



Marine Microbiology Diversity of China and Methodologies of Genetic Diversity Studies

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Marine Microbiology Diversity of China

INTERNATIONAL CENSUS OF MARINE MICROBES

The role of the International Census of Marine Microbes (ICoMM) is to promote an agenda and an environment that will accelerate discovery, understanding, and awareness of the global significance of marine microbes.

- **a total of approx. 5,000-10,000 thousands marine microorganisms living on our earth, but only 5,000 kinds were named.**



Culture collections of Marine Microorganisms around the world

Culture collections	Country	Adress
IMBCC	USA	University of Hawaii, 2525 Correa Road, HIG 131, Honolulu, HI 96822-2219, USA
KMM	Russia	Pacific Institute of Bioorganic Chemistry, Far-Eastern Branch, Russian Academy of Sciences, 690022 Vladivostok, Prospekt 100 Let Vladivostoku 159
MBIC	Japan	Marine Biotechnology Institute Culture Collection, 3-75-1 Heita, Kamaishi, Iwate 026-001
NCMB	UK Scotland	Torry Research Station Aberdeen, Scotland,
RCC	France	Station Biologique, Place G. Tessier, 29680 Roscoff
WCUM	U.S.A.	Center of Marine Biotechnology, 701 E. Pratt Street, Baltimore, MD, 21202



Traditional culturing: 2216E


Extinction culturing: (S. A. Connon and S. J. Giovannoni, 2002)

Gel microdrop: cAMP (Alke Bruns, 2002)



Different ecosystems for marine microorganisms

- **Coastal Ecosystems : Li Yun et al.,2006**
- **estuary ecosystem: Ning Xiurin et al.,2004**
- **coral reefs ecosystems: Dong Junde, et al.,2005**
- **Mangrove Ecosystems : Lin Peng et al.,2005**
- **Deep Sea Ecosystems :Mu Chunhua et al.,2005**

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- Now, our database contains the information of 4627 marine microorganisms

prokaryote : bacillus , actinomycete

eucaryote : fungi (mould , yeast , single-celled algae)

Virus

中国海洋微生物菌种保藏管理中心 - Microsoft Internet Explorer

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Marine Culture Collection 中国海洋微生物菌种保藏管理中心

新闻公告 news / notice / on going project

- 第八届国际海洋生物技术大会召开 2007-4-19
- 南开大学破译一株能“吃”石油的细菌 2007-4-9
- 科学家进行全球海洋微生物普查发现大量 2007-3-23
- 中国工业生物技术发展高峰论坛在天津举 2007-3-21
- 关于召开“2007两岸生物资源与生物 2007-3-13
- 太阳越胀越大 50亿年后将把月球撕成 2007-1-24
- 2006中国海洋环境关键词 渤海污染 2007-1-23

菌种检索 收藏编号 中文名称

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页 显示 30 条记录 共155页/共找到4627条数据

批量修改 数据统计 培养基 添加数据 修改数据 搜索数据 文献数据 添加数据 修改数据 搜索数据 保藏单位 添加数据 修改数据 搜索数据 图像数据 数据列表 添加数据

全选 反选 删除选中的数据

菌株编号	中心缩写	中文名称	拉丁属名	拉丁种名	平台资源号	管理
<input type="checkbox"/> 1C00002	MCCC	海杆菌	Marinobacter	sp.	1535C0001000000562	修改 删除 图
<input type="checkbox"/> 1A00002	MCCC	冷海希瓦氏菌	Shewanella	frigidimarina	1535C0001000000002	修改 删除 图
<input type="checkbox"/> 1A00003	MCCC	红串红球菌	Rhodococcus	erythropolis	1535C0001000000003	修改 删除 图
<input type="checkbox"/> 1A00006	MCCC	巨大芽孢杆菌	Bacillus	megaterium	1535C0001000000006	修改 删除 图
<input type="checkbox"/> 1A00004	MCCC	鳗利斯顿氏菌	Listonella	anguillarum	1535C0001000000004	修改 删除 图
<input type="checkbox"/> 1A00005	MCCC	蜡样芽孢杆菌	Bacillus	cereus	1535C0001000000005	修改 删除 图

