12th International Congress on
Microbial Interaction and Applications of Beneficial Microbes
July 17-18, 2017 Munich, Germany

Keynote Forum

Day 1

Konstantinos Kormas, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Konstantinos Kormas

University of Thessaly, Greece

Bacteria as true residents in the gastrointestinal tract of commercially reared fish

Bacteria are the main symbionts of the gastrointestinal tract (GIT) of practically every macro-organism that has been studied so far. Usually the benefits of this symbiosis are far more significant than the harmful (pathogenic/toxic) symbiotic relations occurring in some animals. Of all the GIT-bacteria systems known to date, aquatic animals are among the least studied. The GIT of commercially reared fish, consist an excellent ecosystem for the investigation of the origin, establishment and growth of their bacteria populations. The major reason for this is that the GIT of reared fish: (1) receives a relatively constant food supply of specific ingredients, serving as the growth medium of the symbiotic bacteria; (2) is characterized by a rather constant suite of *in situ* environmental conditions, which set a stable and known profile of incubation conditions of the symbiotic bacteria; and (3) aquaculture installations come in various systems and can be found in a wide array of locations around the world covering both freshwater, brackish and marine habitats. Available studies to date, depict that: various reared fish species harbor different but specific prokaryotic communities, being shaped by the supplied diet and/or the animal's habitat; have temporally variable symbiotic bacterial communities; populations of reared species have distinct GIT bacterial communities compared to their wild counterparts; there is uncertainty on the fish GIT bacteria origin; and the understudied effect of the individual variability vs. individual-independent, limits us from depicting a true core microbiome for species of reared fish.

Biography

Konstantinos Kormas received his BSc (1994) and PhD (1998) from the Biology Department of the University of Athens, Greece. He worked as a Post-doctoral fellow at the Trondhjem Biological Station, Norway and Woods Hole Oceanographic Institution, USA. Since 2015, he is a Professor of Aquatic Microbial Ecology at the University of Thessaly, Greece. His research focuses on the patterns and processes that underpin the distribution and abundance of microorganisms in different habitats of the aquatic environment, including plankton, benthos and symbionts. He has published more than 80 papers in peer-reviewed journals

kkormas@uth.gr

Notes:

Susanne Zeilinger, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Susanne Zeilinger

University of Innsbruck, Austria

From genes to biocontrol: Unraveling the molecular mechanisms of mycoparasitic fungus-fungus interactions

Mycoparasitic species of the fungal genus *Trichoderma* are among the most successful bio-fungicides in today's agriculture although our understanding of the exact molecular mechanisms of their activity still is fragmentary. The biological control of fungal plant diseases by *Trichoderma* includes direct antagonism of phytopathogenic fungi by mycoparasitism. This mycoparasitic attack comprises sensing of the prey and chemotropic growth towards it followed by overgrowing and killing of the prey fungus. Genome sequence analysis of *Trichoderma* mycoparasites showed an abundance of cell wall lytic enzymes such as chitinases and glucanases essential for prey lysis and degradation and an assortment of genes involved in the formation of secondary metabolites for chemical warfare. The signals activating the mycoparasitic response include surface molecules and surface properties and may also include prey-derived secondary metabolites and other small substances exchanged between the interaction partners. Investigations of *Trichoderma atroviride* will be presented showing that this potent mycoparasite relies on G protein and MAP kinase signaling for triggering of the mycoparasitic response. Results on the role of the Gpr1 7-transmembrane receptor in the recognition of prey-derived signals will be shown as well as data on transcriptome profiling of gpr1-mutants and mutants interrupted in Tmk1 MAP kinase signaling.

Biography

Susanne Zeilinger has studied Microbiology and Genetics from the University of Vienna and during her Diploma thesis she gained experience in fungal enzyme characterization from the VTT Technical Research Center of Finland. She did her PhD from the Technical University of Vienna (TUW) on fungal cellulase gene regulation. As a Post-doctorate she has worked on *Trichoderma* biocontrol at TUW and as a Visiting Scientist at the Institute of Plant Pathology in Portici, Naples, Italy. In 2003, she became the Group Leader in the Research Area of Biotechnology and Microbiology at the Institute of Chemical Engineering at TUW. Since 2015, she is a Full Professor for Microbiology at the University of Innsbruck, Austria. Her research focuses on molecular fungal biology with a special interest in interactions of fungi with other (micro-) organisms, bio-communication and signal transduction.

susanne.zeilinger@uibk.ac.at

Notes:

Raimondas Jasevičius, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Raimondas Jasevičius

