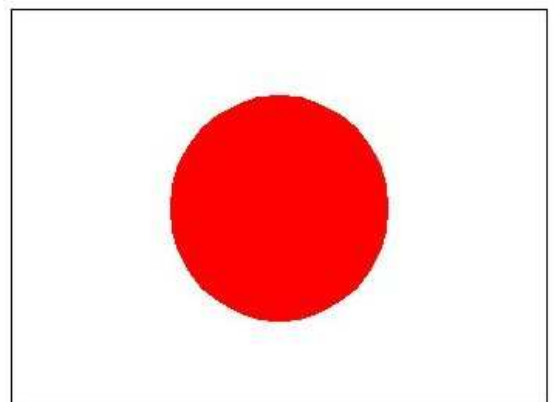


**Laboratory of Microbiology  
Wageningen University, the Netherlands**

# **PhD Study trip 2011**

**April 15<sup>th</sup> – May 1st**

## **China-Japan**



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*Laboratory of Systems and Synthetic Biology*  
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## Summary

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Friday the 15<sup>th</sup> of April turned out to be a good start of a beautiful Dutch spring but was also a perfect beginning for our study trip to Asia (15<sup>th</sup> April-1<sup>st</sup> May). Saturday 9:30 local time, off course without having any good night rest, our party of 20 PhD students and Dr Servé Kengen of the Laboratory of Microbiology arrived at Beijing international airport.

After 1.5 day of free time, including visits to the Forbidden City and the Great Wall, we were warmly welcomed by Dr Dinghuan Hu, the Chief representative of WURChina ([www.wurchina.com/](http://www.wurchina.com/)). This session, held at the main building of The Chinese Academy of Agricultural Sciences ([www.caas.net.cn](http://www.caas.net.cn)), was the Kick-off of our scientific program in China. During the following 3 days we were subsequently hosted by the Department of energy and resources engineering of Peking University ([www.pku.edu.cn/](http://www.pku.edu.cn/)), the Institute of Microbiology Chinese Academy of Science ([www.im.cas.cn/](http://www.im.cas.cn/)) and the College of Resources and Environmental Sciences of the China Agricultural University (group photo) ([www.cau.edu.cn/](http://www.cau.edu.cn/)). After a short visit to the Summer Palace on Wednesday afternoon the group travelled by night train to Shanghai, where only one person caused some stress for the organization by being unable to distinguish Beijing 'south' railway station from Beijing railway station. The next day it was directly from our bed bunks into the chairs of the conference room of the School of Life Sciences and Biotechnology Shanghai Jiao Tong University (<http://life.sjtu.edu.cn/>). A joined symposium of SIPPE-CAS & Fudan University ([www.sippe.ac.cn/](http://www.sippe.ac.cn/) / [www.fudan.edu.cn/](http://www.fudan.edu.cn/)) brought the end of our scientific program in China. After a day of sightseeing we headed for Japan, unfortunately with the exception of 6 participants who travelled directly back to the Netherlands.

Because of the tragic events befalling Japan our the scientific program in Japan was shortened and the intended visits to Yakult Central Institute for Microbial Research and the Department of Biotechnology of the University of Tokyo had been cancelled, thus limiting our visit to the central part of Japan (Kansai region). On Sunday we travelled to Spring8 were on Monday, as a part of our day program, we had a peak at the world's largest third generations synchrotron facility ([www.spring8.or.jp/en/](http://www.spring8.or.jp/en/)). A joined workshop with 4 different departments at Kyoto University ([www.kyoto-u.ac.jp/en](http://www.kyoto-u.ac.jp/en/)) brought us to the old capital of Japan. Our Japanese scientific program ended with a visit to the Graduate school of Biological Sciences of the Nara Institute Of Science and Technology ([www.naist.jp/en/](http://www.naist.jp/en/)). Some additional free time in Kyoto and Osaka, before our departure May 1<sup>st</sup>, allowed us to recover from this intense program.

Throughout our visits we shared scientific knowledge during oral presentations, poster presentations and facility tours and we were able exchange cultures by joined social events. Thus living up to the aim of our study trip: To strengthen existing partnerships, looking for new collaborations and allowing the participating PhD students to broaden their vision in the field of Microbiology.

The organization would like to thank all the involved sponsors and off course the hosting departments in both China and Japan, everywhere we received a very warm welcome. An overview of the scientific program and the sponsors will be available on the web page of the Laboratory of Microbiology ([www.mib.wur.nl/UK/](http://www.mib.wur.nl/UK/))

### The organization

Bram Bielen  
Martin Liebensteiner  
Jimmy Omony  
Mauricio Rocha Dimitrov  
Teun Veuskens  
Edze Westra  
Jing Zhang

## Samenvatting (Dutch)

---

Op Vrijdag 15 April begon de studiereis naar China en Japan voor de AIO's van het Laboratorium voor Microbiologie WUR, toen een groep van 20 AIO's en vast staf lid Dr Servé Kengen vertrok vanuit Schiphol. Zaterdag 9:30 (lokale tijd), na een slapeloze nacht, arriveerde onze groep op Beijing international airport. De eerste twee dagen in Beijing waren grotendeels vrij en zijn goed besteed met een bezoek aan de Verboden Stad en de Chinese Muur.

Op zondagavond werden we hartelijk verwelkomd door Dr Dinghuan Hu, de Chief Representative van WURChina ([www.wurchina.com/](http://www.wurchina.com/)). Deze sessie, die werd gehouden in het hoofdgebouw van The Chinese Academy of Agricultural Sciences ([www.caas.net.cn](http://www.caas.net.cn)), was de Kick-off van ons wetenschappelijk programma in China. Gedurende drie dagen zijn we achtereenvolgens op bezoek geweest bij het Department of Energy and Resources Engineering van Peking University ([www.pku.edu.cn/](http://www.pku.edu.cn/)), het Instituut voor Microbiologie van de Chinese Academy of Science ([www.im.cas.cn/](http://www.im.cas.cn/)) en het College of Resources and Environmental Sciences van de China Agricultural University (zie groeps foto) ([www.cau.edu.cn/](http://www.cau.edu.cn/)). Na een kort bezoek aan het Zomerpaleis van de keizer op woensdagmiddag zijn we als groep per nachttrein van Peking naar Shanghai gereisd. Een persoon wist hier, door op het verkeerde treinstation op de groep te wachten, nog voor flink wat stress bij de organisatie te zorgen; gelukkig was deze persoon nog net op tijd voor vertrek ter plaatse! De volgende dag zijn we onmiddellijk vanuit het trein station naar de conferentiezaal van de School of Life Sciences and Biotechnology van de Shanghai Jiao Tong Universiteit (<http://life.sjtu.edu.cn/>) gegaan. Op vrijdag werd het wetenschappelijk programma in China afgesloten met een symposium georganiseerd door SIPPE-CAS & Fudan University ([www.sippe.ac.cn/](http://www.sippe.ac.cn/) [www.fudan.edu.cn/](http://www.fudan.edu.cn/)). Na een toeristisch rondje door het centrum van Shanghai zijn we per vliegtuig naar Japan gegaan, helaas zonder 6 van onze deelnemers die vanaf hier teruggingen naar Nederland.

Vanwege de recente ramp in Japan was ons programma ingekort en de beoogde bezoeken aan het Yakult Central Institute for Microbial Research en het Department of Biotechnology van de Universiteit van Tokyo waren geschrapt. Aldus zijn we alleen in het centrale deel van Japan geweest (Kansai regio). Op maandag hebben we Spring8 bezocht, waar we de op twee na grootste synchrotron faciliteit ter wereld mochten bezoeken ([www.spring8.or.jp/en/](http://www.spring8.or.jp/en/)). Een workshop met 4 verschillende departementen van Kyoto Universiteit ([www.kyoto-u.ac.jp/en](http://www.kyoto-u.ac.jp/en)) bracht ons naar de oude hoofdstad van Japan. Het Japanse wetenschappelijk programma eindigde met een bezoek aan de Graduate school of Biological Sciences van het Nara Institute of Science and Technology ([www.naist.jp/en/](http://www.naist.jp/en/)). De daaropvolgende vrije dagen in Kyoto en Osaka gaven ons de kans bij te komen van het intensieve programma, voordat we op 1 Mei teruggingen naar Nederland.

Gedurende onze bezoeken hebben wij en onze gastheren wetenschappelijke kennis uitgewisseld door mondelinge presentaties, poster presentaties en rondleidingen. We kregen gelegenheid om onze Chinese en Japanse collega's beter te leren kennen tijdens de vele sociale activiteiten (diners, karaoke, culturele uitstapjes, etc.). Hiermee werd het doel van onze reis verwezenlijkt: Bestaande samenwerkingsverbanden versterken, nieuwe samenwerkingen aangaan en de deelnemende AIO's in de gelegenheid brengen hun algemene kennis van de Microbiologie te vergroten.

The organisatie wil alle sponsors bedanken die deze reis mogelijk hebben gemaakt en natuurlijk de gastheren in China en Japan; we zijn overal bijzonder hartelijk ontvangen. Een overzicht van het wetenschappelijk programma en de sponsors is te vinden op de website van het Laboratorium voor Microbiologie van Wageningen Universiteit en Research Centre ([www.mib.wur.nl/UK/](http://www.mib.wur.nl/UK/)).

### De Organisatie

Bram Bielen  
Martin Liebensteiner  
Jimmy Omony  
Mauricio Rocha Dimitrov  
Teun Veuskens  
Edze Westra  
Jing Zhang

## Sponsors



### Laboratory of Microbiology

The Laboratory of Microbiology (headed by Professor Willem M. de Vos) is engaged in research and education in biotransformations and interactions of microorganisms as well as their control. Moreover, it contributes to the exploitation of the generated knowledge in the application areas of Health & Food, Bioproducts & Energy and Environment & Sustainability. The research is primarily molecule-driven and genomics-based while incorporating systems approaches at all levels. It integrates three important microbial disciplines which are organized into the research groups Bacterial Genetics (led by Professor John van der Oost), Molecular Ecology (led by Professor Hauke Smidt) and Microbial Physiology (led by Professor Fons Stams).

The Laboratory of Microbiology was established close to 100 years ago and has developed a long-standing expertise on bacteria, archaea and viruses. There is a strong emphasis on anaerobic prokaryotes because of their novel and unique properties, their relevance for various industrial application areas, and the developed anaerobic expertise and infrastructure. Present members of the department include approximately 100 international scientists, students and supporting staff. There are active interactions with other Chairs, including that of Systems and Synthetic Biology (<http://www.ssb.wur.nl/UK/>), while many members participate in EU and other international networks via collaborations or joined appointments. For information:

[www.mib.wur.nl/UK](http://www.mib.wur.nl/UK)



### Systems and Synthetic Biology

Our mission is to contribute to the elucidation [from a Systems Biology perspective] of the mechanisms underlying basic cellular processes, evolution and interactions among microbes and between microbes and their environment (including the human host), and to translate this knowledge into applications of biotechnological, medical and environmental interest. For information: <http://www.ssb.wur.nl/UK/>

## Stichting biotechnologie

Stichting Biotechnologie Nederland (SBN) was founded in 1986 to stimulate biotechnology with an emphasis on supporting young scientists, organisation of meetings on biotechnology and participation of Dutch biotechnologists in international activities SBN is a part of the Nederlandse Biotechnologische



Vereniging (NBV, Dutch Biotechnology association) an association of professionals acting in the field of Life Sciences. A valuable network were all 1000 members, from universities, research institutes, intermediate organisation, government, and industry contribute to. The NBV aims at promoting integrated application of scientific disciplines on biological systems for industrial processes and products, energy, pharmaceutical applications, environment and sustainability, agriculture, forensic research, nutrition and healthcare. For information: <http://nbv.kncv.nl/>

## WIMEK

WIMEK (Wageningen Institute for Environment and Climate Research) is the largest institute to participate in the Netherlands Research School for the Socio-Economic and Natural Sciences of the Environment (SENSE).

WIMEK combines a range of natural and socio-economic sciences in studying the flow of substances through the environment and society. Its research programme is focussed on the analysis of the causes and the ecological and societal effects of environmental problems, the development of solutions for sustainable environmental management and nature conservation and the ecological transformation of production and consumption.

The WIMEK research mission: analysis of the causes and the ecological and societal effects of environmental problems originating from substance flows through environment and society, the development of solutions for sustainable environmental management and nature conservation, and the ecological transformation of production and consumption. For information: [www.wimek-new.wur.nl/](http://www.wimek-new.wur.nl/)



## LEBfonds

The LEB funds (or (in Dutch) 'Stichting Fonds Landbouw Export Bureau 1916/1918') stimulates developments in agricultural research – including environmental sciences – at Wageningen UR and the publication of results. Funding is available for activities such as: presentation on an international congress, Ph.D. trips, organizing scientific meetings in the Netherlands for young scientists, printing costs of Ph.D. theses of foreign Ph.D. students without a fixed contract. Applicants for the LEB funds need to be (i) Ph.D. students at Wageningen University, or (ii) young investigators without fixed contracts but connected to Wageningen UR, or (iii) foreign researchers at Wageningen University from developing countries with inadequate financial support, or (iv) guest researchers at Wageningen UR.

# LEBfonds

## VLAG

Founded in 1993, the Graduate School VLAG (Advanced studies in Food Technology, Agrobiotechnology, Nutrition and Health Sciences) is a cooperative endeavour of two universities; Wageningen University, Maastricht University; and five research institutes: WUR Food & Biobased Research, RIKILT-Institute of Food Safety, NIZO Food Research, TNO Quality of Life, and the National Institute for Public Health and the Environment (RIVM), The Netherlands. The disciplines covered by the graduate school are: Nutrition, Food Sciences, Agro-Biotechnology, and Health Sciences. VLAG's two major tasks are: to provide its PhD students with a research and education programme of academic excellence to provide added value to its programme by funding research projects and by acquiring external funding for large-scale multidisciplinary research projects. For information: [www.vlaggraduateschool.nl/](http://www.vlaggraduateschool.nl/)



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The Middelhoven fund was founded in 1995 by Dr. Wout Middelhoven while he turned 60 years old. Wout Middelhoven has been professor at the Laboratory of Microbiology for over 40 years. After his retirement he is still present in the lab on a daily basis. In 2000 he has been rewarded by Wageningen University the "Zilveren Legpenning".

This fund aims to support students and staff members who want to do an internship in the Netherlands or abroad in order to acquire knowledge and experience in microbiology, in particular microbial physiology and ecology.



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## TI Food and Nutrition

TI Food and Nutrition is an alliance of science and industry that generates scientific breakthroughs in food and nutrition, resulting in the development of innovative products and technologies that respond to consumer demands for safe, tasty and healthy foods.

In TI Food and Nutrition the research is flexibly organised in themes and projects, and jointly decided upon and guided by the research and industry partners. All research is carried out in the laboratories of the research partners by multidisciplinary teams. These teams are composed of leading scientists who work together to achieve scientific breakthroughs of high industrial relevance.

In this public-private partnership key players of the (inter)national food industry and academia combine their strengths: CBL, Chr. Hansen, CSM, Danone, DSM, FrieslandCampina, FNLI, Fromageries Bel, Kellogg, Nestlé, Unilever, VION, NIZO food research, TNO, University of Groningen/UMCG, Maastricht University/MUMC and Wageningen UR. The research programme of TI Food and Nutrition is co-funded by the Ministry of Economic Affairs, Agriculture and Innovation. For information: [www.tifn.nl](http://www.tifn.nl).



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## Who we are

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### Wageningen University and Research Centre: For the Quality of Life

Wageningen University and Research Centre (WUR) provides education and generates knowledge in the field of life sciences and natural resources. Wageningen UR aims to make a real contribution to our quality of life. To us, quality of life means both an adequate supply of safe and healthy food and drink, on the one hand, and the chance to live, work and play in a balanced ecosystem with a large variety of plants and animals.

Wageningen UR is a collaboration between Wageningen University, Van Hall Larenstein School of Higher Professional Education and the specialised former research institutes (DLO) from the Dutch Ministry of Agriculture. This combination of knowledge and experience enables Wageningen UR with its 5,600 staff and more than 8,500 students to contribute actively to solving scientific, social and commercial problems in the field of life sciences and natural resources.

Wageningen University has 85 chair groups within 5 departments, viz. AgroTechnology & Food Sciences, Animal Sciences, Plant Sciences, Social Sciences, and Environmental Sciences. Wageningen University offers 18 Bachelor's degree programmes and 30 Master's degree programmes. The scientific quality of Wageningen University is safeguarded by 7 Graduate Schools. Wageningen University is among the top 3 in the worldwide publication index in the field of agriculture and in the top 5 in the areas of plants/ animals and environment.



