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5th World Congress on

Microbial Biotechnology & Vaccine Design

September 17-18, 2018 Lisbon, Portugal

Scientific Tracks & Abstracts
Day 1

30 YEARS OF EXCELLENCE IN MEDICAL PUBLISHING

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The capric acid from *Saccharomyces boulardii* as an antifungal agent: A mechanism study

Anna Krasowska, Jakub Suchodolski and Marcin Lukaszewicz
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Candida albicans is a pathogenic yeast-like fungus that causes exo- and endogenous infections. *C. albicans* strains exhibit multidrug-resistance to commonly used antifungal agents which correlate with overexpression of Cdr and Mdr efflux pumps located in the plasma membrane. Growing resistance of pathogenic *C. albicans* strains to many classes of antifungal drugs has stimulated efforts to find new agents to combat more invasive infections. A selected number of probiotic organisms, *Saccharomyces boulardii* among them, have also been tested as potential biotherapeutic agents. *S. boulardii* is a yeast strain that has been shown to have applications in the prevention and treatment of intestinal infections caused by microbial pathogens. We have similarly shown that *S. boulardii* secretes capric acid (C10:0), which is most effective in inhibiting essential virulence factors of *C. albicans*, especially morphological transition, partial adhesion, as well as biofilm formation. Our latest research on the mechanism of action of capric acid and its influence on the *C. albicans* cells clearly show its interaction with the plasma membrane. Capric acid decreases fluidity, while increasing the potential of the plasma membrane. For these reasons, we have probably not observed antifungal activity of amphotericin B in the presence of capric acid. The antagonism between capric acid and amphotericin B is a strong indication for physicians to not use both compounds simultaneously in the treatment of candidiasis.

Biography

Anna Krasowska is an assistant professor at the Department of Biotransformation, University of Wroclaw, Poland. She is currently involved in the isolation and characterization of biosurfactants produced by arctic microorganisms. She has also examined the activity of lipases and proteases released into the environment by microorganisms isolated from different environments. Her research interests lie in multidrug resistance of pathogenic microorganisms like *Saccharomyces cerevisiae,* yeast and *Candida albicans*.

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The biorefinery based on biotransformation by *Bacillus subtilis* of meal from oilseeds

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The most effective holistic approach of circular economy based on biotransformation of the agricultural biomass, which has been developed in the last few years, is the concept of biorefineries. In the biorefinery approach assuming zero waste, each process stream is exploited to the full through careful fractionation to produce commercially valuable products or through reuse of byproducts and wastes. The biorefinery approach has already been introduced to this area through a consideration of biodiesel and bioethanol, but very interesting seems multitude of other application especially in green chemistry to obtain high value added compounds. The main objective of the recent study is construction of demonstration plant focused on possibilities using GRAS microorganisms such as *Bacillus subtilis* in biotransformation meal remaining after oil extraction from oilseeds and subsequent fractionation. The key to this is the assertion that a complex mixed component material can be exploited in a variety of ways with some components used to produced new materials while others can be directly fractionated and separated into commercially highly valuable materials. Most of high value added products are synthesized in relatively low quantities e.g., biosurfactants making often the production process unprofitable. Thus, after their extraction the remaining biomass must also have an increased value as an end product, which could be complementary feed for animals as *Bacillus subtilis* var natto strains have probiotic properties. The realization of the demonstration biorefinery requires multidisciplinary approach and development of several dedicated methods such as Solid State Fermentation (SSF), fractionation using ecologically friendly solvents such as super critical carbon dioxide and centrifugal partition chromatography.

Biography

Marcin Lukaszewicz is working as an associate professor at the Department of Biotransformation, University of Wroclaw, Poland. He has has done research on the optimization of lipopeptide biosurfactants production, methanogenesis and biocalcification. His research work also includes the model complexes agro-power as an example of dispersed cogeneration based on local and renewable energy sources.

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Shiga toxin-producing *Escherichia coli* distribution and characterization in a pasture-based cow-calf production system

