

International Conference on
ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY
&
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ECOLOGY, ECOSYSTEMS AND CONSERVATION BIOLOGY
July 11-12, 2018 | Toronto, Canada

Poster Presentations

Day 2

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July 11-12, 2018 | Toronto, Canada

Complete genome sequence of *Alkalitalea saponilacus*, an anaerobic haloalkaliphilic bacterium capable of secreting halostable xylanase

Baisuo Zhao, Yanchun Yan and Ziya Liao

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The anaerobic haloalkaliphile *Alkalitalea saponilacus* SC/BZ-SP2T could utilize xylan as sole carbon source and produce propionate as the main fermentation product. The xylanase activity from A. using the combined substrates of 0.4% (w/v) sucrose + 0.1% (w/v) birch xylan was 3.2-fold than that of 0.5% (w/v) sucrose or 0.5% (w/v) birch xylan. The xylanase is halo-stable as it exhibited optimal activity at a broad range of 2-6% NaCl. Its activity was inhibited by Cu^{2+} , Fe^{3+} , Ni^{2+} , Al^{3+} , Mn^{2+} , Co^{2+} , Zn^{2+} and Ca^{2+} while increased 1.16-fold with the addition of Tween 20. In order to get a deep understanding of the potential genetic mechanisms of xylanase secretion and adaptive saline-alkali tolerance, the complete genome sequence of strain SC/BZ-SP2T was performed with the Pacbio SMRT and Illumina Misseq platforms. The genome contained one chromosome, with the total size of 4,775,573 bps, and the G+C content of this strain was 39.27%. A number of genes related to xylan degradation and its complete xylan degradation pathway, xyn A gene of xylanase belonging to a glycoside hydrolase (GH) family 10 and its neighborhood genes were systematically identified. Furthermore, various genes involved in biosynthesis and transportation of osmolytes, as well as genes encoding monovalent cation/proton antiporters, multi-subunit sodium/proton antiporters, F₀F₁-ATP synthases, H⁺-transporting ATPases, Na⁺/solute symporters and K⁺ transport systems were predicted. This genome sequence provides molecular information and elucidation for halo-stable xylanase production, and will be used in the biotechnology.

Biography

The focus of Baisuo Zhao research is bacterial taxonomy and microbial physiology, Molecular mechanisms of gene expression and mutagenesis. He is also interested in studies of molecular microbial ecology including the genetic and the functional diversity of microbial communities. His third research interest on Microbial Genomics & Metagenomics involves in genome analysis of pure isolates and metagenomics from extreme conditions, reactors etc.

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Operational taxonomic units that distinguish soils of crops and fruits in the whole Japan

Andre F Cruz¹, Atsushi Nakao, Junta Yanai, Tetsushi Tanaka², Naoaki Ono and Shigehiko Kanaya

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²Nara Institute of Technology, Japan

The microbial community evaluation constitutes an essential topic to access the soil health conditions, with special regard to the operational taxonomic units (OTU). This data can easily represent the soil bacterial condition and also might distinguish many kinds of environment, such as urban areas, and agricultural soils. As a criterion to set up a “finger-print” for agricultural soils in terms of microbial community, metagenomic profiles from crops and fruit soils had their OTU analyzed after the normalizing their abundance where the sum of each sample was equivalent to 1. The bacterial and fungal genes were the target region evaluated by principal component analysis (PCA). Although some dominant taxonomic groups were constantly present in most of the soils, the OTU within the bacterial and fungal communities were specific according to the land use type (crops or fruits) i.e. each one had a remarkable difference in terms of OTU. Hokkaido prefecture contained most of specific groups, whereas other prefectures were more diverse. Similar profile was found in fungal genes. Within the bacterial genes a few number of OTUs made possible to separate crops and fruit soils, however for the fungal ones a large number was necessary for the same goal. The bacterial representative genera were *Nitrospira* (involved with Nitrogen cycling) and *Arthrobacter*. Whereas the *Fusarium* was the most important fungus in terms of OTU bioindicator.