### Laboratory of Microbiology

The Laboratory of Microbiology (headed by Professor Willem M. de Vos) is engaged in research and education in biotransformations and interactions of microorganisms as well as their control. Moreover, it contributes to the exploitation of the generated knowledge in the application areas of Health & Food, Bioproducts & Energy and Environment & Sustainability. The research is primarily molecule-driven and genomics-based while incorporating systems approaches at all levels. It integrates three important microbial disciplines which are organized into the research groups Bacterial Genetics (led by Professor John van der Oost), Molecular Ecology (led by Professor Hauke Smidt) and Microbial Physiology (led by Professor Fons Stams).



The Laboratory of Microbiology was established close to 100 years ago and has developed a long-standing expertise on bacteria, archaea and viruses. There is a strong emphasis on anaerobic prokaryotes because of their novel and unique properties, their relevance for various industrial application areas, and the developed anaerobic expertise and infrastructure. Present members of the department include approximately 100 international scientists, students and supporting staff. There are active interactions with other Chairs, including that of Systems and Synthetic Biology (led by Prof. Vitor Martins dos Santos) (<http://www.ssb.wur.nl/UK/>), while many members participate in EU and other international networks via collaborations or joined appointments.

### Bacterial Genetics

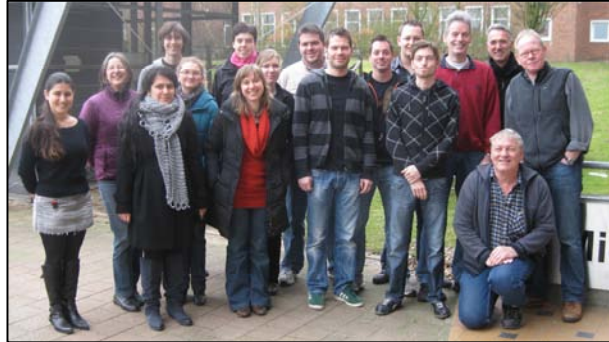
In the Bacterial Genetics research group, molecular techniques are applied to gain insight in the biochemical and genetic adaptation of selected processes in distinct model Archaea and Bacteria. In these analyses a wide variety of biochemical analyses is crucial: *in vitro* transcription, footprinting, crystallization, mutagenesis (directed engineering as well as Laboratory Evolution), analysis of protein-protein interactions, DNA microarray analysis, proteomics. Ongoing research projects are:



- (i) Enzymes & pathways - gene identification & prediction; gene expression; protein purification & characterization; functional optimization of biosensors, biocatalysts and bioconversion routes by random & rational engineering;
- (ii) Regulation & signal transduction - structure-function analysis of specific and global regulators; protein regulators as well as small RNAs (CRISPRs); characterize control at transcription, translation & protein level;
- (iii) Genomics - comparative & functional genomics (transcriptome / proteome / metabolome); integration with physiology and biochemistry (Systems Biology);

## Microbial Physiology

The Microbial Physiology group studies a variety of anaerobic ecosystems. The group studies anaerobic microorganisms that play an important role in biotechnological processes, such as wastewater treatment and soil bioremediation. Through this work they have developed expertise in the biochemical analysis and metabolism of anaerobic microorganisms, along with their isolation and cultivation. Research is currently focused on the following aspects: microbial formation of methane and hydrogen, the importance of the sulfur-cycle for the biological removal of metals and sulphuric compounds, the oxidative and reductive conversion of xenobiotic pollutants, and the use of alternative electron acceptors, such as chlorate and chlorinated organic contaminants, by anaerobic microorganisms, and microbial fuel cells where microorganisms use inert electrodes as terminal electron acceptor.



## Molecular Ecology

Research in the group of Molecular Ecology has, over the last 10 years, focused on the application of molecular methods to



unravel microbial interactions in mainly anaerobic ecosystems, with special emphasis on the mammalian intestine, wastewater treatment reactor sludge, and soil. Molecular ecological approaches, including 16S ribosomal RNA-targeted detection and phylogenetic fingerprinting of microbial communities allowed to complement our current inability to cultivate large fractions of microbial assemblages, and could be used to address biological questions, including the basic question how microbial functioning and diversity is affected by biological and physico-chemical parameters of ecosystems. Recently, state-of-the-art functional genomic and proteomic approaches have been implemented, now allowing for the study of microbe-microbe and microbe-host interaction.

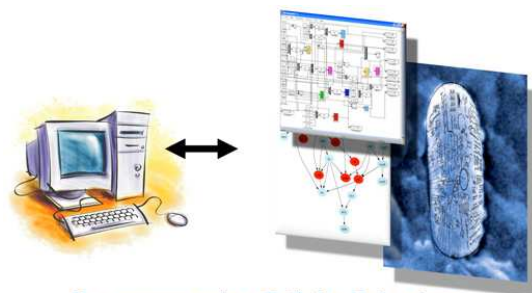
## Systems and Synthetic Biology

Our mission is to contribute to the elucidation [from a Systems Biology perspective] of the mechanisms underlying basic cellular processes, evolution and interactions among microbes and between microbes and their environment (including the human host), and to translate this knowledge [from a Synthetic Biology perspective] into applications of biotechnological, medical and environmental interest.

We aim to develop and apply theoretical frameworks supporting (and relying on) experimental research towards the understanding of the various processes and hierarchies of cellular networks and circuitry.

The Systems & Synthetic Biology Laboratory addresses in an integrated way critical issues and novel biotechnological applications in the areas Health & Food, BioBased Products and Environment.

We carry out our research activities broadly along three major lines: (1) Computational Systems Biology (2) Fungal Systems Biology (3) Synthetic Biology.



Re-programming Cellular Behaviour

## Organizers

---

### **Bram Bielen**

Lab. Of Microbiology, Bacterial Genetics group

### **Martin Liebensteiner**

Lab. Of Microbiology, Microbial Physiology group

### **Jimmy Omony**

Lab. Of Systems and Synthetic Biology,  
Fungal Genomics, Systems and control group

### **Mauricio Rocha Dimitrov**

Lab. Of Microbiology, Molecular Ecology group

### **Teun Veuskens**

Lab. Of Microbiology, Microbial Physiology group

### **Edze Westra**

Lab. Of Microbiology, Bacterial Genetics group

### **Jing Zhang**

Lab. Of Microbiology, Molecular Ecology group

## Information Hosts China/Japan

---

### **Day 4: Beijing**

#### **Peking University**

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College of Engineering

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### **Day 5: Beijing**

#### **Chinese Academy of Science Institute of Microbiology**

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### **Day 6: Beijing**

#### **China Agricultural University**

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Yuan Xu, Ph.D. candidate

Lab of Microbial Ecology

College of Resources and Environmental Sciences

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### **Day 7: Shanghai**

#### **Jiao Tong University**

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### **Day 8: Shanghai**

#### **SIPPE-CAS & Fudan University**

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Institute of Plant Physiology & Ecology,  
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### **Day 11: Kouto**

#### **RIKEN SPring-8 Centre**

Dr. Akeo Shinkai

Harima Institute

Functomics Biology I Research Team

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Phone: +81-791-58-2891

### **Day 12: Kyoto**

#### **Kyoto University**

Prof. Dr. Haruyuki Atomi

Department of Synthetic Chem. and Biol. Chemistry

Graduate School of Engineering

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Phone: +81-75-383-2777

### **Day 13: Nara**

#### **Nara Institute of Science & Technology**

Prof. Dr. Hiroshi Takagi

Graduate School of Biological Sciences

Email: [hiro@bs.naist.jp](mailto:hiro@bs.naist.jp)

Phone: +81 743 72 5420

## Financial Overview

Expenses		Income	
<b>Transportation</b>			
Flight (Group)	25117	Personal (500 pp)	10500
		Rucksack (500 pp)	10000
		Project money (SK)	749
<b>China</b>			
Train Beijing-Shanghai	1854	VLAG (175pp-13p)	2275
Public transport	737	WIMEK (500pp-7p)	3500
		LEB fonds	2500
<b>Japan</b>			
Public transport	801	Microbiology	1355
Shinkansen	1242	TIFN (1p)	500
<b>Subtotal</b>	<b>29751</b>	SBN (NBV)	4000
<b>Accommodation</b>		Middelhovenfund	500
<b>China</b>			
Beijing - 4 nights	1542	Baseclear	200
Shanghai - 2 nights	961	Carl Zeiss	250
Shanghai - 1 night	119	Laboscientific	300
<b>Japan</b>		Rubber BV	538
Osaka - 1 night	272	Thermo fisher	500
Kouto - 1 night	252	Biolegio	150
Kyoto - 4 nights	2330	Infors	250
Osaka - 2 night	554		
Tokyo - cancelation fee	278		
<b>Subtotal</b>	<b>6307</b>		
<b>Additional costs</b>			
Visa costs			
China (20p)	1183		
Japan (3p)	141		
Gifts	503		
Phone rental	83		
Bank costs	98		
<b>Subtotal</b>	<b>2009</b>		
<b>TOTAL</b>	<b>38067</b>		<b>38067</b>

## Participants and Schedule

		Dep.	Beijing						Shanghai			Osaka	Kouto	Kyoto	Nara
		15-4	16-4	17-4	18-4 Mon	19-4 Tue	20-4 We	21-4 Thu	22-4 Fri	23-4 Sat	24-4 Sun	25-4 Mon	26-4 Tue	27-4 Wed	
Name		Day 1	Day 2	Day 3	Day 4	Day 5	Day 6	Day 7	Day 8	Day 9	Day 10	Day 11	Day 12	Day 13	
Kengen	Servé				X	X	X	X	X			X	X	X	
Bielen	Bram							Q	X			X		Q	
Bosma	Elleke								X			Q	X	Q	
Dimitrov	Mauricio				Q	X		Q	X						
Ercan	Onur											Q	X	X	
Falcicchio	Pierpaolo				X	X		Q							
Heshof	Ruud				Q	X						Q	X	X	
Hugenholtz	Floor						Q	X	X						
Groot	Tom					Q	X						Q	X	
Kormelink															
Kutahya	Oylum				Q	X	Q	X							
Liebensteiner	Martin				X	Q	X								
Menschel	Sven					X			Q				Q	X	
Omony	Jimmy				X			Q	X						
Ozuolmez	Derya					Q	X		X						
Quax	Tessa				Q	X			Q			X	Q	X	
Spaans	Bas								Q			X	X	Q	
Timmers	Peer				X		Q	X							
Veuskens	Teun				X							Q	X	Q	
Visser	Michael					Q	X	X							
Westra	Edze								Q			X	X	Q	
Zhang	Jing				X		Q	X					Q		

**X = oral presentation**

**Q = taking notes**

## Report of Scientific and Travel Programme

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### Day 1: Departure from Amsterdam (Schiphol), NL - April, Frid. 15<sup>th</sup>

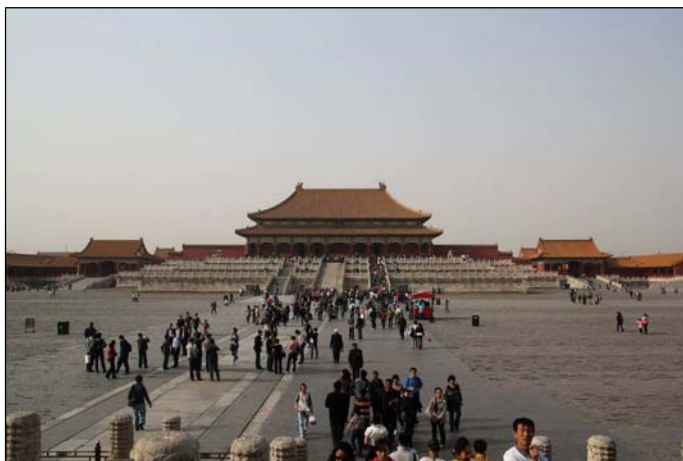
<i>Session</i>	<i>Events<sup>1</sup></i>	<i>ATOD</i>
<b>Morning</b>	<b>Meet at Schiphol at the Burger King</b>	<b>14:30</b>
	Check-in, customs etc.	
	Departure Schiphol <b>Flight KL897Q</b>	<b>17:35</b>
<b>Afternoon</b>		
<b>Evening</b>		

### Day 2: Beijing, CHINA - April, Sat. 16<sup>th</sup>

<i>Session</i>	<i>Events</i>	<i>ATOD</i>
<b>Morning</b>	Arrival Beijing Capital International Airport	<b>08:55</b>
	Travel to the Forbidden City ( <b>luggage in the bus</b> )	<b>10:30</b>
<b>Afternoon</b>	End visiting the Forbidden City	<b>17:00</b>
<b>Evening</b>	<b>Check-in hotel</b>	<b>18:00</b>

#### The Forbidden City

Lying at the center of Beijing, the Forbidden City, called Gu Gong in Chinese, was the imperial palace during the Ming and Qing dynasties. Now known as the Palace Museum, it is to the north of Tiananmen Square. Rectangular in shape, it is the world's largest palace complex and covers 74 hectares. Surrounded



by a six meter deep moat and a ten meter high wall are 9,999 rooms. The wall has a gate on each side. Opposite the Tiananmen Gate, to the north is the Gate of Divine Might (Shenwumen), which faces Jingshan Park. The distance between these two gates is 960 meters, while the distance between the gates in the east and west walls is 750 meters. There are unique and delicately structured towers on each of the four corners of the curtain wall. These afford views over both the palace and the city outside.

### Day 3: Beijing, CHINA – April, Sun. 17<sup>th</sup>

WUR office contact: 010-62118002  
wur.china@wur.nl  
www.wurchina.com

<i>Session</i>	<i>Events</i>	<i>ATOD</i>
<b>Morning</b>	Departure from the hotel	<b>09:00</b>
	Arrival at the <b>Great Wall</b>	<b>10:30</b>
<b>Afternoon</b>	Traveling back to Beijing	<b>15:30</b>
<b>Evening</b>	<b>Meeting with the Dutch Embassy</b> Venue: Room 231, Main Building of CAAS (after entering from the west gate of CAAS the building on the left hand side)	<b>17:00- 18:00</b>
	Greetings and presentation given by Dr. Dinghuan Hu, Chief representative of WUR in China	17:00
	Presentation given by Liu Zhen, sandwich phd student of Wageningen UR and now doing research with Dr. Dinghuan Hu in CAAS.	17:20
	Presentation given by Mr. Jorrit Gosens from Research center for eco-environmental sciences Chinese Academy of Sciences	17:35
	Questions	17:50
	Closure	18:00

#### The Great Wall

The Great Wall of China, one of the greatest wonders of the world, was listed as a World Heritage by UNESCO in 1987. Just like a gigantic dragon, the Great Wall winds up and down across deserts, grasslands, mountains and plateaus, stretching approximately 8,851.8 kilometers (5,500 miles) from east to west of China. With a history of more than 2000 years, some of the sections are now in ruins or have disappeared. However, it is still one of the most appealing attractions all around the world owing to its architectural grandeur and historical significance.





## Day 4: Beijing, CHINA – Peking University - April, Mon. 18<sup>th</sup>

### Prof. Dr. Xiao Lei Wu

Department of Energy and Resources Engineering, College of Engineering, Peking University

### Research areas and interests

1. Molecular microbial ecology, 2. Microbial enhanced oil recovery, 3. Environmental biotechnology, 4. Bioenergy technology

Website: <http://web5.pku.edu.cn/engineering/Faculty/facultyD/Energy/2361.htm>

### Introduction - Department of Energy and Resources Engineering:

The Department of Energy and Resources Engineering was established to address this nation's critical needs in this field by exploring the research frontier of energy and resources engineering. At this time, the Department of Energy and Resources Engineering employs 18 full-time faculty members and several part-time ones. The faculty includes both internationally and domestically recognized scholars and talented young professors.

The department has bachelor, master, and Ph.D. programs, with over 164 students currently in registration. It is leading multiple key projects funded by the "National 973 Program", "the National 863 Program", "the National Science Technology Pillar Program", and "the National Natural Science Foundation Program". An important factor of this department is an emphasis on collaborating with the government and industry in order to provide critical policy and/or technology support. The department's goal is to be a world-class research centre in the field of energy and resources, while supplying top-notch professionals to aid this country.

