The Paradigms They Are a-Changin’:
Past, present and future of your favorite bacteria.

Damien P. Devos
CABD, Uni. Pablo de Olavide,
Sevilla, SP
damienpdevos@gmail.com
Disclaimer

- My point of view and my own only!
- Totally biased
First, there was Chlamydia

“Chlamydozoa” (from the Greek word χλαμύς, meaning mantle or cloak). Originally considered neither protozoa nor bacteria and then regarded as viruses, in the 1960s they were recognized as bacteria. Later, these unique microorganisms were found to be among the most important bacterial pathogens of humankind. Halberstädter's and Prowazek's Chlamydozoa are now called *Chlamydia trachomatis*.

Horn, Ann Rev Micro 2008
Then came *Planctomycetes*

*Pl. Bekefii*

Nandor Gimesi, 1924

*Planctomycetes* = floating fungi
PG-less bacteria

- No PG in Chlamydia (Caldwell et al., 81)
- No PG in Planctomyces, proteinaceus CW (Konig et al., 84)
Gemmata obscuriglobus, a new genus and species of the budding bacteria.

Franzmann PD, Skerman VB.

Abstract

A single strain of a budding bacterium was isolated from freshwater. The strain had a life-cycle, with a multistrichous swarmer stage, and produced a phase-dark inclusion of packed ribosomes and nuclear material. The mol % G + C of the DNA was 64.4 +/- 1.0. A new genus, Gemmata with the type species Gemmata obscuriglobus is proposed. The type strain is UQM 2246.
The occurrence of a membrane-bounded nucleoid in a eubacterial prokaryote is a significant exception to the evidence supporting the prokaryote/eukaryote dichotomous classification of cell structure.
Missing lithotroph identified as new planctomycete

Marc Strous*, John A. Fuerst†, Evelien H. M. Kramer*, Susanne Logemann*, Gerard Muyzer†, Katinka T. van de Pas-Schoonen*, Richard Webb†, J. Gis Kuenen* & Mike S. M. Jetten*

* Department of Biotechnology, Delft University of Technology, Julianalaan 67, 2628 BC Delft, The Netherlands
† Department of Microbiology & Parasitology and the Centre for Microscopy and Microanalysis, University of Queensland, Brisbane, Queensland 4072, Australia
‡ Netherlands Institute for Sea Research, 1790 AB Den Burg, The Netherlands

With the increased use of chemical fertilizers in agriculture, many densely populated countries face environmental problems associated with high ammonia emissions. The process of anaerobic ammonia oxidation ('anammox') is one of the most innovative technological advances in the removal of ammonia nitrogen from

NATURE| VOL 400 | 29 JULY 1999 | www.nature.com
Verrucomicrobia & Lentisphaerae

Vicitallis vadensis gen. nov., sp. nov., a sugar-fermenting anaerobe from human faeces.

Zoetendal EG, Plugge CM, Akkermans AD, de Vos WM.


Lentisphaera araneosa gen. nov., sp. nov, a transparent exopolymer producing marine bacterium, and the description of a novel bacterial phylum, Lentisphaerae.

Cho JC, Virgin KL, Morris RM, Giovannoni SJ.
The PVC superphylum

Very different organism
More controversy!

Wagner and Horn (2006)
3rd cell plan

Fuerst, Ann Rev Micro 2005
Membrane coat like proteins in PVCs

Santarella et al., PLoS B 2010
Prokaryotic endocytosis?

Lonhienne et al., PNAS 2010
Controversy up to ~2013

- PG-less
- FtsZ-less
- Nucleated bacteria
- Membrane system, Membrane coat proteins, Endocytosis
- Melting pot of very different bacteria
- 3rd cell plan, not G-, not G+
Research Topic

Recent advances in the biology of planctomycetes and verrucomicrobia

Submission closed.

About this Research Topic

Planctomycetes and verrucomicrobia exhibit distinctive cellular properties, widespread environmental distribution, unique physiologies, and unusual associations with eukaryotic hosts. Recently the planctomycete and verrucomicrobia research community has begun to expand, stimulated by several key discoveries. ...
1st PVC meeting
Heidelberg, DE 2013

Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum: Exceptions to the bacterial definition?
28 February - 2 March, 2013 | Heidelberg, Germany

ABOUT THE WORKSHOP

The Planctomycetes-Verrucomicrobia-Chlamydiae (PVC) superphylum is an assemblage with different data and phylogeny estimation methods. This EMBO workshop will be for the PVC members. The Workshop will bring together researchers working on such bacteria and evolutionary scenarios. [read more]

Volume 104, Issue 4, October 2013
Special issue on Papers from the 1st EMBO workshop on the Planctomycetes-Verrucomicrobia-Chlamydiae superphylum: Exceptions to the bacterial definition?