Biography

Andre Freire Cruz had focused on evaluation of soil microbial status as indicator of sustainability. He has worked with many agricultural soils, recently has concentrated on fruit orchards in Japan and other countries especially concerning on analysis of microbial growth and activity. He has used many methods to evaluate the soil biology, but actually most of his researches are using metagenome analysis of bacterial and fungal genes and their relation with other soils properties.

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Degradation mechanism for phthalic acid esters (PAEs) degrading bacterium

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Di-(2-ethylehyl) phthalate (DEHP) is the most broadly representative phthalate esters (PAEs) used as a plasticizer and considered an endocrine-disrupting chemical. An efficient DEHP-degrading strain *Rhodococcus ruber* YC-YT1, with salt tolerance (0~12% NaCl), is the first DEHP-degrader isolated from marine plastic debris around coastal saline seawater, which could completely degraded 100 mg/L DEHP within 72 hours. Single factors (pH, temperature, and glucose) analysis and the optimum degradation conditions for the strain were measured by response surface methodology (RSM). According to HPLC-MS analysis, DEHP was transformed by strain YC-YT1 into phthalate (PA) via mono (2-ethylehyl) phthalate (MEHP), and then PA was used for cell growth. Furthermore, YC-YT1 metabolized initial concentrations of DEHP from 0.5 to 1000 mg/L. Especially, YC-YT1 degraded up to 60% of 0.5 mg/L DEHP. Moreover, compared with previous reports, strain YC-YT1 has the largest substrate spectrum, degrading up to 13 kinds of PAEs as well as diphenyl, PA, benzoic acid, protocatechuic acid (PCA), and 1,2,3,3-tetrachlorobenzene. Strain YC-YT1 could adjust its cell surface hydrophobicity (CSH) in the environment and 79.7~95.9% of DEHP-contaminated soil and water was remedied. These results demonstrate that strain YC-YT1 has vast potential to bioremediate various DEHP-contaminated environments, especially in saline environments. The whole genome sequence of strain YC-YT1 was obtained by the PacBio sequencing platform and submitted to GenBank (CP023712), which contained a circular genome and two plasmids. The genes and gene clusters involved in the degradation of PAEs and aromatic compounds, especially the phthalate dioxygenase genes and ring- cleavage dioxygenase genes, which involved the degradation of diphenyl, PCA, benzoate and phthalate were analyzed by comparative genomics analysis. Two genes (*Dehp1199* and *Mehp4077*) encoding DEHP degrading esterases were obtained, condon optimization, expressed and verified. *Dehp1199* is a novel alkaline esterase and the enzymological characteristics were analyzed.

Biography

Yanchun Yan has her expertise in bioremediation of environmental pollution and passion in improving the health and wellbeing. Her research team has been focused on the bioremediation for more than twenty years, and they have isolated more than 60 strains of bacteria or fungi capable of degrading pesticides or environmental estrogen chemicals. The degradation characteristics of the strains and a number of genes or gene clusters encoding key enzymes were investigated. These researches provided significant resources of strains and genes for bioremediation, and lay theoretical foundation for the degradation mechanism of pollutants.

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Clustering analysis of global soil microbe metagenome for characterizing community diversity

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Microbial communities in soil depend on environmental features such as land use and geographic isolation. In this study, we have analyzed soil metagenomes sampled from a wide range in the globe and variety of land use in the context of the environment or ecosystem, from Earth Microbiome Project, containing 4998 samples and 48674 operational taxonomic units (OTUs). The final goal of this work is to discover characteristic microbiota that corresponds to land use and environment. It is worth noting that microbiome OTU data is high dimensional but sparse and many OTUs are phylogenetically related. By taking those factors into consideration, we tried to develop bioinformatics, computational methods as follows:

- (1) Data were labeled into 8 land use categories and applied to Random Forested to reduce variables, and we selected OTUs which relates to land use categories.
- (2) By using these OTUs, the differences between microbial communities were defined and clustered by UniFrac Distance which computes the distance difference based on the phylogenetic information.

The results lead to the interpretation that some clusters are composed of the samples from specific areas and environments, such as cropland in Japan, montane grassland in Mongolia, tundra, and forest, and some of those clusters are characterized by different dominant OTUs, e. g. DA 101, which is known as the one of the most abundant microbial phylotypes. We have concluded that the clusters of individual lands are quite clearly reflecting the ecosystems and can be characterized by the OTUs in the microbial community.

Biography

Tetsushi Tanaka belongs to Computational Systems Biology Laboratory in Nara Institute of Science and Technology and has studied bioinformatics, especially microbiome analysis. He is also familiar with molecular biology and was graduated from Saitama University with a bachelor's degree in Science.

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Metagenomic detection of bacteria and fungi in the atmosphere of Mexico City

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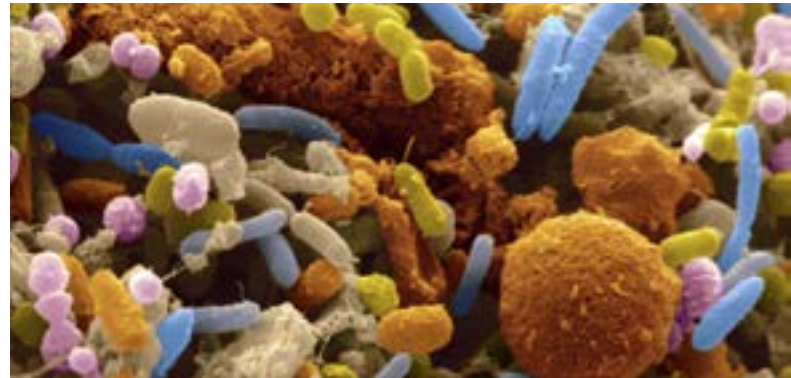
Bioaerosols significantly affect atmospheric processes. The identification of airborne bacteria and fungi has traditionally been performed by retrieval in culture media, but in this way their diversity in the air is underestimated. Advances in DNA sequencing technology have produced a broad knowledge of genomics and metagenomics, so the objective of this study was to efficiently recover microorganisms from the air and standardize monitoring protocols, sample processing and molecular detection of bioaerosols of the Mexico City. To examine this bioaerosols we performed deep sequencing on the 16S rRNA and ITS genes from air samples collected during ten weeks (February to May, 2016) in south of Mexico City. Three samplers were used: a Durham-type spore trap (Durham), a seven-day recording volumetric spore trap (HST), and a high-throughput 'Jet' spore and particle sampler (Jet). A simple and efficient method for collecting bioaerosols and extracting good quality DNA for deep sequencing was standardized. The most abundant bacteria phyla in the air were Actinobacteria, Proteobacteria and Firmicutes. The HST sampler collected the largest amount of airborne bacterial and fungal diversity, however it may be preferred to use one or the other sampler, as each one collected preferentially some groups, i.e. Durham favors the sampling of Cyanobacteria and HST the sampling of Firmicutes. The most abundant fungal phyla in the air were Ascomycota and Basidiomycota. Methods of sampling and processing of samples for metagenomic detection of bacteria and fungi in the air were standardized, which allows a deep exploration of the diversity of airborne bacteria and fungi.

Biography

Nancy Serrano-Silva has her expertise in molecular methods to study microbial communities in environmental samples, mainly soils and air. Currently she is a Postdoctoral Researcher in the Center of atmospheric sciences at National Autonomous University of Mexico. Serrano-Silva and Calderón-Ezquerro have been working since 3 years ago in the implementation of metagenomic to evaluation of air quality (indoor and outdoor) in Mexico City. This is one of the first jobs that report the use of equipment such as the Hirst spore trap and the Durham sampler to collect and identify the microbiota of the atmosphere by using a metagenomic focus.

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From bird monitoring to environmental education