Website: <http://web5.pku.edu.cn/engineering/Departments/2062.htm>

Time	Session	Institution	Topic
09:00	Welcome		
09:15	<b>Prof. Dr. Xiao Lei Wu</b>	Peking University	Plenary Lecture
09:35	<b>Dr. Servé Kengen</b>	WUR	Laboratory of Microbiology (WUR) - an overview
09:55	Guo-Li Lai	Peking University	Construction and screening of metagenomic library for prospecting novel genes encoding cellulases
10:15	Jimmy Omony	WUR	GeneNet: System dynamic analysis of gene networks in fungal systems
10:35	Man Cai	Peking University	Isolation and identification of microorganisms from oil contaminated environments
<b>10:55</b>			<b>Coffee break</b>
11:15	Martin Liebensteiner	WUR	Insight in the physiology of <i>Moorella perchloratireducens</i> , a gram-positive perchlorate reducing bacterium
11:35	Peng Guo	Peking University	Micro fluidic experiment on the mechanism of microbial enhanced oil recovery
11:55	Peers Timmers	WUR	Anaerobic Methane Oxidation for Biological Sulfate & Sulfur Reduction
<b>12:15</b>			<b>Lunch</b>
<b>13:15-14:15</b>			<b>Lab. Tour</b>
14:15	Xin-Biao Wang	Peking University	Degradation of petroleum hydrocarbons and biosurfactant research of a Dietzia strain
14:35	Teun Veuskens	WUR	Application of chlorate reduction as a novel concept for the bioremediation of heavily polluted anaerobic soils
14:55	Chen Weiming	Peking University	Endophytic bacteria isolated from aquatic plant and their potential functions for removal of organic pollutants
<b>15:15</b>			<b>Coffee break</b>
15:35	Pierpaolo Falcicchio	WUR	C-C bond synthesis by thermophilic aldolases
15:55	Sheng-Hua Gu	Peking University	The gut microbiota is a therapeutic target of hyperlipidemia
16:15	Jing Zhang	WUR	Dynamics of early microbial colonisation in gastrointestinal tract of pig
<b>16:35 - 18:00</b>	<b>Poster Session</b>		
18:00	Closure		

## **Report Day 4**

Laboratory of microbiology and biotechnology have been focused on three main fields: petroleum and environmental microbiology and biotechnology; biomass transformation and methanogenesis; and human gut microbiology and microbiome. Additionally they also have a pilot plant for research applications. They work both at the microorganism and community levels. At the microorganism level, the focus is mostly given to the culturability and the metabolism in terms of application of microbial function. At the community level, they investigate the structure and the functions of the microbial community, response of the community to environmental changes and stresses, community evolution, fate and behaviour of the microbial population. Moreover they manipulate the microbial processes by introducing microbial consortium, adjusting nutrients, applying different environmental factors and they try to link the community structure to functions.



### **Summaries of the talks given by our host:**

Guo-Li Lai, Ph.D. student

#### **Construction and screening of metagenomic library for prospecting novel genes encoding cellulases**

Guo is investigating the novel microbial cellulases for butyric acid and bioethanol production. They use metagenomics approach to isolate novel genes encoding cellulases with industrially relevant characteristics from extreme environments like soda-lakes, rabbit cecum, rumens, and non-extreme soils. The environmental samples were used as inoculation material in dry anaerobic digestion system. From each sample, 16S rRNA clone libraries were prepared to investigate the phylogenetic diversity, and T-RFLP was used to investigate the community structure. Additionally geochip and functional gene arrays were used to find the metabolic potential of community and metagenome libraries were constructed for functional gene screening.

Man Cai, Ph.D. student

#### **Isolation and identification of microorganisms from oil contaminated environments**

Man is working on the bioremediation of polluted water and soil contaminated with crude oil and petroleum. Samples were taken from the Shengli oil field, near the Yellow sea. They try to isolate different bacteria that are able to degrade oil, using different media and conditions. Identification of the oil degrading bacteria was done because these isolates could potentially be used for the treatment of oil contaminated sites and enhancement of oil recovery. They are also interested in the engineering the

communities for oil recovery by investigating the community structure and functional activity. He has 48 isolates which had 16S rRNA gene sequenced. The isolates belong to 17 genera and there are several novel species among the isolates. Most of them are related to the Alphaproteobacteria. The fatty acid composition of one of the novel species resembles that of Rhodobacter. They named this new species Polymorphum gilvum.

Peng Guo, Ph.D. student

**Micro fluidic experiment on the mechanism of microbial enhanced oil recovery**

Peng works on micro-fluidic model system for a better oil recovery from porous sandstones. In the normal process, the big oil droplets are stacked in porous sandstones and cannot join to the flow because of narrow pore throat. However within the model system, microorganisms adhere to the big oil droplets in the pores causing them to release from the rock and break into smaller droplets. The formation of biofilms is a major interest. In the new set-up using a microfluid system within a microscope they are able to image a water oil interface. At this stage they are able to get pictures from the oil water interface, but the growth of the bacteria is extremely slow, hampering experiments. Another limitation is the low similarity with the original porous media from which the bacteria were isolated.

Xin-Biao Wang, Ph.D. student

**Degradation of petroleum hydrocarbons and biosurfactant research of a Dietzia strain**

Microbial enhanced oil recovery (MEOR) is the 4<sup>th</sup> generation crude oil recovery technology and makes use of active microorganisms or nutrient injections to degrade the big oil droplets and to enhance the recovery. Xin tries to isolate oil-degrading strains from water flow of oil field for this purpose. Samples were taken from the Daqing oilfield. The isolated strains are checked for degradation of hydrocarbons, n-alkanes, and crude oil and characterized. Amongst the isolated, two homologues of AlkB-rubredoxin fused protein were identified. AlkBr1 expression was induced when grown on C8-C32 alkanes. He showed that the fused rubredoxin domain of AlkBr1 was essential for the hydroxylation of long-chain n-alkanes.

Chen Weiming, Ph.D. student

**Endophytic bacteria isolated from aquatic plant and their potential functions for removal of organic pollutants**

The modern bioremediation technologies are relying on solar energy, applied in situ, less expensive and have better public acceptance. Plants, microorganisms and plant-microbe combinations are used for this purpose. Chen is working on the capabilities of endophytic bacteria, which is a plant associated microorganism, on remediation. He is specifically interested in the microorganisms living on aquatic plants. He took samples on the Guanting Reservoir, which was the major source of tap water for Beijing before 1997, when other sources were searched for this purpose, due to pollution of this reservoir. 21 isolates from different parts of the plants were characterized. Most of them belonging to the genera Pseudomonas and Enterobacter. Some of them are capable of nitrogen fixation. The difference with bacterial isolated from land plants in oil contaminated sites is that there mainly Alphaproteobacteria are found, while in the Guanting Reservoir aquatic plants mainly Gammaproteobacteria were detected.

Sheng-Hua Gu, Ph.D. student

**The gut microbiota is a therapeutic target of hyperlipidemia**

The gut microbiota functions as protection against pathogens, acts in developing homeostasis of immune system, helps metabolism with the fermentation of non-digestible dietary residues and so on. Within this context Sheng investigates the effect of Berberine, a chinese herb, on human gut microflora, and try to find if human gut microbiota has any effect on the function of berberine. Berberine is determined to function as antibiotic, antitumor, cardio protective, anti-diabetes, and lipid-lowering. The hypolipidemic effect of BBR was found to be generated in the gastrointestinal tract. Hamsters are used as model organism and berberine is administered intragastrically and intraperitoneally. The influence of berberine on a high fat diet is studied with this model organism.

**Day 5: Beijing, CHINA – Institute of Microbiology - Chinese Academy of Science - April, Tue 19<sup>th</sup>**

The Institute of Microbiology, Chinese Academy of Sciences (IMCAS) was founded on December 3, 1958. It is a national comprehensive research institution that performs a wide spectrum of basic and applied research in the field of microbiology. IMCAS is committed to three missions: basic and applied research targeting national strategic needs and world-class frontier sciences, thinking tank for the government, and graduate student training. Based on the long term goals of the CAS's Knowledge Innovation Project, which the IMCAS joined in 2001, it has established five key laboratories or departments, namely State Key Laboratory of Microbial Resources, CAS Key Laboratory of Systematic Mycology and Lichenology, Department of Industrial Microbiology and Biotechnology, Department of Agricultural Microbiology & Biotechnology, and Department of Pathogenic Microbiology and Immunology.

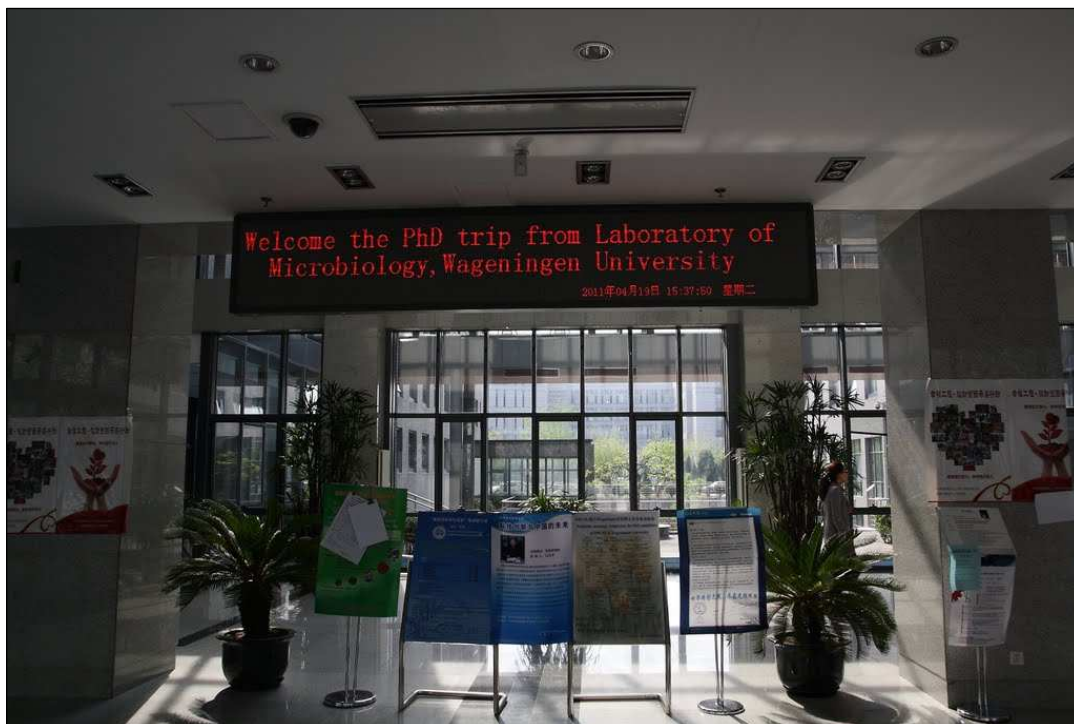
The institute harbors supporting centers/platforms to serve scientific researches, i.e. the culture collection center, the microbial analytical center, the center for technology and information, and the high-throughput screening platform. The culture collection center harbors the largest fungal herbarium in Asia with over 400,000 specimens, and the biggest culture collection in China, with 17,000 isolates of microorganisms. The institute offers a broad range of academic programs that lead to postgraduate degrees. Currently, there are 314 graduate students enrolled in various programs toward doctoral (198) and master's degrees (116).

Three national academic societies, Chinese Society of Microbiology, the Mycological Society of China, and Chinese Society of Biotechnology, are affiliated to the institute. IMCAS is also the seat of editorial offices for four journals, *Acta Microbiologica Sinica*, *Chinese Journal of Biotechnology*, *Microbiology*, and *Mycosystema*. The Institute has a specialized library with a collection of more than 60,000 books.

As the national leading research institution in the field of microbiology, the IMCAS is committed to the advancement of science and technology. During the past 40 years since its establishment, the IMCAS has been honored for more than 170 national and ministry-acknowledged scientific awards, among them, 29 awards were from the national government. More than 3,000 scientific papers and 100 monographs were published, of which over one third were published on Science Citation Index journals, including "Science", "Cell", etc.

The institute is committed to serving national and international needs. This commitment is reflected in research and practical activities located off campus in communities throughout China. It is realized also through worldwide research cooperation, training ex-changes, and student exchange programs. The IMCAS has established a network of international collaborations that involves scientists from the US, Canada, Australia, Japan, Singapore, Russia, United Kingdom, France and other European countries. The international orientation of the institute is an indispensable precondition for its scientific excellence and competitiveness. Website: <http://english.im.cas.cn/>

<b>Time</b>	<b>Session</b>	<b>Institution</b>	<b>Topic</b>
09:00	Welcome		
09:10	<b>Prof. Dr. Li Huang</b> (Executive deputy director)	Institute of Microbiology (Chinese Academy of Science)	Institute of Microbiology (CAS) - an overview
09:30	<b>Dr. Servé Kengen</b>	Wageningen University	Laboratory of Microbiology (WUR) - an overview
09:50	Jinjing Wang	Institute of Microbiology (Chinese Academy of Science)	Oleaginous yeast <i>Yarrowia lipolytica</i> mutants with a disrupted fatty acyl-CoA synthetase gene accumulate saturated fatty acid
10:10	Ruud Heshof	Wageningen University	Novel enzyme tools for production of functional oleochemicals from unsaturated lipids
10:30	Cheng Lu	Institute of Microbiology (Chinese Academy of Science)	Cryptic antibiotic clusters of streptomycetes and their expression
<b>10:50</b>	<b>Coffee break</b>		
11:10	Pierpaolo Falcicchio	Wageningen University	C-C bond synthesis by thermophilic aldolases
11:30	Gang Li	Institute of Microbiology (Chinese Academy of Science)	Mechanism of Influenza virus infection
11:50	Tessa Quax	Wageningen University	Archaeal virus-host interactions
<b>12:10</b>	<b>Lunch</b>		
<b>13:15-14:15</b>	<b>Lab. Tour</b>		
14:15	Na Wu	Institute of Microbiology (Chinese Academy of Science)	The association between the colon microbes and colorectal cancer
14:35	Mauricio Rocha Dimitrov	Wageningen University	Adaptive capacity and functionality of multitrophic aquatic ecosystems
14:55	Zijuan Chen	Institute of Microbiology (Chinese Academy of Science)	Cold adaptation of <i>Methanobrevibacter</i> psychrophilic R15, a psychrophilic archaea from Tibetan
<b>15:15</b>	<b>Coffee break</b>		
15:35	Oylum Kutahya	Wageningen University	The population dynamics of mixed Gouda cheese starter culture
16:15	Sven Menschel	Wageningen University	Peptide utilization in <i>Lactococcus lactis</i>
<b>16:15-17:15</b>	<b>Lab Tour</b>		
17:30-17:45	Photo!		
18:00	Closure		
Evening	Dinner		



### ***Report Day 5***

The Institute of Microbiology, Chinese Academy of Sciences (IMCAS) was founded on December 3, 1958. It was a fusion of Beijing Laboratory of Microbiology, CAS, and the Institute of Applied Mycology, CAS. Resource subjects of the institute are: microbial ecology, fermentation, microbial enzymology, molecular virology, and molecular microbial genetics. IMCAS has 62 different research groups, around 430 staff members, including 5 CAS academicians, 94 professors and associate professors, and 8 postdoctoral research fellows. They have 166 PhD students and 90 Msc. students.

The IMCAS has the equipment for sequencing to facilitate strain identification of their own isolates and that of others. The institute also has the storage capacity for a large amount of isolated strains. The application orientated aim of the IMCAS resulted in the development of a antimicrobial product called 'nizin'. In addition, it also resulted in the collaboration of IMCAS with several companies (examples: DSM; NESTEC, Switzerland; Shell, UK; and domestic companies for the optimization of fermentation processes) and universities throughout the world.

#### Summaries of the talks given by our host:

Jinjing Wang

##### **Oleaginous yeast *Yarrowia lipolytica* mutants with a disrupted fatty acyl-CoA synthetase gene accumulate saturated fatty acid**

The focus of this research is lipid accumulating yeasts and their potential use for biofuel production. Yeast can accumulate lipids between 40-70% of their cell composition. A reaction that converts fatty acid to fatty acyl-CoA is catalysed by the enzyme acyl-CoA synthetase. Subsequently, the fatty acyl-CoA is normally oxidized to CoA and CO<sub>2</sub>. However, Jinjing Wang created a acyl-CoA synthetase mutant in order to observe the effect.

She used a pTAC plasmid for creating the mutant. The insertion of the plasmid makes the mutants more resistant to relative high amounts of CuSO<sub>4</sub>. No additional antibiotics are necessary for selection. Although the mutants have a minor decrease in growth (probably due to the treatment), they have an increased saturated:unsaturated fatty acid ratio and increased total lipid content in the cell. Moreover, the synthetase appears to be involved in fatty acid transportation. However, the mutant still has a small synthetase activity. The reason for this is yet unknown.

Cheng Lu

##### **Cryptic antibiotic clusters of *Streptomyces* and their expression**

This study is driven by the search for new antibiotic substances. Genome information was used to find new antibiotics. They looked at the gene cluster of nikkomycin and disrupted one gene in this cluster in order to completely inhibit the synthesis of nikkomycin. The aim is to stimulate the organism in producing an alternative antibiotic while nikkomycin synthesis is inhibited. Therefore, wild type (WT) and mutant were compared in the synthesis of products.

Mutants were selected by colour differences. Mutants were white while the WT was grey. A candidate compound was found which was able to inhibit microbial growth. However, identification of the compound has yet to be done and the production of the compound by the organism is low. If the candidate compound turns out to be a new antibiotic production optimization is required.

Gang Li

##### **Mechanism of influenza virus infection**

The heat shock protein 70 (Hsp 70) plays an important role in the defending the cell from the influenza virus. Hsp70 can interact with viral polymerase subunits PB1 and 2, but not PA. Moreover, Hsp70 was found in the cytoplasm and is transported to the nucleus when the cell is infected by the influenza virus. Hsp70 is able to affect the polymerase by its interaction. The polymerase complex is disrupted resulting in decreased viral factors NP and M1 (*in vitro*).

*In vivo* studies were performed on BALB/c mice, where Hsp70 was infused with tat protein. The infected mice were treated once a day with Hsp70-tat. Infected mice that were given the treatment of Hsp70-tat showed less infection and had a prolonged survival rate compared with the controls. The potential of Hsp70 as an anti-malaria drug is therefore apparent.

Na Wu

##### **Multiple Displacement Amplification for Detection of *Mycobacterium tuberculosis* in Sputum Samples**

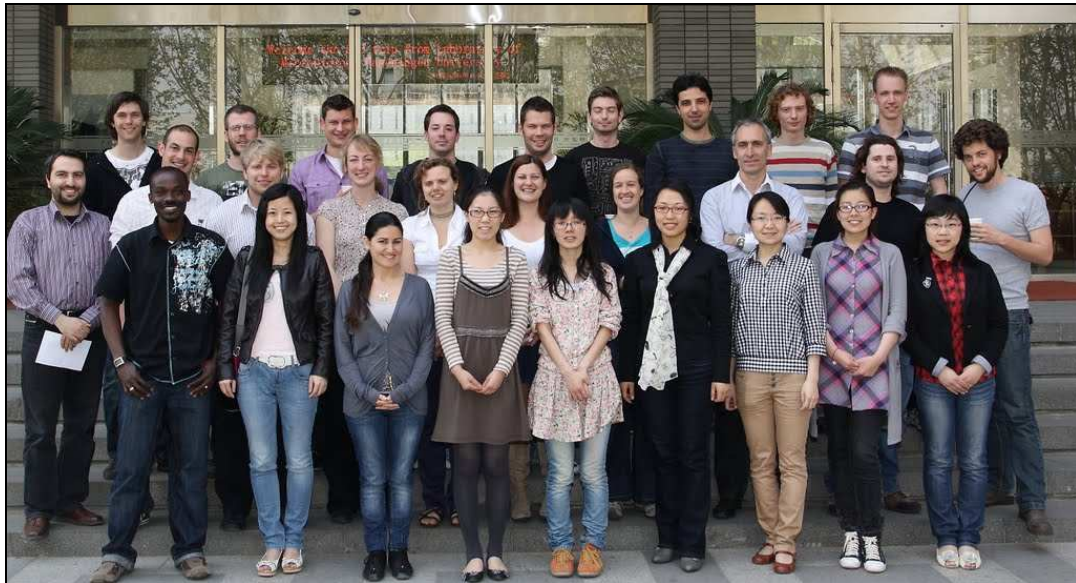
Within this study the multiple displacement amplification PCR (MDA-PCR) is compared with a normal PCR approach on the basis of its applicability for determining tuberculosis infections. MDA-PCR was found to be more specific. For both screening methods healthy patients had a negative test result, indicating that none of the two approaches is producing false positives.

Zijuan Chen

**Cold adaptation of *Methanolobus psychrophilic* R15, a psychrophilic archaea from Tibetan plateau**

In order to study the cold adaptation of the *Methanolobus psychrophilus*, a strain R15, isolated from the Zoige wetlands in China was sequenced (size: 3Mb, 46% GC content and 3096 predicted proteins). Rna sequences were used to describe the gene expression. The dominant COG expression was altered with the change in temperature – 66% of genes were differently expressed (18°C vs. 4°C)

Heat shock proteins and two component systems (TCS) appeared to have an increased expression in cold conditions, indicating they are important in cold adaptations. Chemotaxis proteins are typical TCS and were found to be upregulated in 4°C compared to 18°C. Moreover, flagella synthesis genes were also upregulated. Movement of this organism appears to be important when temperatures decrease.



**Day 6: Beijing, CHINA – China Agricultural University - April, Wed. 20<sup>th</sup>**

**Prof. Dr. Yahai Lu**

Lab of Microbial Ecology, College of Resources and Environmental Sciences, China Agricultural University

The **Lab of Molecular Ecology** – MPI Partner Group, China Agricultural University (CAU), was co-founded in Sep. 2006 by the Max Planck Institute for Terrestrial Microbiology of Marburg and the Key Laboratory of Plant and Soil Interactions of the Ministry of Education of China (MOE), which is affiliated to the College of Resources and Environmental Sciences at CAU. The faculty of the lab consists of one professor, chair professor, assistant professor and post doctor respectively, besides eight Ph.D. candidates and seven M.S. candidates. **Prof. Yahai Lu**, the **director of the lab** and the obtainer of the National Outstanding Youth Funds, was awarded both the title of "New Century Excellent Talents" and "Changjiang Scholar" by the MOE in 2006.

The main topic of the lab is the microbial mechanisms of the environmental processes, which includes:

1. Molecular microbial ecology
2. Microbial diversity and their ecological functions in soil.
3. The microbial mechanisms of the carbon and nitrogen cycles.
4. Microbial remediation.

Date	Session	Institution	Topic
April, Wed. 20 <sup>th</sup>	<b>China Agricultural University</b>		
9:00	Welcome		
9:15	<b>Prof. Dr. Yahai Lu</b>	CAU	Laboratory of Molecular Ecology (CAU) - an overview
9:35	<b>Dr. Servé Kengen</b>	WUR	Laboratory of Microbiology (WUR) - an overview
9:55	Yuan Xu	CAU	Using <sup>13</sup> CH <sub>4</sub> to detect <sup>13</sup> C-using bacteria and their related nitrogen transformation microbes after nitrogen fertilization in rice soil microcosm
10:15	Tom Groot Kormelink	WUR	Comparative genomics of regulatory networks in Gram-positive bacteria
10:35	Chen Zhang	CAU	Microbial Structure and Function of Anaerobic Bioreactor Sludges
<b>10:55</b>	<b>Coffee break</b>		
11:15	Martin Liebensteiner	WUR	Insight in the physiology of Moorella perchloratireducens, a gram-positive perchlorate reducing bacterium
11:35	Lei Cheng	CAU	Molecular characterization of hexadecane-degrading methanogenic consortium
11:55	Derya Ozuolmez	WUR	Microbial interactions in marine anoxic sediments: competition or teamwork?
<b>12:15</b>	<b>Lunch</b>		
<b>13:45</b>	Zhe Lv	CAU	Isolation and characterization of RC-I methanogens from rice soils
13:55	Michael Visser	WUR	Syntrophic growth of anaerobic communities using C1 substrates
<b>14:15-14:45</b>	<b>Lab. Tour</b>		
14:45 - 15:00	Photo!		
15:00	Closure		
following	<b>Free time &amp; <u>transfer to the train station (public transport)</u></b>		
20:15	check-in at the train station Beijing South		
21:21	departure from Beijing South night bullet train D321 (Beijing-Shanghai)		

## **Report Day 6**

China Agricultural University (CAU) has 2 campuses, 1049 professors in its team and giving education to 14488 undergraduate, and 5420 graduate students. There are 6 microbiological labs at CAU: Biological Science, Agronomy and Agrobiotechnology, Animal Science and Technology, Veterinary Medicine, Food science and nutritional engineering and the lab of Molecular Ecology. This lab is quite new, it was started by Prof Yahai Lu in 2004. The lab was supported by MPI Bremen in 2006. Prof Yahai Lu was awarded with the Changjiang Scholar by the Ministry of Education in China in 2007. The lab of Molecular Ecology in the year 2011 consists of 1 professor, 1 adjunct professor, 1 associate professor, 1 assistant professor, 8 PhD, and 8 MS students. The research topics of the lab are microbial remediation, carbon and nitrogen cycles, and microbial ecology. They mostly work on the methane production and emission (oxidation) in the rice fields via microbial transformations. The reason is that China produces an amount of rice that can feed around half of the population of the planet. The downside of this is the methane production in these rice fields which contributes greatly to the global warming (around 10%). Understanding the ecosystem can reduce methane emission eventually. The lab is interested in all microbial functional groups that contribute to this methanogenesis (i.e. fermenting, syntrophic and methanogenic microorganisms). They use  $^{13}\text{CH}_4$  labelling in the field, and stable isotope probing (SIP) for quantification and characterization of microbial consortia involving the process. They also apply SIP-metagenomics to understand the ecophysiology and interactions. They work on methanotrophs in rice rhizosphere with this combined SIP-metagenomics approach. They also work with a GMO rice plant that has higher rice yield but also higher methanogenesis and AOM activity.

### **Summaries of the talks given by our host:**

Yuan Xu:

#### **Using $^{13}\text{CH}_4$ to detect $^{13}\text{C}$ -using bacteria and their related nitrogen transformation microbes after nitrogen fertilization in rice soil microcosm**

Crop residues, photosynthetic aquatic biomass and root exudates make up the organic carbon available for methane production via microbial transformation. The methane produced in rice rhizosphere is either diffused to the atmosphere through the aerenchyma or oxidized. Nitrogen fertilization enhances rice production but ammonium also enhances aerobic methane oxidation. Yuan hypothesized that soluble organic compounds and carbon dioxide produced during methanogenesis is shared via trophic interactions with nitrifiers and dinitrifiers. They took samples from a rice field in Hangzhou, China. They investigate the interactions based on functional gene screening by QPCR and they found out that nitrogen stimulates the methane oxidation with predominately Methanococcaceae as methanogen and hydromicrobium and nitrosomonadales as the responsible bacteria for respectively denitrification and ammonium oxidation.

Chen Zhang

#### **Microbial Structure and Function of Anaerobic Bioreactor Sludges**

Anaerobic degradation of complex organic matter involves three steps with alternative pathways: First the degradation of polymers to fatty acids, alcohol and lactate, then the conversion of these degradation products to  $\text{C}_1$  compounds and acetate, and finally methane and carbon dioxide production. They investigate the effect of the temperature range on methane production on two mixed inocula - pig manure and sludge, and chicken manure and sludge- in anaerobic reactors. Population dynamics, GC, and HPLC results of cultivations at 35C and 55C showed that chicken manure sample adapted to a high temperature by the succession of the archaeal and bacterial community. The archaeal community of the pig manure sample didn't change significantly at high temperature indicating another adaptation mechanism. The GC and HPLC data also shows that they use different pathways for methane production at 35C and 55C. The population dynamics data of two samples show different adaptation strategies even at the same temperature.

Lei Cheng:

#### **Physiological and Molecular Characterization of hexadecane-degrading methanogenic consortium**

At the moment there is a low petroleum recovery and people are looking into better recovery methods as petroleum consumption increases every year. Methanogenic enrichment cultures of crude oil degradation studies show that archaeal and bacterial communities can degrade hydrocarbons to methane. The hydrocarbon degradation requires acetogens in the first degradation of hexadecanes to acetate and carbon dioxide, and requires methanogens for further decomposition to methane. Which types involved and especially initiated the hydrocarbon degradation remains unknown. Lei studies hydrocarbon degradation with enrichment cultures in two steps. First she prepared a pre-enrichment culture with a lag and growth phase of 2-3 months where already 75% of the hexadecane was degraded. Then she made a second transfer where less hexadecane was degraded (around 25%) In the third transfer, a larger inoculum was used which was incubated at 35 and 55 degrees Celsius. Community analysis was based on clone libraries on each transfer. Phylogenetic affiliations and numbers of sequences retrieved from pyrosequencing were used to quantify the relative abundances. In this second transfer, the community of methanogenic hexadecane degradation contain both archaeal and bacterial T-RFs with a larger diversity coming from bacteria. Anaerolineaceae species were dominant on the first pre-enrichment culture, but decreased in 2<sup>nd</sup> and 3<sup>rd</sup> transfers. Of the methanogens, Methanosaeta, Methanoculleus and Methanogenium dominated in the enrichments. Responsible hexadecane degraders were concluded to be acetoclastic and hydrogenotrophic Archaea.

Zhe Lv

#### **Isolation and Characterization of RC-1 methanogens from rice soils**

From rice soils three enrichments were obtained: HZ254, HZ393 and HZ713. All were incubated at 50 degrees Celsius with hydrogen and carbon dioxide in the gasphase. By cloning and sequencing the phylogenetic relationships need to be determined. The focus of this presentation was on the RC-1 methanogen from the enrichment HZ254. In this enrichment only archaeal DNA was detected. The 16S rRNA gene of RC-1 was sequenced. The sequenced gene fragment of 258 bp, shows the highest homology, 91 %, with the Methanocellales. An mcrA functional gene tree also showed that it clustered in the 'rice cluster 1' (Methanocellales). Some characteristics of this strain:

- NaCl Range: 0-5 g/L, Optimum: 0-1 g/L
- Acetate required, Yeast extract not required but stimulating growth
- Resist lysis at 0-0.5% but become fragile at 0.5%
- SDS%>=1%: Intact cell hardly observed
- Flagellum-like structures were present but no motility observed
- Temperature range 37-60 degrees Celsius
- pH optimum at 6.8 (at 55 °C)
- Substrate utilization: formate 40mM. others 10-20mM
  - Growth: H<sub>2</sub>/CO<sub>2</sub> +
  - No Growth: Formate, Acetate, Propionate Butyrate, Pyruvate, Lactate, Methanol, Ethanol, Propanol, Butanol, Cyclopentanol, Glycerol, Methylamine, Trimethylamine
- Antibiotics(100ug mL<sup>-1</sup>)
  - Growth: Penicillin-G, Kanamycin, Ampicillin
  - No growth: Apramycin, Rifamycin, Chloramphenicol, Neomycin

With this information a novel species is proposed: *Methanocella conradii* HZ254, named after Ralf Conrad.

**1. National Collaborations:**

Nanjing, Chinese Academy of Science

Xiaolei Wu's lab, Peking University (for methane production and oxidation)

Prof. Yahai Lu Lab, China Agricultural University

**2. International Collaborations:**

Max-Planck Institute, Terrestrial Microbiology Group

Xiaolei Wu's lab, Peking University

**3. Industrial Collaborations:**

China Petrochemical Corporation (Sinopec Group)

China National Petroleum Corporation (CNPC)



## **Day 7: Shanghai, CHINA – School of Life Sciences and Technology of Shanghai Jiao Tong University**

### **Prof. Dr. Liping Zhao**

Laboratory of Mol. Microbial Ecology & Ecogenomics, Jiao Tong University

### **Dr. Xiaojun Zhang**

Key Laboratory of Microbial Metabolism, College of Life Science and Biotechnology, Jiao Tong University

### **Introduction:**

School of Life Sciences and Biotechnology ( SLSB ) of Shanghai Jiao Tong University (SJTU) was jointly established by SJTU and Chinese Academy of Sciences (Shanghai Branch) in February 1997 on basis of the former Departments of Biological Science and Technology (established in 1986) and Biomedical Engineering (established in 1979). After more than ten years of rapid development, the School has earned high reputation and significant recognition in several research areas in the world including Biochemistry and Molecular Biology, Genetics, Microbiology, Biomedical Engineering and Bioengineering. The school has acquired substantial education and research resources.

### **Organization:**

#### **Departments:**

Department of Bioscience and Biotechnology  
Department of Bioengineering  
Department of Biomedical Engineering  
Department of Bioinformatics and Biostatistics

#### **Institutes:**

Bio-X Center  
Institute of Neuroscience

#### **Training Center:**

The Experimental Teaching Center For Life Science

### **Key Laboratory in the School of Life Science and Biotechnology:**

#### **Key Laboratory of Microbial Metabolism, Ministry of Education**

Headed by Professor Deng Zixin, academician of the Chinese Academy of Sciences, this lab is dedicated to build a world-class scientific and technological innovation platform for microbial drugs innovation and microbial strain improvement. Currently, this lab has become an important base of Chinese microbiology, especially in the fundamental and applied field of microbial metabolism.

**Research interests:** anabolism, catabolism and metabolic interactions.

#### **Key Laboratory of Genetics of Developmental and Neuropsychiatric, Ministry of Education**

Headed by Professor He Lin, academician of the Chinese Academy of Sciences, this lab is focusing on neuropsychiatric disorders and other genetic diseases. Also the lab is dedicated to reproductive, developmental and genetic mechanisms in human, animal and plants, targeting to provide both theoretical and technical basis for early diagnosis and individual treatment of human disease, as well as the solution to food security.

