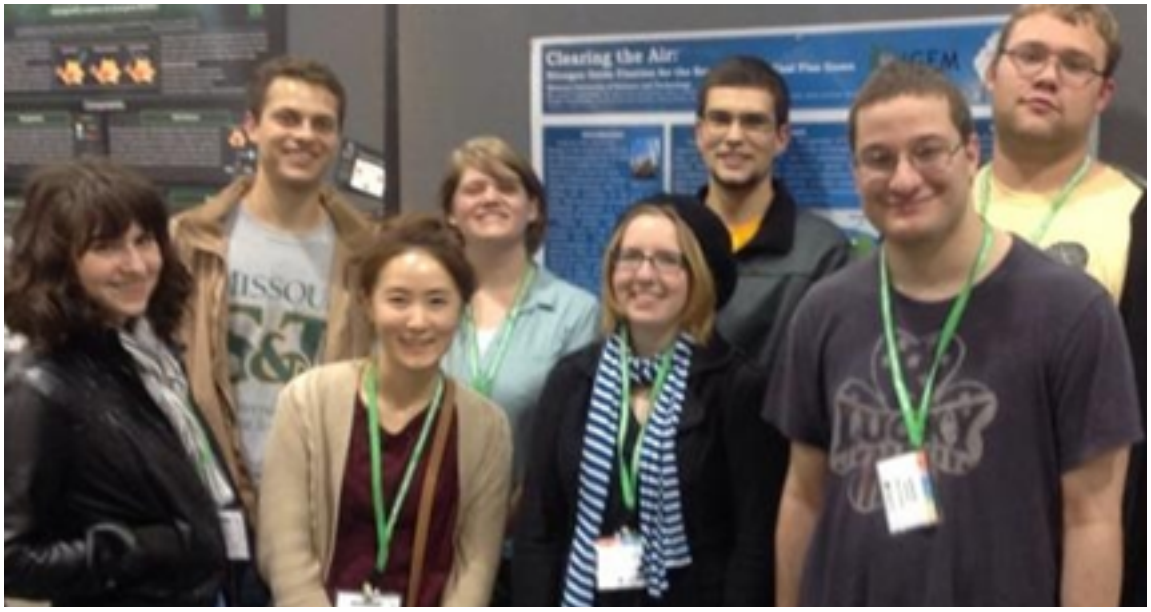
Bats are a vital part of the ecosystem in the United States, providing immeasurable services in terms of pest control, fertilization, and pollination throughout their range. In 2007, a new bat disease was introduced to the United States and has since been spreading rapidly and causing mortality rates as high as 90% in some hibernacula. This disease termed White Nose Syndrome (WNS), caused by Pseudogymnoascus destructans(formerly Geomyces destructans), works though several ways to disturb the bats' hibernation, metabolism, and skin integrity, ultimately leading to the death of most of the affected individuals.

Fighting this pathogen has proven to be quite difficult, very little research had been done on the immune response of bats and key aspects of this fungus, which is widespread throughout Europe, leaving scientists to play catch-up while millions of bats succumbed to WNS. To make matters worse, it has been found that P. destructans is quite tolerant to changes in its food source, that bats may have a depressed immune response during hibernation, and that many compounds that could be used to fight the fungus are harmful to the native cave flora.

The 2014 Missouri S&T iGEM competition team at the Giant Jamboree in Boston! Photo by Bob Phelan of Missouri S&T.



For the above reasons, we have decided to try to defend the bats rather than aggressively attack the fungus, hoping to slow the fungus and its effects to give the bats more time to make it through the winter and fight off the fungus naturally. We are currently exploring means to detect and inhibit the destructive enzymes of the fungus while developing a fungistatic expression pathway to slow the fungus. We hope that with this three-pronged approach, we will be able to successfully defend bats while disturbing the natural habitat as little as possible.

