Society for Microbial Ecology and Disease

SOMED NEWSLETTER

Winter 2012

Message from the President

The 28th November 2012

Dear SOMED members,

After the very successful meeting in Valencia this past summer, we are now looking forward to our meeting in Kosice in September of 2013. A very exciting program is being put together and I encourage all of you to attend this meeting. I think that we all recognize that human microbial ecology is no longer a "niche" area of microbiology, but represents a mainstream effort to understand the role that microbes play in both health and disease. The very successful effort to elucidate the human microbiome has drawn a new group of scientists into the realm of microbial ecology, including immunologists, systems biologists, bioinformatics specialists and oncologists. We now have the tools to identify all of the genes within a specific environment and to determine the metabolome as well. Among the most exciting current studies are those focused on the role of the microbiome of the GI tract in the development of the host immune response, which organisms may be beneficial within the GI and vaginal microbiome as potential probiotic agents and equally as important are studies to determine whether members of the human microbiome contribute in a causal fashion to the development of chronic inflammatory or neoplastic diseases. It seems reasonable to assume that the actual names of the organisms present within a particular microbiome is not as important as what the microbiome, in total, is contributing to interactions with the human host. Data suggests that the phenotypes that have been used in the past to define a particular genus or "species" may actually represent a multiplicity of genetically different organisms that all behave in a similar fashion,

rendering names less important than the metabolic activity and cross talk with eukaryotic cells.

Members of SOMED are playing an instrumental role in moving the entire field of human microbial ecology forward by collaborating with other scientists representing a variety of different disciplines. SOMED has an online journal in which members can publish their findings quickly. We need to take advantage of this journal, Microbial Ecology in Health and Disease (MEHD) because it has been the traditional outlet for our scientific work and because several of our members recently invested their own money to purchase the journal on behalf of SOMED. The survival of our journal depends on how often and how well we use it, so I encourage all of you to consider publication in MEHD as a fundamental part of your commitment to microbial ecology.

As a final note, I would like to inform the membership that the SOMED meeting for 2014 will be held as a collaborative meeting with the Anaerobe Society of the Americas in Chicago, Illinois. I am working closely with the President of ASA to work out the format for this meeting and will provide additional details as they become available. This meeting is an important step for SOMED because we have not held a meeting in the United States for over a decade. If we are to grow and prosper as a society, we need to include scientists from all nations as active members of our society and I believe that the 2014 meeting will allow SOMED to demonstrate the important role it plays in furthering our understanding of microbial ecology and to attract new members.

I send all of you my warm best wishes for the upcoming holiday season and wish all of you the best for a healthy and prosperous New Year.

Andy Onderdonk

President, SOMED

NEWS FROM THE SOMED JOURNAL

Microbial Ecology in Heath and Disease (MEHD)

The 8th November 2012

Year 2012 has been a good one for our journal. We have succeeded in attracting a substantial number of excellent manuscripts and have also printed abstracts etc, from some meetings The thematic cluster "Autism Spectrum Disorders" covering most of the lectures given at a symposium, entitled, "From gut to brain – with focus on autism spectrum disorders", arranged at the Nobel Forum in Stockholm in May 2012, turned out to be a great success.

Now I am planning for the year to come. My main intention is to get MEHD into PubMed. I am pleased by telling you that we will be there if we slightly increase the number of papers published. Be sure, I have several ideas for reaching that goal – and you are parts of my ideas. Simply spoken, if each of you will send the next relevant paper to be published in MEHD, we will reach PubMed.

Surely, I have other ideas as well. Realizing that our next SOMED meeting is will be in September 2013, I think time has come to focus upon the topic of "Probiotics". Our meeting in Yokohama convinced me about huge variations in regulatory rules worldwide, creating problems for researchers as well as producers. Letters from you, describing your own experience – and problems – in this field will be put into a new mailbox, entitled "Letters to the Editor". You will find more about other ideas in my next Editorial in MEHD.