修改 删除 图



Microbial aspects of biodiversity

- It is almost impossible to quantify the abundance of an uncultured organism
- The possibility to perform environmental genomics opens a perspective to assess the potential of yet uncultured microorganisms



Methodologies of Genetic Diversity Studies


Genetic diversity


Genetic diversity is an important part of biodiversity.

In large scale, genetic diversity means the summation of every kind of genetic information carried by all the organisms on the earth.

In small scale, genetic diversity means the gene variation in the same species, which include genetic variance in the groups with significant difference of the same species and that in the same group.

Genetic diversity provides the basis to the evolution of life and differentiation of species.

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- 1) Know the hereditary structure of natural population, which contains the genetic variance in the same natural population and between the natural populations (such as: gene frequency, the number of loci for every gene, the number of allele for every loci). Higher level of genetic diversity means higher stability of the population structure.
 - 2) Establish gene pool of the Germplasm resource , which is an important way to protect the Rare and Endangered organisms
 - 3) This study is important for higher effectively cultivating : high quality, stable, yield and stress resistance .

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- 4) Great potential will be shown with the develop of genetic diversity research about extremophiles. Because of their special physiological functions, extremophiles can survive in and adapt to some extreme environments, such as high or low temperature, extremely salty, acidic or alkaline conditions, as well as high p ressure etc. They can also, with their unique metabolic pathway formed in special environments, p roduce many special bioactive substances, such as extremozymes and antibiotics. These bioactive substances showed considerable usefulness and great potential in many areas, such as medicine, food, agriculture, chemical engineering and environmental p rotection.
 - 5) provide scientific basis for constructive protection plan for genetic diversity through objective estimate.

Methodologies of Genetic Diversity

Protein: isozyme

PLFA: Phospholipid fatty acid

DNA: RFLP, SSR, RAPD, ARDRA, ISSR, AFLP, DGGE/TGGE, T-RFLP, DNA sequence,

ARDRA: amplified rDNA restriction analysis

ARDRA for bacteria consists of the amplification of the 16S rRNA gene, followed by separate restriction digestion with different restriction enzymes (*HhaI*, *MboI* and *RsaI et al*). This yields restriction patterns which in combination result in ARDRA profiles which enable differentiation between most species. And with a library of ARDRA profiles, obtained from well-identified bacterial strains, the combination of the obtained fingerprints is designated an ARDRA profile which can be compared.