**Research interests:** molecular mechanism of human's Neuropsychiatric Disorders, pathogenesis with the interaction of nutrition, environmental and genetic factors, genetic development and molecular mechanism of major bone diseases etc.

### National Testing Center for Molecular Characterizations of GMOs

Headed by Professor Zhang Dabing, this center is dedicated to reveal the molecular characterizations of genetically modified organisms (GMOs) and develop methods and standards for testing GMOs.

**Research interests:** new methods and standards on characterizing GMOs, and database and reference materials for GMO analysis.

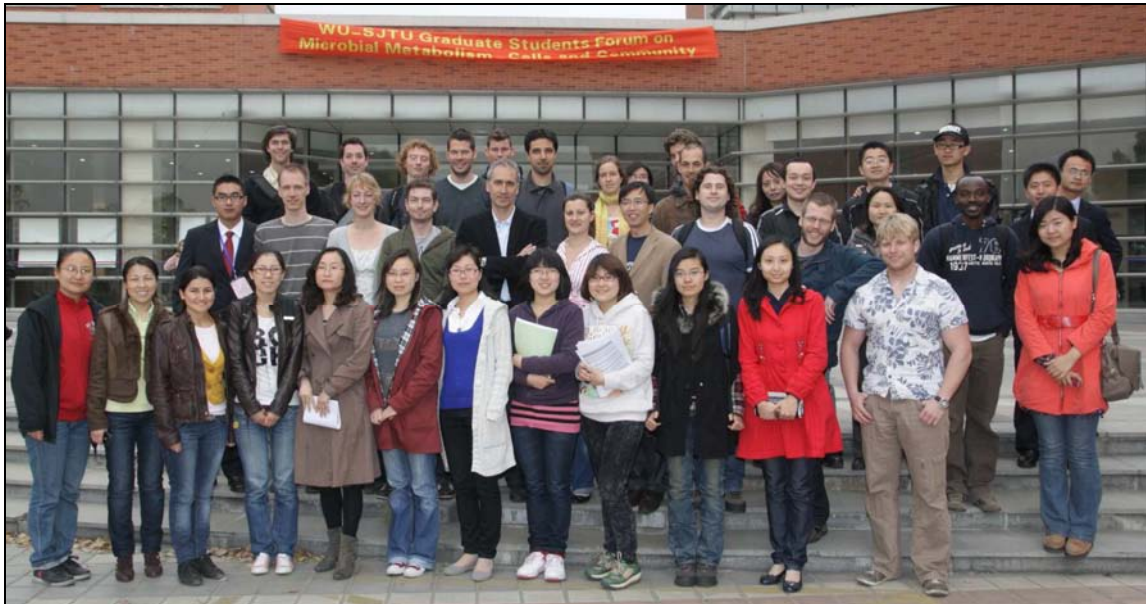
Date	Session	Institution	Topic
<b>April, Thu. 21<sup>th</sup></b>	<b>Shanghai Jiao Tong University, School of Life Science and Biotechnology</b>		
7:15	arrival at Hongqiao Station Shanghai night bullet train D321 (Beijing - Shanghai)		
7:15-9:15	bustransfer to Shanghai Jiao Tong University (SJTU), School of Life Science and Biotechnology, Key laboratory of MOE on Microbial metabolism		
9:15	Welcome		
9:30	<b>Prof. Dr. Liping Zhao</b>	SJTU	Shanghai Center for Systems Biomedicine (SJTU) - an overview
9:50	<b>Ass. Prof. Dr. Servé Kengen</b>	WUR	Laboratory of Microbiology (WUR) - an overview
10:10	SJTU speaker 1 : Tingting Wang	SJTU	Structural Comparison of Gut Microbiota between Patients with Colorectal Cancer and Healthy Volunteers
10:30	Coffee break		
10:50	WUR Speaker 1: Floor Hugenholtz	WUR	Gut microbiomics of SCFA metabolism
11:10	SJTU speaker 2: Xinwei Yang	SJTU	Ferric uptake regulator Fur plays roles in regulating anaerobic respiration in <i>Shewanella piezotolerans</i> WP3
11:30	WUR Speaker 2: Jing Zhang	WUR	Dynamics of early microbial colonization in gastrointestinal tract of pig
11:50	SJTU speaker 3: Zhonghui Gai	SJTU	Characterization of carbazole catabolism genes from <i>Sphingobium yanoikuyae</i> XLDN2-5
12:10-13:10	Lunch		
13:25-14:25	Lab. Tour		
14:25	WUR Speaker 3: Michael Visser	WUR	Syntrophic growth of anaerobic communities using C1 substrates
14:45	SJTU speaker 4: Hongyan Ren	SJTU	Bacterial community comparison of injection water and surrounding production wells in a long-term water flooding petroleum reservoir
15:05	WUR Speaker 4: Peer Timmers	WUR	Anaerobic Methane Oxidation for Biological Sulfate & Sulfur Reduction
15:25	SJTU speaker 5: Ying Chen	SJTU	Genetic and Functional characterization of a simulated, active AOM-SR consortia
15:45	Coffee break		
16:05	WUR speaker 5: Oylum Kutahya	WUR	The population dynamics of mixed Gouda cheese starter culture
16:25	SJTU speaker 6: Fei Su	SJTU	Comparative genome analysis of the thermophilic strain, <i>Bacillus coagulans</i> 2-6: An excellent producer of platform chemicals
16:45-17:45	Poster Session		
17:45	Closure		
18:00	dinner & get-together		
21:00	bus transfer & late check-in		
			Hope hotel (500 Zhaojiabang Road, Shanghai China)

## **Report Day 7**

### **WU-SJTU PhD Students Forum on Microbial Metabolism – Cells and Community**

School of Life Sciences and Biotechnology (SLSB) of Shanghai Jiao Tong University (SJTU) was jointly established by SJTU and Chinese Academy of Sciences (Shanghai Branch) in February 1997 on basis of the former Departments of Biological Science and Technology (established in 1986) and Biomedical Engineering (established in 1979). The school has the following departments, centers and institutes: Bioscience & Biotechnology, Bioengineering, Biomedical Engineering, Bioinformatics, Center of Experimental Teaching for Life Science, Bio-X Center and Institute of Neuroscience. SLSB has a proficient and competent team of teaching and research with about 180 members including 47 professors and 62 associate professors. More than 1,200 students are currently enrolled in SLSB, being 326 master students and 284 Ph.D. students. International exchange and collaboration are taken very seriously and are considered very important to improve the level and quality of education and broaden an international perspective for students. Therefore, the goal of SLSB regarding international exchange and collaborations is, by 2020, to have at least 50% of its students with an international experience. After more than ten years of rapid development, the School has earned high reputation and significant recognition in several research areas in the world including Biochemistry and Molecular Biology, Genetics, Microbiology, Biomedical Engineering and Bioengineering.

The whole program was well organized and distributed during the day. Some Ph.D. students from both sides had an opportunity to present their work, but there was also a poster session where all Ph.D. students from Wageningen University had to present their poster. Many posters from SJTU were presented as well. The WU group had also the opportunity to visit different facilities from different research groups. The day ended with a warm and pleasant “part” organized by the SJTU Students Union in order to provide a nice atmosphere for interaction between the Chinese and foreign people.



#### Summaries of the talks given by our host:

SJTU speaker 1 : Tingting Wang

##### **Structural Comparison of Gut Microbiota between Patients with Colorectal Cancer and Healthy Volunteers**

This project focuses on the effect of colorectal cancer (CRC) on the gut microbial community. Colorectal cancer is considered to be a rising social problem in China. CRC takes about 10-20 year to develop CRC. The presents of aberrant crypt foci (ACF) can be the first signs of CRC development. Difference in the gut microbial composition was studied in a ACF rat model. Rats (12 males) were treated either with Dimethylhydrazine (DMH) saline, to induce CRC, or a saline solution as control. Fresh faeces were collected 1,3 and 7 weeks after induction. Samples were analysed by PCR (16S rRNA V3 region), DGGE, PCA 454 Pyro sequencing. Key variables were found using PLS – DA model. The relative contribution of the *Ruminococcus* genus appeared to be higher in precolorectal lesions with respect to the control. Additionally a microbiome wide study was performed on male CRC patients. Data was analysed using PCA and MANOVA test redundancy analysis showed some OTU's to be significant. A reduction in the butyrate producing bacteria was reveal (16S rRNA PCR).

SJTU speaker 2: Xinwei Yang

##### **Ferric uptake regulator Fur plays roles in regulating anaerobic respiration in *Shewanella piezotolerans* WP3**

In this study the role of the pleiotropic transcription factor Fur is investigated. Fur is involved, amongst others, in the regulation of iron homeostasis and redox stress response. It can act as a negative regulator (direct) and/or as positive regulator (indirectly). A Fur deletion mutant was used to investigate the regulatory mechanisms of Fur on the regulation of anaerobic respiration by *S.piezotolerans*. Fur deletion mutant showed an up-regulation of iron acquisition and utilization genes, additionally Fur deletion mutants showed low cytochrome c levels.

SJTU speaker 3: Yang Lu

##### **Purification and Crystallization of Flavin Reductase Involved in Desulfurization by *Mycobacterium goodii* X7B**

This study focuses on the biodesulfurization (BDS) of dibenzothiophene (DBT). DBTs are abundant in crude oil. BDS, using microorganisms, promises to be a more cost effective alternative compared to Hydrodesulfurization (HDS), a widely spread but costly method used in refineries to desulfurize crude oil. The oxidative cleavage of the C-S bonds of DBT is by Flavin reductates (DszD) is the first enzyme step in the BDS of DBT. In this Study the DszD gene of *M.goodii* X7B was amplified by PCR and cloned the pEt24a Vector. The vector was cloned in the E.coli expression strain BL21 (DE3). Expression of DszD was induced by IPTG, sub-sequentially cells were cooled to 22°C, to prevent inclusion bodies. The enzyme was purified by size exclusion chromatography. SDS-PAGE and enzyme assay conferment the proper expression of an active enzyme. Crystallisation formation is still in progress, finally crystals will be sent to the Shanghai Synchrotron Radiation facility, China.

SJTU speaker 4 : Hongyan Ren

##### **Bacterial community comparison of injection water and surrounding production wells in a long-term water flooding petroleum reservoir.**

This project focuses on the microbial enhanced oil recovery( MOER) of existing oil reservoirs and in particular in the Shengli oil field, situated on the Yellow river delta in the Shandong province. This oil field that is the second of China is deep around 1200 m and has a temperature of 69°C. About 2/3 of the oil present in a reservoir cannot be extracted with the actual technology. There are several strategies to increase the amount of extracted oil including, gasification, water injection and MEOR.

MOER consist in an injection of a microbial community in the oil field where the MO can use oil for growth. The firs consortia was isolated from the flooding water and the community was characterized by 16S

rRNA amplification and subsequent sequencing. A total of 106 OUT'S were present in the injection water and the sequencing evidence the presence of species that rarely have been identify in an oil field including *Pelomonas* and *Weissella*.

SJTU speaker 5: Ying Chen

**Genetic and functional characterization of a stimulated, active AOM-SR consortia**

This study aims at the elucidation of the interaction of Anaerobic Methane Oxidation(AOM) and Sulphate Reducing (SR) consortia in marine environments.

Methane production is associated with several geochemical processes in particular occurring in deep ocean environments. The consortia characterized in this study was isolated at around 1200m and then enriched before the subsequent characterization. From 16S rRNA amplification and sequencing was revealed the presence of a new halophilic bacteria of genus *Methylophaga*. the draft map of this new bacteria is drawn and work is going on for the full genome annotation.

SJTU speaker 6: Fei Su

**Comparative genome analysis of the thermophilic strain, *Bacillus coagulans* 2-6: an excellent producer of platform chemicals**

This study aims at the genome analysis of a new strain of *Bacillus coagulans*, *Bacillus coagulans* 2-6.

The organisms of this species are well known at industrial level to be good producer of Lactic acid and in medicine to increase the immune response to viral challenges .

The genome of *B.coagulans* 2-6 is 3.6 Mbp and it represents the smaller genome for Bacillus genus. It contains 325 unique genes representing the 13.5 % of the total genome and those genes are associated with secondary metabolites with a potential applications in industry or medicine.

**1. National top research groups:**

- Intestinal Microbiota and Health:  
Liping Zhao, Shanghai Jiao Tong University  
Lanjuan Li, First affiliated hospital of Zhejiang University  
Weiyun Zhu, Nanjing Agriculture University
- Food Fermentations  
Jian Chen, Jiangnan University
- White Biotechnology  
Zixin Deng, Shanghai Jiao Tong University
- Synthetic & Systems Biology  
Linzhang Lin, Tsinghua University  
Yanhe Ma, Institute of Microbiology (CAS)  
Lei Wang, Nankai University

**2. International collaborations:**

- Pascal Simonet - Ecole Centrale de Lyon, Université de Lyon.
- Asa Frostergard - Lars Bakken, Norwegian University of Life Sciences

**3. Industrial Collaborations**

- Nestle
- Danon
- Shanghai Coking wastewater treatment Company

## Day 8: Shanghai, CHINA – SIPPE-CAS & Fudan University

### Prof. Zhihua Zhou

Institute of Plant Physiology & Ecology, Shanghai Institutes for Biological Science, CAS

### Ass. Prof. Zhe-Xue Quan

School of Life Sciences, SIPPE-CAS & Fudan University

**Institute of Plant Physiology and Ecology (IPPE)** was formed by the integration of the former Shanghai Institute of Plant Physiology and Shanghai Institute of Entomology, CAS, in 1999.

Aiming at cutting edge of biological sciences and developmental strategies of agriculture, environment and resources, the research in IPPE is focused on functional genomics and molecular physiology of plants, microorganisms and insects, plant-insect-microbe interactions, and molecular ecology.

IPPE has established exchange and collaborative programs of various forms with many research, educational and industrial institutions at home and abroad. It has substantial collaboration with the National Genome Research Center.

### Key Laboratory of Synthetic Biology

#### (Institute of Plant Physiology and Ecology – Chinese Academy of Science)

The Key Laboratory of Synthetic Biology was established in Chinese Academy of Science in 2008 through reorganization of the Laboratory of Molecular Microbiology, The laboratory currently consists of 7 research groups including 12 principal investigators and about 70 graduate students. The director of laboratory is Prof. Guo-Ping Zhao and the academic committee director is Prof. Sheng-Li Yang.

The Laboratory aims at the cutting-edge research in synthetic biology to address global challenges in areas related to energy, human health and the environment. The research subjects include characterization and design of functional biological parts, processing systems and organisms, production of biomaterial and energy molecules through modification and synthesis of biosystems as well as innovation of synthetic biotechnology.



Date	Session	Institution	Topic
<b>April, Fri. 22<sup>th</sup></b>	<b>Chinese Academy of Science (CAS), Shanghai Institute of Plant Physiology &amp; Ecology</b>		
9:00	Welcome		
9:15	<b>Prof. Zhihua Zhou</b>	SIPPE-CAS	Shanghai Institute of Plant Physiology & Ecology - an overview
9:35	<b>Associate Prof. Dr. Zhe-Xue Quan</b>	Fudan University	School of Life Sciences (Fudan University) - an overview
9:55	<b>Assistant Prof. Dr. Servé Kengen</b>	WUR	Laboratory of Microbiology (WUR) - an overview
10:15	Dan-Ping Mao	Fudan University	Coverage evaluation of commonly used primers for 16S rRNA in bacteria
10:35	Coffee break		
10:55	Floor Hugenholtz	WUR	Gut microbiomics of SCFA metabolism
11:15	Xiao-Ran Li	Fudan University	Microbial diversity analysis using pyrosequencing of small-subunit ribosomal RNA without PCR amplification
11:35	Mauricio Rocha Dimitrov	WUR	Adaptive capacity and functionality of multitrophic aquatic ecosystems
11:55	Danning Zeng	Fudan University	Change of bacterial population in drinking water treatment process
12:15	Lunch		
13:15-14:15	Lab. Tour		
14:15	Derya Ozuolmez	WUR	Microbial interactions in marine anoxic sediments: competition or teamwork?
14:35	HaoKui Zhou	SIPPE-CAS	Comparative analysis of metagenomes in two lab-scale biogas digesters by 454 sequencing
14:55	Jimmy Omony	WUR	GeneNet: System dynamic analysis of gene networks in fungal systems
15:15	Ning Liu	SIPPE-CAS	Microbiome of fungus-growing termites: a new reservoir for mining lignocellulase genes
15:35	Coffee break		
15:55	Abraham Bielen	WUR	Systems Biology of <i>Caldicellulosiruptor saccharolyticus</i> : Analysis of the metabolic network leading to hydrogen formation
16:15	Ruofan Wang	SIPPE-CAS	Isolation of <i>Clostridium perfringens</i> strain W11 and its modification for biohydrogen production
16:35	Elleke Bosma	WUR	Developing a high-temperature and low-cost microbial white biotechnology production platform for green chemicals
16:55 - 17:55	Poster Session		
17:55	Closure		
19:00	dinner & get-together		

## Report Day 8

Prof. Chengshu Wang

### **Shanghai Institute of Plant Physiology & Ecology – an overview**

The former Institute of Plant Physiology was founded in 1944. It has been contributing to not only plant physiology research, but also the initiating and promoting molecular genetics research of plants and microorganisms in China. Then, in 1959, the former Shanghai Institute of Entomology, which has been studying on insect taxonomy, physiology, co-evolution, pesticide resistance and sex hormones, was founded. Institute of Plant Physiology and Ecology (IPPE) was formed by the integration of the former Shanghai Institute of Plant Physiology and Shanghai Institute of Entomology in 1999. Aiming at cutting edge of biological sciences and developmental strategies of agriculture, environment and resources, the research in IPPE is focused on functional genomics and molecular physiology of plants, microorganisms and insects, plant-insect-microbe interactions, and molecular ecology. At IPPE, almost 650 people works, 9 academicians, 210 staff scientists, 57 supporting staff, 320 graduate students and 40 post-doc fellows. Besides, it includes 4 laboratories, which are Plant Molecular Genetics, Synthetic Biology, Insect Development and Evolutionary Biology, and Photosynthesis and Environmental Biology. In addition to this, they have National Center for Gene Research and Insect museum in IPPE.