Karolinska Institute,

Tore Midtvedt, ***Editor-in-Cief***

Upcoming meetings 2013-2014 and recent references of interest for the SOMED members:

2nd ESCMID Conference on The Impact of Vaccines on Public Health

22 - 24 March 2013, Prague, Czech Republic

The **2nd ESCMID Conference on the Impact of Vaccines on Public Health** is tailored to specialists or physicians in training in infectious diseases, clinical microbiology, hygiene, public health, vaccinology and other disciplines dealing with all aspects of vaccination.

The scientific progamme will present the latest research across a broad range of topics including:

Pneumococcal vaccines and their implementation strategy	**Vaccines for adults**	**Paediatric and adolescent vaccination**	**Novel vaccine targets**
Vaccines and women: more than a gender issue	**Hepatitis**	**Technological challenges**	**Vaccine policies**
The role of WHO-Europe	**The role of ECDC**	**Innovative vaccines for old diseases**	**Developing countries**
Vaccines for viral haemorrhagic fevers			

For more information about the scientific programme, click here.

ESCMID Attendance Grants

ESCMID provides a number of attendance grants preferentially for ESCMID "young scientist members". The grant covers the registration fee, but not travel or accommodation costs. Please submit your application before **14 February 2013** online through the Conference website.

Scientific Secretariat	**Conference Secretariat**
Giuseppe Cornaglia	ICO
Dept. of Pathology & Diagnostics	Marco Moschin Via Lorenzo
University of Verona	Marcello 32
Phone +39 045 802 71 96	30126 Lido di Venezia Italy
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giuseppe.cornaglia@univr.it	E-mail: ico@icorganization.it

www.worldnutrition2013.com
worldnutrition2013@vibocongresos.com

Dates for your agenda:

Deadline for abstracts submission: January 20th, 2013; **Early Registration:** Before March 20th, 2013

The fifth ***FEBS Advanced Lecture Course on Human Fungal Pathogens*** will be held May 25-31, 2013 in Nice, France. The course will cover the latest topics in fungal pathogenesis. The deadline for pre-registration and abstract submission has been set to February 15th, 2013. The course is open to PhD and postdocs as well as senior scientists (PIs, staff scientists). Attendance will be limited to 120 PhDs and post-docs and 40 senior scientists, selected by the Scientific Advisory Board on the basis of pre-registration and abstract. More information: http://www.pasteur.fr/hfp2013
Thanks to the support of FEBS and FEMS, about

20 fellowships will be accorded to help graduate students and post-doctoral fellows attend the meeting. More information: http://www.pasteur.fr/infosci/conf/hfp2013/Bursaries.html.

Chair of HFP2013: Christophe d'Enfert

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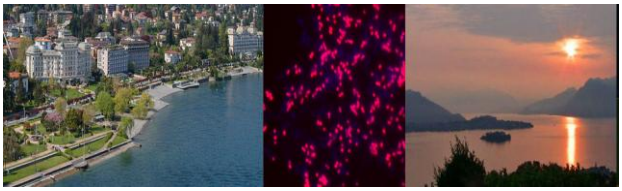
"**International Symposium on *Francisella Tularencis* and Tularemia" will be held in Urgup, Nevsehir, Turkey between 19 - 22 June 2013.**

The symposium web page is opened and can be reached the following web page address: http://www.tularemiasymposium2013.com.

President of The Symposium: Prof. Mehmet Doganay, M.D. , Professor in Inf. Diseases, Dept. of Infectious Diseases, Faculty of Medicine, Erciyes University,38039 Kayseri Turkey, Email. mdoganay@erciyes.edu.tr; Phone. +90 352 4374901-22055; Cell phone. +90 533 3682042; Fax. +90 352 4375273.

that will be held in Stresa, on the shore of Lake Maggiore (Italy).



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Eurobiofilms 2013 will take place between 9th – 12th September 2013 in Gent, Belgium, organized by Tom Coenye, Johan van Eldere and Patrick van Dijck

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The **36th International Congress of the Society for Microbial Ecology and Diseases – SOMED 2013 CONGRESS -** will be held between **24th-26th September 2013** in the University city of Kosice, European Capital of Culture 2013.