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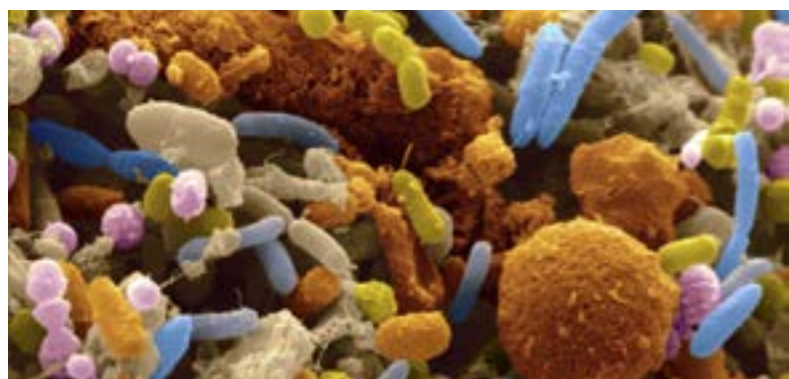
The quality of people's knowledge of nature has always had a significant influence on their approach to wildlife and nature conservation. However, direct interactions of people with nature are greatly limited nowadays, especially because of urbanization and modern lifestyles. As a result, our segregation from the natural world has been growing. In this light, we have developed a unique technology of camera monitoring that offers to generate enormous amounts of high-quality biological and engineering data with minimum effort and allows the public to be involved in scientific research in undemanding ways. In particular, we have developed and tested a method of automatic camera monitoring that allows the collection of unique knowledge on breeding biology in cavity-dwelling animals. This system enables the remote acquisition, storing and sharing video, audio, and text data on everyday animal activities inside bird boxes, and live-streaming animal life on websites. The technology developed has potential to be applied across the world and society, and it can be incorporated into multiple scientific fields, including education, environmental and computer science, ecology, and social science. This approach offers a powerful open door for moving youngsters and others to have a fabulous time figuring out how to act like researchers and gives expansive chances to building up the until now disregarded instructive potential of Citizen Science.

Biography

Marketa Zarybnicka has her expertise in ecology, behaviour and conservation of birds and small mammals. Her researcher on Boreal owl in air-polluted areas in the Czech Republic has gradually transformed into a Citizen Science project that aims for camera monitoring of bird nesting and collecting of biological data with the help of the public.

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Destructive effects of mining on people's life in the village of Lashtaghan in South Iran

Atefeh Gholami

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The limestone mine is located in Lashtaghan, a village located in Hormozgan province in the south of Iran. The amount of sulfur and chlorine produced by the mining operation, as well as the sound of the mine explosion, have caused serious environmental issues, noise pollution and neurological diseases for the local habitants. In order to overcome these problems, this study aimed to investigate a new location for the mine in an area outside the village. To this end, 21 samples were taken from the Asmari formation and alluvia and were investigated from the viewpoint of petrography and chemical analysis (XRF). The results showed that the new proposed location with an area of 4 km² in Asmari formation had a considerable limestone ore reserve. Moreover, due to further distance from the salt dome, the amounts of sulfur and chlorine were significantly lower than that in the mine. The impact of noise pollution on the local people was also reduced owing to the long distance from the village.

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Actinobacterial endophytes: Beneficial partners for agriculture and medicine

Christopher Franco

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Actinobacteria are well recognized as prolific producers of bioactive metabolites that have diverse functions depending on their chemical structures and concentration. Many of these 'talented' actinobacteria have been found within their host plants as endophytes- each with their own roles. They were isolated from crop plants-wheat barley, oats, rice, lucerne, medics, peas, faba and soya beans chickpea, tomato, potato and Australian native plants and trees. Low nutrient media in multiple plates and incubation times of up to 16 weeks revealed large numbers of new species and one new genus. Next-gen sequencing informs us that there are a larger number of genera that were previously isolated. Nevertheless, new species were screened by RP-HPLC-Photodiode array against a proprietary database to reveal-new chemical structures. We have isolated novel antibiotics active against multidrug-resistant Gram-positive bacterial strains as well as with broad-spectrum activity. Their functional versatility coupled with their internal location makes them preferred candidates for biocontrol agents. Screening 2000 strains directly onto plants indicate the poor correlation between *in vitro* antipathogenic activity, and also the importance of the priming effect in induced systemic resistance. Ultimately, their ability to increase crop yield in the field is critical and this depends on a multitude of factors including stability and delivery and the relative cost of the inoculant. Other endophytic actinobacteria isolated from legume plants showed synergy with rhizobia when added to the seed to increase biological N Fixation by up to 70% and grain yields by 40%.