Picture source: featuredcreature.com

iGEM 2015 team

NCTU_ Formosa

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Project

Have you ever thought that E.coli which display antibody can be used as a detector? Our project is to fulfill this unbelievable thing.
In our daily lives, risks or threatening factors could be underlying in our surroundings. Hence, detecting these threats becomes a significant task. Among all the detecting, the one that will directly affect human beings is about detecting antigen so called immunoassay. However, t hey all face a common problem called random orientation of receptors , such as antibody. Random orientation means that the cristallisable fragment of antibodies don't stand straight on the detecting chip , in this case is gold chip. Under this situation, the antigen could not bind with antibodies efficiently, which results in low yield and inaccurate results. This severe problem has never been solved .Although there have been many scientists focused on this issue.
Here is where our idea will have a significant impact. If we can use an E.coli to display antibodies on its surface, with the aid of E.coli., antibodies can stand straight on detecting chip. As a result, we fix the problem of random orientation and improve the binding efficiency of antigens on antibodies.

Our Team

Our team is consisted of students from different ages. We have senior to consult, but most of the time the project is mainly lead and organized by freshmen. Students majoring in biotechnology, biology science, bioengineering, ecology, aquaculture, computer and mathematics work together almost a year, due to the same passion for a challenge in biology field.

Our project is mainly based on ferritin, which genetically encoded nanoparticles in cells, and thermosensitivity regulators or structures, such as TCS, RNA thermometer and intein, which can response to temperature changes and regulate the downstream gene expressions. When low frequency electromagnetic wave comes, intracellular ferritin kernel resonance occurs, generating heat. At this time, thermosensitivity regulators was stimulated to activate the downstream gene expression, achieving the goal of what we want.

iGEM 2015 team

OUC-China

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As a matter of fact, we have considered some application in future. For example, we can control our E.coli in water pipe to dismiss the harmful biofilm by means of RF signal, while chemical signal is limited, or produce Exopoly Saccharides(EPS) to flocculate yeast when fermentation completed, in order to simplify filtration and avoid chemical substances in food industry.

Obviously, our platform has great potential for building a bridge between electronic area and biological application, and it's excited to imagine that we could control creatures like bacteria just by using an App on our smart phones to release drug.We can also use the platform we structure to replace pesticide, form the guidepost in mining accidents and so on.

Project Overview

Fermented foods form an integral part of various cultures all over the world. These were accepted as high nutrition foods long before we knew what microbes were or how fermentation worked. Foods made out of fermented rice are staples in almost all of South India and Sri Lanka, with idli and dosa being over the most widely consumed throughout the Indian subcontinent. While the process of fermentation in the preparation of these foods already enriches the dishes with some essential vitamins and amino acids, these regions still suffer from high levels of malnutrition due to a heavy dependence on rice and a lack of other food sources, which itself stems from socioeconomic issues.

iGEM 2015 team

Paris_ Bettencourt

Biology Project

We, the iGEM Paris-Bettencourt team 2015, are trying to tackle this problem of malnutrition in the region while celebrating the cultural heritage of fermented foods, by engineering strains of yeast and bacteria. Those microorganisms, when used for food fermentation, will enrich it with essential nutrients either present in low quantities or not present in these foods.

We are planning to work on vitamins that are lacking in fermented rice, including: vitamin A, B2, B9 and B12. Further, mineral deficiencies (the lack of iron, iodine or zinc for instance) is also a big concern. We plan to make them more bioavailable by producing enzymes that degrade antinutrients such as phytic acid, which chelates minerals.

Next, since the over expression of nutrients by the microorganisms will tend to counter select them, we are designing a system that will mimic cell differentiation. First some cells will not produce anything and will grow fast, then a fraction of them will differentiate to produce one nutrient at a time. That way, there will be cells to produce each nutrients but slowly growing, as well as cells producing nothing but growing fast.