Focus areas are current advances in clinical microbiology, dietary modulation of the GIT ecosystem, the effect of antibiotics on microbial ecology, host microbe interactions and the role of biofilms in health and disease.

More information with the hyperlink http://www.somed2013.org/

Organising Secretariat: SOMED2013CONGRESS;

Phone: +421 918 707371;Fax: +421 41 4000123
E-mail: info@somed2013.org; www.somed2013.org

Person of contact: Alojz Bomba DVM, DrSc. Institute of Experimental Medicine, Faculty of Medicine Pavol Jozef Safarik University in Kosice Trieda SNP 1, 040 11 Kosice, Slovak Republic tel.: +421 55 64 24 606, fax: +421 55 64 20 253, mobile: +421 905 947 032

The Joint SOMED – ANAEROBE Meeting, 2014, June 29th- July 1st, Chicago, IL U.S.A.

A Joint Meeting with the Society for Microbial Ecology & Disease- *Anaerobe 2014* will be held ***at the Westin River North Hotel in Chicago***

This will be a joint meeting with SOMED, in which our member Dr. Andrew Onderdonk is the current President. We feel there are a lot of commonalities of interest between the two groups and will serve as a forum to maximize European and American researcher's interaction. Proposals for sessions should be emailed to the ASA office. A Call for Abstracts will be published in the Spring.

Ronald Goldman, Ph.D., *Anaerobe Society*;
E-mail:asa@anaerobe.org; www.anaerobe.org

Recent references of interest for the SOMED members:

Nature. 2012 Jun 13;486(7402):215-21.

doi: 10.1038/nature11209.

A framework for human microbiome research.

Human Microbiome Project Consortium.

Collaborators (248)

Abstract

A variety of microbial communities and their genes (the microbiome) exist throughout the human body, with fundamental roles in human health and disease. The National Institutes of Health (NIH)-funded Human Microbiome Project Consortium has established a population-scale framework to develop metagenomic protocols, resulting in a broad range of quality-controlled resources and data including standardized methods for creating, processing and interpreting distinct types of high-throughput metagenomic data available to the scientific community. Here we present resources from a population of 242 healthy adults sampled at 15 or 18 body sites up to three times, which have generated 5,177 microbial taxonomic profiles from 16S ribosomal RNA genes and over 3.5 terabases of metagenomic sequence so far. In parallel, approximately 800 reference strains isolated from the human body have been sequenced. Collectively, these data represent the largest resource describing the abundance and variety of the human microbiome, while providing a framework for current and future studies.

Comment in: Microbiology: Learning about who we are. [Nature. 2012]

PMID: 22699610 [PubMed - indexed for MEDLINE]

PMCID: PMC3377744 [Available on 2012/12/14]

Nature. 2012 Jun 13;486(7402):207-14. doi: 10.1038/nature11234.

Structure, function and diversity of the healthy human microbiome.

Human Microbiome Project Consortium.

Collaborators (248)

Abstract

Studies of the human microbiome have revealed that even healthy individuals differ remarkably in the microbes that occupy habitats such as the gut, skin and vagina. Much of this diversity remains unexplained, although diet, environment, host genetics and early microbial exposure have all been implicated. Accordingly, to characterize the ecology of human-associated microbial communities, the Human Microbiome Project has analysed the largest cohort and set of distinct, clinically relevant body habitats so far. We found the diversity and abundance of each habitat's signature microbes to vary widely even among healthy subjects, with strong niche specialization both within and among individuals. The project encountered an estimated 81-99% of the genera, enzyme families and community configurations occupied by the healthy Western microbiome. Metagenomic carriage of metabolic pathways was stable among individuals despite variation in community structure, and ethnic/racial background proved to be one of the strongest associations of both pathways and microbes with clinical metadata. These results thus delineate the range of structural and functional configurations normal in the microbial communities of a healthy population, enabling future characterization of the epidemiology, ecology and translational applications of the human microbiome.