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Evaluation of biodiesel quality and lipid production by *Synechocystis sp.* grown under different culture conditions

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In this study, the effects of different types of carbohydrates, vitamins and amino acids, temperature, photoperiod (light/dark cycle), initial pH, NaCl, NaNO₃, sodium thiosulphate pentahydrate on biomass and lipid productivity of *Synechocystis sp.* were investigated. Maximum lipid productivity was achieved under the following conditions: light/dark period (24-0) (Biomass productivity: 75 Mg/L day, lipid productivity: 24 Mg/L day), sodium thiosulphate 1mM (BP: 125, LP: 32.42), initial pH 7 (BP: 109, LP: 22.89), NaNO₃ (LP: 0.5 g/l), sucrose % 1 (BP: 194 LP: 71.93), glycine % 0.1 (BP: 130, LP: 40), biotin (BP: 155, LP: 26.85) and temperature 30°C (BP: 111, LP: 33.42). The fatty acid profiles of the selected cyanobacterial strain grown in this condition were determined using GC analysis and compared with control subjects to further validate biodiesel quality. Fatty acid profiles of the cyanobacterial cell were used to estimate biodiesel quality parameters including saturated fatty acid (%), mono unsaturated fatty acid (%), poly unsaturated fatty acid (%), degree of unsaturation, saponification value (mg/g), cetane number, long chain saturated factor, cold filter plugging point (°C), cloud point (°C), pour point (°C), allylic position equivalent, bis-allylic position equivalent, oxidation stability (h), higher heating value, kinematic viscosity (mm²/s), density (g/cm³).

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Linking soil microbiome to sustainability

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Sustainable agriculture depends on healthy soil and soil microbial diversity and thus must focus on managing soil microbes to deliver more efficient ecosystem services to crops. Moreover, intensified crop production demands integrated nutrient management systems to maintain agricultural productivity and protect the environment. Using beneficial native microbes that promote plant health and quality, and recycling crop residues with low environmental impact are ultimate practices for sustainable food and energy production. In this study we use biological native resources (beneficial bacteria and fungi) and recycling organic residues for sustainable crop production. Our studies have shown that sugarcane endophyte bacteria and fungi, when inoculated in plantlets, promote sugarcane plants growth, quality, and health (microorganisms antagonistic to sugarcane pathogens). Subsequently, following the crop cycling production, our studies on recycling of crop residue as a sustainable practice, showed that the combination of sugarcane residue (vinasse), rich in carbon, nitrogen, and potassium when applied together with inorganic fertilizer, emits more nitrous oxide than inorganic fertilizers through nitrification process carried out by bacteria. In order to mitigate N_2O emissions, we showed that the use of inhibitors of nitrification is a practical solution and, more importantly, these compounds do not affect soil-borne microbial community diversity.

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ESKAPE active antibiotics avoiding resistance development

Brice Felden

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Infections caused by bacteria with developed resistance to nearly all antibiotic classes are critically spreading. They represent a major cause of mortality and morbidity worldwide, and urgently require new compounds into clinical practice. Here we present cyclic pseudo mimetic antibiotics bactericidal against ESKAPE human multi-resistant clinical isolates and stable in human sera. Modified, unnatural amino acids are required for stability and antibacterial activity on infected mice. These novel antibiotics trigger bacterial deformity, induce cell wall dissolution and alter membrane permeability. Two are active against methicillin and vancomycin resistant *Staphylococcus aureus* on a mice sepsis model and also on a skin infection model. Upon prolonged exposure to the antibiotics in-vitro and in infected mice, multi-resistant *S. aureus* did not develop resistance. Three-dimensional structures of the lead compound with and without modified amino-acids provide structural insights on its activity.