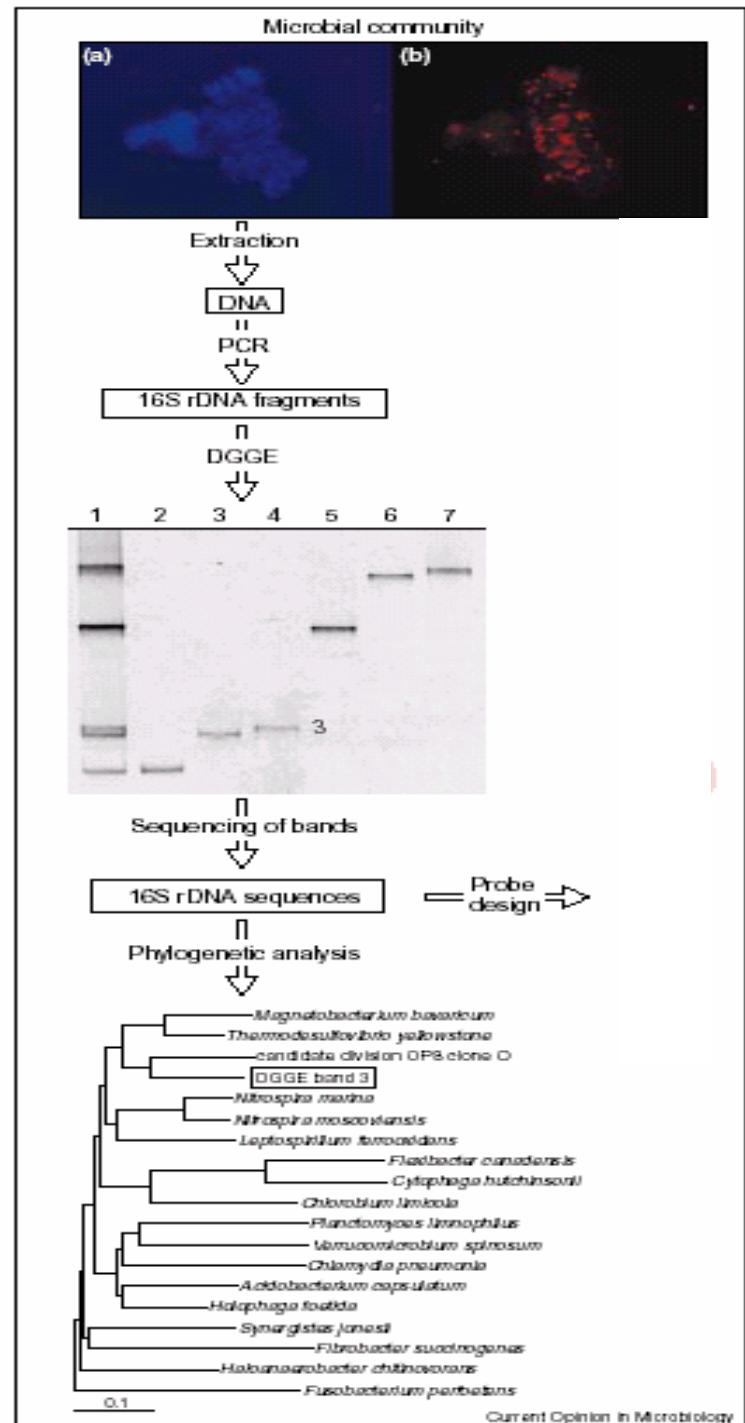
Song Zhigang, 2006--A primary study on population biodiversity of Marine microorganisms from east China sea

DGGE /TGGE

Since 1994, after the introduction of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in environmental microbiology these techniques are now routinely used in many microbiological laboratories worldwide as molecular tools to compare the diversity of microbial communities and to monitor population dynamics.

Su Yunhuan,2006--Investigation on bacterial diversity of deep-sea sediments from Pacific Arctic

Tan Tianfeng,2006--Construction of Marine Oil Biodegradation Bacterial Consortium and Its Dynamic Change in the Process of Oil Consumption



T-RFLP

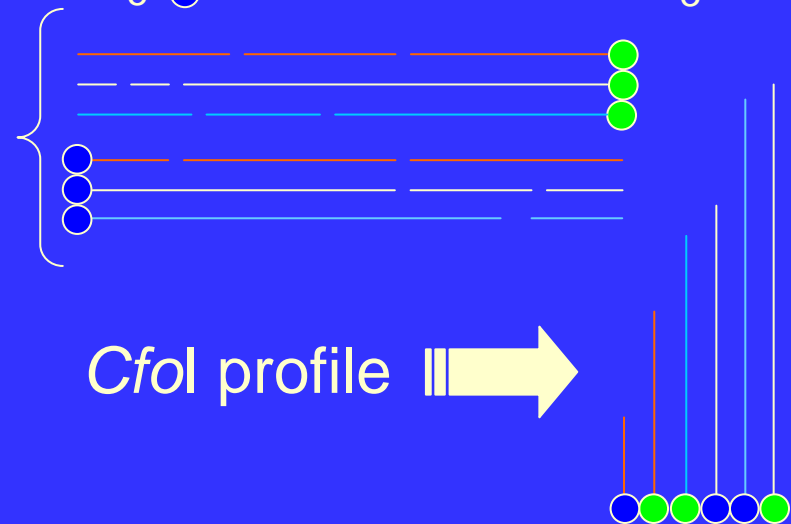
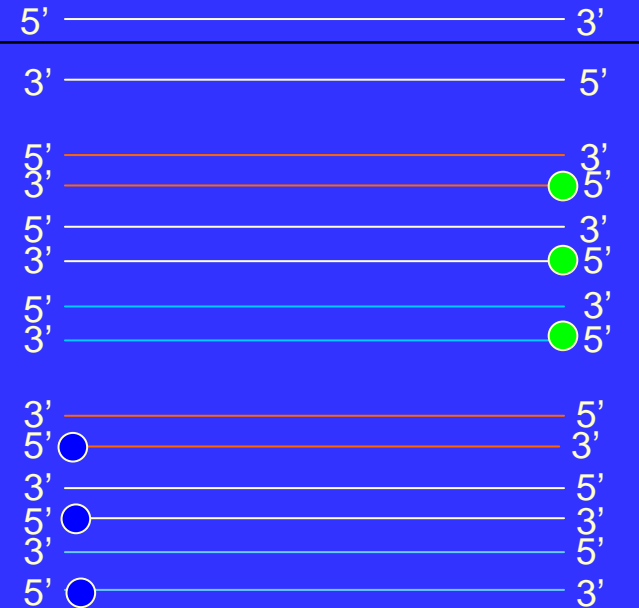
Extraction of community DNA or RNA from environmental samples

PCR amplification of 16S rRNA gene with fluorescent primers (HEX, FAM or TET.)

3. Digestion with one or more restriction enzymes (e.g. *CfoI*, *AluI*)

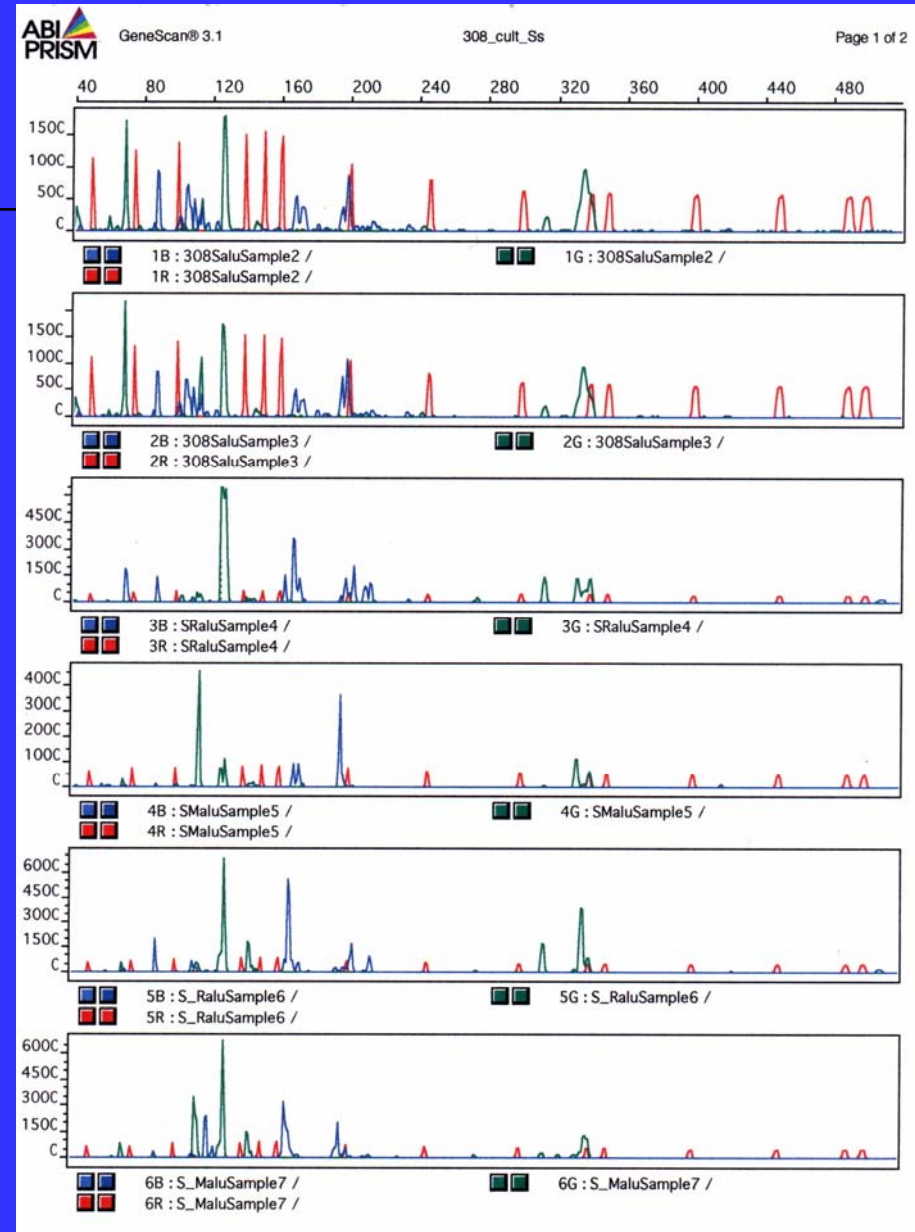
4. Detection and sizing of labelled terminal fragments by capillary or gel electrophoresis

