

1856th Conference

Annual Biotechnology 2018



Annual Biotechnology Congress

July 23-24, 2018 | Vancouver, Canada

Scientific Tracks & Abstracts

Day 1

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Characterizing constitutive promoters in yeast

Sabrina Schulze

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Design and establishment of new biosynthetic pathways in yeast are important goals in synthetic biology. Therefore, promoters with predictable and reproducible protein expression levels independent of the protein of interest are needed. Data presented here show a library of constitutive promoters expressing two different fluorescent proteins in diverse conditions. We compare expression levels for episomal and chromosomal location, different growth media and different growth times. GFP and RFP are quantified via fluorescence spectroscopy and flow cytometry.

Biography

Sabrina Schulze has completed her PhD in Medical Sciences at the University of Aberdeen (UK) followed by a Postdoctoral Associate position at the University of Pittsburgh (USA). In 2017, she joined the group for synthetic biosystems at Potsdam University (Germany).

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Bioethics and arguments for and against the human consumption of genetically modified foods in the scientific literature

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In 1994, the FDA approved the first genetically modified food, the Flavr Savr tomato that was introduced to the fresh food market for consumption by the public, however, it was not commercially viable and two more years later was retired from the fresh food market. Since then the advances of modern biotechnology and genetically modified foods have had a great growth and adoption at a global level and considered of great value to society. However, there are controversies and public concern about transgenic foods and crops, which focus on food security and environmental conservation, whether the consumer has the right or not to choose, if they are needed to face hunger in the world now or in the future, on intellectual property rights and ethics. In this work, a systematic review of the scientific literature on pros and cons in relation to the use of genetically modified organisms for planting and human consumption was made, and an analysis of the findings from the bioethical perspectives, which allowed us to make a synthesis with which we established what is most appropriate regarding this subject in the light of bioethical principles. In summary we can say that 70% of the articles reviewed, see the need to regulate the use and application of GMOs and 44% of the articles support a regulation of biosafety. In other words, most countries, seek to follow the same rules of control and prevention for the consumption of foods derived from genetically modified organisms to avoid any risk to human health or environment. Our main recommendation is to continue scientifically founded research on genetically modified foods and to evaluate them through an International Committee periodically, to detect early negative effects on ecology, economy and human and animal health.

Biography

Rosa Martha Desentis Mendoza for more than 30 years has been dedicated to research in the science of food for more than 30 years, started with fresh tropical fruit studying its conservation, later with probiotic microorganisms, also antioxidant enzymes to form polymers with great antioxidant effect. For three years he has been researching genetically modified foods, especially seeds, from a bioethical perspective. Most countries seek to follow the same rules of control and prevention for the consumption of foods derived from genetically modified organisms to avoid any risk to human health or the environment. Evaluations should not only start from an economic base, but from the care of the most important capital of humanity, which is the human product and the ecology that sustains it .

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Development of an integrated method for utilizing seaweed and seaweed waste to grow fungal marine biomass for bioproducts

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In the last two decades the interest in biotechnology has focused on obtaining products of commercial importance from residual biomass. At present, there are no studies that have been carried out to evaluate the feasibility of taking waste from the seaweed to feed marine fungi and extract of these hydrophobic proteins hydrophobins (HPs) and the Single Cell Protein (SCP). Marine fungi are a diverse group of opportunistic and obligate marine organisms. In these fungi, new metabolites of biotechnological interest and hydrolytic enzymes have been detected. In this study, the growth of 10 strains of Ascomycetes marine fungi and filamentous (NBCR collection), was evaluated. So, the concentration of intracellular protein, of the preselected fungi, fed with wastes from the algae industry (waste A), and with the brown alga *Macrocystis pyrifera*, was evaluated. The highest protein concentrations were obtained with *Asteromyces cruciatus* and *Dendryphiella salina*. In the case of *A. cruciatus*, it was possible to increase the protein content 1.7 folds using *M. pyrifera* and the waste A. In the case of *D. salina*, the protein content in *M. pyrifera* and in residue A was increased 3.1 and 1.9-fold, respectively. The experimental response surface design, Box-Behnken, predicted that optimum growth conditions for the case of *A. cruciatus* fed with *M. pyrifera*, should be: 30°C, pH 5.0 and 0.5% salinity. The presence of HPs, in *A. cruciatus* (1.230-1.560 mg/L) and *D. salina* (1.560 -2.110 mg/L), using *M. pyrifera*, as a carbon source, were preliminarily evaluated.

Biography

Catalina Landeta Salgado is a Biologist from the Catholic University of Ecuador, has a magister in Environmental Management and Auditing from the Polytechnic University of Catalonia, Spain, a magister in Energy Engineering, mentioning biofuels from the Catholic University of Chile. She is currently a PhD candidate in Chemical Engineering and Biotechnology at the University of Chile. She has worked for more than four years in nationally recognized research projects in Ecuador. The achievements in their results could help the development of the only bioethanol pilot plant, from agroindustrial waste, in Ecuador.