Comment in: Microbiology: Learning about who we are. [Nature. 2012]

PMID: 22699609 [PubMed - indexed for MEDLINE]

Nature. 2012 Oct 4;490(7418):55-60. doi: 10.1038/nature11450. Epub 2012 Sep 26.

A metagenome-wide association study of gut microbiota in type 2 diabetes.

Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, Liang S, Zhang W, Guan Y, Shen D, Peng Y, Zhang D, Jie Z, Wu W, Qin Y, Xue W, Li J, Han L, Lu D, Wu P, Dai Y, Sun X, Li Z, Tang A, Zhong S, Li X, Chen W, Xu R, Wang M, Feng Q, Gong M, Yu J, Zhang Y, Zhang M, Hansen T, Sanchez G, Raes J, Falony G, Okuda S, Almeida M, LeChatelier E, Renault P, Pons N, Batto JM, Zhang Z, Chen H, Yang R, Zheng W, Li S, Yang H, Wang J, Ehrlich SD, Nielsen R, Pedersen O, Kristiansen K, Wang J.

Source: BGI-Shenzhen, Shenzhen 518083, China.

Abstract

Assessment and characterization of gut microbiota has become a major research area in human disease, including type 2 diabetes, the most prevalent endocrine disease worldwide. To carry out analysis on gut microbial content in patients with type 2 diabetes, we developed a protocol for a metagenome-wide association study (MGWAS) and undertook a two-stage MGWAS based on deep shotgun sequencing of the gut microbial DNA from 345 Chinese individuals. We identified and validated approximately 60,000 type-2-diabetes-associated markers and established the concept of a metagenomic linkage group, enabling taxonomic species-level analyses. MGWAS analysis showed that patients with type 2 diabetes were characterized by a moderate degree of gut microbial dysbiosis, a decrease in the abundance of some universal butyrate-producing bacteria and an increase in various opportunistic pathogens, as well as an enrichment of other microbial functions conferring sulphate reduction and oxidative stress resistance. An analysis of 23 additional individuals demonstrated that these gut microbial markers might be useful for classifying type 2 diabetes.

Comment in : Genomics: Resident risks. [Nature. 2012]

PMID: 23023125 [PubMed - in process]

Nature. 2011 May 12;473(7346):174-80. Epub 2011 Apr 20.

Enterotypes of the human gut microbiome.

Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, Fernandes GR, Tap J, Bruls T, Batto JM, Bertalan M, Borruel N, Casellas F, Fernandez L, Gautier L, Hansen T, Hattori M, Hayashi T, Kleerebezem M, Kurokawa K, Leclerc M, Levenez F, Manichanh C, Nielsen HB, Nielsen T, Pons N, Poulain J, Qin J, Sicheritz-Ponten T, Tims S, Torrents D, Ugarte E, Zoetendal EG, Wang J, Guarner F, Pedersen O, de Vos WM, Brunak S, Doré J; MetaHIT Consortium, Antolín M, Artiguenave F, Blottiere HM, Almeida M, Brechot C, Cara C, Chervaux C, Cultrone A, Delorme C, Denariaz G, Dervyn R, Foerstner KU, Friss C, van de Guchte M, Guedon E, Haimet F, Huber W, van Hylckama-Vlieg J, Jamet A, Juste C, Kaci G, Knol J, Lakhdari O, Layec S, Le Roux K, Maguin E, Mérieux A, Melo Minardi R, M'rini C, Muller J, Oozeer R, Parkhill J, Renault P, Rescigno M, Sanchez N, Sunagawa S, Torrejon A, Turner K, Vandemeulebrouck G, Varela E, Winogradsky Y, Zeller G, Weissenbach J, Ehrlich SD, Bork P.

Source: European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany.

Erratum in : Nature. 2011 Jun 30;474(7353):666.