International collaborations are CAS & Max-Planck-Society Partner Group (Germany), Shanghai Institutes for Biological Sciences (SIBS)-UC Berkeley Molecular Life Science Research Center SIBS-Penn State University (the USA)-Shanghai Jiaotong University Center, SIBS-ETH Center on Cassava Biotechnology (Switzerland), Joint-laboratory with Keygene (The Netherlands).

National collaborations are China National Rice Research Institute, Shanghai Chensen Botanical Garden, Shanghai Research Center of Industrial Biotechnology, SIBS- Huzhou Industrial Biotechnology Center.

Assoc. Prof. Dr. Zhe-Xue Quan,

### **School of Life Sciences (Fudan University)**

As an introduction, a brief history of molecular microbial ecology, which was started with Woese's revolution, three domains theory by phlogenetics taxonomy of 16S/18S rRNA was mentioned. Then, universal primers and technics of microbial population analysis, which were clone library, DGGE, T-RFLP, and pyrosequencing were told. The next topic was diversity of ammonia-oxidizing microorganisms that contained aerobic and anaerobic, aerobic archaea. The group defined the fifth ANAMMOX genus, *Candidatus jettenia asiatica*, among the Planctomycetes. Their further aims are enrichment of anaerobic ANAMMOX microorganisms with sulfate reduction and design specific primers for each ANAMMOX bacteria genus. In another study, communities of ANAMMOX bacteria and archaea were identified in Changjiang Estuary in China. And they want to define affecting factors of the quantity of ANAMMOX bacteria and archaea. Furthermore, they would like to develop PCR kit for detection soil health. In the last study, the group monitored the changing of microbial populations in different swimming pools treated with non-chlorine disinfectant and also in drinking water treatment process.

Dan-Ping Mao

### **Coverage Evaluation of Commonly Used for 16S rRNA in Bacteria**

Zhou Quan works in the Laboratory of Prof. Quan, in his presentation he spoke over the improvement of primers, for this he gave a short introduction over PCR, factors that are effecting PCR and the limitations of former studies in this field of research. For his study, 16s rRNA sequences from databases (Ribosomal Database Project, metagenomic databases) were collected, bacterial sequences were sought out, primer binding sites identified and the uncoverage rate of primers was calculated. The work bases of the work of Daims *et al* (1999).

Xiao-Ran Li

**Microbial diversity analysis using pyrosequencing of small-subunit ribosomal RNA without PCR amplification**

In the presentation of of Xiao-Ran Li, working at Molecular Microbial Ecology at Fudan University, methods for microbial community analyses and their drawbacks were discussed. As a result the method of using pyrosequencing of small-subunit ribosomal RNA without PCR amplification was presented, which has the advantage of the reflection of the activity of the microbes, avoids PCR bias and allows quantitative analysis of three domains.

Danning Zang

**Change of bacterial population in drinking water treatment process.**

The research of Danning Zang focuses on the analysis of bacterial communities present in the Chinese drinking water. Although the current treatment process includes steps in which chlorine, chloramine and ozone are used to promote coagulation, kill microbes and oxidize organic carbons a variety of microorganisms (especially alpha- and beta-proteobacteria and the bacteroidetes) are still found to be present in the Chinese tap water. Danning Zang wants to follow and analyse the bacterial community after each step in the treatment process, thereby getting a better understanding of the effect of each step on the bacterial community. The final goal would be to optimise the Chinese drinking water treatment process and to improve the quality of the tap water.

HaoKui Zhou

**Comparative analysis of metagenomes in two lab-scale biogas digesters by 454 sequencing**

The aim of this study is to compare species present in 2 anaerobic fermentation systems of agricultural wasteproducts that lead to the production of biogas, and to relate the species present to the composition of the biogas. The efficiency of biogas production is dependent on the composition of the anaerobic microflora in the biogas digester. Using 454 sequencing, the taxonomic compositions of the microflora in the biogas reactors were determined. The effects of different conditions on hydrogen yield were investigated during anaerobic fermentation of kitchen wastes. The variation of the heterotrophic microflora in the hydrogen producing process was monitored. A high efficiency of cellulose degradation was observed in the anaerobic fermentation system, which suggests that there are abundant novel cellulases expressed by the microflora. However, since most microorganisms in the system are unculturable it is difficult to isolate any novel cellulase genes from pure cultures. Metagenomic methods are used to screen for novel cellulase genes from the microbial community.

Ning Liu

**Microbiome of fungus growing termites: a new reservoir for mining lignocellulase genes**

The research of Ning Liu focuses on finding new enzymes that degrade lignocellulose to improve its utilization in the production of biofuels. Lignocellulose is rather resistant to degradation, which makes it hard to release the easy-to-degrade mono- or di-saccharides stored in lignocellulose. Bacterial species specialized in lignocellulose degradation probably contain enzymes capable of lignocellulose degradation. Another difficulty is the abundance of pentose sugars such as xylose in lignocellulose, which are more difficult to ferment. In this research (1) the abundance of bacterial species in the termite gut (an environment containing a steep pH gradient, redox gradient and substrate gradient) were analysed under different feeding conditions and (2) from the metagenome a xylose converting enzyme was identified, cloned, purified and tested for activity.

- (1) 16S rRNA was used as a phylogenetic marker. On a diet of xylan, cellulose and glucose Bacteroidetes were dominant. On a diet of xylose Firmicutes were dominant. On a diet of wood Spirochaetes were dominant.
- (2) A fosmid library was constructed to identify candidate genes involved in lignocellulase degradation and pentose sugar utilization. Based on the metagenome sequences XylE7, an enzyme capable of converting xylose was found. This enzyme has an optimal pH of 8.5, an optimal Temperature of 55 C and an activity of 700 U/mg at pH 7.5 and T=55 C.

Ruofan Wang

**Isolation of *Clostridium perfringens* strain W11 and its modification for biohydrogen production.**

The research of Ruofan Wang focuses on biological hydrogen production. By making use of DGGE profiles, they analysed the bacterial composition of anaerobic mixed cultures present in their bioreactors. They found that the species most abundantly present are belonging to the genera *Bacillus* and *Clostridium*. In addition they developed a PCR based screening method making use of the *hydA* gene, the gene encoding a hydrogenase, to identify the actual hydrogen producers. It was discovered that both *C. perfringens* and *C. beijerinckii* contributed to hydrogen production in the reactor but that *C. perfringens* was the dominant producer. Next, they developed all kinds of mutants of this strain to optimize the hydrogen production and to develop a safe working strain. They were able to get an 50% increase in hydrogen production (2.31 mol/mol hexose instead of 1.53mol/mol hexose ).

**Day 9: Shanghai, CHINA, arrival in Osaka, JAPAN - April, Sat. 23<sup>rd</sup>**

<i>Session</i>	<i>Institution</i>	<i>Events</i>	<i>ATOD</i>
<b>Morning</b>		Check out hotel	<b>9:00</b>
		Sightseeing around Nanjing road( <b>luggage in the bus</b> )	<b>10:00</b>
<b>Afternoon</b>		End of sightseeing	<b>14:00</b>
		Arrival Shanghai Pudong Airport	<b>15:30</b>
		Departure Shanghai Pudong Airport NH 154 23APR PVG KIX	<b>18:20</b>
<b>Evening</b>		Arrival Osaka kansai International Airport	<b>21:35</b>
		Kansai Airport <b>Ltd Express Rapid</b>	<b>21.59</b> <b>22.30</b>
		Departures to hotel: Checkinn at Hotel Chuo*	<b>22:59</b> <b>23:30</b>

**Day 10: Arrival in Osaka, JAPAN - April, Sun. 24<sup>th</sup>**

	<i>Institution</i>	<i>Events</i>	<i>ATOD</i>
<b>Morning</b>		Travel to Kouto	Departure 9:00 Take midosuji Line at Dobutsuen-mae metro station (M22) (near hotel) to Shin Osaka station (M13) ~30 min  Take Kodama train <b>K743</b> departure from Osaka <b>10.39</b> <b>direction Hiroshima</b> (end station) Arrival <b>AIOI station 11.43</b>  Bus departure from AIOI <b>12.37 to Spring-8 Kouto</b> . Name bus line: AIOI station-Harima-Kagaku-kouen-toshi line Arrival at Spring-8 at 13.13
<b>Afternoon</b>	Guest house in SPring-8 campus.		Check-in time is 16:00-22:00  Free
<b>Evening</b>			Free

## Day 11: Kouto, JAPAN – RIKEN Spring-8 Centre

### Contact

#### Dr. Akeo Shinkai

Harima Institute, Functomics Biology I Research Team, RIKEN SPring-8 Centre

SPring-8 is a large synchrotron radiation facility which delivers the most powerful synchrotron radiation currently available. Consisting of narrow, powerful beams of electromagnetic radiation, synchrotron radiation is produced when electron beams, accelerated to nearly the speed of light, are forced to travel in a curved path by a magnetic field. The research conducted at SPring-8, located in Harima Science Park City, Hyogo Prefecture, Japan, includes nanotechnology, biotechnology and industrial applications. The name "SPring-8" is derived from "Super Photon ring-8 GeV" (8 GeV, or 8 giga electron volts, being the power output of the ring).

SPring-8 was opened in 1997 to industrial, academic and government users, domestic and international. Any user whose application is accepted may use the facility.

SPring-8 is managed by RIKEN, with the Japan Synchrotron Radiation Research Institute (JASRI) in charge of operation, maintenance and promotion of use.

Synchrotron radiation (SR) is an electro-magnetic wave emitted from an electron traveling at almost the speed of light, toward its running-direction when its path is bent by a magnetic field. Synchrotron radiation is characterized by useful features; brightness, high directionality and variable polarization. SPring-8, the world's largest third-generation synchrotron radiation facility, provides the most powerful synchrotron radiation currently available. SPring-8's ultra-brilliant synchrotron radiation gives researchers exciting opportunities for advanced research in materials science, spectroscopic analysis, earth science, life science, environmental science, industrial applications and so forth.

### History:

**October 1988** - Japan Atomic Energy Research Institute and RIKEN established a collaborative team for the synchrotron radiation facility research and development.

**June 1989** - Harima Science Garden City in Hyogo Prefecture was chosen as the construction site.

**December 1990** - Japan Synchrotron Radiation Research Institute (JASRI) was founded.

**November 1991** - Construction on SPring-8 was initiated.

**October 1994** - The "Law Regarding Promotion of Common Use of the Synchrotron Radiation Facility" was implemented and JASRI was assigned as the "Organization for promoting the study and use of synchrotron radiation."

**March 1997** - Generation of synchrotron radiation was confirmed.

**October 1997** - SPring-8 was opened for users.

**October 2005** - Japan Atomic Energy Research Institute withdrew from the management of SPring-8 and management by two bodies, JASRI and RIKEN, began.

**July 2006** - "Law Regarding Promotion of Common Use of the Synchrotron Radiation Facility" was revised to "Law for the Promotion of Public Utilization of the Specific Advanced Large Research Facilities" and the "Organization for promoting the study and use of synchrotron radiation" was dismantled.

**March 2007** - JASRI was selected as the Registered Institution for Facilities Use Promotion.

**October 2007** - The tenth anniversary of operations at SPring-8, an anniversary ceremony and a symposium, were held.

**June 2009** - SPring-8 welcomed its 100,000th user since it was opened in October 1997

Date	Session	Institution
April, Mon. 25 <sup>th</sup>		SPring-8
9:00	Welcome	
9:15	Dr. Tetsuya Ishikawa,	Director of RIKEN Harima Institute and RIKEN SPring-8 Center
9:35	Dr. Servé Kengen	Laboratory of Microbiology (WUR) - an overview
9:50	Dr. Seiki Kuramitsu	Director of SR System Biology Research Group, RIKEN SPring-8 Center (T. thermophilus HB8 whole cell project)
10:10	WUR speaker 1 Tessa Quax, M.Sc.	Archaeal virus-host interactions
10:30	6) Dr. Thirumananseri Kumarevel,	> Senior Research Scientist of Biometal Science Laboratory & Advanced > Protein Crystallography Group, RIKEN SPring-8 Center > (Structural Biology of RNA polymerase and/or transcription factor)
10:50	Coffee break	
11:15	Dr. Akeo Shinkai,	> Team Leader of Functomics Biology I Research Team, SR System Biology > Research Group, RIKEN SPring-8 Center > (Transcriptional regulation of T. thermophilus HB8)
11:35	WUR speaker 2 Bram Bielen, M.Sc.	Systems Biology of <i>Caldicellulosiruptor saccharolyticus</i> : Analysis of the metabolic network leading to hydrogen formation.
11:55	7) Dr. Koji Yonekura,	> Associate Chief Scientist of Biostructural Mechanism Laboratory, RIKEN > SPring-8 Center > (Cryo-electron microscopy, Flagella)
12:15	WUR speaker 3 Edze Westra, M.Sc.	Prokaryotic antiviral defense mediated by CRISPR RNA
12:35	Lunch	
13:30-15:30	Tour	
15:30	Coffee break	
16:00	4) Dr. Yoshitaka Bessho,	> Team Leader of Functomics Biology II Research Team, SR System Biology > Research Group, RIKEN SPring-8 Center > (tRNA modification)
16:20	WUR speaker 4 Bas Spaans, M.Sc.	Biological hydrogen production beyond current limits
16:40	5) Dr. Kenji Fukui,	> Research Scientist of Functomics Integration Research Team, SR System > Biology Research Group, RIKEN SPring-8 Center > (DNA repair)
17:00	Closure	
17:28-18:09	Bus Spring-8 to AIOI	Departure bus from <b>Spring-8 Kouto</b> 17.28 to <b>AIOI</b> arrival 18.09 AIOI station-Harima-Kagaku-kouen-toshi line
18:46-19:54	Train AIOI to Kyoto	<b>Hikari</b> train departure <b>H486</b> from <b>AIOI</b> 18.46 to end station Tokyo arrival <b>Kyoto</b> station 19.54
20.00 – 20.30	Metro Kyoto	From Kyoto station ( <b>K11</b> ) on Karasuma Line to Karasuma Oike station ( <b>K08</b> ), change for Tozai Line ( <b>T13</b> ). Get off at Sanjyo Keihan station ( <b>T11</b> ). Walk to hotel Sunset Inn
20:30	Check in Kyoto SUNSET INN	
21:00	Dinner	

## **Report Day 11**

RIKEN SPring-8 Centre is located at the Harima Institute in Kouto (Hyogo prefecture, Japan) and started operating in 1997 for use by industrial, governmental and academic researchers. The Centre is divided into 3 groups, which are again divided into several research groups. In the afternoon of our visit, promotion material was handed out, a promotion video was shown and we were given a tour around the facilities in which some remarkable features of the buildings and devices were further explained. All in all, seeing and hearing about the SPring-8 institute was highly interesting. All the (high-quality) talks were given by post-doctoral researchers and showed the wide variety of possibilities given by SPring-8. Our stay in the Institute's own guest houses was comfortable, and taking a walk on Sunday afternoon in the beautiful surroundings was very pleasant.