Cheng Haiying et al.2006---16S rRNA genes comparative analysis of microbial community in nutrient injected oil reservoir by the T-RFLP method *CfoI*



T-RFLP profile: Electropherogram

- Different fragments come from different organisms
- Different organisms may share a common terminal fragment size
- Peak height “in principle” correlates to the abundance of a group of organisms



Pros and cons of T-RFLP

LIMITATIONS

- Biases inherent to PCR-based techniques
- Data generated depend on the choice of restriction enzymes
- A large group of organisms may share the same terminal fragment size
- Apparent size may differ from actual size and varies with the type of genetic analyser

ADVANTAGES

- Straightforward technique
- High reproducibility at each step of the process
- Highly precise (if not always accurate)
- Digital data can be objectively processed

Ribosomal Database Project II - Release 9 - Microsoft Internet Explorer

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Ribosomal Database Project II






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Release 9.50 :: May 2, 2007 :: 368,406 16S rRNAs
(More on Release 9 and monthly updates is available in the [release notes](#).)

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 [RDP video tutorials](#)

RDP Analysis Tools

-  [myRDP](#) - Align and Classify your 16S rRNA sequences. Use the RDP Pipeline to process sequence libraries from raw sequencer output to analysis.
-  [Tree Builder](#) Create a phylogenetic tree.
 -  [Hierarchy Browser](#) - Browse a phylogenetic hierarchy and compile a list of 16S rRNA sequences for download or use.
 -  [Classifier](#) - Assign 16S rRNA sequences to our taxonomical hierarchy.
 -  [Library Compare](#) - Compare two sequence libraries using the RDP Classifier.

News 

05/02/2007
RDP 9, Update 50 Released. Seqmatch results can be downloaded as a tab-delimited text file and imported into a spreadsheet program. [\[more\]](#)

04/03/2007
RDP 9, Update 49 Released. Upgraded Tree Builder now includes bootstrap confidence estimates. [\[more\]](#)

Internet

DNA sequence:

- Database of rRNA: <http://rdp.cme.msu.edu/>
- special functional genes



Thank you