Patricia Baltasar, François Elvinger, Monica Ponder, William Swecker and Korine Kolivras
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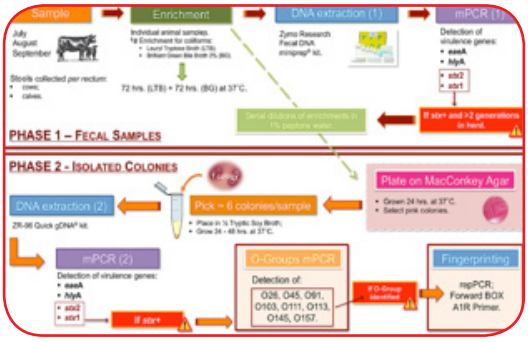
Escherichia coli is part of the normal gastrointestinal microbiota of many animals, especially cattle. While most strains are commensal, Shiga toxin-producing *E. coli* (STEC) can cause severe human illness. Persistent carriers and environmental contamination may be responsible for maintenance of STEC in cattle. Prevalence and distribution of *E. coli* virulence genes (stx1, stx2, hlyA and eaeA) were assessed in a cow-calf pasture-based system. Angus cows (n=90) and their calves (n=90) were kept in three on-farm locations and fecal samples were collected at three consecutive time-points (July through September, 2011). After enrichment, sample detection of stx1, stx2, eaeA and hlyA was done by multiplex PCR (mPCR). Fecal samples positive for stx genes were obtained from 93.3% (84/90) of dams and 95.6% (86/90) of calves. Age class (dam, calf) and spatial distribution of cattle and sampling time-point influenced prevalence and distribution of virulence genes. Of 293 stx-positive fecal samples, 744 *E. coli* colonies were isolated. Virulence patterns of isolates were determined through mPCR: stx1 was present in 41.9% (312/744) of isolates, stx2 in 6.5% (48/744), eaeA in 4.2% (31/744) and hlyA in 2.4% (18/744). Prevalence of non-O157 STEC was high among isolates: 33.8% (112/331) were O121, 3.6% (12/331) were O103, 1.8% (6/331) were O113. One isolate (0.3%) was identified as serotype O157. Repetitive element sequence based-PCR (rep-PCR) fingerprinting was used to study genetic diversity of stx-positive isolates. Rep-PCR fingerprints were highly similar, supporting the hypothesis that strains are transmitted between animals, but not necessarily from a dam to its calf. Highly similar STEC isolates were obtained at each sampling time-point, but isolates from dams were more diverse than those from calves, suggesting that strain-to-strain differences in transfer may exist. Furthermore, fingerprints from O121 isolates closely resembled those of test isolates from in human outbreaks.



Biography

Patricia Baltasar has an impressive background in veterinary medicine, public health and research. Her excellent analytical, communication, people skills, coupled with a strong command of epidemiology have been critical in consistently reflecting the highest academic standards. She has a solid record of publications and presentations and has established a sound trajectory towards a career focused in the “One Health” concept.

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Evaluation of antimicrobial peptides in fermented breast milk

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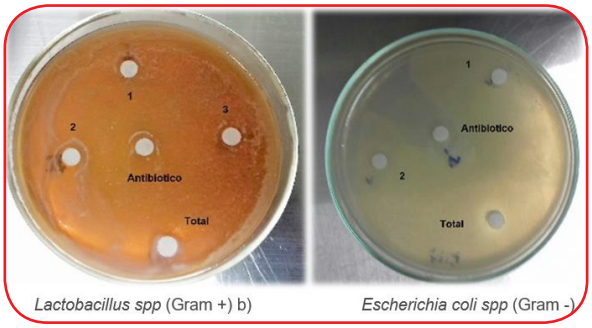
Autonomous University of San Luis Potosí, Mexico

Introduction & Aim: The antibiotic resistance is a world problem due to genetic modification of microorganisms rendering them ineffective. This increases the spread of infections in the population and it has become an alarming public health problem. A promising solution to solve this problem is the use of antimicrobial peptides obtained from natural sources such as Breast Milk (BM), therefore the aim of this investigation is to evaluate the antimicrobial activity of peptides obtained from the fermentation of BM using probiotic bacteria found in the same one.

Methodology: Three samples of BM was pasteurized and inoculated with *Bifidobacterium* spp., *Lactobacillus* spp., and *Streptococcus* spp. genera which were isolated from BM through selective mediums and incubated at 37 °C under anaerobic conditions for 37 hours. The whey proteins amount was determined by Bradford method. The whey proteins were visualized in acrylamide gel at 16% concentration. The separation of whey proteins was done by size exclusion chromatography with Poly (allyl dextran]-co-N,N'-methylenebisacrylamide) within 25-75 microns resin and it was quantified with the Bradford method and visualized in SDS-PAGE. The antimicrobial characteristics of the protein fractions were evaluated on Gram negative and positive bacteria using disks impregnated of whey protein fractions.

Findings: The fermentation of milk stopped at the exponential phase of bacterial growth. The range of weight of whey proteins was 10-75 kDa and a significant low weight proteins concentration. In all cases, four fractions were obtained in the chromatography separation, nevertheless only one contained proteins lower than 10 kDa. The antibiogram assay determined microbiological inhibition of whey proteins in both the Gram-positive and negative bacterial genera.