So we will be using techniques such as pathway engineering to produce bigger amounts of nutrients that already exist in rice or in the organisms. For the nutrients that are totally absent, such as vitamin A, we will use cloning methods to introduce new pathways into the microbial genomes. Since multiple enzymes are usually needed, we think of using chromosomal landing pads to insert them

iGEM 2015 team

Slovenia_HS

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Wiki:
http://2015.igem.org/Team:Slovenia_HS
Webpage:
hsigem.si

We are the first high school team from Slovenia to compete at iGEM and are very excited to face the challenges synthetic biology poses. After a demanding selection process consisting of a research challenge and interviews the team was formed and consists of eight pupils attending secondary educational institutions across Slovenia. Our research is performed at the National Institute of Chemistry of Slovenia and the Faculty of Chemistry and Chemical Technology, University of Ljubljana, under supervision of knowledgeable and encouraging mentors.

We have decided to tackle a very imposing ecological problem that is becoming more and more threatening. Fossil fuels, such as oil and gasoline, have gained popularity in the beginning of the 20th century. It is estimated that we have spent between 100 and 135 billion tons of oil since 1850 and the demands are still increasing. Fossil fuels are used in cars, airplanes and other vehicles, to power electricity plants, to heat our homes

Our society is largely dependent on them, but fossil fuels take millions of years to form and are therefore a non-renewable resource. According to some projections, we only have enough oil for the next 40 years, so it is becoming increasingly necessary to find an alternative method of obtaining fuels.

Our first thought was to make use of butanol. Research has already shown that because of its long chain and consequent nonpolarity, butanol could, amongst other uses, replace gasoline in internal combustion engines. In nature, many organisms have been proven to be able to produce butanol by converting glucose into acids and then converting acids into alcohols. This organisms, mostly bacteria of the Clostridium genus (Clostridium acetobutylicum, Clostridium beijerinckii and Clostridium saccharoperbutylacetonicum), however, have complex metabolism, slow conversion rate and are often hard to grow in laboratories or for industrious use. For these and other reasons, they are unsuitable for larger butanol production. On the other hand, bacteria E. coli have relatively simple and strikingly fast metabolism, already researched and utilized mechanisms for genetic manipulation and are easy to grow and cultivate, making them the perfect laboratory and industrial organisms.

Laboratory for Environmental Sciences and Engineering at the National Institute of Chemistry

in Ljubljana has been engaged in advancing processes that enable conversion of waste and renewable raw materials into energy for a long time now, but they have recently also developed a mechanism for direct biological conversion of waste to hydrogen by the means of using microorganisms. A series of intermediate products is produced, glycerol and high concentrations of butanoic acid amongst others. Incidentally, these are the two most important substances for our E. coli conversion mechanism, as we could boost their butanol production and achieve good conversion rates and high yield of butanol for biofuel, by genetically manipulating the E. coli bacteria into performing only the second phase of butanol production found in Clostridium bacteria (acids to alcohols conversion).

By using this waste products we could make use of all of the components involved in this processes, while also producing the much-needed biofuel,thus

[Team photo of Slovenia_HS]

completing the circle of waste recycling, all while being eco-friendly. Our aim is to compose an optimized system of bioreactors with which we will be able to produce pure butanol as well as successfully use all side products formed. In the first stage the biogas will be isolated out of organic waste and the remaining sediment shall be used as natural fertilizer. At the same time the butanoic acid formed will be redirected in another bioreactor where it will be converted into biobutanol.

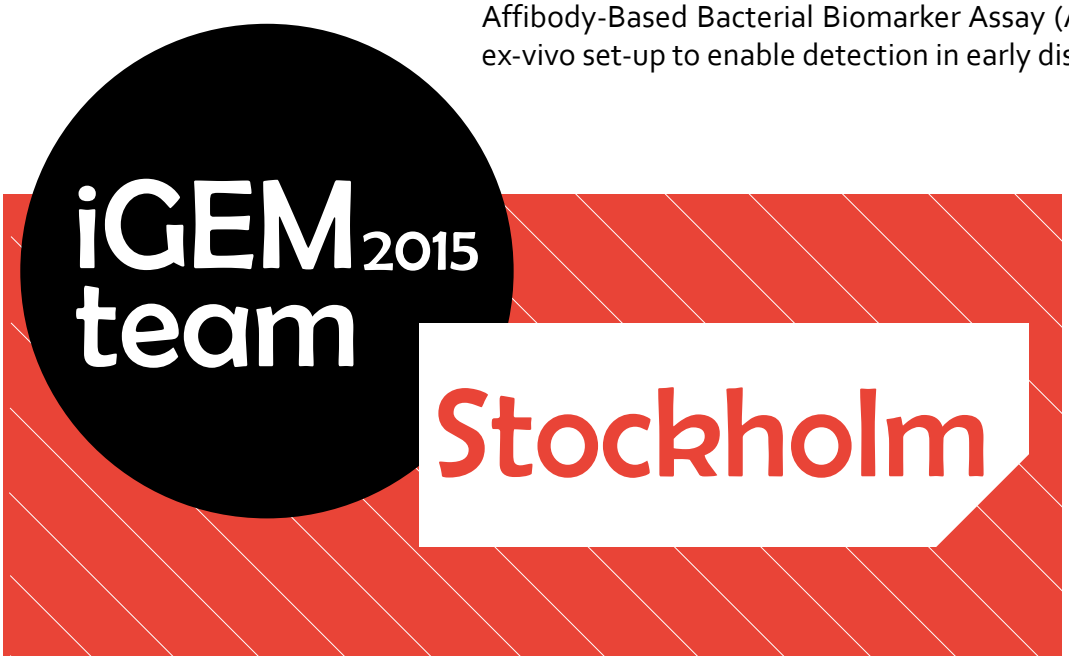
We are currently facing some challenges, as there the isolation of the exact genes we need is not an easy task, but are optimistic about our progress.

We are also looking for other teams with similar projects for possible collaborations, so if you are interested, we encourage you to contact us.

(Written by Nina Jerala, member of iGEM HS Slovenia team)

Introducing ABBBA

The iGEM Group Stockholm is the fourth team from Sweden to join the iGEM competition. The team is a cooperation consisting of students from Karolinska Institutet, the Royal Institute of Technology and Stockholm University. Using the strengths of synthetic biology, we want to design a bacterial detection system for low concentrations of soluble protein biomarkers in human body fluids. Our detection system is an Affibody-Based Bacterial Biomarker Assay (ABBBA) using an ex-vivo set-up to enable detection in early disease stages.



Our goal is fast and simple detection of protein biomarkers for lung cancer.

Cancer is among the primary causes of death, especially in industrialized countries. Certain cancer types such as lung cancer are among the most deadly cancers worldwide. 1800 thousand cases of lung cancer were estimated globally in 2012 with most prevalence in the less developed regions [1]. These cases are majorly caused by the cancer type known as non-small cell lung cancer (NSCLC) [2]. Smoking, a widely known risk factor for lung cancer has seen a decline in many of the more developed countries. At the same time, many of the less developed countries have seen a steady increase in smoking over the last decades which could lead to a coming apex in lung cancer incidence for these countries [3]. In addition, air pollution has been associated to NSCLC, accounting for an estimated 11% of cases in Europe [4]. With the growing urbanization this will most certainly become a major cause of lung cancer globally.

Detection of lung cancer is costly and disease verification often late.

Tomography is the most common verification method for lung cancer [5]. This method for diagnosis is expensive and leaves a risk of false positive diagnosis. The cost on the healthcare system for regular lung cancer check-ups is very high and makes this technique only accessible to wealthy countries and societies. One particularly disturbing factor is that many cancer cases are detected at late disease stages, often even metastatic stages [5].

A cheap and easily applicable diagnostics for early diagnose is required.

At this point, we, the iGEM team Stockholm, want to step in and make a difference. We will design a bacterial system for biomarker detection in body fluid samples. In a proof-of-principle experiment, we will target the carcinoembryonic antigen (CEA) which circulating in increased concentrations in blood during NSCLC [6]. For our bacteria-based detection system, the genetic construction is based on the principle of chimeric antigen receptors (CARs) which are used in clinical phase III trials for the efficient activation of T cells against B-cell malignancies. CARs consist of the single chain variable part of an antibody which is fused to the transmembrane CD3 domain, a co-receptor of the T-cell receptor. After antigen binding, CARs have been shown to stimulate a potent T-cell response and hence killing of malignant tumor cells. Transferring the principle of CARs from T-cells, we want to sensitize bacteria by creating a novel receptor, called the bacterial antigen receptor (BAR).

Instead of antibody-fragments, affinity proteins called affibody molecules are fused to a bacterial transmembrane domain. This BAR will stimulate a signaling over the bacterial membrane into the cytosol for further amplification by feed-forward loops. The creation of a BAR forms the basis for our ABBBA. For ABBBA, we plan to assess both fluorometric and electronic detections methods.

By modifying ion-channels in the bacteria cell membrane, we aim to set up a highly-sensitive quantifiable way of biomarker detection which is competitive to canonical assays such as ELISA. As a tool for successful diagnosis, we imagine several proteins besides CEA being screened for by different strains of bacteria to confirm diagnosis and prevent false positive results.

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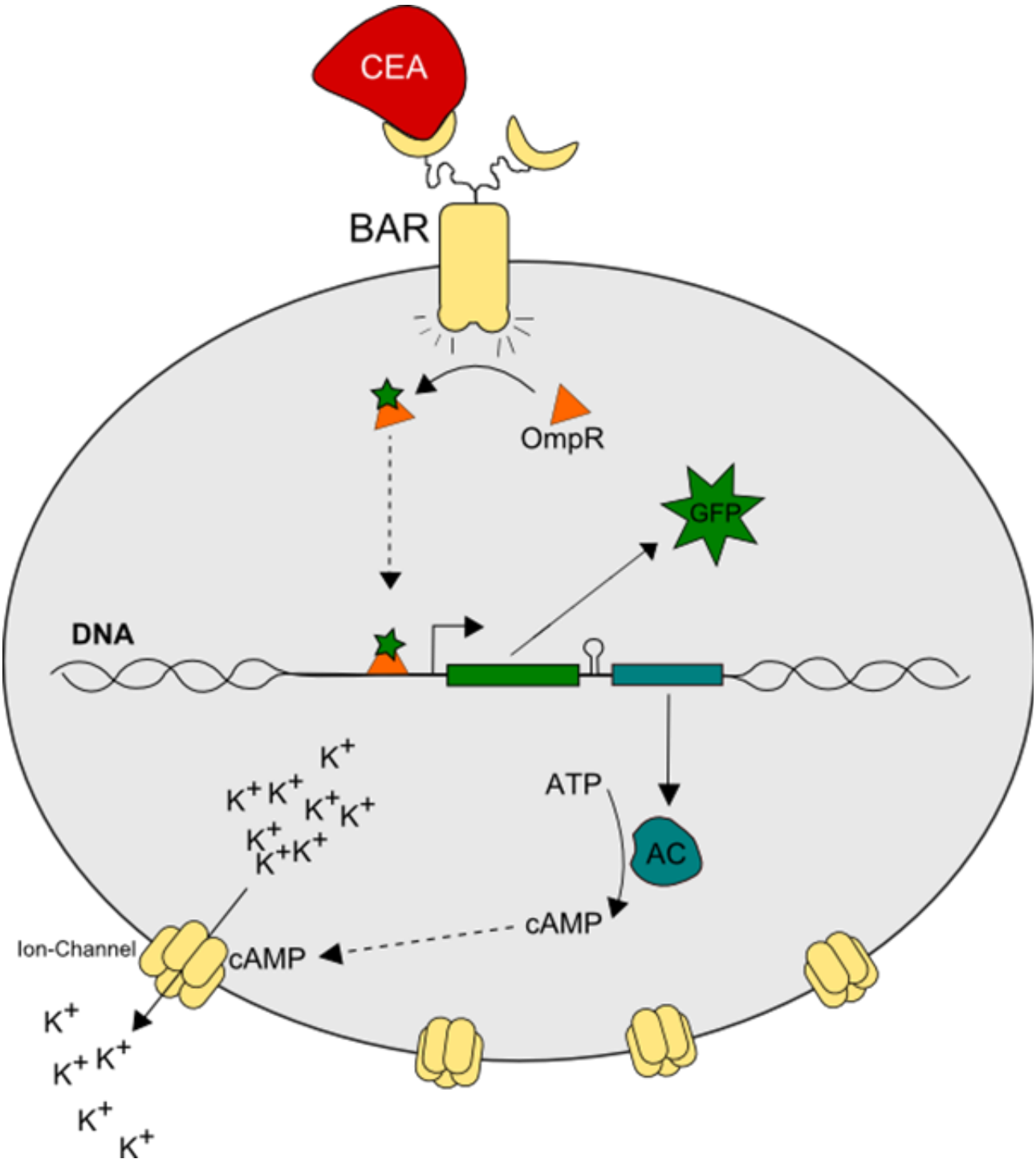

Figure: The Affibody-Based Bacterial Biomarker Assay (ABBBA), a novel tool for disease biomarker detection.

The disease biomarker (here: CEA) can specifically and sensitively bind to the bacterial antigen receptor (BAR), a fusion protein consisting of an affibody binder molecule and a bacterial transmembrane domain. The binding triggers the signal transduction into the cytoplasmic space allowing the phosphorylation of OmpR to OmpR-P which targets the promotor region of a genetic locus coding for a fluorometric molecule (here: GFP) allowing a fluorometric read-out and for adenylate cyclase (AC). The expression of AC will amplify our extracellular signal by producing the secondary messenger cAMP which can specifically bind to newly engineered mononucleotide ion channels resulting in ion efflux and a change in electric current.

iGEM 2015 team Toulouse

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[A way to save bees from Varroa]

The first parasite cause of bees' death in US and Europe is the Varroa, an external mite that uses the honey bees as hosts, that weakens their wings and even kill them by sucking out their blood. It is a serious matter in the beekeeper world.

Indeed, current treatments against Varroa that are chemicals, are becoming less and less efficient, and not very convenient to use because of the possibility to harm the quality of the honey and to stress the bees. Therefore, it is becoming more and more difficult to deal with.

iGEM Toulouse 2015

[Team Photo & Logo]

This is why we thought of a microorganism system that would both attract and kill the Varroa in the beehive, with a high-controlled regulation process, because we would want it to work during specific periods. This idea would lead to a more efficient fight against the varroa, and more respectfull of the bees and the quality of honey.

So far, we have already identified the molecules to produce, and built an hypothetical genetic construction, and we still have to work more precisely on the metabolic pathways. Plus, we have to overcome some challenges : bacteria survivability, cyclic regulation, biocontainment, etc.

What really drives us is that we got in touch with many biologists, specialists and associations of beekeepers from Toulouse and other French cities, that are eager to collaborate and share information with us, and find our project very promising, even if there are some tough biological challenges !

[This is the description of pictures]

We are looking forward to starting our project experiments by the beginning of June :)
By the meantime, we should have our project name and logo !

Valencia_UPV

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Our team

We are students of the Polytechnic University of Valencia. We are glad of our age and degree variety, with members covering all courses (from 1st to 4th) of different Bachelor Degrees: Biotechnology, Industrial Engineering, Biomedical Engineering and Electronics Engineering. Nationally, the 2006-UPV team was the first team involved in the competition, and this year it will be our duty again, to represent Spain and its young scientists.
Our meetings started at the end of February with the support of teachers and counselors. After a long phase of brainstorming and research, we finally took a project decision. Today, we keep working on it with illusion and excited about the priceless experience of defending it at the Jamboree. Of course, we are also encouraged by the success of the last year

The Project

Synthetic biology might sound too much technical or scientific to mean anything else apart from biology or genetics. However, during our brainstorming period, we realized that many of our ideas could have a great impact on society, and this is what our project is about. Our idea is based on how synthetic biology, provides us with skills to make our small contribution in order to improve our society.
After changes and changes, we finally had our project. Our aim is to produce substances of high sanitary interest (vaccines, drugs, vitamins...), in a sustainable biological system supported on a compact device, which is also portable, automatic, controlled, individualized, affordable, and robust enough to still work in extreme conditions.