Abstract

Our knowledge of species and functional composition of the human gut microbiome is rapidly increasing, but it is still based on very few cohorts and little is known about variation across the world. By combining 22 newly sequenced faecal metagenomes of individuals from four countries with previously published data sets, here we identify three robust clusters (referred to as enterotypes hereafter) that are not nation or continent specific. We also confirmed the enterotypes in two published, larger cohorts, indicating that intestinal microbiota variation is generally stratified, not continuous. This indicates further the existence of a limited

number of well-balanced host-microbial symbiotic states that might respond differently to diet and drug intake. The enterotypes are mostly driven by species composition, but abundant molecular functions are not necessarily provided by abundant species, highlighting the importance of a functional analysis to understand microbial communities. Although individual host properties such as body mass index, age, or gender cannot explain the observed enterotypes, data-driven marker genes or functional modules can be identified for each of these host properties. For example, twelve genes significantly correlate with age and three functional modules with the body mass index, hinting at a diagnostic potential of microbial markers.

PMID: 21508958 [PubMed - indexed for MEDLINE]

Nature. 2010 Mar 4;464(7285):59-65.

A human gut microbial gene catalogue established by metagenomic sequencing.

Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR, Li J, Xu J, Li S, Li D, Cao J, Wang B, Liang H, Zheng H, Xie Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Le Paslier D, Linneberg A, Nielsen HB, Pelletier E, Renault P, Sicheritz-Ponten T, Turner K, Zhu H, Yu C, Li S, Jian M, Zhou Y, Li Y, Zhang X, Li S, Qin N, Yang H, Wang J, Brunak S, Doré J, Guarner F, Kristiansen K, Pedersen O, Parkhill J, Weissenbach J; MetaHIT Consortium, Bork P, Ehrlich SD, Wang J.

Collaborators (36)

Source: BGI-Shenzhen, Shenzhen 518083, China.

Abstract

To understand the impact of gut microbes on human health and well-being it is crucial to assess their genetic potential. Here we describe the Illumina-based metagenomic sequencing, assembly and characterization of 3.3 million non-redundant microbial genes, derived from 576.7 gigabases of sequence, from faecal samples of 124 European individuals. The gene set, approximately 150 times larger than the human gene complement, contains an overwhelming majority of the prevalent (more frequent) microbial genes of the cohort and probably includes a large proportion of the prevalent human intestinal microbial genes. The genes are largely shared among individuals of the cohort. Over 99% of the genes are bacterial, indicating that the entire cohort harbours between 1,000 and 1,150 prevalent bacterial species and each individual at least 160 such species, which are also largely shared. We define and describe the minimal gut metagenome and the minimal gut bacterial genome in terms of functions present in all individuals and most bacteria, respectively.

Comment in: A gut feeling for disease. [Nat Rev Genet. 2010]

For all SOMED members and friends,

Merry Christmas and

a Happy and successful New Year 2013!

SOMED MEMBERSHIP 2013 APPLICATION FORM

First name: **Surname**:

Dept/Laboratory/Center:

Institution/Company: **Street/P.O.Box**:

Postal code: **City**: State: Country:

Phone: Fax: E-mail:

I authorize the inclusion of my data in the SOMED Membership Directory as above detailed.
Date Signature

□ **Regular membership: EUR 40 (or USD 55)**

□ **Corporate membership: EUR 400 (or USD 550)**

□ **Student membership: EUR 20 (or USD 25)** *(Please add student status certification)*

□ **Supporting membership: EUR 1000 (or USD 1350)**

Please send your payment to the **SOMED Treasurer, Professor Eugenia Bezirtzoglou**, by:

□ Bank transfer to: **EUGENIA BEZIRTZOGLOU**
PIRAEUS BANK, Athens, Greece
IBAN: GR04 0172 3510 0053 5103 0344 567 - **BIC**: PIRBGRAA

□ By Cheque to: **EUGENIA BEZIRTZOGLOU**

Please send the cheque by registered mail to:

Prof. Eugenia Bezirtzoglou
Faculty of Agricultural Development
Dept. Food Science and Technology
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2 Fleming Street, 163 45
Ano Ilioupolis, Athens, Greece

Please fax (+30 25 52041191) or send by e-mail (empezirt@yahoo.gr) this form to Prof. Bezirtzoglou