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Nutritional and cultivational aspects of *Flammulina velutipes* (Curt. Fr.) Sing. under Punjab conditions

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Flammulina velutipes was maintained on Potato-Dextrose Agar (PDA) slants and used for physiological, nutritional and cultivational studies. The culture showed white to cream coloured mycelium on seven different agar media with fine and strand hyphae on Wheat extract, PDA and Malt extract medium while thin and silky character was seen on Czapeck's and Richard's medium. Among the synthetic media, Richard's medium showed best growth. *F. velutipes* yielded maximum biomass on Wheat extract medium at pH 6.5 when incubated at 25°C for 20 days. Nutritional studies using Richard's medium showed that glucose and mannitol were the preferred C-sources while ammonium nitrate and glutamic acid were the preferred N-sources. Among the macro-elements, calcium supplementation improved biomass yield while molybdenum was most effective among the trace elements tested. For cultivation, different substrates were used including wheat straw, paddy straw, cotton waste, corncobs, sawdust and moong bean waste. Maximum yield was obtained on wheat straw supplemented with 15% wheat bran (BE 14.28%). Minimum number of days for completion of spawn run was of 19 days in case of cotton waste, corncobs, moong bean waste. Pinheads were observed in paddy straw and corncobs but no mature fruit bodies developed. Nutritional analysis showed that the fruit bodies were rich in proteins containing 27.57% crude protein out of which 81.65% was digestible, however soluble fraction of protein-4.5%, crude fat-4.25%, fibre-9.35% and ash-9.25% on dry weight basis was found. The dried powder of this mushroom contained 0.031 mg/100g β -carotene and 2.26mg/100g vitamin E.

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Shell Petroleum Company and the environment in Nigeria

Hurso Adam

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This presentation uses data from field interviews with 47 respondents in the Niger Delta region of Nigeria. The interviews were carried out conducted through in-depth interviews one to one and focus group sessions. This paper examines the nexus between the environment, conflict, and security in the Niger Delta region of Nigeria. The study has raised some valid and insightful questions concerning how different views promote their notions and visions of the oil extraction, particularly regarding exploration, environmental pollution, security, and development. The questions were timely and established an increased understanding of the nature of the environmental conflict in Nigeria by excavating the nexus between the central government, oil companies, and communities. The paper will also highlight how both the government and MNCs responded to such developmental issues as the environment and the social security of the local communities in the oil-rich Niger Delta. The specific objective of the presentation is: a) to discuss the oil-based conflicts in Nigeria's Niger Delta region triggered by environmental destruction; b) to examine the responses of the government and local and international oil companies to the demands of the community regarding environmental protection or clean-up, and the development and security of the inhabitants of the Niger Delta. The riverine communities experiencing the infernal quaking of the wrath of gas flares which have been in operation and burning, 24 hours a day non-stop for the last fifty years. No one community in the Niger Delta comfortably drinks water anymore from cement wells. The multinational and local oil companies and the Nigerian federal government have left the owners with no compensation after taking all the massive acreage of land. The lands, streams, and creeks are mostly polluted seemingly beyond easy remediation. The gas flaring, illegal oil refining, corroded oil supply blast and spillages contributed to the severe risks to the ecosystem and human life in the Niger Delta, which the government and the oil companies neglected for so long. The Ogoniland clean-up necessitated by the reality on the ground, one of the activists I interviewed in the Niger Delta had this to say: In the Niger Delta, the ecosystem has been depleted: water is polluted and the environment everywhere is in total degradation. No one community in the Niger Delta comfortably drinks water anymore. Apart from the government leaving the owners with no compensation after taking all the massive acreage of land, there is a huge amount of unemployment as a result. The Niger Delta environment has suffered tremendous damage during the militants' violent conflict with the Nigerian security forces, especially from the recent destabilization and the setting fire to the oil pipelines.

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Effect of heavy metals (Ni, Cr, Cd, Pb and Zn) on nitrogen content, chlorophyll, leghaemoglobin and seed yield in chickpea plants in India

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The present research had been conducted to study nitrogen content, chlorophyll, leghaemoglobin and seed yield in chickpea plants. All the plants of chickpea were grown in three pots while were as at and for each treatment, there were 3 replicates were removed 60, 90 and 135 DAS after seeding of chickpea respectively. Chromium was found to be the least phytotoxic and significantly at ($P \leq 0.05$ and 0.01) among all the single metal treatments increased the percentage of nitrogen of root and shoot and chlorophyll, leghaemoglobin and seed yield at all the three concentration among all dose. Among all the combination of metal treatments, Ni⁺, Cr⁺, Cd⁺, Pb⁺, Zn was found to be the most phytotoxic and significantly ($P \leq 0.05$ and 0.01) reduced the percent of nitrogen content, chlorophyll, leghaemoglobin and seed yield in of chickpea. Plant materials were analyzed for different parameters along with the determination of heavy metal accumulation by the collected samples of *Cicer arietinum* L. The data revealed that after 60, 90 and 135 DAS maximum nitrogen content, maximum chlorophyll, leghaemoglobin and seed yield was recorded by chickpea as compare to control.