To put it simply, it looks like a portable pharmacy, but with a simple plant appearance. Its characteristic, make this plant the ideal system to be taken to, for instance, poor or isolated regions. Furthermore, portability is not the only goal. The importance resides also in the high level of information that could be stored inside the plant's genome. Then, just pushing a few buttons, the user would be able to control the plant's production, so it would be possible to get the needed solution in the suitable moment.

How does this work?

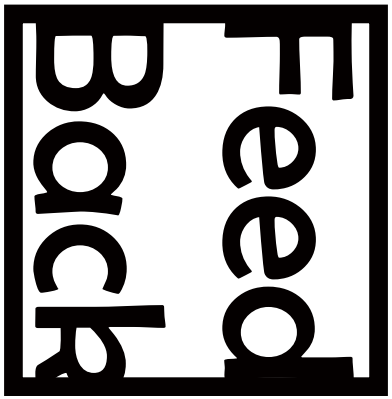
Theoretically, our plant would have on its genome the necessary genes to encode a wide range of drugs. We have thought about testing an antibody, a vaccine, an antiviral and a valuable protein from milk. In this way having one seed, you can grow it and produce what you need once at a time or even create a new plant with the same characteristics, as the information to make the drugs is encoded on its genome.
The main idea is that the stimuli, that the plant will receive to create the protein, is a light source. More specifically, light from different colors. Depending on the order and type of the pulses given, it will produce one or another drug.
The difficulty of this approach is the optimization of the process. We want that with few stimuli, the plant would be able to produce all the range of information stored on its genome. A biological and logical circuit had to be designed in order to achieve this purpose.

The biological circuit:

It is based in two main blocks toggle switches and recombinations. We will construct a library of toggle switches that will work with red and blue light with different binding domains. With the first impulse one of the two first genetic switchers will produce a recombinase that will take out the homologous switcher and also produce the next two toggle switchers. Hence the next pulse of light will control the production of one drug. In this way it is possible to produce four different drugs depending on the type and order of the light pulses. However, theoretically this circuit strategy can be exploited to codify information of many hundreds of products and the production of any of them will be controlled by the light impulses. The limiting step is the number of recombinases and binding domains available.

Depending on the drug it would be or not necessary to purify it, but in the case that it is not needed, the bud, for instance, can be eaten to ingest the drug. Studies of kinetics and efficiency must be also done to improve the process.

Our team will go step to step in the lab improving the circuit, from its simple features to the most complex ones, in order to make a proof of concept of our project. We will try to show that our design would work and would be useful in plenty of situations.



Thanks for your support

Feedback

1.Is this issue useful for your team?
A. Yes. It may help.
B. No. I cannot see any important reference value to my own team, because each situation differs.
C. Maybe a little.

2. How many passages are suitable for each issue?
A. Not more than 5.
B. 6-8
C. 9-12
D.13-15
E.15-20

3. How often should we publish Newsletter?
A. Weekly.
B. Biweekly. (The same as last year)
C. Triweekly.
D. Monthly.

4. Is is necessary to add new content besides project & update?
A. Yes. (Run to 5)
B. No (Run to 6)

5. What contents can be added in Newsletter (multiple-choice) ?
A. Discussion on bioethics.
B. Experts' interviews.
C. Summary information for Biobricks.
D. Wiki technology.
E. Art & Design.
F. Others _____(Please let us know your idea)

6. Are there any problems you have encountered? Would you like to write them down on Newsletter so that other readers can help you?

7. Any suggestions after reading this issue? Help us to make the Newsletter better!

Thank you for your support.
Please complete the feedback form and send it to us: igemxmu@gmail.com