Vilnius Gediminas Technical University, Lithuania

Numerical modeling of the mechanical interaction of a bacterium

The behavior of non-biological spherical particles can be readily modeled with the discrete element method. The size of the particles thereby plays an important role in particle or particle system behavior. For micron-sized particles the attractive force becomes dominant, thus specific knowledge is needed regarding it. This knowledge can be applied not only for non-biological, but also for biological similar sized objects, such as cells. This can extend the implementation, the understanding and possible applications of the discrete element method even up to the molecular dynamics level. In this work, we introduce models for cell interaction, basing on experience from modeling the interaction of ultrafine particles. The cell is thereby considered as a colloid particle, where an idealization with continuum mechanics is applicable. The model parameters for the cells are taken from known physical experiments performed with spherical *S. aureus* bacteria. The presented model is universal, and can be applied for the modeling of the dynamics of possibly other cell types as well. The investigation of the dynamics of a single bacterium may help to understand the behavior of a system of bacteria (e.g. biofilm formation) as well as the transmission of infections in the air. One of the important factors influencing the stability of a bacterial structure, but also important in the context of an infection is the adhesion force. Detailed results on the sticking process of a bacterium are presented. A characterization of the influence of repulsive and attractive forces on the bacterium is given. The obtained results are shown in terms of force displacement diagrams as well as a function of the interaction and sticking time history. For the modeling of the system behavior the sticking process of 10,000 bacteria is considered.

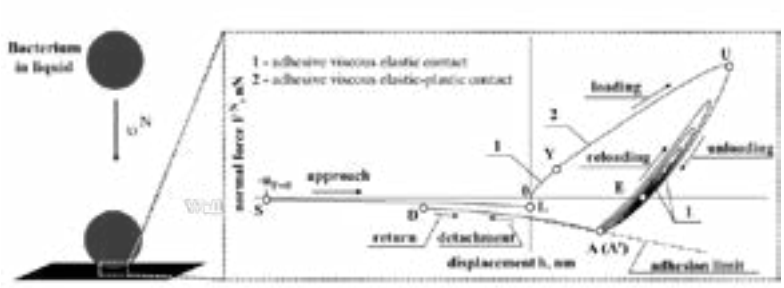

Figure 1: Scheme for the motion of the bacterium close to the wall. Adhesive viscous elastic-plastic sticking process model applied.

Biography

Raimondas Jasevičius has completed his PhD from Vilnius Gediminas Technical University (VGTU) and Post-doctoral studies from Vilnius University, Lithuania. He is a Senior Researcher, Institute of Mechanics and is an Associate Professor, Department of Printing Machines, VGTU. He has built an adhesive dissipative interaction model after years of experience in research with Otto von Guericke University and Berlin Technical University, Germany. He has more than 18 published articles in reputed journals.

raimondas.jasevicius@vgtu.lt

12th International Congress on
Microbial Interaction and Applications of Beneficial Microbes
July 17-18, 2017 Munich, Germany

Keynote Forum

Day 2

Andreas Vilcinskas, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Andreas Vilcinskas

University of Giessen, Germany

Insect-derived beneficial microbes for industrial applications

Industrial (white) biotechnology focuses on the biotransformation of raw materials into useful industrial products, predominantly using microbes and/or enzymes. Insects, the most diverse group of organisms on the earth, owe part of their evolutionary success in extreme habitats to their own version of white biotechnology-symbiosis with microorganisms. The presentation highlights how the industrial biotechnology toolbox can be expanded by developing insect-associated microbes as biological resources for the production of enzymes and as tools in their own right, e.g. for the conversion of biomass. Focusing on selected examples such as the black soldier fly *Hermetia illucens*, the burying beetle *Nicrophorus vespilloides* or the clothes moth *Tineola bisselliella* it is demonstrated how advanced and complementary methods covering biochemistry (bioassays, proteomics), molecular biology (genomics, RNA-Seq and candidate gene-centered analysis of insect hosts and their microbiota) and cell biology (cell cultures, enzyme assays, biotechnology-based processing) are used to decipher the interactions between insect species occupying unique ecological niches and their microbiota, emphasizing the partitioning of adaptive processes between the host and symbionts to convert biomass more efficiently.

Biography

Andreas Vilcinskas is a Professor of Applied Entomology and Director of the Institute for Insect Biotechnology Justus Liebig University Giessen, Germany. His fields of research are insect biotechnology; development of innovative approaches for the control of pest and vector insects; insect immunity, ecology and evolution; invasion biology; and genome biology and epigenetics of insects.

Andreas.Vilcinskas@agrar.uni-giessen.de

Notes:

Robert Czajkowski, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Robert Czajkowski

University of Gdansk and Medical University of Gdansk, Poland

Biological control of plant pathogens with the use of beneficial bacteria and lytic bacteriophages - fact or fiction?