Dr. Tetsuya Ishikawa

### **Director RIKEN SPring-8 Centre**

SPring-8 is an abbreviation for Super Photon ring 8 GeV and it consists of a 1436m long ring structure with 62 ports leading to research hubs, making it the world's largest synchrotron radiation (SR) facility, functioning as a 'super microscope'. Electrons are generated by an electron gun, accelerated and then stored in the storage ring, where the electrons emit SR that is sent through the ports to the research hubs. Currently, RIKEN and JASRI (Japan Synchrotron Radiation Research Institute) are constructing XFEL (X-ray Free Electron Laser), which gives an extremely coherent and small-wavelength light. At RIKEN, XFEL can be combined with SPring-8, which will create an even more powerful tool for for example solving thus far unsolved molecular structures. Dr. Ishikawa mentions that the desire of Japanese researchers to make such small and coherent light beams fits with their "tradition to make everything compact", thereby referring to the famous Japanese Bonsai trees.

Dr. Seiki Kuramitsu

### **Whole-cell project of an extremely thermophilic organism**

The aim of the group is to understand basic biological properties in a cell based on 3 dimensional structure and function of all molecules. In addition to this, transcriptome (mRNA expression), proteome (protein expression), and metabolome (metabolite dynamics) analyses are performed to investigate biological system. *Thermus thermophilus* HB8, extremely thermophilic bacterium, is studied as a model organism in the group, because *T. thermophilus* has small genome and less proteins, but high thermostable proteins. Besides, its genome is also available. Functionally unknown 113 genes are identified and all biological phenomena in a cell are simulated.

Dr. Kumarevel

### **Structural Biology of RNA polymerase and/or transcription factor**

This group analyses the structure of RNA polymerase and its function with use of the Spring8 facilities. They are currently looking at the function of Gfh1, which has a proofreading function in elongation, and its inhibition function towards the RNA polymerase. Gfh1 is responsible for the positional change of the T-state (Tight) to the R-state (Ratcheted). They found Gfh1 is responsible for a 50 degrees shift in the RNA polymerase which blocks the elongation.

Dr. Akeo Shinkai,

### **Transcriptional regulation of *T. thermophilus* HB8**

The aim of the project is structural and functional analysis of transcription factors and to observe the phenotype as the results of transcriptional changes in *Thermus thermophilus* HB8 as a model organism. *T. thermophilus* HB8 is poorly characterized, and has roughly 600 functionally unknown proteins. Decreasing the activity of one set of genes, while increasing the activity of another is often regulated by transcription factors. One group of transcription factors is CRP/FNR superfamily proteins, of which there are 4 representatives in *T. Thermophilus*. *CRP is catabolite gene activator which is also cAMP dependent. CRP-regulated genes are screened and identified by the group. Moreover, one of these regulators is stationary*

phase-dependent regulatory protein (SdrP), its activity increased at times of nutrient depletion. SdrP gene candidates were screened, structure and function of the protein was identified.

Dr. Koji Yonekura

#### **Cryo-electron microscopy, Flagella**

Bacteria swim by rotating helical flagellar filaments. The rotary motor at the base of the filament drives the rotation of this helical propeller. For chemotaxis and thermotaxis, bacteria alternate their swimming pattern between run and tumble to change their swimming directions. Left- and right-handed helical forms are produced by supercoiling caused by a mixture of two distinct protofilament conformations, L- and R-type. The group examined the structures of the L- and R-type straight filaments by cryo-electron microscopy and helical image reconstruction at  $\sim 10\text{-\AA}$  resolution, which revealed four radially arranged domains of flagellin. Flexible changes were found in the conformation of flagellin within the filament, which were shown on figures at the presentation.

Dr. Bessho

#### **tRNA modification**

tRNA modification in *T. thermophilus* is the main target in this project. This organism has 47 different tRNAs. They come in 4 different shapes: trans-, chiasmic-, clover- and L-shaped. They modified 37 tRNAs with help of a -1 frame shift. Spring8 facilities help in analysing the produced structures to understand how these tRNAs work. By use of fluorescence light they visualize the crystal structure. The main idea is that the electron waves are deformed when passing through the structure and the deformed waves are measured. Then inverse Fourier transformation formulas are used in novel algorithms to solve the structures.

Dr. Fukui,

#### **DNA repair**

Dr. Fukui loves to play basketball and is a big fan of the mascot of Nara which is called Sento-kun. This mascot looks like a big baby with an antler. After this lovely introduction he starts his presentation by telling they are investigating the Small MutS Related domain of *T. thermophilus* MutS2 enzyme. These enzymes are involved in the DNA mismatch repair system. They solved the crystal structure of the *T. thermophilus* MutS enzyme and tested the biochemical properties of the protein as in pKa-value, optimal pH and temperature and they looked for homologues. Via this way they discovered MutS2 enzyme looks like a MutS enzyme, but lacks the mismatching recognition domain of a MutS and contains an extra C-terminal region which is called the small MutS-related (Smr) domain.



## **Day 12: Kyoto, JAPAN - Kyoto University**

### **Kyoto University, Kyoto**

<http://www.kyoto-u.ac.jp/en>

#### **Contact**

##### **Prof. Dr. Haruyuki Atomi**

Department of Synthetic Chemistry and Biological Chemistry, Graduate School of Engineering Kyoto University.

#### **Groups joining the Wageningen UR/Kyoto University workshop 2011**

##### **Department of Synthetic Chemistry and Biological Chemistry, Biological Chemistry Course, Biochemical Engineering Field**

##### **Prof. Haruyuki Atomi**

<http://www.sc.t.kyoto-u.ac.jp/en>

Chemistry is a science that seeks to explain, at a molecular level, the properties of substances and the changes they undergo. At the same time, it is also the technical art of manipulating substances at a molecular level to endow them with particular properties.

The 21st century is shaping up to be a new age of chemistry. This is because many technical issues connected closely with the continued survival of humanity—relating to energy, information, biological phenomena, medicine, and the environment—can be understood at a molecular level, or in the language of chemistry. Synthetic chemistry offers unlimited potential for the development of functional materials. Biological chemistry involves not only the elucidation of biological phenomena, but also their utilization and modification.

The fundamental purpose of the Department of Synthetic Chemistry and Biological Chemistry is to push the boundaries of a new scientific domain (chemical biology) centred around the disciplines of synthetic chemistry and biological chemistry, and to reshape it as a richly creative, comprehensive precision science. It is also striving to promote sound and balanced views of nature and life, and to help establish new industrial platform technologies for the development of a sustainable society.

##### **Graduate school of Agriculture, Division of Applied Life Sciences, Lab. of Fermentation Physiology and Applied Microbiology**

##### **Prof. Jun Ogawa**

<http://www.hakko.kais.kyoto-u.ac.jp/lab-e/index-e.html>

Enzymes have been generally accepted as superior catalysts in organic synthesis. Microorganisms in particular have been regarded as treasure sources of useful enzymes. The synthetic technology using microbial enzymes or microorganisms themselves is called microbial transformation. In designing a microbial transformation process, one of the most important points is to find a suitable enzyme for the reaction of interest. Various kinds of novel enzymes for specific transformations have been discovered in microorganisms and their potential characteristics revealed. Our research activities on the discovery of novel enzymes for the production of biologically and chemically useful compounds are summarized as follows:

- Production of useful lipids by filamentous fungi
- Microbial nitrile degradation and its application
- Microbial production of optically active compounds
- Functional analysis and application of novel microbial enzymes

**Institute for Chemical Research, Division of Environmental Chemistry,  
Molecular microbial Science Laboratory**

**Associate Prof. Tatsuo Kurihara**

[http://www.scl.kyoto-u.ac.jp/~mmsicr/mmstojp/Top\\_en.html](http://www.scl.kyoto-u.ac.jp/~mmsicr/mmstojp/Top_en.html)

Structure and function of biocatalysts, in particular, pyridoxal enzymes and enzymes acting on xenobiotic compounds, are studied to elucidate the dynamic aspects of the fine mechanism for their catalysis in the light of recent advances in gene technology, protein engineering and crystallography. In addition, the metabolism and biofunction of sulfur, selenium, and some other trace elements are investigated. Development and application of new biomolecular functions of microorganisms are also studied to open the door to new fields of biotechnology. For example, molecular structures and functions of psychrophilic enzymes and their application are under investigation.

**Graduate School of Human and Environmental Studies, Department of Interdisciplinary Environment,  
Molecular Studies on Chemical and Biological Environments, Environmental Molecular Life Science.**

**Associate Prof. Hideaki Miyashita**

[http://www.h.kyoto-u.ac.jp/jinkan/index\\_e.php](http://www.h.kyoto-u.ac.jp/jinkan/index_e.php)

The 20th century saw dramatic progress in science and technology that greatly expanded the potential for human beings. This progress created a number of new problems that remain unsolved today: pollution, energy resources, ethnic conflicts, wealth discrepancies, and urban problems. The wave of globalization and information technology that appeared at the end of the century created new problems that can no longer be addressed by established ideas and approaches.

To address these seemingly intractable global problems effectively, new approaches to scholarship that go beyond traditional divisions in academic fields are needed. Scholarship in the 21st century must take traditional scholarship into a new paradigm that emerges from a new vision of human beings and a new vision of scholarship. To achieve this goal, new scholarship cannot be defined simply as an "interdisciplinary" or "comprehensive" grouping of established fields. Rather, to reach this goal, new scholarship must focus developing "comprehensive knowledge" to create new fields of study from various related fields, as well as to offer practical solutions to the issue of "creating sustainable societies" and to advance research on "coexistence between human beings and limited natural resources" and "mutual coexistence of human beings."

The Graduate School of Human and Environmental Sciences is organized into the three departments: the Department of Human Coexistence with "human beings" as its key concept, the Department of Cultural Coexistence with "civilization" as its key concept, and the Department of Interdisciplinary Environment with "nature" as its key concept. This organization will contribute to new views of human beings, nature, and civilization, which will, in turn, foster a new scholarship that is capable of responding to the urgent and essential task of creating a sustainable society.

	Events	ATOD
<b>Morning</b>	Travel to Kyoto University Yoshida Campus	9:00 Pickup by Dr. Takaaki Sato depart from hotel to Sanjo(Kyoto) trainstation Take Train to Demachiyanaagi (Keihan Line) (~5min) Walk to Yoshida Campus (~20)

Date	Session	Institution	Topic
April, Tues. 26th		Kyoto university	
10:00	Introduction/welcome Prof. Haruyuki Atomi Assistant Prof. Servé Kengen Prof. Haruyuki Atomi		Welcome address Laboratory of Microbiology (WUR) - an overview  Introduction from the Katsura group.
10:50	Wageningen/Kyoto University	.	.
11:10	Edze Westra	Wageningen University	Prokaryotic antiviral defence mediated by CRISPR RNA
11:30	Takaaki Sato	Kyoto university	Unique metabolism involving archaeal Rubiscos
11:50	Small break		
12:00	Onur Ercan	Wageningen University	Zero-Growth of Lactic acid Bacteria; Plant-Microbe Interactions and Increased 4 Heterogeneity
12:20	Satoshi Ohkubo	Kyoto university	Ecological distribution of chlorophyll d and Acaryochloris spp. (Cyanobacteria)
12:40	Bas Spaans	Wageningen University	Biological hydrogen production beyond current limits
13:00	Lunch & Facility tour on Yoshida Campus		
14:30	Makoto Hibi	Kyoto university	Novel microbial enzyme systems for future industry
14:50	Elleke Bosma	Wageningen University	Developing a high-temperature and low-cost microbial white biotechnology production platform for green chemicals
15:10	Jun Ogawa	Kyoto university	Unique microbial metabolisms for functional food production
15:30	Teun Veuskens	Wageningen University	Application of chlorate reduction as a novel concept for the bioremediation of heavily polluted anaerobic soils
15:50	Small break		
16:00	Hideaki Miyashita	Kyoto university	Isolation of oil-producing microalgae for the biofuel production.
16:20	Ruud Heshof	Wageningen University	Novel enzyme tools for production of functional oleochemicals from unsaturated lipids
16:40	Tatsuo Kurihara	Kyoto university	Function of phospholipids containing eicosapentaenoic acid in the bacterial cell membrane
17:00	Closing remarks & Get together		

## **Report Day 12**

Haruyuki Atomi

### **Isolation of oil-producing microalgae for biofuel production**

Biochemical Engineering Lab, Department of Synthetic Chemistry and Biological Chemistry, Graduate school of Engineering

The Biochemical Engineering Lab led by professor Haruyuki Atomi is located at the new campus Katsura of Kyoto University. Professor Haruyuki Atomi focuses on microorganisms from extreme environments, especially on *Hyperthermophiles*.

Hideaki Miyashita

### **Ecological distribution of chlorophyll d and Acaryochloris spp. (Cyanobacteria)**

Environmental Molecular Life Science, Department of Interdisciplinary Environment, Graduate School of Human and Environmental Studies

Satoshi Ohkubo

### **Unique microbial metabolisms for functional food production and probiotics**

S. Ohkubo presented his work on chlorophyll d which in opposite to chlorophyll a from plants and chlorophyll b from algae seems to be a distinguishable form of chlorophyll from red algae. Absorption spectra compared to other chlorophyll were performed and phylogenetic analysis of algae sequences showed a fraction of 1% of chlorophyll of total chlorophyll in *Acaryochloris* spp.

Jun Ogawa

### **Lab. of Fermentation Physiology and Applied Microbiology, Graduate school of Agriculture**

J. Ogawa is associated with the graduate school of agriculture of Kyoto University. Aim is to apply microbial functions in functional foods. First of all my microbial transformation to produce functional food nutrients. Secondly by using microbial enzymes to add extra functions to food. And finally by probiotics. J. Ogawa focuses specifically on polyunsaturated fatty acids and is screening for the production of unusual fatty acids in mutant libraries. Conjugated fatty acids like linoleic acid are found to reduce the body fat content. Biohydrogenation of linoleic acid to stearic acid can occur in anaerobic bacteria. They manage to produce linoleic acid in *Escherichia coli* by heterologous expression of multicomponent enzymes from *Lactobacillus plantarium*.

Makoto Hibi

### **Novel microbial enzyme systems for future industry**

Takaaki Sato

### **Unique metabolism involving archaeal Rubiscos**

T. Sato studies the role of Rubisco homologues in archaea. Rubisco is an enzyme with a function in the Calvin cycle and is generally found in plants, algae and other autotrophs. In *Thermococcus kodakarensis* a Rubisco homologue is found, but this organism is a heterotroph and does not have a Calvin cycle. After an extensive screen the Rubisco homologue was detected in more Archaea. When a tree is constructed based on their sequence the archaeal Rubisco's form a distinct group different from the plant and bacterial Rubisco's. It was found that in all archaeal genomes containing Rubisco, two other genes are specifically present: E2b2 and DeoA. DeoA has Nucleoside 5' Mono Phosphate (NMP) phosphorylase activity. It is concluded that archaeal Rubisco's function in a novel AMP metabolic pathway.

Associate Prof. Tatsuo Kurihara

### **Function of phospholipids containing eicosapentaenoic acid in the bacterial cell membrane**

Molecular Microbial Science Laboratory, Division of Environmental Chemistry, Institute for Chemical Research,

The group of T. Kurihara works on the cryophilic gram negative *Shewanella livingstonensis* Ac10, isolated from Antarctica, with a growth temperature optimum between 4 and 25°C. For cold adaption eicosapentaenoic acid-(EPA)phospholipids have been identified as a key molecules for growth. Analysis of membrane fluidity and morphology of an EPA defected mutant gave limited insight, while EPA knockout had a defect in cell division which could be restored with 3% NaCl. The presented hypothesis is that EPA-phospholipids are important for cell division at low temperatures to facilitate the folding of membrane proteins.



## **Day 13: Ikoma, JAPAN – Nara Institute of Science Technology**

**Nara institute of Science and technology, Ikoma**

<http://www.naist.jp/en/>

### **Contacts:**

**Prof. Hiroshi Takagi, Ph.D.**

Graduate School of Biological Sciences Nara Institute of Science & Technology

**Dr. Nobuyuki Yoshida, Assistant Professor**

Graduate School of Biological Sciences Nara Institute of Science & Technology

**Dr. Iwao Ohtsu, Assistant Professor**

Graduate School of Biological Sciences Nara Institute of Science & Technology

**The Graduate School of Biological Sciences**

<http://bsw3.naist.jp/eng/courses/index.html>

The Graduate School of Biological Sciences offers an exciting international research environment, with research groups led by dynamic faculty members undertaking advanced research to address fundamental questions in cellular and molecular biology, plant sciences, and systems biology. As in all NAIST's graduate schools, there is a strong emphasis on interdisciplinary research, particularly in terms of the use of information science techniques in genomics and bioinformatics. This research is helping to clarify some of the basic phenomena of living things, leading to discoveries that will be of benefit to humanity in future. The Graduate School of Biological Sciences is one of the top institutes in Japan in attracting research funds, testifying to its high national and international reputation.