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Use of combined strategy of light intensities and wavelength to enhance the biomass and lipids production on the microalga *Acutodesmus obliquus*

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The quality of light, such as wavelength and the intensity affect the performance of the algal growth and lipids production. Moreover, these variables affect both the quantity and the lipid profile. To study the interrelation among these variables, *Acutodesmus obliquus* (*Scenedesmus obliquus* UTEX 393) was cultivated in Bold 3N medium modified with 75% nitrogen at 25°C, pH 6.8, 125 rpm, and a photoperiod of 18/6h. The illumination was provided by a light-emitting diode surface mount device extensions (LED SMD) emitting red ($\lambda=620-750\text{nm}$), yellow ($\lambda=570-590\text{nm}$), green ($\lambda=495-570\text{nm}$) and violet ($\lambda=380-450\text{nm}$) lights. Additionally, each culture was illuminated at different light intensities ($I_1=40\mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$, $I_2=65\mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ and $I_3=90\mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$). The extraction method was microwave assisted (MW) using hexane: chloroform: methanol in proportions 1:2:3. All samples were analyzed with gas chromatography coupled to mass spectrometry (GC-MS). The results showed that the biomass production is directly proportional to the light intensity under the parameters established, e.g. at $90\mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ violet, yellow and red light showed the major biomass production, violet light produced minor amount of lipids when there was a major light intensity and *A. obliquus*, under the parameters established, is a good producer of palmitate, linolenate and linoleate methyl ester.

Biography

Edisson Tello Camacho is a Chemist. He received his master's degree in Chemical Science from the National University of Colombia with an emphasis on natural products, bioprospecting, and organic synthesis. In 2012 and 2013, he developed a research internship in the synthesis of natural products at the University of Nottingham, United Kingdom. Currently, he is Assistant Professor at the Department of Chemical Engineering at Universidad de La Sabana, Colombia and supports the Bioscience PhD program at the same university. He is also the Leader of the Bioprospecting Research Group at Universidad de La Sabana, where he focuses his research on marine natural products chemistry, searching for cytotoxic and antimicrobial compounds and working in biotechnology. Finally, he has been awarded with the Early Career Chemist award from the ACS in 2015, a laureate PhD thesis in 2013 and Meritorious Magister Thesis in 2008.

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The use of hairy roots for validation of CRISPR/Cas plasmid constructs and genome functional analysis in composite plants

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Statement of the Problem: Since the inception of CRISPR/Cas based plant genome engineering, *Agrobacterium tumefaciens*-mediated plant transformation procedures have been frequently used for crop improvement. Once CRISPR/Cas-sgRNA plasmid constructs are synthesized and before commencing plant transformation, validation of the constructs is indispensable. So far, sequence analysis sometimes coupled with agro-infiltration procedures are being employed for the same. However, in recalcitrant crops such as the cucurbitaceae, agro-infiltration procedures are either ineffective or impossible. Alternatively, validation of CRISPR/Cas-sgRNA cassettes and characterization of edited gene/promoter/ sequences in *A. rhizogenes* induced hairy roots seem reliable and time saving.

Methodology & Theoretical Orientation: The CRISPR/Cas-sgRNA plasmid constructs were mobilized into ATCC15834 or K599 *A. rhizogenes* strains to transform tomato and potato, or melon and cucumber explants, respectively. Genomic DNA was extracted from kanamycin resistant roots, PCR amplified with gene specific primers, PCR products were restriction digested, cloned and Sanger sequenced.

Findings: Mostly, we observed deletion of DNA sequences located in the sgRNA target regions, upstream of the proto spacer adjacent motif (PAM). Sometimes, deletions/substitutions/ of nucleotides both up- and downstream to the PAM or removal of the whole DNA sequence between two sgRNA target sites were observed. Although the same CRISPR/Cas-sgRNA cassette was used in tomato and potato, the types of insertions/deletions (indels) showed significant variations. In cucumber, where two independent CRISPR/Cas-sgRNAs were designed to target promoter sequences, with an assumption that the downstream gene would be up-regulated, more than two-fold transcript increment of the gene were observed, in the promoter-edited roots compared with the WT.

Conclusion & Significance: Before implementing whole plant transformation procedures, validation of CRISPR/Cas-sgRNA plasmid constructs in *A. rhizogenes* induced hairy roots could save time. Validation of CRISPR/Cas-sgRNA plasmid constructs and genome engineering/functional/ analysis in *A. rhizogenes* has induced hairy roots and/or composite plants seems vital and efficient.

Biography

Bekele Abebie has his expertise in Horticulture, especially postharvest physiology of cut flowers and plant molecular biology. Since Sep 2017, as a postdoctoral student, he has been working on developing methodologies for validation of CRISPR/Cas-sgRNA plasmid constructs and promoter functional studies in *A. rhizogenes* induced hairy roots, in some vegetable crops of the solanaceae and cucurbitaceae. In addition, he used *A. tumefaciens* mediated plant transformation protocols for developing virus resistance plants via CRISPR/Cas-genome editing, and the regenerated plants are being evaluated. Currently, he is developing transformation protocols for evaluating the effectiveness of CRISPR/Cas-genome editing technology in banana composite plants, which is expected to give a way for developing banana plants resistant to *Fusarium* wilt disease, via genome editing.