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Do more with less: Industrial food and agriculture waste valorization

Christopher Simmons, Yigal Achmon, Jesus Fernandez-Bayo, Jean Vander Gheynst, and James Stapleton
University of California, USA

Food, agriculture, and the environment are intricately connected. In order to sustain a world with a population of 9 billion people by 2050, agriculture and food processing will have to maximize resource utilization. As such, food waste can be utilized either as a soil amendment to enhance sustainable agricultural advantages, or as a sustainable energy source. There is an ongoing effort to reduce the use of hazardous chemicals in soil pest management, and to use instead agricultural waste amendment is one possible solution to the problem. One of the environmentally-friendly processes is anaerobic soil disinfestation (ASD), that when coupled with passive solar heating, is also known as biosolarization. We have used industrial tomato processing waste, which is a common waste stream in California, in a bio-solarized application. By combining laboratory studies with field trials we were able to elucidate the complex biological system of biosolarization. The results showed that our laboratory system that simulates biosolarization, can predict the soil microbial behavior in the field. The laboratory results were later translated into field trials that showed the ability of biosolarization to control pests in a fast and environmental friendly procedure. The project will help to open new sustainable venues for future industrial food waste valorization.

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***In-vitro* evaluation of heavy metal tolerance and biosorptive potential of two native strains of *Bacillus cereus* against Nickel and Cobalt**

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Heavy metal contamination is a major global environmental issue and industrial effluents are commonly used for irrigation. Increasing industrial rate in the modern world is responsible for the increase in the concentration of these heavy metals. The present study was designed to isolate and evaluate some indigenous heavy metal tolerant bacteria from textile effluents of Faisalabad Pakistan. Out of 30 positive samples, two isolates were selected showing maximum tolerable concentration and multi-metal resistance to Ni and Co and were named AMIC2 and AMIC3. Molecular characterization confirmed AMIC2 as (*Bacillus cereus*, accession number LT838345) and AMIC3 as (*B. cereus*, LT838346). Biosorptive potential was accessed using Inductively Coupled Plasma-Optical Emission Spectroscopy and it was found that AMIC2 reduced Ni (48.4%, 49%) and Co (70.6%, 73.6%) after 24 and 48 hours respectively whereas AMIC3 reduced Ni (50.6%, 51.8%) and Co (71.8%, 73.2%) after 24 and 48 hours respectively. Fourier transform infrared spectroscopy was used to analyze the functional groups and overall nature of chemical bonds in isolates while Scanning Electron Microscope was performed to detect outer morphological changes in bacteria in response to metal stress. Results suggested that bacteria possessed significant biosorptive potential and may be used for the development of bioremediation agent in future.

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New deltas formation in large water reservoirs of the globe

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Formation of new delta-like landscapes at the places where rivers flow into the large reservoir we consider as the important and major scientific and economic problem. This process is estimated to be universal having a global character. However, new landscapes, which are formed by delta type, are vary considerably depending (first of all) on climatic conditions. At the same time, this process is especially characteristic for rivers with large sediment load, which is often observed in arid, sub-arid and in sub-humid regions. And landscapes peculiarities and rate of their formation depend on hydrological and hydrochemical regimes of rivers and reservoirs where this process takes place. So in this presentation the processes of new deltas formation are discussed in more detail in the temperate climate of Ukraine and in arid and semiarid climate of Central Asia, where we carried out our research for some decades. Schematic observations are made in other regions of the world as well. Problem analysis was carried out using remote sensing data (Landsat satellite imagery) and ground-based observations. Using satellite images made it possible to trace the process in time and space over a long period. Translating of satellite pictures with the assistance of particular programming gave a possibility to direct the zone of the recently framed scenes and roughly to analyze soil and vegetation protests that were indicated by ground checking in the repositories.

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