Conclusion & Significance: It was confirmed the proteolitical activity of probiotics genera on BM and the consequent liberation of broad spectrum antimicrobial peptides.



Lactobacillus spp (Gram +) b) *Escherichia coli spp* (Gram -)

Biography

Diana Martinez is a PhD student in the Autonomous University of San Luis Potosi, Mexico. Her research interest is in antimicrobial peptides, bacterial studies, etc. She is working under Professor Enrique Maldonado at the UASLP in Mexico.

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Recycling waste CO_2 to valuable resources through microbial electrosynthesis

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Anthropogenic and industrial activities have led to a rapid rise in the atmospheric CO_2 concentrations leading to increased global warming. A new approach that has emerged in recent years is that of Microbial Electrosynthesis (MES), which relies on chemolithoautotrophic bacteria that can uptake electrons directly or indirectly (via H2) from the cathode of an electrochemical cell to catalyze the reduction of CO_2 into fuels or value-added chemicals. Gas-liquid mass transfer is one of the limiting factors in MES, mainly because of the low solubility of gaseous CO_2 in solution. To overcome this limitation, we developed dual-function electro-Catalytic and macro Porous Hollow-Fiber (CCPHF) cathodes that act as an electron donor for chemolithoautotrophs as well as a diffusive material to facilitate direct delivery of CO_2 gas to chemolithoautotrophs through the pores in the hollow fibers. Using the CCPHF cathode we observed a Faradic efficiency of 77% for the production of CH_4 from CO_2 through hydrogenotrophic methanogens when CO_2 was delivered directly through the pores of the CCPHF cathode, compared to 3% when gaseous CO_2 was bubbled into the solution. We also successfully demonstrated that the rates of product formation can be enhanced by using Carbon Nanotubes (CNTs), which increases CO_2 adsorption capability and enhances microbe-electrode interactions. Modification of the CCPHF cathodes with CNTs resulted in 70% increase in acetate production rate from CO_2 in MES using the homo acetogenic bacterium Sporomusa ovata. The use of CCPHF cathodes in MES research is a significant breakthrough. The high specific surface area of the CCPHF cathode maximizes the diffusion of CO_2 gas, and the high surface-area-to-volume ratio of the CCPHF cathode architecture solves the issue of cathode packing density for large-scale applications. Most importantly, using CCPHF cathodes make the MES process highly attractive for on-site carbon capture and utilization.

Biography

Pascal E Saikaly has received his Bachelors in Biology and Masters in Environmental Technology from the American University of Beirut, Lebanon. He has completed his PhD in Environmental Engineering from the University of Cincinnati and pursued his training as a Post-doctorate at North Carolina State University. He is currently working as an Associate Professor at King Abdullah University of Science and Technology. His research interests include microbial electrochemical systems, membrane bioreactors, electro-microbiology and advanced materials for water and energy applications. He has more than 74 refereed journal articles.

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Diversity of microbial communities associated with mercury contamination in the Colombia's Amazon region

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The use of mercury (Hg) in gold mining is a disturbance process that severely affects the ecosystems of the Colombian Amazon. In environments contaminated with Hg, microbial transformations (reduction and methylation) are the main mechanisms of metal speciation. There are few studies that evaluate the composition of microbial communities and their relationship with biotic and abiotic variables in Hg contaminated areas. In this work we have analyzed, through massive sequencing with Illumina Miseq, the structure of bacterial communities in waters, soils and sediments with different degrees of intervention with gold mining, in two locations of the Colombian Amazon Tarapaca-Amazonas (low intervention) and Taraira-Vaupes (high intervention). We found that in both locations the microbial composition is similar, predominating the Phylum Proteobacteria, Acidobacteria, Actinobacteria and Chloroflexi, which includes genera resistant to Hg. The comparison of the diversity indices for the two localities indicates that in Tarapaca the average richness of OTUs was generally higher than in Taraira, although with a high dispersion, attributable to the differences in richness between sample types and sampling sites, samples from aquatic ecosystems have communities with less richness, which increases in sediments and forest soils. Additionally, the interaction between locality and sample type is also evident in the degree of divergence between the regions the soil and sediment samples are more similar between the two locations than the respective water samples. Among the environmental variables that modulate the composition of the community between localities are the textures of the support (sand and clay). And other environmental variables are Na and K that modulate the composition by the type of samples (water versus soil and sediment). Regarding the variables mercury and methyl-mercury (CH3Hg), its effect is not global but site-specific. This could be due to the ability of Hg to be immobilized with other elements and form stable non-bioavailable molecules.