Issue Editors: Damien P Devoe, Christian Jogler, John A. Fuerst
ISSN: 0003-6972 (Print) 1572-9699 (Online)

VENUE

Erlangen, IFB 267 Room 3111
University Erlangen-Nuremberg
Heidelberg SE

Register Now

We look forward to welcoming you in Heidelberg!

Meet other participants on facebook

14 articles, ~30 authors
Gemmata 3D reconstruction

Sections 250nm
Technai F30 300kv (FEI)
Dual axis tilt series
IMOD
1130 slices/5

Santarella et al., PLoS B 2010
Variation of, but no exception to, Gram(-) cell plan

- **E. coli**
- **Chlamydiae**
- **P. marina**
- **I. pallida**
- **anammox**
- **P. limnophilus**
- **G. obscuriglobus Type I**
- **G. obscuriglobus Type II**
- **P. dejongei (V)**
- **C. flavus (V)**
- **V. spinosum (V)**

Devos TiM 2013
Planctomycetes do possess a peptidoglycan cell wall.

Jeske O¹, Schüler M², Schumann F³, Schneider A⁴, Roedeker C¹, Jogler M¹, Boßlischweiler D², Rohde M⁵, Mayer C⁴, Engelhardt H², Spring S³, Jogler C¹.

Anammox Planctomycetes have a peptidoglycan cell wall.

van Teeseling M G¹, Mesman R J¹, Kuru F², Espaillat A³, Cava F³, Brun Y V⁴, VanNieuwenhze M S⁵, Kortal B⁵, van Nifrik L¹.

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Ostiautaceae of the Verrucomicrobial Subdivision 4.

Rast P¹, Glockner F G⁷, Roedeker C¹, Jeske O¹, Wiegard S¹, Reinhardt B³, Schumann F³, Rohde M⁵, Spring S³, Glockner F G⁷, Jogler C², Jogler M¹.
Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum: New model organisms

2 - 4 June, 2015 | Carmona (Sevilla), Spain

The Planctomycetes-Verrucomicrobia-Chlamydiae (PVC) superphylum is an assemblage of bacterial phyla which is consistently recovered as a monophyletic group with different data and phylogeny estimation methods. This conference will be the second one to focus on the characterization and fundamental understanding of the PVC members. The Workshop will bring together researchers working on such bacteria and provide a broad coverage of these exceptional bacterial taxa and evolutionary scenarios. The PVC superphylum has more recently emerged as fascinating subjects for research in evolutionary cell biology, ecology and biotechnology, and human health.

Register Now

We look forward to welcoming you to Sevilla!
Frontiers SI
Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!

- 12 articles
- 86 authors
- 13 countries
  - Netherlands, Portugal, USA, Malaysia, UK, Germany, Switzerland, Austria, Spain, France, Finland, Greece, New Zealand
Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!

Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning
John Vollmers, Martinique Frentrup, Patrick Rast, Christian Jogler and Anne-Kristin Kaster

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision
Patrick Rast, Ines Glückner, Christian Boeckeler, Olga Jeske, Sandra Wiegand, Richard Reinhardt, Peter Schumann, Manfred Rohde, Stefan Spring, Frank O. Glückner, Christian Jogler and Mareike Jogler

Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum
Elena Rivas-Marin, Inès Canosa and Damien P. Devos

The S-Layer Protein of the Anammox Bacteria Kuenenia stuttgartiensis is Heavily O-Glycosylated
Muriel C. F. van Teeseling, Daniel Maresch, Cornelia B. Ral Rudolf Figl, Friedrich Altmann, Mike S. M. Jetten, Paul Messner, Christina Schäffer and Laura van Niftrik

Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvylglucosamine Reductase/UDP-N-Acetylmurametil-Alanine Ligase Fusion Enzyme from Verrucomicrobiun spinosum DSM 4136T
Kubra F. Naqui, Delphine Patin, Matthew S. Westley, Michael A. Savka, Renwick C. J. Dobson, Han Ming Gan, Hélène Barreteau, Didier Bianot, Dominique Mengin-Lecreux and André O. Hudson

Frontiers SI

Fuerstia marisgermanicae gen. nov., sp. nov., an Unusual Member of the Phyllum Planctomycetes from the German Wadden Sea