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Video Presentation

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Detection of Rotavirus genotypes with conventional PCR in a group of Iraqi children with acute viral gastroenteritis

Hiba Sabah Jasim

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Statement of the Problem: Rotaviruses are one of the major causes of acute viral gastroenteritis in children under 5 years old worldwide, the highest mortality is observed in developing countries. The genome of the rotavirus is composed of 11 segments of double-stranded RNA, according to the antigenic characteristics of the middle layer protein VP6 the virus can be classified into A to I serogroups, the most common serogroup that can cause more than 90% of the rotavirus infections in human is the rotavirus A. This study aimed to detect the rotavirus genotypes in the infected children with acute viral gastroenteritis as this disease causes many deaths in children and cost the country a lot of money for treatment, additionally if the diagnosis of the virus is early the disease will be under control.

Methodology and Theoretical Orientation: This study was conducted during March 2017 to September 2017; the study included 200 stool samples collected from hospitalized children with acute gastroenteritis. Samples were of two groups, 150 stool sample of patient with acute viral gastroenteritis, the other 50 stool samples were collected from healthy children also under 5 years old, The result considered positive if ELISA and/or conventional PCR gave positive result, while the result considered negative if both of them gave negative result.

Findings: The incidence of the rotavirus in the patient group was (70/150) while only two cases (2/50) of the control group showed positive result with rotavirus, the most prevalence serotype was G2P serotype with (40/150) in the patient group, additionally this serotype was the only serotype that was detected in control group in both two cases that showed positive result with rotavirus.

Conclusion and Significance: Rotavirus genotyping is a major risk factor of acute viral gastroenteritis in children under 5 years old as the percentage of the virus was high.

Recommendation: Prophylaxis and treatment of the infants and children under 5 years old is very important especially for children that attend hospitals.

Biography

Hiba Sabah Jasim she was graduated from the college of science, University of Baghdad, Department of Life Sciences, specialized microbiology, appointed in the Medicine College, University of Baghdad, branch of microbiology in 2005, and then obtained Master degree from the same branch in 2009. And thus become a faculty in the medicine college. In 2013 got the scientific title lecturer and then she was accepted in the medicine college, University of Al- Nahrain department of microbiology and received her PhD degree in January 2018.

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Targeting therapy of hepatocarcinoma by a peptide directed doxorubicin/miRNA liposome

Yingchun Hou

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Hepatocellular carcinoma (HCC) is a severe malignant disease to threaten human life safety, and current chemical therapeutic methods are usually developed with low efficacy and high side effects because they have no enough specific targeting to cancer cells and cannot inhibit the multiple drug resistance (MDR) of chemical therapeutics. HCSP4, a 12aa peptide was screened out in our lab using the bio-panning method from a phage displayed peptide library, and it binds to HCC cells with high specificity and sensitivity. In our study, to develop a HCC targeting chemical therapeutic delivery system with high HCC therapeutic efficacy, low side effects and satisfactory resistance for MDR, HCSP4 and miR101 were used to construct the HCC targeting DOX (doxorubicin) delivery liposome system, HCSP4-Lipo-miR101-DOX. The results in vitro showed that HCSP4-Lipo-miR101-DOX presented the much enhanced cytotoxicity to HepG2 cells and HepG2/ADR cells (DOX resistant HCC cells). To explore the mechanism by that HCSP4-Lipo-miR101-DOX presents the reversal of MDR of DOX, the expression of the genes were of the potential to be the targets of miR101 was detected with western blot. The result indicated that the expression of some genes associated with membrane transportation and cancer growth was significantly inhibited, such as ABCC5, COX-2, P-gp, VEGF, STX1A, and EZH2. The results above suggested that the HCSP4 conjugated DOX delivery system, HCSP4-Lipo -miR101-DOX is of the great promising potential to be developed as an important efficient drug system for the therapy of HCC with low recurrence, its mechanism against MDR is discussed in the study. This approach is also an important strategy can be referenced for other cancer therapeutics study.

Biography

Yingchun Hou has completed his MD and PhD degrees in 1997 at The Fourth Military Medical University, China. He has his experience as Postdoctoral Scholar, Postdoctoral Research Associate and Senior Scientist in USA NIH and other institutions from 1998 to 2006. From January 2006 to date, he holds the position of Professor and PI in Shaanxi Normal University, China. His researches focus on the molecular and cellular biology of cancer, published papers more than 100, and got 10 of Chinese patents approved. He concluded and created the theory of spatiotemporal cell biology and its core frame, triple W and signal basin in the world firstly. He is the Associate Chairman for the Shaanxi Society for Genome and Health, the Member of the American Society for Biochemistry and Molecular Biology, and the Member of American Society for Microbiology. His current research projects include the functions of tumor associated genes and signal regulation and the target to cancer cells and the targeting therapy for cancers.

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