### **Groups joining the WUR/NAIST Microbial workshop 2011**

#### **Department of Systems Biology**

##### **Applied Stress Microbiology**

**Prof. Hiroshi Takagi**

<http://bsw3.naist.jp/eng/courses/courses305.html>

We are engaged in the research and education with a goal of developing new bioindustry on the basis of microbial bioscience. Specifically, we search, analyse and improve the various functions and mechanisms of microorganisms including yeasts, fungi, bacteria, actinomycetes, algae, etc. from molecular, metabolic and cellular aspects and thus attempt have deeper insight into microbial functions.

It is also our goal to apply the results of these basic studies to construction of useful strains of microorganisms (yeasts, bacteria, etc.), production of valuable substances (enzymes, amino acids, carotenoids, optically chiral alcohols, etc.) and development of promising technology (bioremediation and bioprevention, etc.).

## **Systems Microbiology**

**Prof. Hirotada Mori**

<http://bsw3.aist-nara.ac.jp/eng/courses/courses302.html>

Due to the enormous amount of information, collected about E. coli over the past half century, it is the best understood organism in biology, not just for bacteria. It has led the understanding of biology at the molecular level and is the clear system of choice to act as a test bed for Systems Biology. No organism can rival E. coli in the amount of baseline information and experimental tractability for the technologies required by this undertaking. Solving the E. coli cell will provide critical new insights into the fundamental nature of life. And it will contribute to basic understanding not only of bacterial cell but of plant and animal cells, with significant benefits to biotechnology, industry and human health.

## **Genomics of Bacterial Cell Functions**

**Prof. Naotake Ogasawara**

<http://bsw3.naist.jp/eng/courses/courses303.html>

With the availability of complete genome sequences, microbial research has entered a new era, to understand various cellular functions as a network of proteins encoded on the genome. We study the basic cellular functions of model bacteria, Bacillus subtilis and Escherichia coli, as a system. Therefore, we are implementing novel research methods such as whole genome expression analysis using DNA chips, analysis of trace amounts of protein by mass spectrometry, and analysis of protein localization in cells by fluorescence microscopy.

## **Microbial Molecular Genetics**

**Prof. Hisaji Maki**

<http://bsw3.naist.jp/eng/courses/courses301.html>

At our laboratory, it has been studied how the genetic information is precisely transmitted from parents (parent cells) to offspring (daughter cells) and, conversely, which processes are involved in the mutation induced by inaccurate transmission of genetic information. We are also exercising our best efforts in education of young students highly interested in basic issues related to the DNA transaction and molecular mechanisms for evolution of organisms to help them become independent investigators.

## **Department of Plant Biology**

### **Plant Differentiation and Morphogenesis**

**Prof. Akiho Yokota**

<http://bsw3.naist.jp/eng/courses/courses107.html>

Organic substances which serve as a source of food and fossil fuel are formed by photosynthesis in plants. We are conducting research aimed at alleviating the two major factors restricting the photosynthesis by plants to elevate the productivity of photosynthesis. One of these two factors is RuBisCO, which is the most important enzyme involved in photosynthesis and catalyzes the formation of organic substances from CO<sub>2</sub>. The rate of the reaction catalyzed by RuBisCO is quite low, and the capability of this enzyme to recognize CO<sub>2</sub> is low, thus reducing the overall efficiency of photosynthesis. The second factor is stress due to strong light and dryness, affecting the plants seriously. If the stomata of the plant is closed due to dryness, photosynthesis does not occur. Excessive light energy can produce oxygen radicals, injuring the plant cells and eventually leading to injuring of the plant. If plants with high performance RuBisCO and resistance to stress (due to strong light and dryness) can be developed, they will remarkably increase the production of food and other resources and will also contribute to covering the deserts (currently seen in many areas on the globe) with trees.

	Events	ATOD
<b>Morning</b>	Travel to NAIST	7:00 Departure Take Tozai Line at at Sanjo Keihan metro station (T11) (~2 min from hotel) to Karasuma Oike station (T13) change to Karasuma line (K08) and get off at Kyoto train station (K11) ~20 min  7:46 Express bound for Nara (Kintetsu Nara) 8:22 Arrival at Takanohara station 8:45 Nara Kotsu bus bound for NAIST (NAIST students will wait for us at Takanohara station) 9:10 Arrival at NAIST
<b>Late Afternoon</b>	Travel to Kyoto	17:00 Bus back to Takanohara station Express bound for Kyoto (Kintetsu) Metro back to hotel

### WUR/NAIST Microbial workshop 2011

Date: April 27, 2011

Venue: Large Seminar Room, NAIST

Date	Session	Institution	Topic
April, Wed. 27th		Nara institute of Science and technology, Graduate School of Biological Sciences, Department of Systems Biology	
9:55	Opening remarks by Assist. Prof. Dr. Nobuyuki Yoshida (Takagi's lab)		
10:00	Brief introduction of NAIST by Prof. Dr. Hiroshi Takagi (Takagi's lab)		
10:15	Brief introduction of the Laboratory of Microbiology, WUR by Assist. Prof. Dr. Servé Kengen		
10:30	Akira Nishimura	Ph. D. student of Takagi's lab	"Oxidative stress induced arginine/nitric oxide synthesis and its physiological role in <i>Saccharomyces cerevisiae</i> "
10:50	Sven Menschel	Ph.D. student of WUR	"Peptide utilization in <i>Lactococcus lactis</i> "
11:10	Rikiya Takeuchi	Ph. D. student of Mori's lab	"Functional structure of the genes working on the central metabolic pathways in <i>E. coli</i> based on genetic interactions"
11:30	Small break		
11:45	Tom Groot Kormelink	Ph.D. student of WUR	"Comparative genomics of regulatory networks in Gram-positive bacteria"
12:05	Lay Ei	Ph.D student of Ogasawara's laboratory	"Functional analysis of the Veg protein that stimulates biofilm formation in <i>B. subtilis</i> "
12:25	Onur Ercan	Ph.D. student of WUR	"Zero-Growth of Lactic acid Bacteria; Plant-Microbe Interactions and Increased Heterogeneity"
12:45	Lunch at the University Cafeteria		
13:30	Poster session		14 students from WUR and 11 students from NAIST
14:30	Ryo Nasuno	Ph. D. student of Takagi's lab	"Structural and functional analyses of a novel N-acetyltransferase, Mpr1 involved in oxidative stress tolerance in yeast"
14:50	Ruud Heshof	Ph.D. student of WUR	"Novel enzyme tools for production of functional oleochemicals from unsaturated lipids"
15:10	Small break		
15:20	Lai Pey Jiun	Ph. D. student of Maki's lab	"Effects of inverted repeats on DNA replication fork: biochemical studies with a fully reconstituted oriC plasmid DNA replication in vitro"
15:40	Tessa Quax	Ph.D. student of WUR	"Archaeal virus-host interactions"
16:00	Short lab tour		
17:00	Leave NAIST		

## Report Day 13

Prof. Dr. Takagi

### **Description of the institute/group and general things**

NAIST was established in 1991 and is composed of three graduate schools (Information Sciences, Materials Sciences and Biological Sciences), with in total around 1000 graduate students. There are collaborations and exchanges with 19 countries, more than 10% of the students is international and 25% of the NAIST-students goes abroad. After graduating from their master, 25% of the students proceeds with a PhD and about 75% of the students finds a job in industry. From the students who finished their PhD at NAIST in 2008, around 30% moves on to a post-doc position, around 25% finds a job in industry and 25% goes back to their former employer. The NAIST Graduate School of Biological Sciences belongs to the top institutes of Japan. It consist of 23 laboratories, which are divided into three groups (Plant Biology, Medical Biology and Systems Biology). We visited the Systems Biology department; the speakers during the day were from the laboratories of Prof. Takagi (Applied Stress Microbiology), Prof. Maki (Microbial Molecular Genetics), Prof. Ogasawara (Genomics of Bacterial Cell Functions) and Prof. Mori (Systems Microbiology). The whole day was very nicely organized, with many interesting presentations and a lively poster session. Subsidy was provided by the local government, which financed a tasty lunch and our bus ride to and from the institute.

Rikiya Takeuchi, PhD student of Mori's lab

### **Functional structure of the genes working on the central metabolic pathways in *E. coli* based on genetic interactions**

The goal of this project is to elucidate a functional genetic network in *E. coli* based on similar functions of genes, which is done via the mapping of genetic interactions (GIs). For the GI-mapping, conjugation is used to create double knock-outs in a high-throughput way. From the 'Keio-collection' donor cells carrying an F-plasmid with kanamycin resistance and a single gene deletion are used to 'mate' with recipient cells carrying another single gene deletion and chloramphenicol resistance. This is done via 'mating plates', having a maximum of 1536 colonies per plate. After mating, colonies are screened on the different antibiotics for double knock-outs. From the growth of double mutants compared to growth of single mutants GI-scores can be calculated, after which Pearson Correlation Coefficient is used to calculate functional similarities. Using this system, genes in the same pathway were often identified as similar, but also new interactions were discovered which need to further investigated.

Lay Ei, PhD student of Ogasawara's lab

### **Functional analysis of Veg protein that stimulates biofilm formation in *B. subtilis*.**

The group of Prof. Ogasawara focuses on the basic cellular function of model bacteria *B. subtilis* and *E. coli*. This research project is focussing on the biofilm formation of *B. subtilis*. In *B. subtilis* an extracellular poly saccharide (EPS) and an excreted protein TasA are the primary components of the extracellular matrix in its biofilms. Matrix production during biofilm formation is governed by multiple physiological and populational signals. The investigators identified a small Veg protein responsible for biofilm formation, which is highly conserved among gram-positive bacteria. In *B. subtilis* high transcription levels during the vegetative growth phase have been reported, and its product localizes on the entire nucleoid. No biofilm formation was observed for a *veg* knockout mutant in *B. subtilis*. Overexpression of the *veg* resulted in complex structure formation of the colonies, and transcriptome analysis revealed that both EPS and TasA were strongly induced. Thus confirming that the identified Veg protein activates biofilm formation under the appropriate conditions.

Ryo Nasuno, Ph.D. student of Takagi's lab

**Structural and functional analyses of a novel N-acetyltransferase, Mpr1 involved in oxidative stress tolerance in yeast**

This group is focussing on the stress response and adaptation mechanisms in yeast. They specifically look at the novel enzyme Mpr1. Mpr1 is a novel N-acetyltransferase that detoxifies the toxic proline analogue azetidine-2-carboxylate. Furthermore, Mpr1 has also been found to be a novel antioxidant enzyme that protects the cells from oxidative stress by controlling ROS levels. So far they discovered that Mpr1 catalyzes *N*-acetylation of AZC, GSA and *cis*-4-hydroxy-L-proline and that it is also involved in antioxidation by GSA *N*-acetylation and stress induced arginine synthesis. It was found that Mpr1 connects the proline and arginine metabolism. They are currently working on the determination of the tertiary structure of Mpr1 via x-ray crystal structure analysis. Furthermore, they are looking into the catalytic reaction mechanism, e.g. the identification of the catalytic residues. Finally, they are trying to determine the exact order of substrate binding and they currently think that the reaction proceeds through a sequential mechanism.

Lai Pey Jiun, Ph.D. student of Maki's lab

**Effects of inverted repeats on DNA replication fork: biochemical studies with a fully reconstituted *oriC* plasmid DNA replication *in vitro***

In this study the aim is to investigate the effect of inverted repeats on DNA replication. The hypothesis is that the presence of inverted repeats can lead to genome instability during replication due to the formation of non-B-type helices (e.g. Z-DNA, cruciform DNA, etc.). A plasmid with *OriC* sequence (theta replication) and a *TerB* sequence downstream of the *Ori*, that blocks replication in one direction, is used. This leads to theta replication that goes in the anti-clockwise direction for only a short stretch (where it runs into the *TerB* sequence) and the remainder (~3/4) of the plasmid is replicated in the clockwise direction. A palindromic repeat of 246 nt is inserted halfway between the *TerB* and *OriC* sequence, such that the DNAP complex that replicates in the clockwise direction encounters the palindromic sequence. At high salt and high Temperature, cruciform DNA is formed. Yet, no effect of the palindromic sequence on DNA replication *in vitro* was found, possibly due to the high length of the palindromic sequence. It was discussed whether this *in vitro* system resembles the *in vivo* situation, where the *ssb* protein binds the lagging strand and may prevent secondary structure formation in the DNA. Future work in this project includes monitoring lagging strand synthesis, where effects of the palindromic sequences might be more pronounced.



Day 14: Kyoto, JAPAN – free time

**Background on Kyoto** (from wikipedia)

Kyoto is a city in the central part of the island of Honshū, Japan. It has a population close to 1.5 million. Formerly the imperial capital of Japan, it is now the capital of Kyoto Prefecture, as well as a major part of the Osaka-Kobe-Kyoto metropolitan area.

Kyoto is one of the few Japanese cities that still has an abundance of prewar buildings, such as the traditional townhouses known as *machiya*. However, modernization is continually breaking down the traditional Kyoto in favor of newer architecture, such as the Kyoto Station complex.

Kyoto became a city designated by government ordinance on September 1, 1956. In 1997, Kyoto hosted the conference that resulted in the protocol on greenhouse gas emissions that bears the city's name.

Although ravaged by wars, fires, and earthquakes during its eleven centuries as the imperial capital, Kyoto was spared from the firebombing of World War II. With its 2000 religious places- 1600 Buddhist temples and 400 Shinto shrines, as well as palaces, gardens and architecture intact, it is one of the best preserved cities in Japan. Among the most famous temples in Japan are Kiyomizu-dera, a magnificent wooden temple supported by pillars off the slope of a mountain; Kinkaku-ji, the Temple of the Golden Pavilion; Ginkaku-ji, the Temple of the Silver Pavilion; and Ryōan-ji, famous for its rock garden. The Heian Jingū is a Shinto shrine, built in 1895, celebrating the Imperial family and commemorating the first and last emperors to reside in Kyoto. Three special sites have connections to the imperial family: the Kyoto Gyoen area including the Kyoto Imperial Palace and Sento Imperial Palace, homes of the Emperors of Japan for many centuries; Katsura Imperial Villa, one of the nation's finest architectural treasures; and Shugaku-in Imperial Villa, one of its best Japanese gardens.



**Day 15: Kyoto and travel to Osaka, JAPAN**

Session	Events	ATOD
<b>During the day</b>	Travel from Kyoto to Osaka	Depart from Sanjo(Kyoto) trainstation (~2min from hotel) Take train to Yodoyabashi (Keihan Line, Limited express) (~51min) Take Midosuji Line at Yodoyabashi subway station (M17) to Dobutsuen-mae station (M22) Take exit (2 or 4), walk to the hotel Check in time 12PM Checkout 11 AM

**Day 16: Osaka, JAPAN**

**Background on Osaka** (from wikipedia)

Osaka is a city in the Kansai region of Japan's main island of Honshū, a designated city under the Local Autonomy Law, the capital city of Osaka Prefecture and also the biggest part of Keihanshin Area, which is represented by three major cities of Japan, Kyoto, Osaka and Kobe. Located at the mouth of the Yodo River on Osaka Bay, Osaka is the third largest city by population after Tokyo and Yokohama. For reference, Keihanshin Area is the second largest area in Japan by population and one of the largest metropolitan areas highly ranked in the world, with nearly 18 million people, and by GDP, the second largest area in Japan and the seventh largest area in the world. Historically the commercial capital of Japan, Osaka functions as one of the command centers for the Japanese economy. The ratio between daytime and night time population is 141%, the highest in Japan, highlighting its status as an economic center. Its nighttime population is 2.6 million, the third in the country, but in daytime the population surges to 3.7 million, second only after Tokyo. Osaka used to be referred to as the "nation's kitchen" in feudal Edo period because it was the centre of trading for rice, creating the first modern future exchange market in the world.



**Day 17: Leaving from Osaka, JAPAN back to Amsterdam, NL**

	<i>Institution</i>	<i>Events</i>	<i>ATOD</i>
<b>Morning</b>		Check out hotel	<b>6:30</b>
		Take Nankai Ltd Express Rapid to Kansai international airport	<b>7:00</b>
		Arrivel at Kansai international airport train station	<b>8:00</b>
		Departure at Kansai international airport Flight number: <b>KL868L</b>	<b>10:30</b>
		Arrivel at schiphol airport, Amsterdam	<b>15:25</b>