Characterization of Outer Membrane Proteome of Akkermansia muciniphila Reveals Sets of Novel Proteins Exposed to the Human Intestine
Noora Ottman, Laura Huuskoenen, Justus Reunanen, Sjef Boeren, Judith Klievink, Hauke Smidt, Clara Belzer and Willem M. de Vos

Development of Genetic Tools for the Manipulation of the Planctomycetes
Elena Rivas-Marin, Ines Canosa, Eduardo Santero and Damien P. Devos

Developing Techniques for the Utilization of Planctomycetes As Producers of Bioactive Molecules
Olga Jeske, Frank Surup, Marcel Ketteniö, Patrick Rast, Birthe Förster, Mareike Jogler, Joachim Wink and Christian Jogler

Helena M. B. Seth-Smith, Pantelis Katharios, Nancy Dourala, José M. Mateos, Alexander G. J. Feht, Lisbeth Nufet, Maja Ruetten, Maricruez Guevara Soto and Lloyd Vaughan

Planctomycetes as Novel Source of Bioactive Molecules
Ana P. Graça, Rita Calisto and Olga M. Lage

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision
Patrick Rast, Ines Glückner, Christian Boeckeler, Olga Jeske, Sandra Wiegand, Richard Reinhardt, Peter Schumann, Manfred Rohde, Stefan Spring, Frank O. Glückner, Christian Jogler and Mareike Jogler

Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum
Elena Rivas-Marin, Inès Canosa and Damien P. Devos

The S-Layer Protein of the Anammox Bacteria Kuenenia stuttgartiensis is Heavily O-Glycosylated
Muriel C. F. van Teeseling, Daniel Maresch, Cornelia B. Ral Rudolf Figl, Friedrich Altmann, Mike S. M. Jetten, Paul Messner, Christina Schäffer and Laura van Niftrik

Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvylglucosamine Reductase/UDP-N-Acetylmurametil-Alanine Ligase Fusion Enzyme from Verrucomicrobiun spinosum DSM 4136T
Kubra F. Naqui, Delphine Patin, Matthew S. Westley, Michael A. Savka, Renwick C. J. Dobson, Han Ming Gan, Hélène Barreteau, Didier Bianot, Dominique Mengin-Lecreux and André O. Hudson

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision
Patrick Rast, Ines Glückner, Christian Boeckeler, Olga Jeske, Sandra Wiegand, Richard Reinhardt, Peter Schumann, Manfred Rohde, Stefan Spring, Frank O. Glückner, Christian Jogler and Mareike Jogler

Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum
Elena Rivas-Marin, Inès Canosa and Damien P. Devos

The S-Layer Protein of the Anammox Bacteria Kuenenia stuttgartiensis is Heavily O-Glycosylated
Muriel C. F. van Teeseling, Daniel Maresch, Cornelia B. Ral Rudolf Figl, Friedrich Altmann, Mike S. M. Jetten, Paul Messner, Christina Schäffer and Laura van Niftrik

Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvylglucosamine Reductase/UDP-N-Acetylmurametil-Alanine Ligase Fusion Enzyme from Verrucomicrobiun spinosum DSM 4136T
Kubra F. Naqui, Delphine Patin, Matthew S. Westley, Michael A. Savka, Renwick C. J. Dobson, Han Ming Gan, Hélène Barreteau, Didier Bianot, Dominique Mengin-Lecreux and André O. Hudson

Three Novel Species with Peptidoglycan Cell Walls form the New Genus Lacunisphaera gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision
Patrick Rast, Ines Glückner, Christian Boeckeler, Olga Jeske, Sandra Wiegand, Richard Reinhardt, Peter Schumann, Manfred Rohde, Stefan Spring, Frank O. Glückner, Christian Jogler and Mareike Jogler

Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum
Elena Rivas-Marin, Inès Canosa and Damien P. Devos

The S-Layer Protein of the Anammox Bacteria Kuenenia stuttgartiensis is Heavily O-Glycosylated
Muriel C. F. van Teeseling, Daniel Maresch, Cornelia B. Ral Rudolf Figl, Friedrich Altmann, Mike S. M. Jetten, Paul Messner, Christina Schäffer and Laura van Niftrik

Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvylglucosamine Reductase/UDP-N-Acetylmurametil-Alanine Ligase Fusion Enzyme from Verrucomicrobiun spinosum DSM 4136T
Kubra F. Naqui, Delphine Patin, Matthew S. Westley, Michael A. Savka, Renwick C. J. Dobson, Han Ming Gan, Hélène Barreteau, Didier Bianot, Dominique Mengin-Lecreux and André O. Hudson
Damien Paul Devos,
The Research Topic you recently contributed to is attracting interest from the community, below you can see its current impact numbers.

**Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!**

12 ARTICLES
16,090 TOTAL VIEWS
1,875 DOWNLOADS
45 SHARES
Resolving the controversies

Superphylum status now amply accepted
Variation of Gram – cell plan
PG present
Pubmed & genomes trends

Planomycetes

Verrucomicrobia

Lentisphaerae

Genomes deposited in Gold

PVC bacteria: New model organisms!

Ecology and biotechnology:
- Carbon and nitrogen cycle on earth
- Methane oxidation (anammox)
- Biomolecules
- Antibiotics

Human health:
- Chlamydiae
- Verrucomicrobia
  - gastrointestinal homeostasis
  - Immune system
  - Cell development
  - Obesity
- Planctomycetes

Evolutionary cell biology:
- Deviate from 'classical' bacteria characters and definition
- Origin of those characters
PVC genetic tools

Characterization of Planctomyces limnophilus and development of genetic tools for its manipulation establish it as a model species for the phylum Planctomycetes.
Jogler C, Göckner FO, Kolter R.

Random transposon mutagenesis of Verrucomicrobiun spinosum DSM 4136(T).
Domman DB, Steven BT, Ward NL.

Development of Genetic Tools for the Manipulation of the Planctomyces

Bona Rivas-Marin¹, Inés Canosa², Eduardo Santac² and Damien P. Devos³*

Characterization of a planctomycetal organelle: a novel bacterial microcompartment for the aerobic degradation of plant saccharides.
Erbilgin O, McDonald KL, Kerfeld CA.

Transposon mutagenesis of Planctomyces limnophilus and analysis of a pckA mutant.
Schreier HJ, Dejtsisakdi W, Escalante JO, Brailo M.
Happening right now!

3x researchers
10 countries
21 talks

Planctomycetes-Verrucomicrobia-Chlamydiae bacteria:
New model organisms in the omics era

Porto, Portugal
10 – 12 May 2017
The future is bright!

Let’s ask for money!
Open Questions & Future Research

● Evolution: Diverse group of bacteria
  – ‘Ancestral’ bacteria or Long Branch Atraction? Rapid evolution?
  – How was diversity generated from Last PVC Common Ancestor (LPCA)?

● Cell biology
  – Endomembrane system (how? When, dynamic?)
  – Membrane coat proteins (link with eukaryotes → LGT?)
  – Tubulovesicular network

● Link to human (and animal) health
  – Verrucomicrobia and Planctomycetes

● Earth system
  – Including kelp

● Bioproduction and bioremediation
Prokaryotic connected vesicles

Acehan et al., JCS 2014; Boedeker et al., Nat Coms 2017
Defensive extrusive ectosymbionts of Euclotidium (Ciliophora) that contain microtubule-like structures are bacteria related to Verrucomicrobia

Petroni et al. PNAS 2000
The bacterial pore complex

The bacterial ‘mitochondrion’

Isolation and characterization of a prokaryotic cell organelle from the anammox bacterium *Kuenenia stuttgartiensis*

Neumann *et al*. Mol Micro 2014
Verrucomicrobia were detected in 180 out of 181 soils examined, with members of the class Spartobacteria dominating verrucomicrobial communities in nearly all biomes and soil depths. The relative abundance of Verrucomicrobia was highest in grasslands and in subsurface soil horizons, where they were often the dominant bacterial phylum. Although their ecology remains poorly understood, Verrucomicrobia appear to be dominant in many soil bacterial communities across the globe, making additional research on their ecology clearly necessary.
some bacterial relationships were always recovered and strongly supported regardless of the model implemented such as a Chlamydiae/Planctomycetes clade (PC), a Fibrobacteria, Bacteriodetes, Chlorobi + Gemmatimonadetes monophyly (labeled clade “A” in Fig. 4), a Proteobacteria (Alpha, Beta, and Gamma) + Nitrospirae group (or clade “B” in Fig. 4) and a Deferribacteres, Chrysiogenetes, Thermodesulfbacteria, + Delta/Epsilon Proteobacteria clade (clade “C” in Fig. 4).

Lasek-Nesselquist and Gogarten (2013) MPE
From an evolutionary perspective, two chlamydia-like bacteria deserve special attention, the uncultured “Candidatus Piscichlamydia salmonis” and “Candidatus Clavochlamydia salmonicola.” “Ca. Piscichlamydia salmonis” is particularly interesting because it currently represents the deepest branch in the Chlamydiae, i.e., it might still share features of the last common ancestor of all chlamydiae, which are absent in all other chlamydial lineages. “Ca. Clavochlamydia salmonicola” is the closest relative of the Chlamydiaceae (Figure 1) and might thus represent a transitional stage between the highly adapted human and animal pathogens of the Chlamydiaceae and all other chlamydia-like bacteria. Novel approaches and technologies such as whole-genome amplification and pyrosequencing might facilitate genome analysis of these organisms in the near future.
Gemmata obscuriglobus UQM2246 tax214688 NCBI 7756p (7756 proteins)

The protein sequences in FASTA format used in this analysis can be downloaded [here](http://pvcbacteria.org/pvcbase/). The complete table is also available as [XLSX](http://pvcbacteria.org/pvcbase/) format for downloading.

<table>
<thead>
<tr>
<th>NAME / ID</th>
<th>Description</th>
<th>Organism</th>
<th>Protein Length (aa)</th>
<th>Best PHAST Hit</th>
<th>Uniprot Accession</th>
<th>Best PHAST Hit Gene</th>
<th>Best PHAST Hit GO terms</th>
<th>Best PHAST Hit Keywords</th>
<th>Best PHAST Hit EC number</th>
<th>Signal_Peptide</th>
<th>TMDB</th>
<th>Disorder %</th>
<th>Biological Functions</th>
<th>InterPro GO terms - Molecular Function</th>
<th>InterPro GO terms - Biological Process</th>
<th>InterPro GO terms - Cellular Component</th>
</tr>
</thead>
</table>
| ATP-dependent helicase Gemmata obscuriglobus 700 Q4AYV7 [Cov=38.1%] [Exp=86-184] akd55 | ATP-dependent helicase Gemmata obscuriglobus DDX55 | GO:0005224: ATP-binding; IA:0010000908 helicase activator; IA:0010000908 DNA binding; IA:0010000908 ATP binding | ATP-binding; Helicase activity; DNA binding; RNA binding | EC:3.6.4.13 | 0 [80%] | 2.8% | Q4AYV7, [Cov=38.1%] [Exp=86-184] | 0.000000 | DEAD/DEAH box helicase domain | GO:0005224: ATP-binding; IA:0010000908 helicase activator; IA:0010000908 DNA binding; IA:0010000908 ATP binding | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEAH box helicase domain | DEAD/DEA
PVC blast

PVCbase BLAST

Nucleotide databases
- Akkermansia muciniphila
- Blastopirellula marina
- Chlamydia felis
- Chlamydia trachomatis
- Chlamydia abortus
- Chlamydia pecorum
- Chlamydia psittaci
- Chthoniobacter flavus
- Clamydia pneumonae
- CoralloMargara akujimensis
- Gemmata obscuriglobus
- Isosphaera pallida
- Lentisphaera araneosa
- Methylocaldiphilum fumaricicum
- Methylocaldiphilum infernum
- Opitutus terrae
- Parachlamydia acanthamoebae
- Pedosphaera parvula
- Phycisphaera mikurensis
- Pirellula staleyi
- Planctomycetes brasilienensis

Protein databases
- Akkermansia muciniphila
- Blastopirellula marina
- Chlamydia pneumonae
- Chlamydia psittaci
- Chlamydia trachomatis
- Chlamydia pecorum
- Chlamydia felis
- Chthoniobacter flavus
- CoralloMargara akujimensis
- Gemmata obscuriglobus UQMM2246
- Isosphaera pallida ATCC43644
- Lentisphaera araneosa HTCC2155
- Methylocaldiphilum fumaricicum SolV
- Methylocaldiphilum infernum V4
- Opitutus terrae DSM112046
- Parachlamydia acanthamoebae UV7
- Pedosphaera parvula Efri514
- Phycisphaera mikurensis NBRC102666
- Pirellula staleyi DSM0006
- Planctomycetes brasilienensis ATCC49424
2020?

Nijmegen?

Lausanne?
Previous PVC meetings
Heidelberg, DE 2013 - Sevilla, SP 2015

43 participants; 8 keynotes
16 countries

27 participants; 4 keynotes
10 countries

The 1st EMBO workshop on PVC bacteria-Planctomycetes-Verrucomicrobia-Chlamydiae superphylum: exceptions to the bacterial definition?


Research Topic
Planctomycetes-Verrucomicrobia-Chlamydiae bacterial superphylum: New model organisms!