Biography

Gladys Cardona has completed her Master's degree in Biological Science and PhD in Biological Systems. She has experience in microbial ecology in Amazonian ecosystems, especially in forest soils to look for microorganisms that promote growth, bioremediation and restoration.

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Application of a γ-polyglutamic acid flocculant to water treatment

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Gamma-polyglutamic acid (γ-PGA) has received considerable attention for environmental applications. γ-PGA can be produced by fermenting soybeans using the bacterium Bacillus subtilis found in foods such as natto (Figure 1), which is considered a delicacy in Japan. Most biopolymer applications are directly linked to their potential to respond to changes in the environment in which they are dissolved. An approach aimed at understanding the structural changes, conformation and associations of polymer chains, as well as their practical applications, is of great scientific interest. This work focuses on the extraction and quantification of γ-polyglutamic acid from natto, a fermented soybean food. The γ-PGA extraction method using methanol proved to be more efficient than extraction with ethyl alcohol and acetone. The extraction of γ-PGA using methanol yielded 4.72 g kg-1 of natto. After, a conventional jar test apparatus was used for flocculation experiments. The commercial coagulants used in the coagulation-flocculation-sedimentation tests were aluminum sulfate (16% Al2O3) and PAC (9.59% Al2O3). The levels of coagulants were established based on preliminary tests and recommended by the WTP, but the parameters of pH and temperature of the raw water were not changed. The optimum operating conditions for bioflocculant treatment were determined by the jar test procedure and, in this case, the γ-PGA was used directly in its powder form for the jar test. The tests were performed using raw water from the Salto de Pirapora Water Treatment Plant (WTP) in the state of São Paulo, Brazil. The performance of PGA bioflocculant was superior to that of the other coagulants. In the dry season, 65 mg L^{-1} of new formulation γ-PGA removed 93.12% of apparent color, and residual turbidity was 3.38 NTU.

Biography

Valquiria Campos is a B.Sc. in Geology at University of São Paulo; D.Sc. in Geology at Geoscience Institute at the São Paulo University and she held Postdoctoral in Chemical Engineering at São Paulo University. A full Professor since 2009 at São Paulo State University (UNESP), Institute of Science and Technology, Sorocaba, Brazil. The actual laboratory in which she is working is in the Department of Environmental Engineering of the Polytechnic School. She is focused on understanding hydrogeochemistry processes and related impacts on water supply and demand, water quality, agriculture, and impacts to other sectors of society.

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Let's quench the quorum: Indigenous microbial flora with quorum sensing inhibition potential

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Quorum Sensing (QS) is a communicating mechanism among bacteria and a vital factor in enhancing resistance against most of the antibacterial agents. Gram-negative bacteria have been reported to use N-acyl Homoserine Lactones (AHLs) as QS signals. This cell-cell communication system plays a critical role in the coordination of their gene expression and thus in the formation of the biofilms. Therefore, Quorum Quenching (QQ) is a promising new alternative for the control of infections in multi-drug resistant bacteria. It is basically enzymatic interruption of QS and poses fewer resistance risks. In this study, bacterial strains were isolated from the soil samples of Margala hills in Islamabad and its QQ ability was analyzed against the pathogenic *Pseudomonas aeruginosa*. Specific genes encoding the QQ enzymes were screened and confirmed via PCR and sequencing. Strategy for enhanced production of these enzymes in *E. coli* was devised and proceeded for further evaluation. Our results has predicted and verified the AHL degrading enzymes, lactonases and acylases in the novel identified bacterial strains. Genes encoding the particular AHL degrading enzymes were fully sequenced and for phylogenetic analysis of these novel strains, 16S rRNA sequencing has been done and a comparative analysis with the already known bacterial strains was performed. Currently we are working on enhanced production of these AHL degrading enzymes and their sustainable expression in the *E. coli*. The QQ-associated genes can be potential transgenes in other most suitable hosts to produce large amount of QQ enzymes. And they could potentially be used to inhibit biofilm formation in the MDR bacteria which is not only a big concern in the health sector but also a major issue in the Membrane Bioreactors (MBR) where microbial biofilm causes bio-fouling.

Biography

Fazal Adnan is an assistant professor at the Atta-ur- Rahman School of Applied Biosciences, National University of Sciences and Technology. He has completed his Bachelor's degree in Biotechnology from the University of Peshawar and MPhil in Industrial Biotechnology from the Government College University, Lahore. During his stay at the Institute of Molecular Microbiology in Giessen, he investigated role of protein and RNA-based regulators in the photo-oxidative stress response mechanisms of alpha-proteobacteria Rhodobacter sphaeroides.

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