It is forecasted that the world population will reach 10 billion people by 2050. Overpopulation, climate instability and plant pest and diseases are directly responsible for increasing global hunger. It is estimated that more than 60% of the human population is starving and plant diseases play a major role in food shortages worldwide. Global loss of staple crops due to plant pathogens is predictably estimated to be as high as even 40 percent. Potato (*Solanum tuberosum* L.) is one of the most important staple food crops worldwide and the fourth main food crop after rice, maize and wheat. The area of potato cultivation is rapidly increasing especially in developing regions. In Europe potato has always been recognized as an significant food crop. Intensive potato cultivation together with the international potato tuber market may result in the increased risk of transmission and spread of potato diseases that lead to decrease of crop quality and yield. Diseases caused by pectinolytic bacteria: blackleg during potato cultivation and soft rot of potato tubers in storage and transit are among the most important bacterial diseases leading to substantial losses in potato production in Europe and worldwide. Traditional pathogen control methods based on chemical and physical applications are insufficient to cure infected potato tubers from pectinolytic bacteria as well as they are unable to prevent spread of the pathogens in the field. Biological (environmentally friendly) control of plant pathogens could be an alternative to chemical and physical approaches. We are eager to develop new biological control strategies based on the use of beneficial bacteria and bacteriophages in order to prevent buildup of the pathogen populations in potato tubers. This presentation acknowledges past and present work on biological control of potato pathogens – pectinolytic bacteria, with the major focus on research leading to commercialization.

Biography

Associated Professor at University of Gdansk, Poland. He is a graduate of Intercollegiate Faculty of Biotechnology, University of Gdansk and Medical University of Gdansk in Gdansk (2006). In 2006 he received a year-fellowship from EU Marie Curie Early Stage Research programme and from 2006 till2007 he worked as a visiting scientist at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany. Scholar of doctoral studies at the Netherlands Institute of Ecology, the Royal Netherlands Academy of Sciences in Wageningen, the Netherlands (2007-2011). Postdoctoral researcher at Wageningen University and Research Center - Plant Research International in Wageningen, the Netherlands (2011- 2012), Assistant Professor in the Department of Biotechnology in the Intercollegiate Faculty of Biotechnology, University of Gdansk and Medical University of Gdansk (2012-2016). In 2013 received a fellowship from the Ministry of Science and Higher Education for outstanding young scientists (2013-2016) and in 2014 fellowship from The Foundation of Polish Science in the EU Skills Mentoring Programme. Between 2013 and 2015 was a Secretary of Polish Society of Experimental Plant Biology, Presently, a member of The Council of Young Scientists at the Ministry of Science and Higher Education and a member of editorial board of BioTechnologia and Journal of Plant Pathology.

Robert.czajkowski@biotech.ug.edu.pl

Notes:

Zajac Vladimir, Appli Micro Open Access 2017, 3:2(Suppl)
DOI: 10.4172/2471-9315-C1-004

Zajac Vladimir

Cancer Research Institute BMC SAS, Slovakia

Participation of bacteria and yeasts in the AIDS process: evolutionary view

We have identified HIV-like sequences homologous with HIV-1 isolates for about 90% and HIV-like proteins in bacteria/yeasts in a cohort of 80 AIDS patients from Slovakia, USA, Kenya and Cambodia. Based on these results, we assume that HIV is an integral part of humans from the beginning of our existence and bacteria and yeasts are natural hosts of HIV, thereby affording affinity to T cells. The results obtained and the subsequent analysis have led us to believe that on the epidemic of "Black Dead" in the 14th century participated except *Yersenia pestis* and other agents, and thus in our view he is HIV. This version corresponds to the means of human-to-human transmission, speed and intensity of the epidemic. This epidemic took place in Europe, parts of Asia and North Africa,but not in America and sub-Saharan Africa. The victims of the Black Death epidemic were individuals with a damaged immune system due to violation of symbiosis between the prokaryotic and eukaryotic kingdom in their body. The epidemic was so devastating, because resulted also in the elimination of HIV carriers. Those who survived had delta 32 mutation in the CCR5 co-receptor, which is predominantly expressed in T cells, macrophages, dendritic cells, and eosinophils. A mutation to prevent participants from *Yersenie pestis* infection, but the smallpox virus and HIV infection, as well. The "Black Dead" epidemic results in an increase in the number of CCR5 delta 32 mutations in the Caucasus population to 10%, in some areas to 15-20%. This epidemic on the other side as "sanitary process" led to the restoration of balance between the two kingdoms in the human body and to the recovery of most of the human population. In Sub-Saharan Africa, this epidemic and subsequent "sanitation process" has not taken place and that's why HIV-related genetic information has not been eliminated in the population. Therefore, there is no CCR5Δ32 mutation in this population and the level of HIV genetic information is much higher than in other parts of the world. Options to remedy this situation in Sub-Saharan Africa are under discussion. Confirmation of the presented hypothesis can bring new insight into AIDS, especially in Africa, and open up new possibilities in diagnostics and therapy of this syndrome.

Biography

Vladimir Zajac has completed his PhD. in 1982 at the Cancer Research Institute of Slovak Academy of Sciences in Bratislava (Slovakia), where he worked as the Head of Department of Cancer Genetics from 1996 to 2010. He joined the Medical Faculty of the Comenius University as Associate Professor of Genetics in 2007. He has published 72 papers mostly in reputed journals and he was editor of the book "Bacteria, viruses and parasites in AIDS process" (InTech, 2011).

vladimir.zajac@savba.sk

Notes: