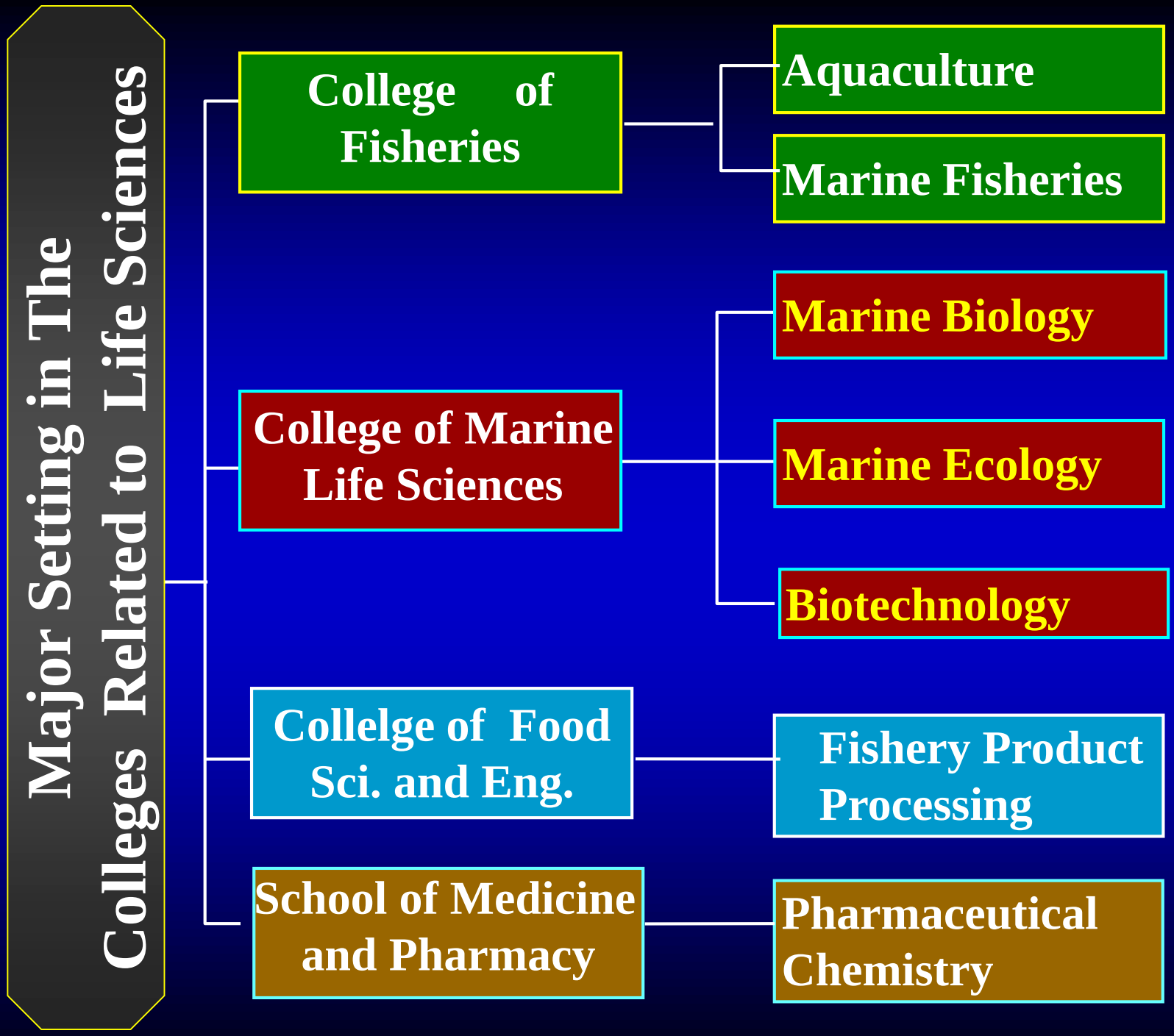
College of Marine Life Sciences

2017.06.16

The College was established in 1930.


Major Setting in The Colleges Related to Life Sciences
College of Fisheries
Aquaculture
Marine Fisheries
College of Marine Life Sciences
Marine Biology
Marine Ecology
Biotechnology
Collelge of Food Sci. and Eng.
Fishery Product Processing
School of Medicine and Pharmacy
Pharmaceutical Chemistry

Doctoral and Master's Degree Programs in

- Biology

- Aquaculture

- Food Sciences and Engineering

- Pharmacology

Main Courses for “Marine Biology”

Botany
Zoology
Microbiology
Marine Biology
Marine Ecology
Biodiversity
Anatomy & Phylogenetics
Histology and Embryology
Developmental Biology
Human & Animal Physiology
Plant Physiology
General Immunology
Cell Biology
Genetics
Molecular Biology

Mathematics
Physics
Biostatistics
Inorganic &Analytical Chemistry
Organic Chemistry
Biochemistry
Oceanography

Gene Engineering
Cell Engineering
Microbial Engineering
Modern Biotechnology
Genomics
Bioinformatics

Faculty, Staff and Students

128 Faculty members and staff

- 37 Professors
- 34 Associate professors

About 1300 students

- 500 graduate students
- 700 undergraduate students

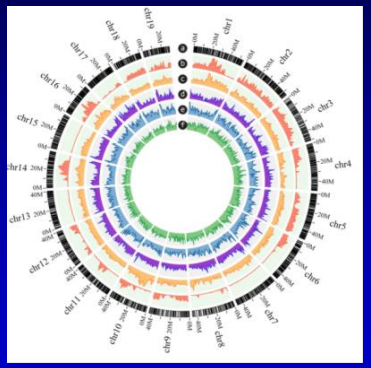
In the past 5 years

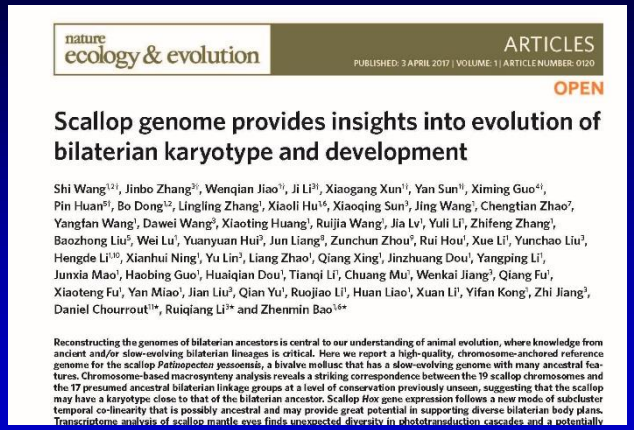
- Ca. 350 New Projects
- Funds: 170 million yuan
- 900 Academic Papers, 11 Books
- 140 Authorized Patents
- ESI 1%: Plants & Zoology; Biology & Biochemistry; Environment &E cology

Main Research Areas

- Genetics and breeding of farmed species
  fish, shellfish, crustacean, seaweed
- Developmental biology and Evolution
- Cell and tissue engineering
- Marine natural products and biomaterials
- Marine Ecology
- Biological Oceanography

I. Genetics and Breeding of Farmed Species





nature ecology & evolution — ARTICLES

PUBLISHED: 3 APRIL 2017 | VOLUME: 1 | ARTICLE NUMBER: 0120

OPEN

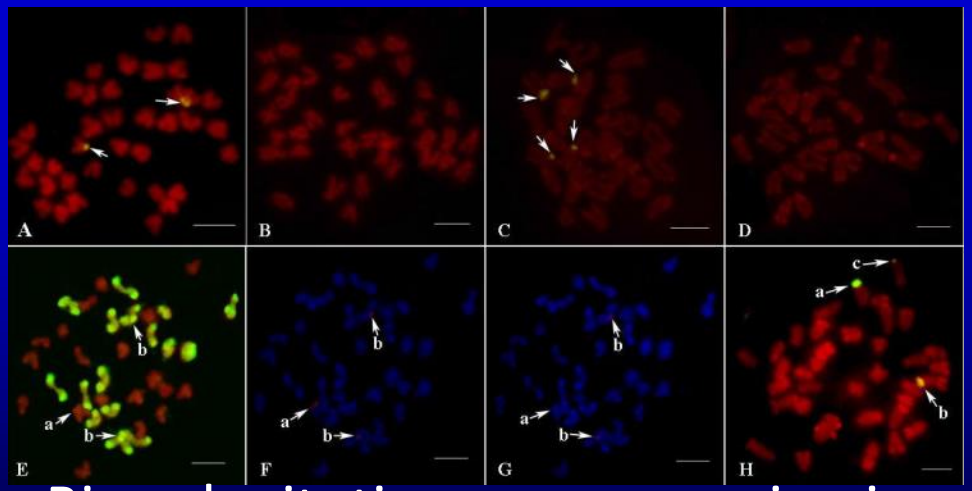
Scallop genome provides insights into evolution of bilaterian karyotype and development

Shi Wang[12], Jinbo Zhang[3], Wenqian Jiao[1], Ji Li[3], Xiaogang Xun[1], Yan Sun[1], Ximing Guo[4], Pin Huan[5], Bo Dong[12], Lingling Zhang[1], Xiaoli Hu[16], Xiaoqing Sun[3], Jing Wang[1], Chengtian Zhao[7], Yangfan Wang[1], Dawei Wang[8], Xiaoting Huang[1], Ruijia Wang[1], Jia Lv[1], Yuli Li[1], Zhifeng Zhang[1], Baozhong Liu[5], Wei Lu[1], Yuanyuan Hui[3], Jun Liang[8], Zunchun Zhou[7], Rui Hou[1], Xue Li[1], Yunchao Liu[3], Hengde Li[1,10], Xianhui Ning[1], Yu Lin[3], Liang Zhao[1], Qiang Xing[1], Jinzhuang Dou[1], Yangping Li[1], Junxia Mao[1], Haobing Guo[1], Huaiqian Dou[1], Tianqi Li[1], Chuang Mu[1], Wenkai Jiang[3], Qiang Fu[1], Xiaoteng Fu[1], Yan Miao[1], Jian Liu[3], Qian Yu[1], Ruojiao Li[1], Huan Liao[1], Xuan Li[1], Yifan Kong[1], Zhi Jiang[3], Daniel Chourrout[11]*, Ruiqiang Li[3]* and Zhenmin Bao[1,6]*

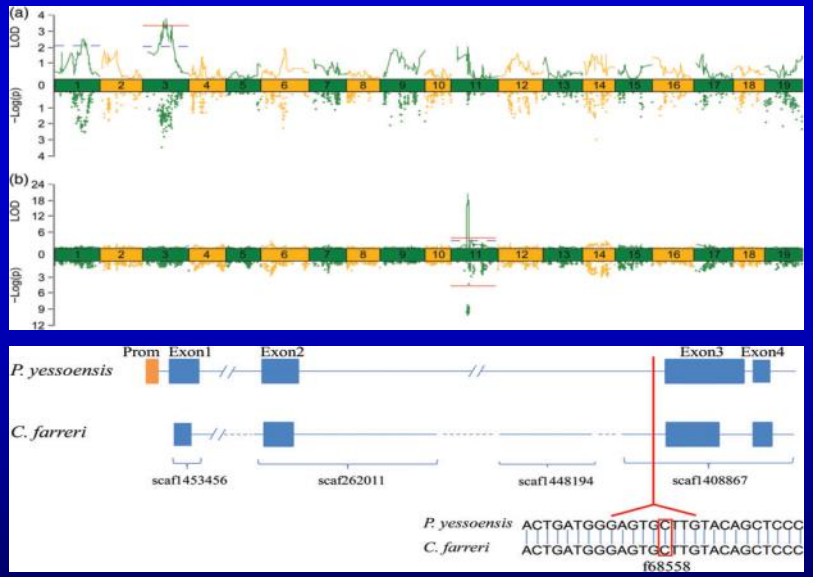
Reconstructing the genomes of bilaterian ancestors is central to our understanding of animal evolution, where knowledge from ancient and/or slow-evolving bilaterian lineages is critical. Here we report a high-quality, chromosome-anchored reference genome for the scallop *Patinopecten yessoensis*, a bivalve mollusc that has a slow-evolving genome with many ancestral features. Chromosome-based macrosynteny analysis reveals a striking correspondence between the 19 scallop chromosomes and the 17 presumed ancestral bilaterian linkage groups at a level of conservation previously unseen, suggesting that the scallop may have a karyotype close to that of the bilaterian ancestor. Scallop *Hox* gene expression follows a new mode of subcluster temporal co-linearity that is possibly ancestral and may provide great potential in supporting diverse bilaterian body plans. Transcriptome analysis of scallop mantle eyes finds unexpected diversity in phototransduction cascades and a potentially

Dean
Prof. Zhenmin Bao
zmbao@ouc.edu.cn

Scallop Genome evolution
_**Nture Ecology & Evolution 1, 0120 (2017)**

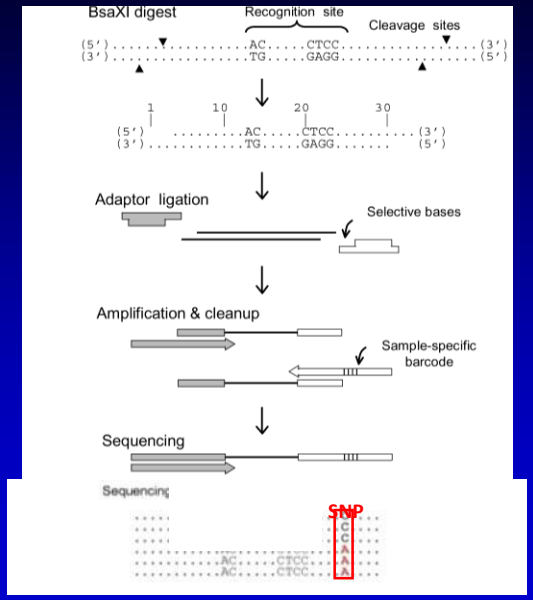


Biased mitotic gene conversion in hybrid scallop
BMC Evolutionary Biology, 10:6



QTL and association analysis of scallop traits
DNA Research, 21:85-101

Genomic tools for whole genome scan in non-model aquatic organisms



2b-RAD and RAD typing: efficient genotyping tools for whole genome scanning.

Nature Methods, 9:808-810, 2012; Nature Protocols, 12, 279–288 (2017)

Genetic breeding platform

“Haida Golden”scallop (*Patinopecten yessoensis*)

“Penglaihong II” (*Chlamys farreri*)

2. Fish Genetics and Breeding Technology

Research Interests

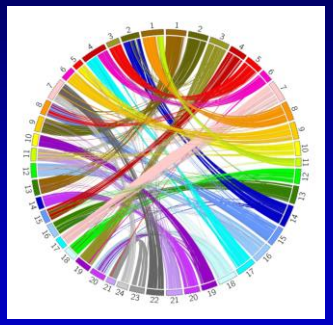
- Genetics and genetic breeding of farmed marine fishes.
- Molecular mechanism of sex determination in fish.
- Embryonic Stem Cells (ESC)and Germ Stem Cells (GSCs) of flounder.
  ----Identification and transplantation for **surrogate reproduction**

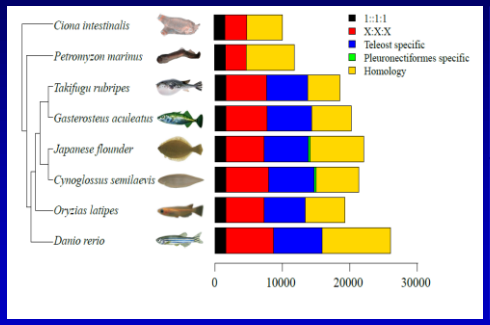
Prof. Quanqi Zhang

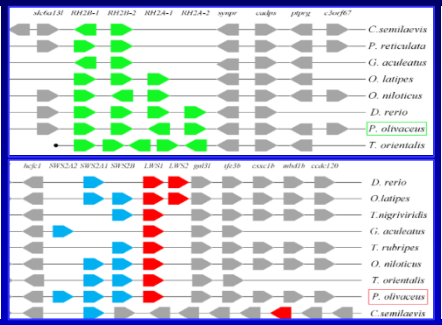
Email: qzhang@ouc.edu.cn

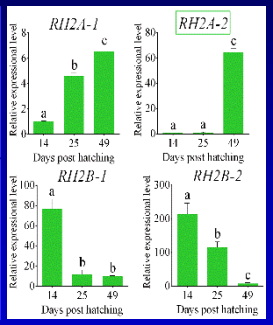
Tel: 0532-82031806

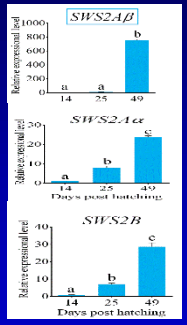
The Haploid Genome Reveals Visual System Adaptation to The Benthic Life Style in Japanese Flounder



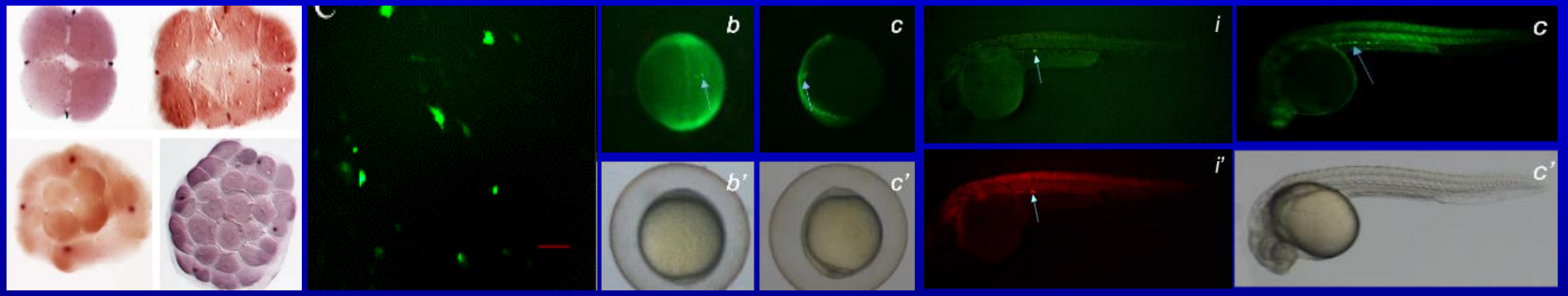








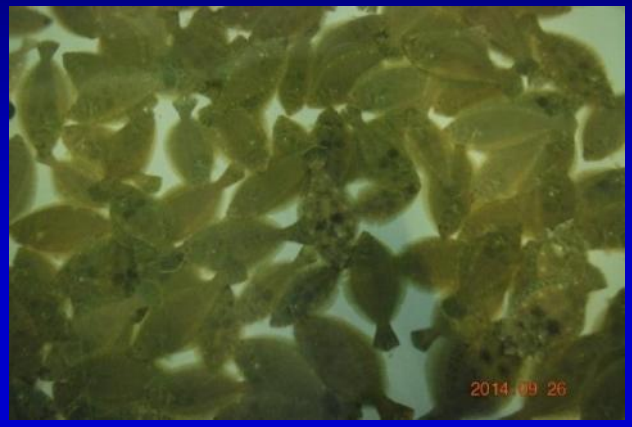
Identification and interspecific transplantation of PGCs in flatfish



Genetics and breeding of flounder

- Transcriptomic analysis
- QTLs analysis, high density map construction over 5800 SNPs

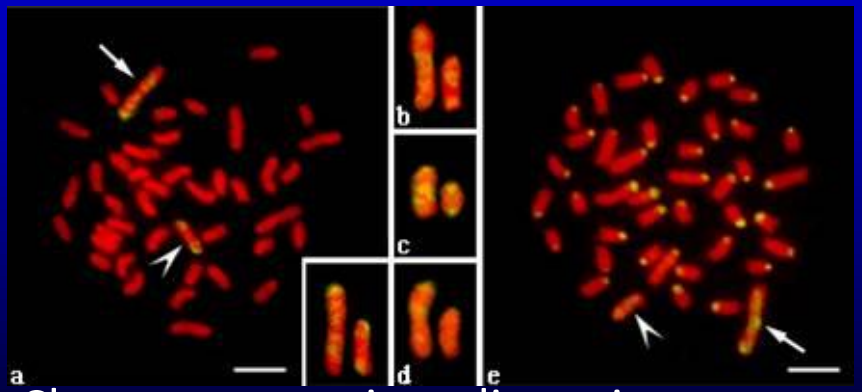
Whole female breeding



Normal family

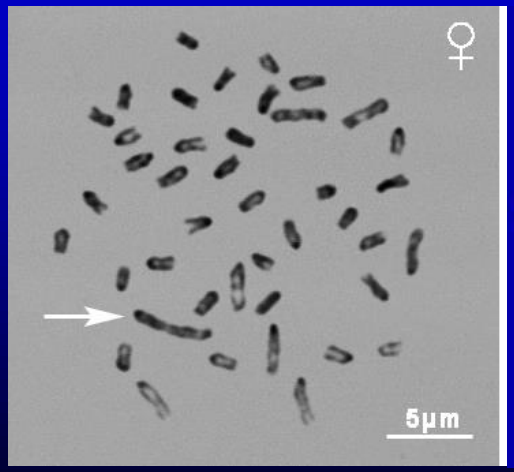
All female family

Sex control of Sole



Chromosome micro-dissection and painting

Molecular mechanism of sex determination



Identification and transgenic of ESC and GSC

3. Seaweed Genetics and Breeding

biodiversity of macroalgae

Prof. Yunxiang Mao
yxmao@ouc.edu.cn

Morphology

Chondrophycus intermedius

Ceramium kondoi

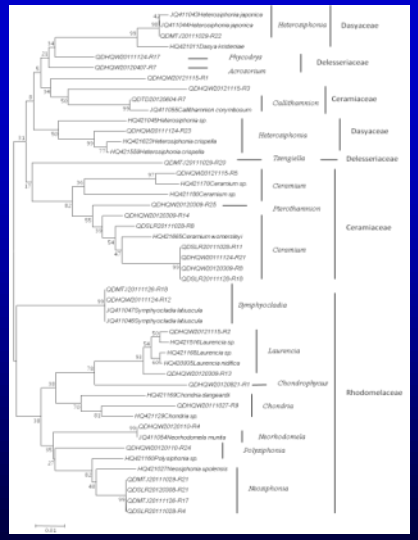
Ulva laetevirens

Sargassum horneri

Gelidium japonicum

DNA barcoding

Sampling sites



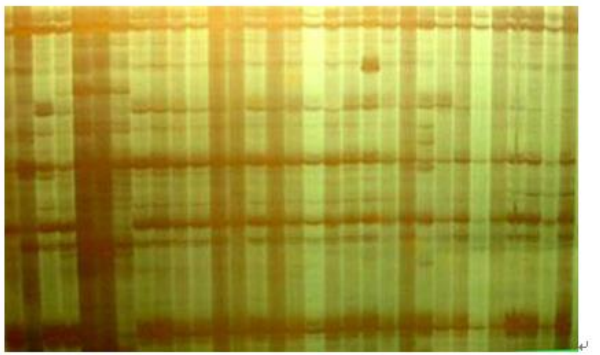
NJ tree of UPA sequences of Ceramiales (Red algae)

Specimen_voucher	No.	Species	Lat_Lon	date	Country	orf frame
JZW-20111118-1	KC411833	*Ulva australis*	36.40N 120.17E	18-Nov-11	China	18-903
JZW-20111118-3	KC411834	*Ulva australis*	36.40N 120.17E	18-Nov-11	China	14-898
JZW-20111118-4	KC411835	*Codium fragile*	36.40N 120.17E	18-Nov-11	China	14-899
JZW-20111118-5	KC411836	*Ulva laetevirens*	36.40N 120.20E	18-Nov-11	China	30-829
JZW-20111118-6	KC411837	*Ulva australis*	36.40N 120.20E	18-Nov-11	China	32-815
JZW-20111118-8	KC411838	*Ulva flexuosa*	36.40N 120.20E	18-Nov-11	China	12-816
HQW-20110902-1	KC411839	*Ulva flexuosa*	36.30N 120.20E	2-Sep-11	China	6-832
HQW-20110902-2	KC411840	*Ulva flexuosa*	36.30N 120.20E	2-Sep-11	China	288-815
HQW-20110902-3	KC411841	*Ulva australis*	36.30N 120.20E	2-Sep-11	China	242-769
HQW-20110902-4	KC411842	*Ulva laetevirens*	36.30N 120.20E	40788	China	291-818
HQW-20110902-5	KC411843	*Ulva australis*	36.30N 120.20E	2-Sep-11	China	268-800
HQW-20110902-6	KC411844	*Ulva flexuosa*	36.30N 120.20E	2-Sep-11	China	24-836
JZW-20111215-1	KC411845	*Codium fragile*	36.40N 120.17E	15-Dec-11	China	43-851
JZW-20111215-2	KC411846	*Ulva linza*	36.40N 120.17E	15-Dec-11	China	67-875
JZW-20111215-3	KC411847	*Ulva australis*	36.40N 120.17E	15-Dec-11	China	44-853
HQW-20110710-1	KC411848	*Ulva prolifera*	36.30N 120.20E	10-Jul-11	China	22-872
TWL-20110412-1	KC411849	*Monostroma arcticum*	36.30N 120.24E	12-Apr-11	China	60-871

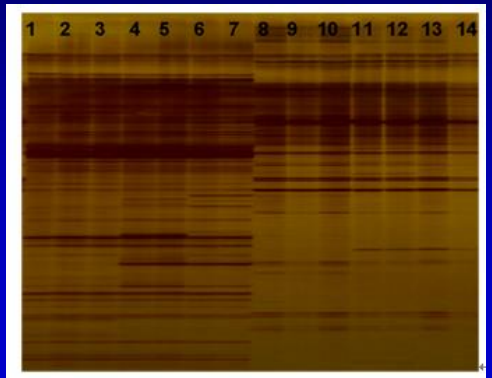
Sequences No. of Gene Bank

Studies on the genetic diversity and genetic breeding of Gracilariaceae species

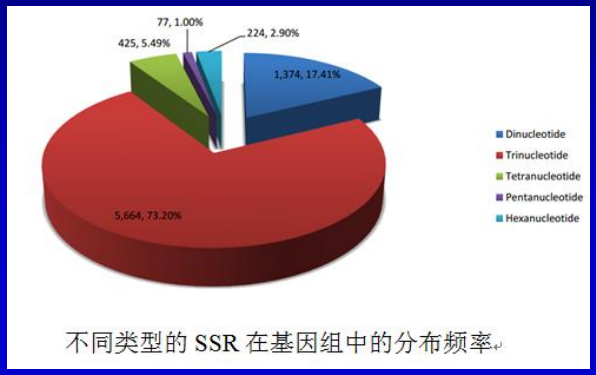
Prof. Zhenghong Sui
suizhengh@ouc.edu.cn



龙须菜 AFLP 聚丙烯酰胺凝胶凝胶电泳图

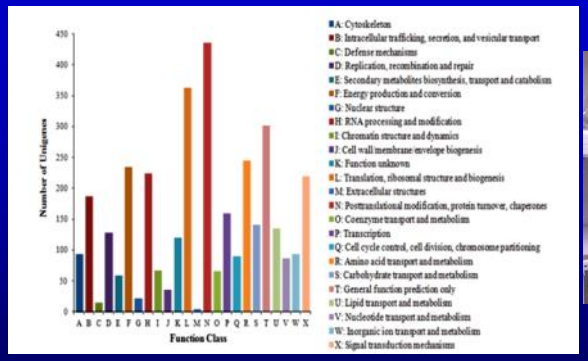


龙须菜RSAP聚丙烯酰胺凝胶电泳图



不同类型的 SSR 在基因组中的分布频率

Different molecular markers were exploited to elucidate the genetic diversity of Gracilariaceae species, such as AFLP,RSAP, SSR and SNP techniques.



Genetic analysis and molecular marker assistant breeding was used during the development of cultivar with outstanding traits.

Cultivation and conservation of seweed

Prof. Tao Liu
liutao@ouc.edu.cn

Hybridization and selection of Laminaria
The largest alga culture in the world

The germplasm conservation of seaweed

Eucheuma

Kappaphycus

4. Seaweed molecular pathology

Prof. Gaoge Wang
liutao@ouc.edu.cn

Contact information：
gaogewang@hotmail.com
wgaoge@ouc.edu.cn

Interactions of pathogenic bacteria and economically cultivated alga S*accharina japonica, including:*

-- Identifying the pathogenic bacteria or virulence of *S. japonica* diseases.

-- Investigating the mechanism of defense responses caused by pathogenic bacteria or virulence

S. japonica

Sporeling nursery

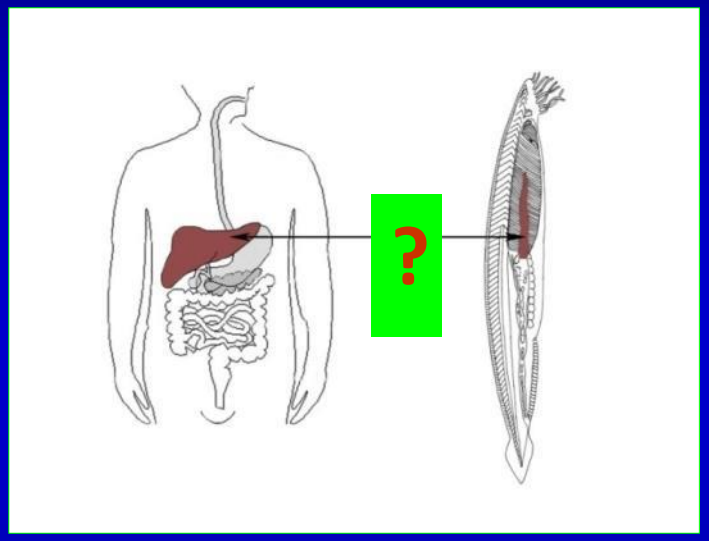
Disease outbreaks at two stages

Adult diseased sporophytes near the harvest time

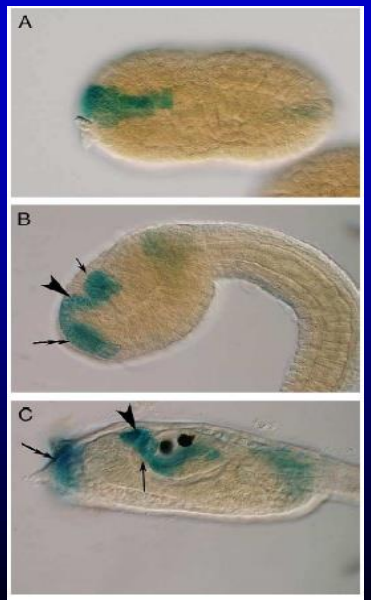
II. Evolution and tissue engineering

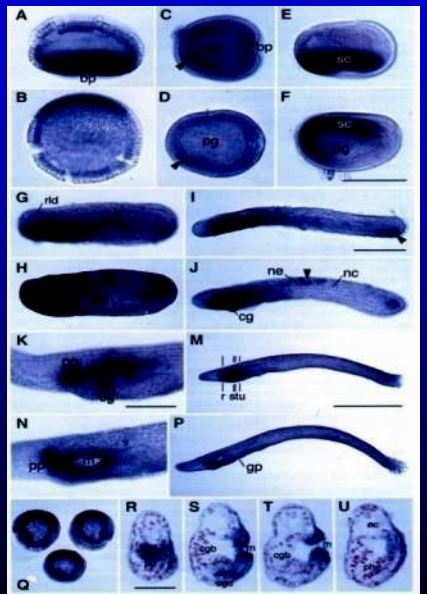
1. Comparative and developmental immunology of marine animals -- using Amphioxis as model

Prof. Shicui ZHANG
E-mail: sczhang@ouc.edu.cn



Through comparative analysis of conserved sequences, expression and functions of genes to study the origin of human organs and tissues





2. Marine fish cytotechnology and tissue engineering

Prof. Tingjun Fan
Tel：+86-532-82031637
Email：tjfan@ouc.edu.cn

Research interests:

- Marine fish cytotechnology
- Human corneal tissue engineering
- Innate immunology of marine invertebrates

Achievements:

- Established 17 tissue cell lines from marine fish, and performed intensive investigations in cell-virus interaction, transgenic and vaccine;
- Constructed various kinds of human corneal tissues from non-transformed human corneal cells and scaffold including fish collagen composite scaffold, which could maintain corneal clarity in various animal models;
- Characterized the properties of phenoloxidase from various marine invertebrates, mechanisms involved in immunostimulants and endocrine disruptors.

III. Marine natural products and biomaterials

Research properties: focus on the development of marine bioactive substance, from biochemical, molecular mechanism, cellular level to animal model, establish the technological system for the development and industrialization of marine biomedical materials.

- Marine biomaterials
- Marine enzyme
- Marine biological and biochemical products

1. Biomedical materials based on chitin and chitosan

Prof. Boqin Han
Tel： +86-532-82032105
E-mail: baoqinh@ouc.edu.cn

chitosan → (**chitosanase**) → **Chitosan oligosaccharide**

Hemostatic material

“CHIMEHERB” artificial skin for treatment of skin burn

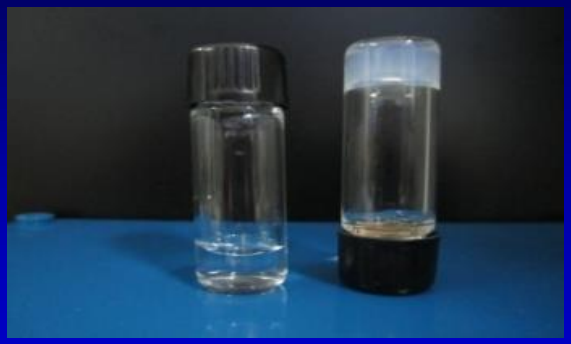
‘HAIMING” ointment

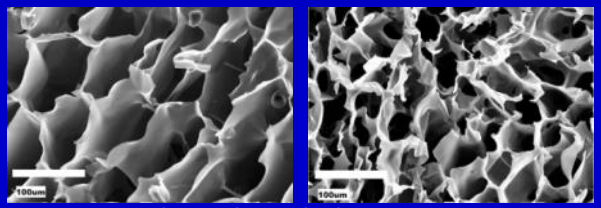
Prof. Xiguang Chen

xgchen@ouc.edu.cn

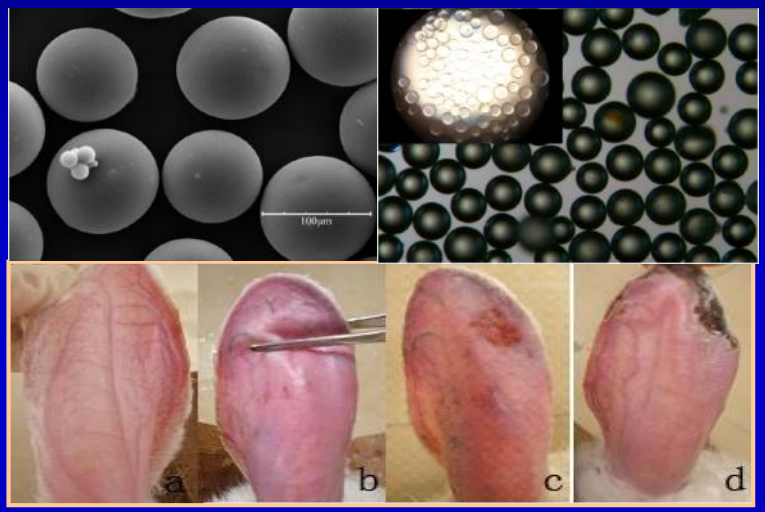
H_2O

Liquid swellable chitosan fiber

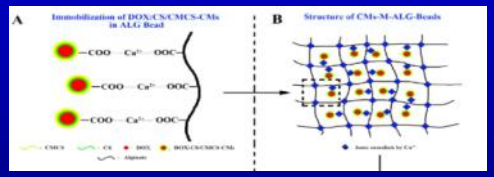


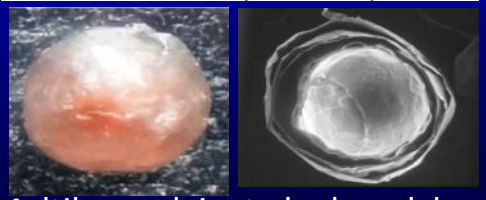


Hydroxybutyl chitosan
Thermo-sensitive hydrogel
Wang et al. (2013) J Mater Sci, 48

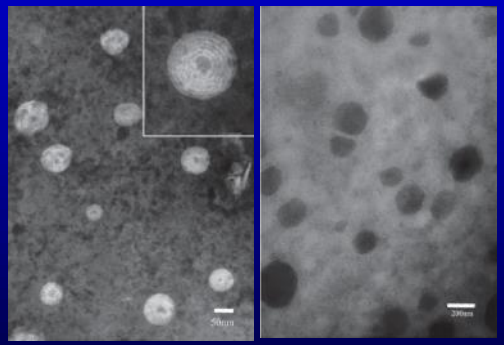


Chitosan microspheres as potential embolic agent
Zhou et al. (2014) Carbohydr Polym, 113

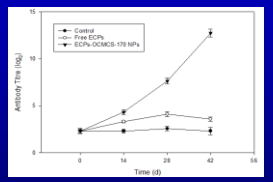




Multilayer alginate hydrogel beads for oral delivery. Feng et al (2014) Biomacromolecules, 15



Multilayer HA-transfersome for transdermal delivery. Kong et al. (2015) Chem Commun, 51

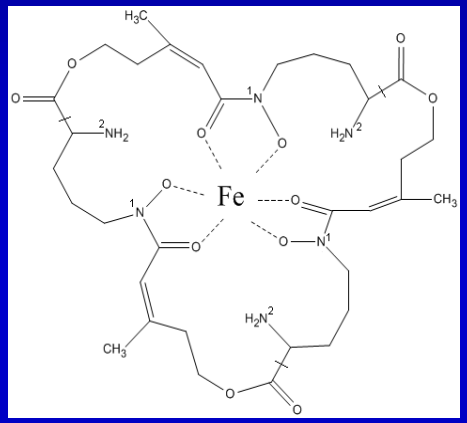


Oleoyl-carboxymethy-chitosan nanoparticles for oral vaccine delivery
Liu et al (2012) Carbohydr Polym, 89

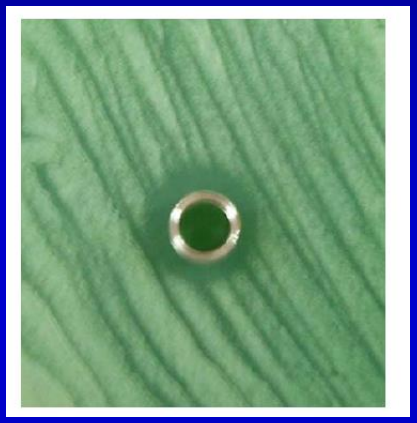
2. Bioactive substances from marine yeasts

Prof. Zhen-Ming Chi
E-mail: chi@ouc.edu.cn

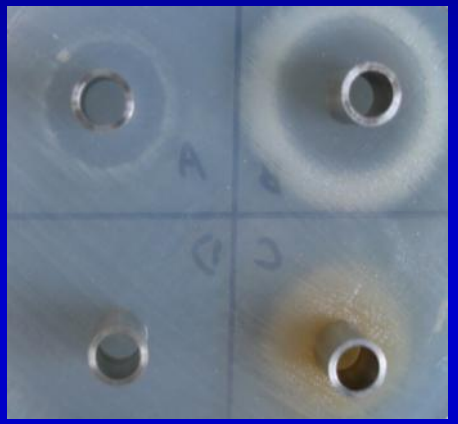
Production and metabolic regulations of bioactive substances from marine yeasts



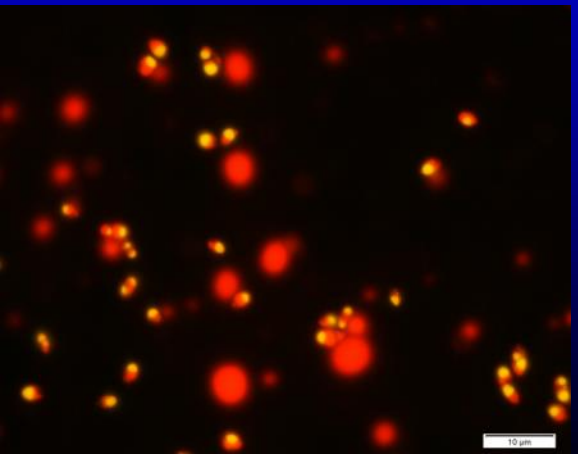
Siderophore



Killer toxin



Antimicrobial activity



Lipid and alkanes produced by marine yeasts

Polymalate produced by marine yeasts

3. Marine Enzymes: Basic and Applications Research

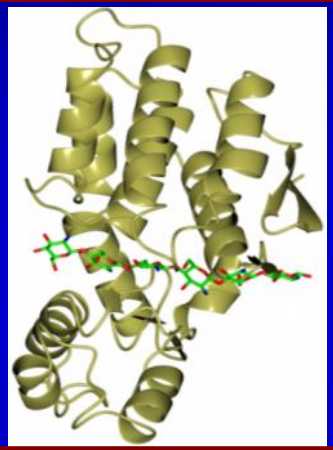
Prof. Weizhi Liu: liuweizhi@ouc.edu.cn

Research Interests

1). Novel polysaccharides degrading enzyme and their application in the generation of oligosaccharide.

2). Adhesive proteins/enzyme and their application in medical adhesive material area.

1.Determination of the first chitosanase-substrate complex. (PDB: 4OLT, 4QWP)



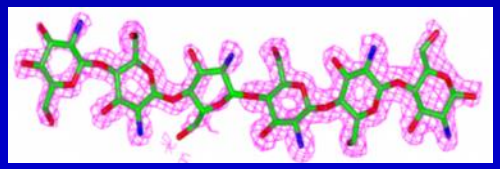


Fig 1. The first crystals of the chitosanase OU01-substrate complex and the degradation mechanism

Lyu Q, et al, Biochemical Journal (2014); BBA- General Subjects, 2015

2. Adhesive proteins derived from scallop byssus was analyzed in the first time, which will facilitate the development of new medical adhesive material.

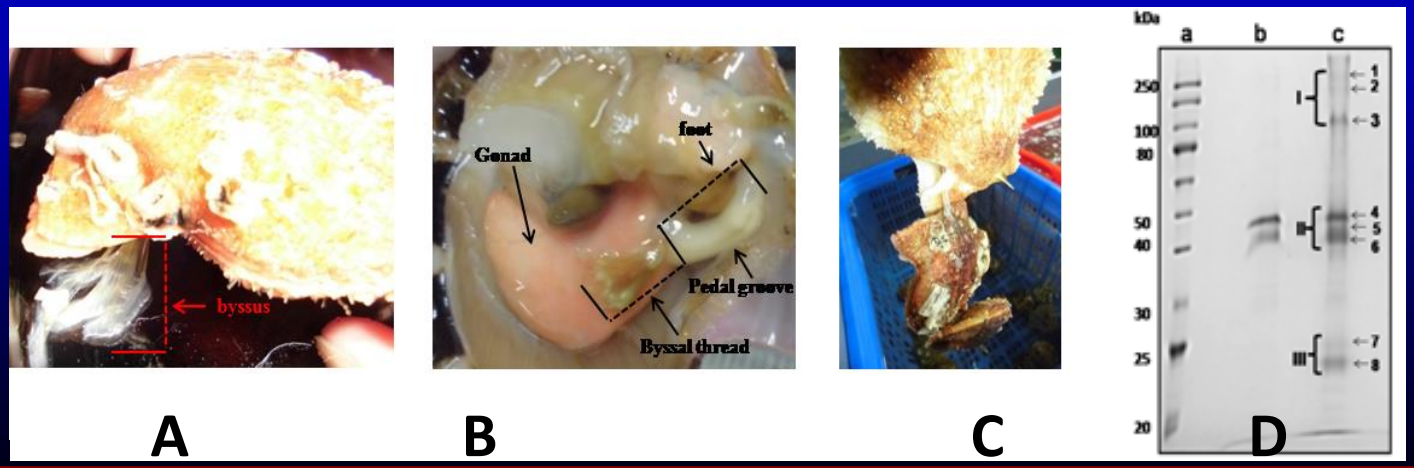


Fig 2. Scallop byssal protein

(A-C: The morphology photos of scallop byssus; D: The whole extracted scallop byssal protein)

Miao Y, et al, Mar Biotechnol (NY). 2015

IV Marine Ecology and Biological Oceanography

1. Anthropogenic effects on marine ecosystems

Prof. Xuexi Tang:
E-mail:
tangxx@ouc.edu.cn

The lab's research is focused on low-trophic level organisms to address questions related to water, pollutant and climate. We use quantitative and experimental approaches to elucidate the importance of biotic and abiotic factors influencing different biota' dynamics in both field and laboratory-settings.

Research interests

Marine environmental ecology

1. Experimental eco-toxicology: The typically marine environmental pollutants on low-trophic biota: effects, mechanisms and biomarkers

2.Field studies: Comprehensive investigation and feature evaluation on the coastal China

3.Bio-restoration aiming at the degraded seaweed bed using macroalgae and seagrass

The goal of much of the work is to understand and predict interactions between water systems, climate change, and ecosystem function and services in estuaries and coasts, and to elucidate the possible ecological mechanism involving in the process.

2. Ecotoxicological effect of endocrine disrupting chemicals in coastal waters

Prof. Shaoguo Ru

Email: rusg@ouc.edu.cn

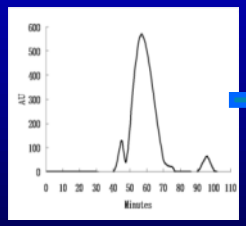
Research Area

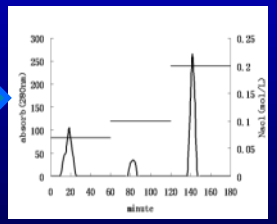
- Ecotoxicological effect and underlying mechanisms of endocrine disrupting chemicals
- Development and application of biological detection method for endocrine disrupting chemicals
- Ecological risk assessment of endocrine disrupting chemicals on the marine fishery resource populations

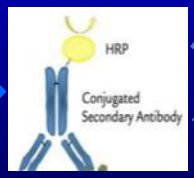
flounder

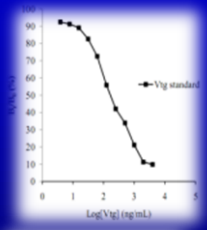
Sebastes schlegeli

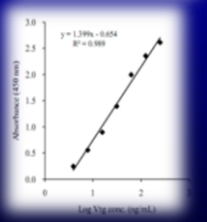
greenling











3. Microbial oceanography

Research Interests

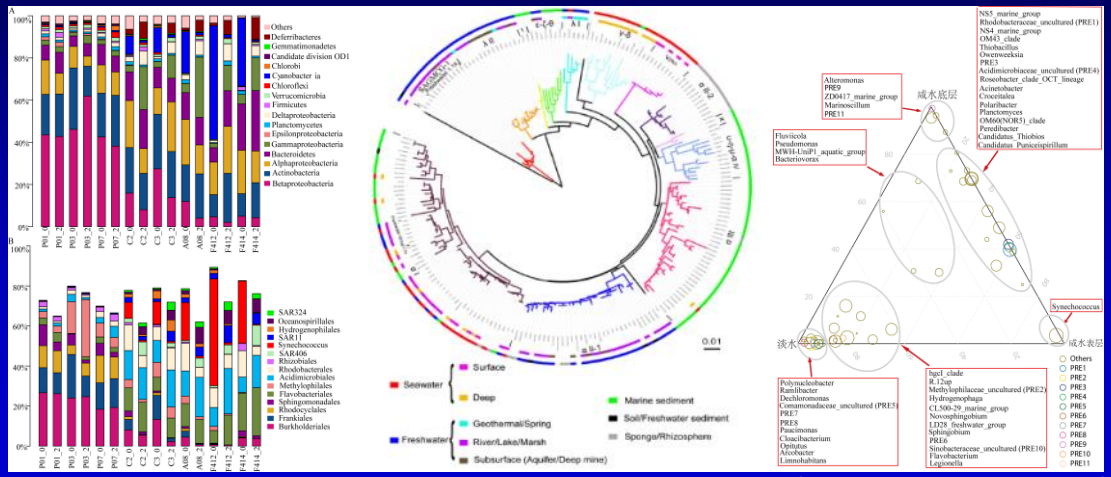
- Microbial community structure and co-occurrence patterns in typical sea areas
- Roles of microbes in biogeochemical cycles
- Adaptation mechanisms of marine microorganisms
- Quorum sensing and quorum quenching of marine bacteria
- Cultivation of novel marine bacteria

Prof. Xiao-Hua Zhang

xhzhang@ouc.edu.cn

1）Microbial community structure in typical sea areas

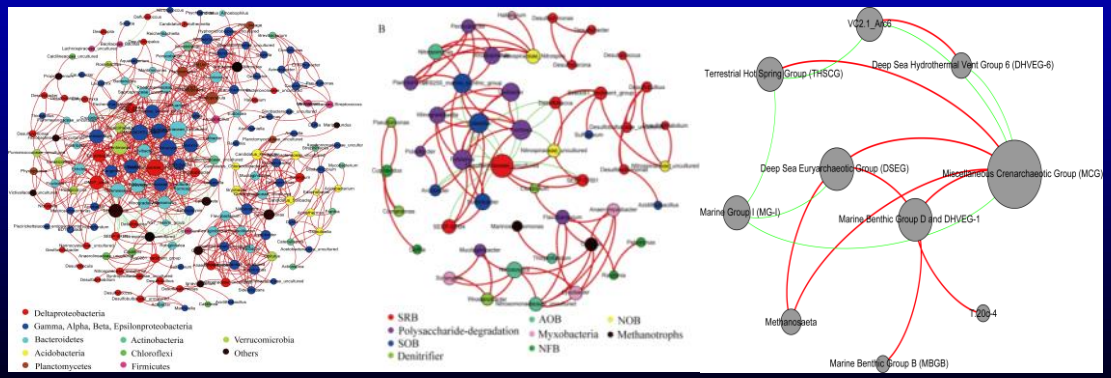
- Different areas of Chinese marginal seas harbor distinctive microbial community structures, which were controlled by different environmental factors.



Liu et al. 2014. FEMS Microbiol Ecol; Liu et al. 2015. Microb Ecol.

2） Microbial co-occurrence patterns

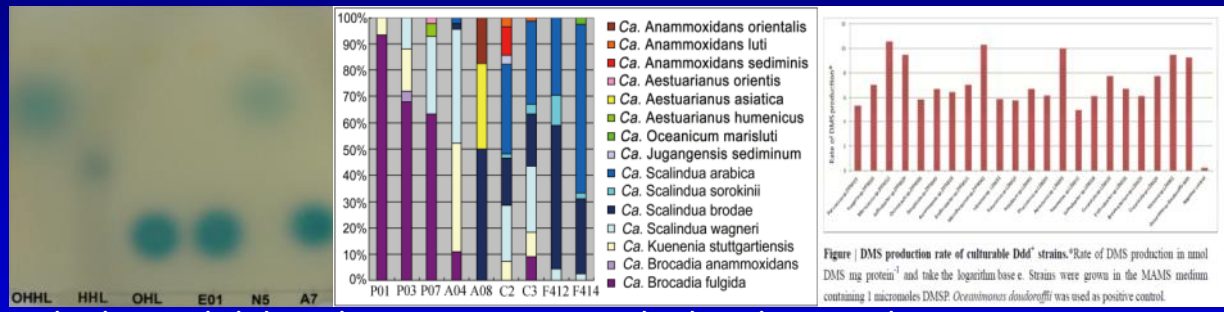
- Microbial co-occurrence patterns in sediments of Chinese marginal seas;
- SRB and SOB, SRB and nitrite-oxidizing bacteria, nitrogen fixation and denitrifying bacteria had significant correlation at marginal sea sediments.



Liu et al. 2014. Syst Appl Microbiol

3） Roles of microbes in biogeochemical cycles

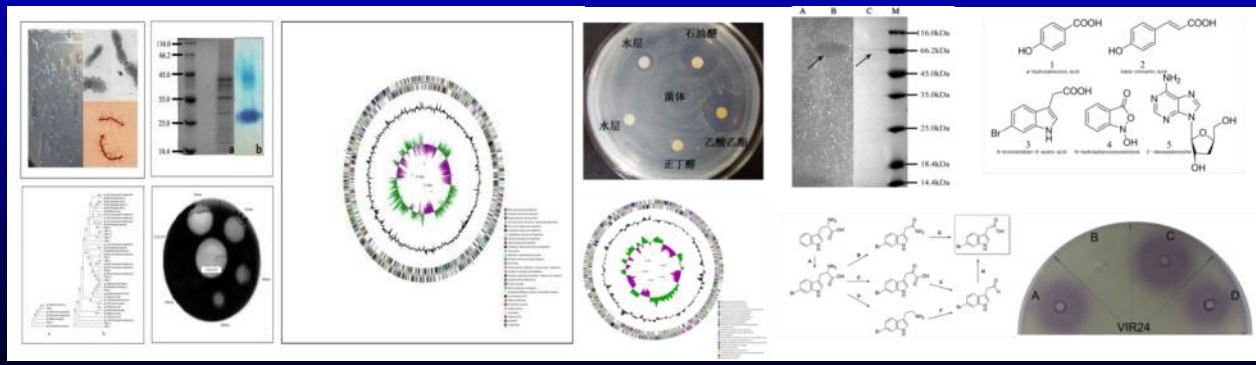
- Bacterial quorum sensing in regulation of particulate organic carbon degradation;
- Anammox bacteria in the Pearl Estuary and the impact of environmental factors;
- DMSP catabolism by bacteria isolated from East China Sea.



Todd et al., 2017, Nature Microbiology; Abdul et al., 2015,FEMS Microbiol Ecol; Fu et al., 2015, JGR-Oceans.

4） Adaptation mechanisms of marine bacteria

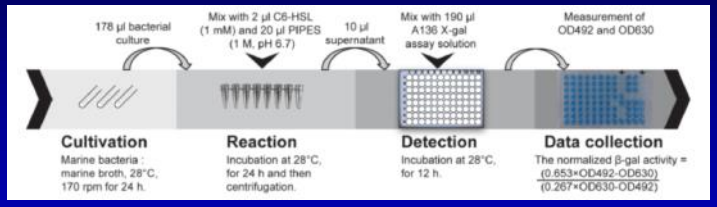
- Polysaccharide degradation properties of *Catenovulum agarivorans* adapting to eutrophic environments
- Competitive properties of *Pseudoalteromonas flavipulchra* adapting to various adverse environments

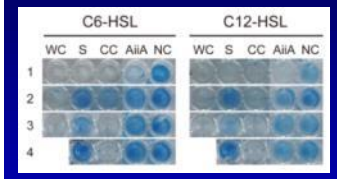


Shi et al., 2012. J Bacteriol; Cui et al., 2014. Mar Drug; Yu et al., 2013. BMC Genomics

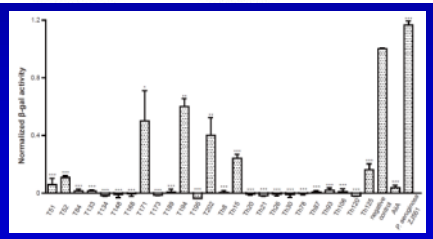
5） Quorum sensing and quenching of marine bacteria

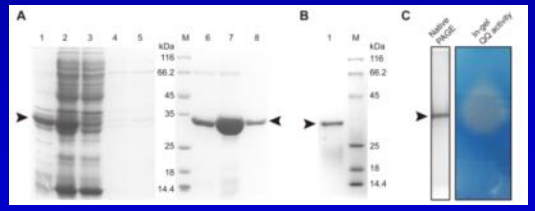
- Established a sensitive and high-throughput method for identifying QQ bacteria
- Identified a novel marine AHL lactonase MomL





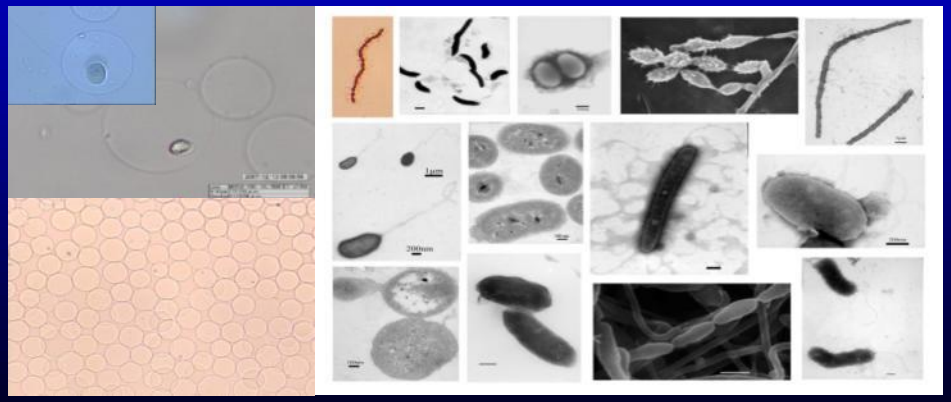
Tang et al., 2013. Sci Rep; Tang et al., 2014. Appl Environ Microbiol





6） Cultivation of novel marine bacteria

- Established a new high-throughout cultivation method for marine bacteria
- Published 30 novel bacteria, including 10 novel genera and 20 novel species
- Established a culture collection center (Marine Culture Collection, Ocean University of China, MCCO)

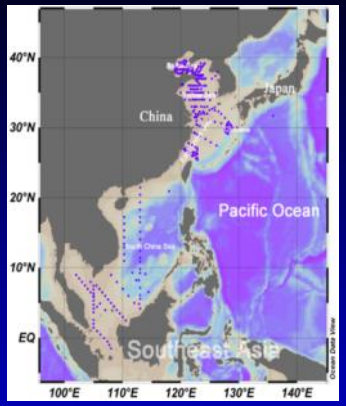


Website： http://iunh.v099.10000net.cn/bio/index.jsp

4. Diversity and Ecology of Virioplankton, Pico-, Nano-, and Micro-plankton

Prof. Min Wang,
mingwang@ouc.edu.cn

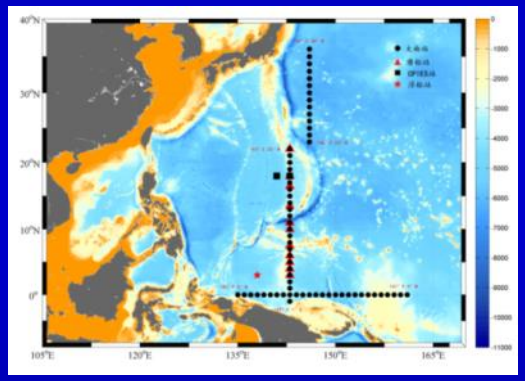
Asso. Prof. Yong Jiang,
yongjiang@ouc.edu.cn

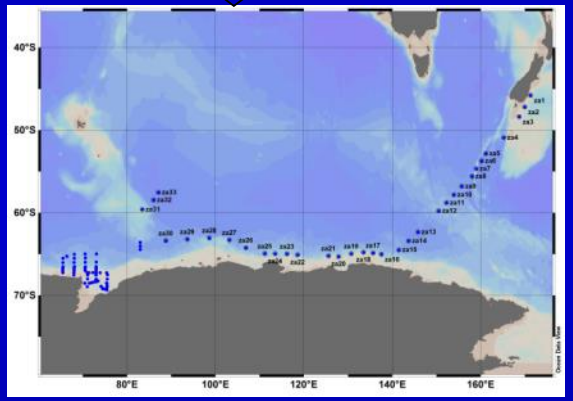


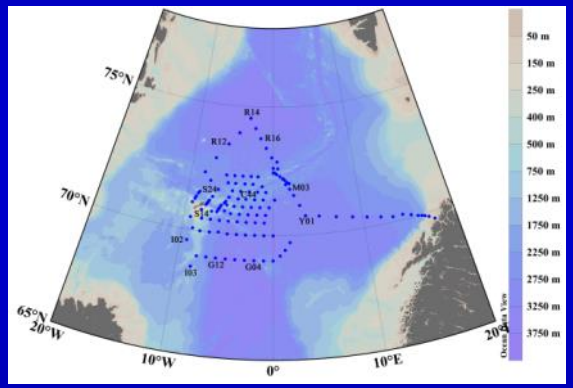
Chinese marginal seas
to deep Pacific Ocean

Antarctic Ocean

Nordic Sea
Arctic Ocean







Research Interests:

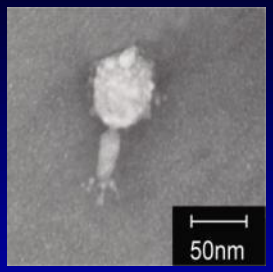
1) Abundance of microbial populations and their relationship with environmental parameters

2) Diversity of viroplankton and its relationship with enviromental parameters ;

3) Marine phage isolation and characterization

4) Diversity of picoeukaryote community and its relationship with environmental parameters

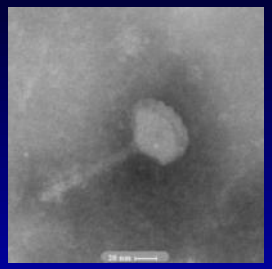
Marine phage Isolation and Characterization



H188, *Myovirida*

Host：*Vibrio kanaloa*

50,364 bp, 76 ORFs.

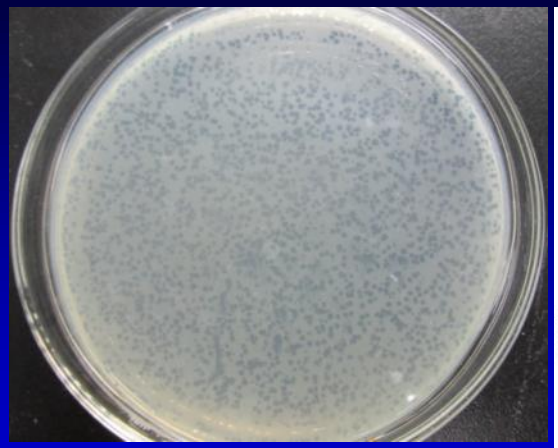


PHq0, *Siphoviridae*

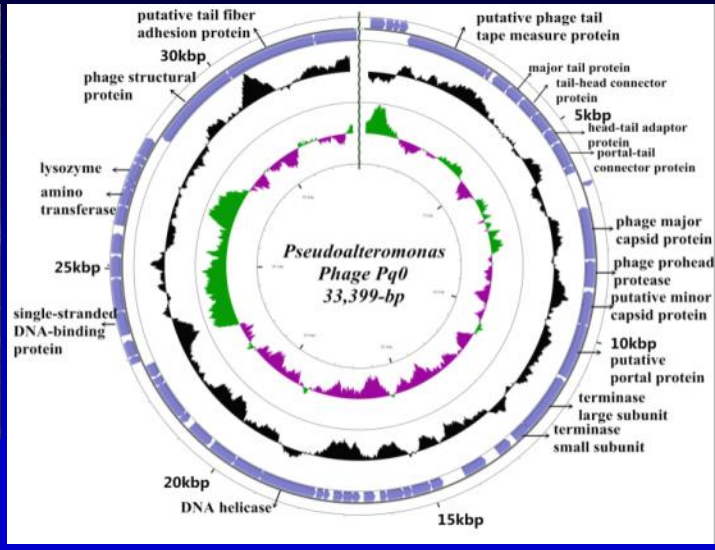
Host: *Pseudoalteromonas*

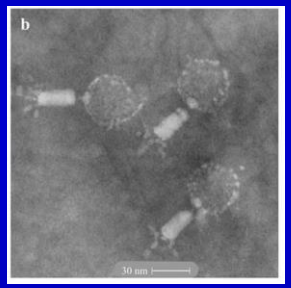
33,399-bp, 56ORFs

(Wang et al. 2015. Curr Microbiol. DOI:10.1007/s00284-015-0919-2)



Bacteriophage plaque of PH103

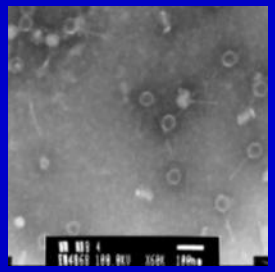




PH101, *Myoviridae*

Host:*Pseudoalteromonas*

131,903bp, 228 ORFs

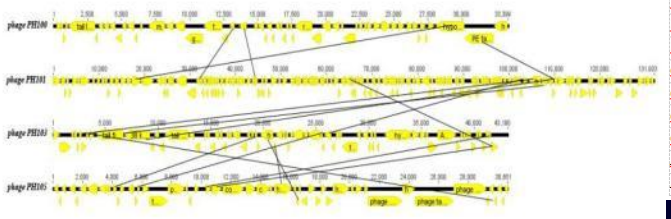


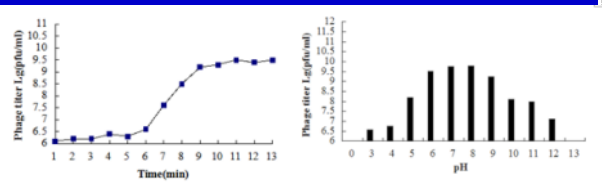
H103, Siphoviridae

Host: *Pseudoalteromonas*

43,190bp, 75 ORFs

(Wang et al. 2015. Curr Microbiol, DOI 10.1007/s00284-015-0896-5.)





One-step growth curve of phage PH101.

Fig. 4 pH stability of phage PH101

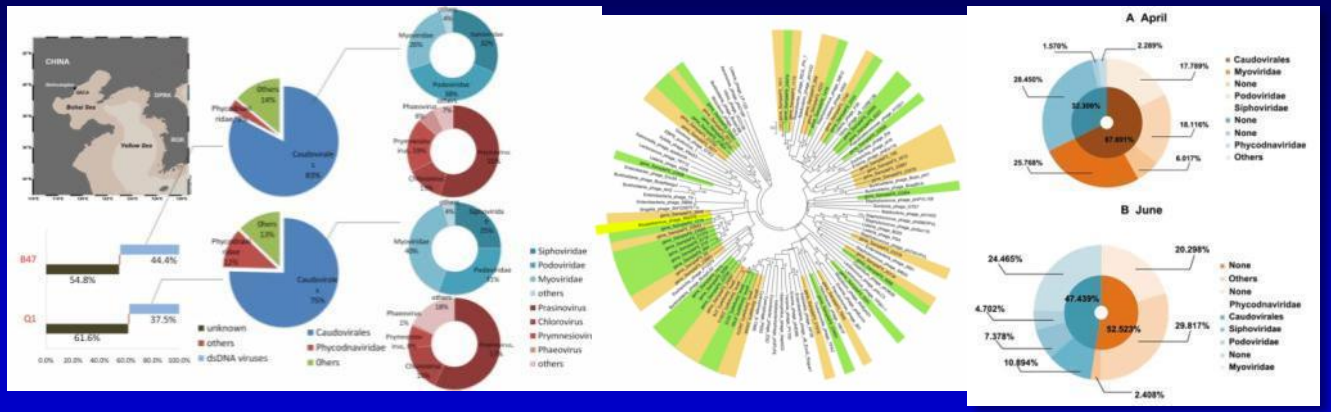
Table 4 Phages with common genes with *Pseudoalteromonas* Phage PH101 by BLASTP (e <10⁻⁵)

Phage name	Phage family	Genome length (bp)	GenBank accession number	Common genes with PH101
Shewanella sp. phage 1/4	Myoviridae	133824	NC_025436	30
Shewanella sp. phage 1/40	Myoviridae	139004	NC_025470	21
Salmonella phage PVP-SE1	Myoviridae	145964	NC_016071	11
Vibrio phage ICP1	Myoviridae	125956	NC_015157	19
Vibrio phage helene 12B3	unclassified	135982	NC_021067	16
Vibrio phage PWH3a-P1	unclassified	129155	NC_020863	14
Cronobacter phage CR9	Myoviridae	151924	NC_023717	10
Citrobacter phage Moogle	Myoviridae	87999	KM236239	9
Cronobacter phage CR3	Myoviridae	149273	NC_017974	9
Cronobacter phage CR8	Myoviridae	149126	NC_024354	7
Enterobacteria phage phi92	Myoviridae	148612	NC_023693	10
Escherichia phage EC6	Myoviridae	86231	JX560968	9

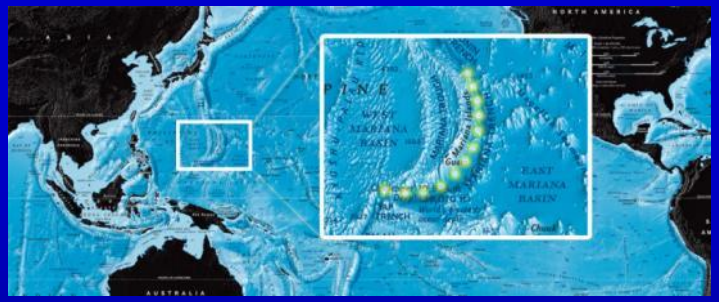
ORF	Start	Stop	Strand	Function	Conserved domain	Conserved domain accession
8	4114	5472	+	Phage structural protein	DUF3383	pfam11863
9	5490	5978	+	hypothetical protein	DUF3277	pfam11681
12	6743	8050	+	hypothetical protein	HemX superfamily	cl19375
14	9672	10358	+	HNH homing endonuclease	HNHc superfamily	pfam13392
19	13478	14182	+	hypothetical protein	VgrG	COG3501
23	16219	17139	+	hypothetical protein	DUF2612 superfamily	pfam11041
24	17154	19409	+	hypothetical protein	SGNH_hydrolase	cd00229
37	29299	26828	-	DNA polymerase I	DNA_pol_A superfamily	pfam00476
38	31308	29296	-	T7-like phage primase	GP4d_helicase	cd01120
51	35370	35714	+	hypothetical protein	PLN02197	PLN02197
55	36291	36803	+	hypothetical protein	LT_GEWL	cd00254
62	39678	40169	+	hypothetical protein	PRK06508	PRK06508
68	42548	43498	+	Phage-associated homing endonuclease	HNHc	cd00085
69	43783	44268	+	Phage protein	AP2	cd00018
75	46389	47234	+	Ribose-phosphate pyrophosphokinase	PRTases_typeI	cd06223
76	47221	47784	+	HNH homing endonuclease	HNH_3	pfam13392
77	47787	49340	+	Nicotinamide phosphoribosyltransferase	PBEF_like	cd01569
81	52586	53092	+	Endonuclease V	Pyr_excise	pfam03013
85	54255	54446	+	hypothetical protein	TopoIIA_Trans_ScTopoIIA	cd03481
103	63736	63089	-	hypothetical protein	HNHc	cd00085
106	64953	64168	-	Adenine-specific methyltransferase	AdoMet_MTases	cd02440
119	69979	69050	-	hypothetical protein，PREDICTED	Laps	pfam10169

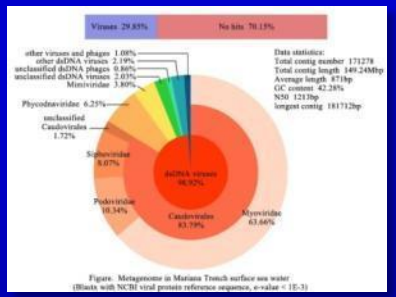
Metagenomic diversity of the viroplankton

The Metagenomic diversity of the virioplankton in response to Red Tide in aquaculture zone

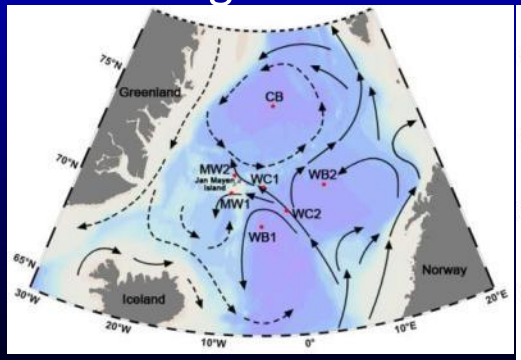


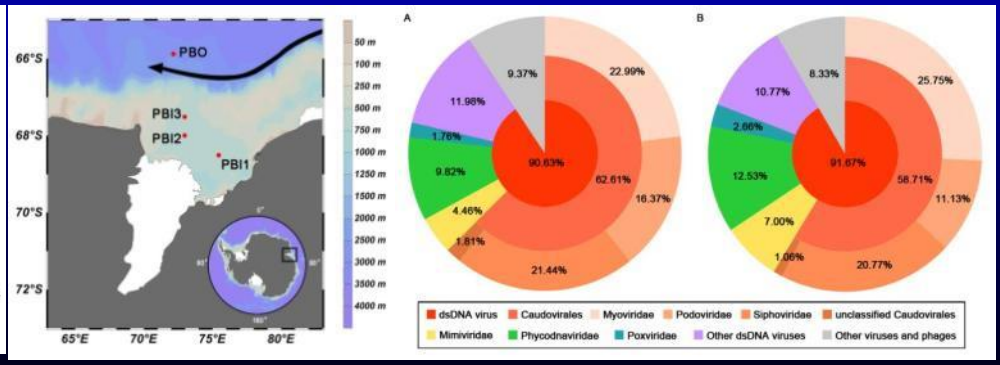
Distribution of Viral Communities in the Mariana Trench





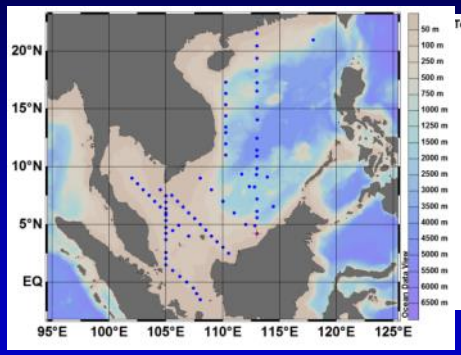
Viral Diversity in Polar region

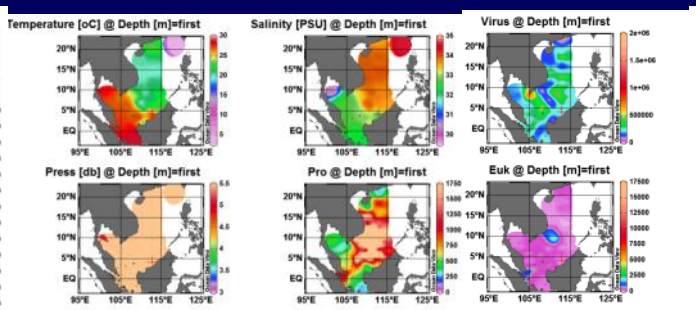


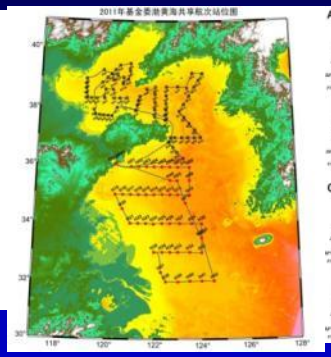


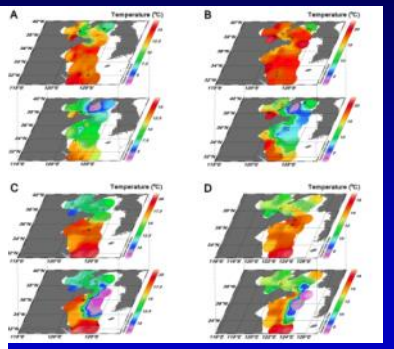
Distribution of viroplankton and pico-plankton

Seasonal and spatial distribution of virioplankton in the Marginal Seas of China

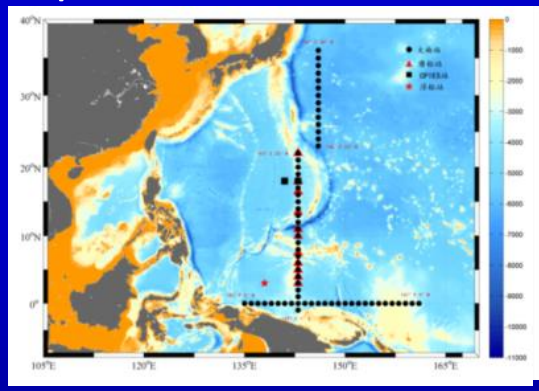


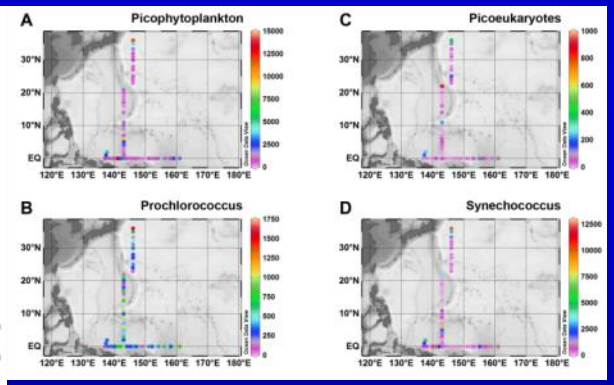




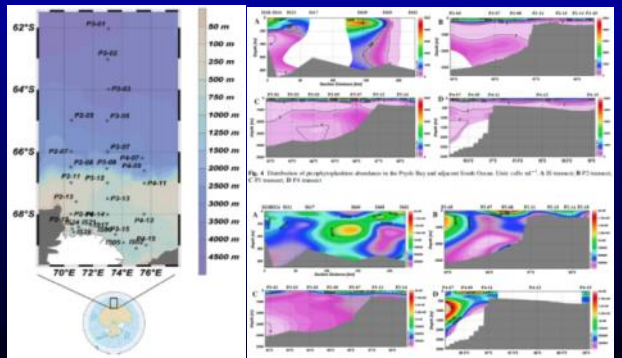


Distribution of viroplankton pico-plankton in Pacific Ocean



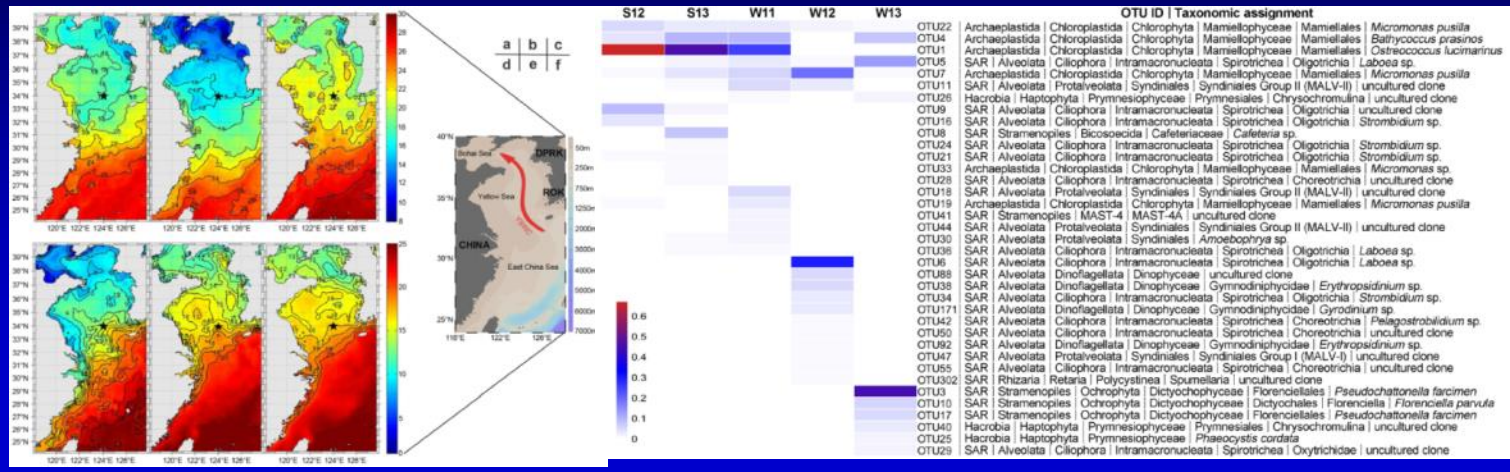


Distribution of marine viruses and their potential hosts in Prydz Bay and adjacent Southern Ocean, Antarctic



Diversity of eukaryote community

Community composition of eukaryotes in response to changes in the Yellow Sea Warm Current



Diversity of eukaryotic community in the Mariana Trench

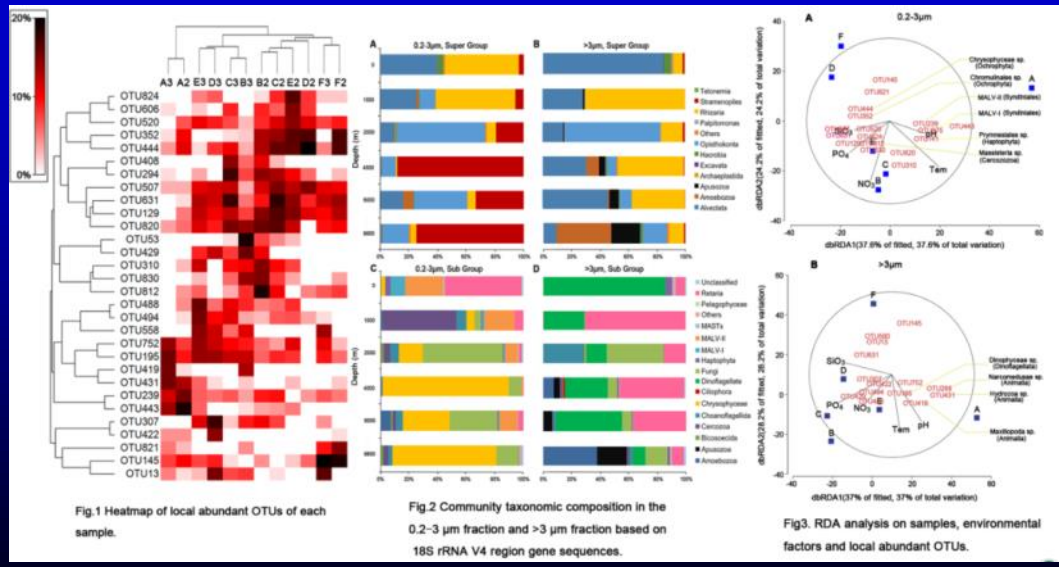


Fig.1 Heatmap of local abundant OTUs of each sample.

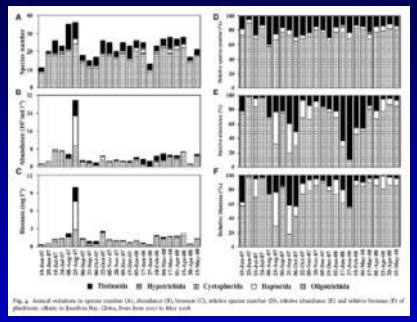
Fig.2 Community taxonomic composition in the 0.2–3 μm fraction and >3 μm fraction based on 18S rRNA V4 region gene sequences.

Fig3. RDA analysis on samples, environmental factors and local abundant OTUs.

Community study of planktonic ciliated in coastal area

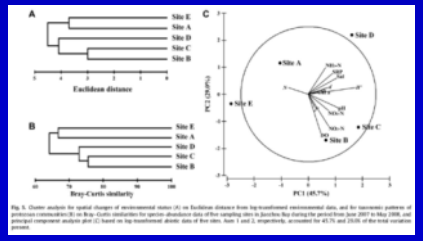
Seasonal variation of planktonic ciliate communities

Jiang et al. (2011) Journal of the Marine Biological Association of the United Kingdom



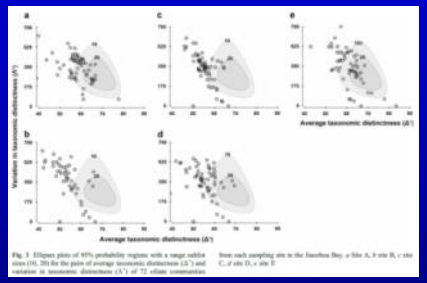
Using spatial pattern of planktonic ciliate communities as indicators to assess water quality

Jiang et al. (2011) Marine Pollution Bulletin



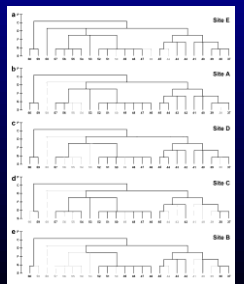
Application of taxonomic relatedness for bioassessment using ciliates

Jiang et al. (2012) Environmental Science and Pollution Research; Xu et al. (2011)



Discriminating EQS using the taxonomic relatedness with in a small pool of planktonic ciliates

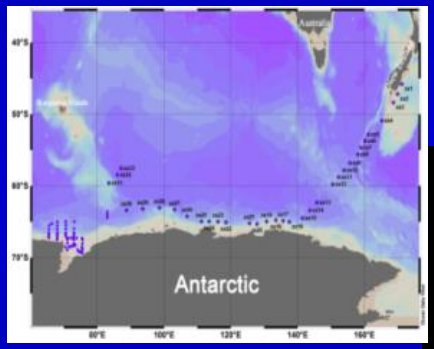
Jiang et al. (2014) Science of the Total Environment

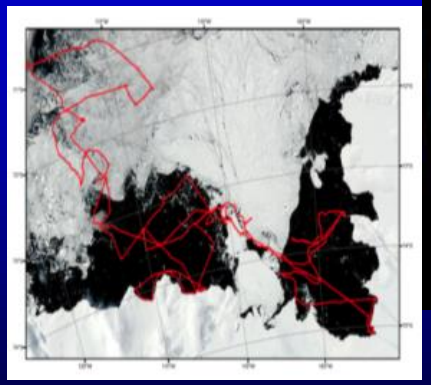


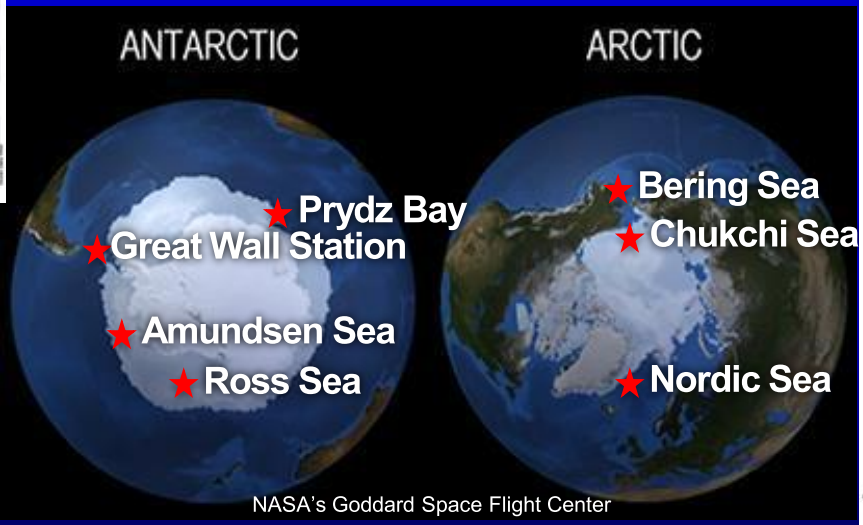
Community study of plagic ciliated microzooplankton in bipolar

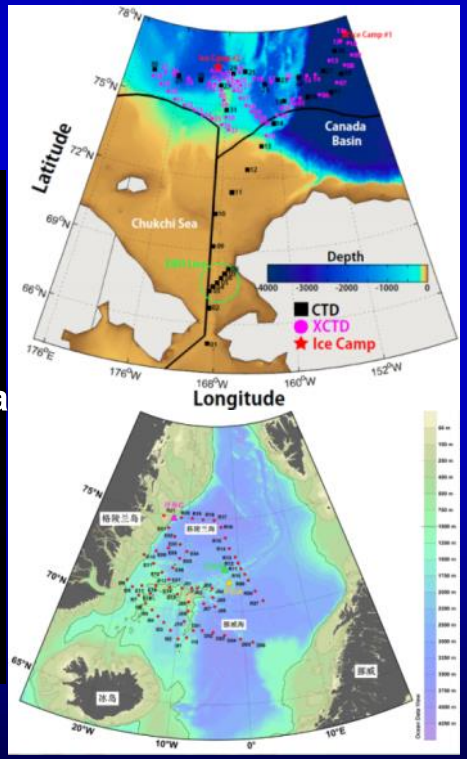
R/V Xuelong's Track (2014–2016)

R/V Araon's Track (2010–2016)









Jiang et al. (2013) Ecological Indicators; Jiang et al. (2014) Progress in Oceanography; Jiang et al. (2015, 2016) Deep-Sea Research Part II; Jiang et al. (2017) Polar Biology

5. Ecological functions of benthos









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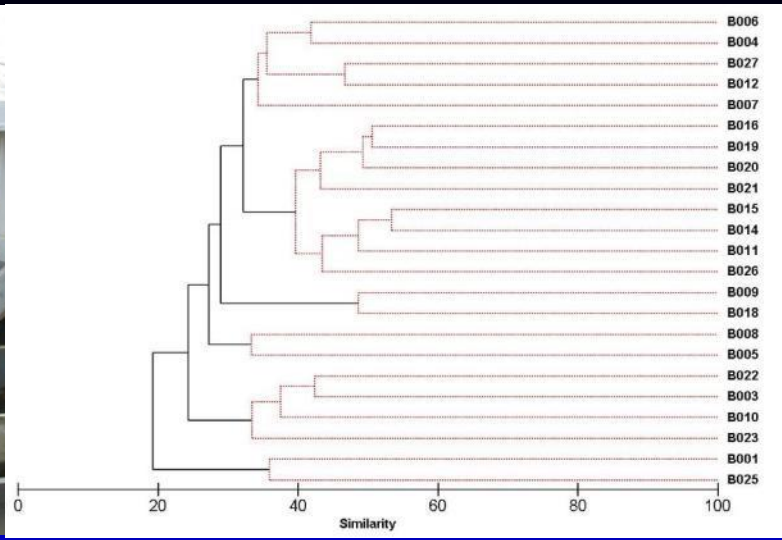
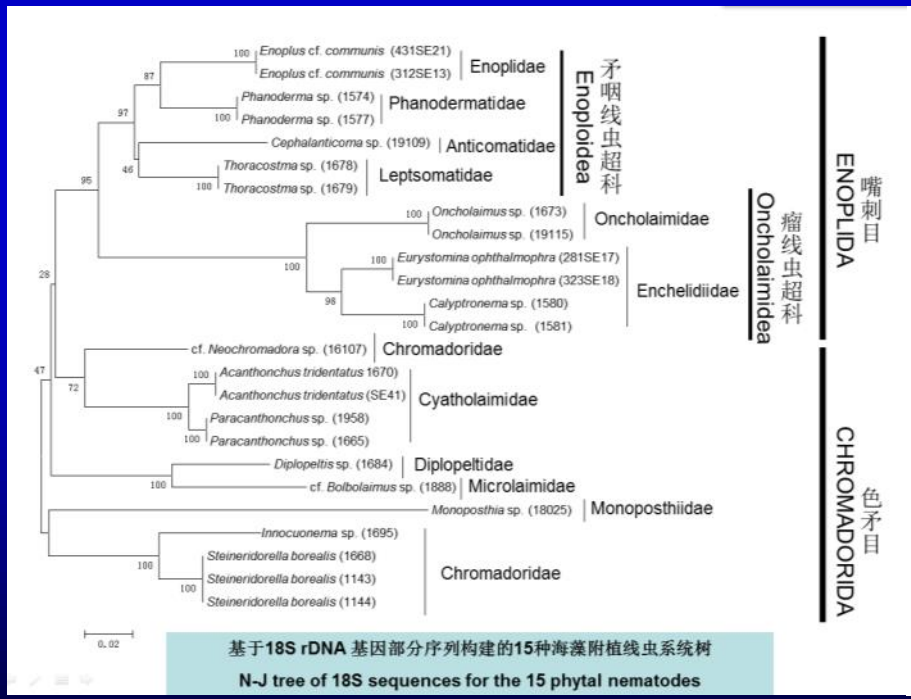
Research Interests

- Biodiversity of benthos (temperate, subtropical, tropical and polar areas)
- Secondary production of benthos
- Benthic food web dynamics
- Benthic-pelagic coupling
- Effects of marine pollution on benthic community
- Effects of ocean acidification on benthos
- Benthic size spectra
- Taxonomy of marine meiofauna
- DNA barcoding for marine nematodes

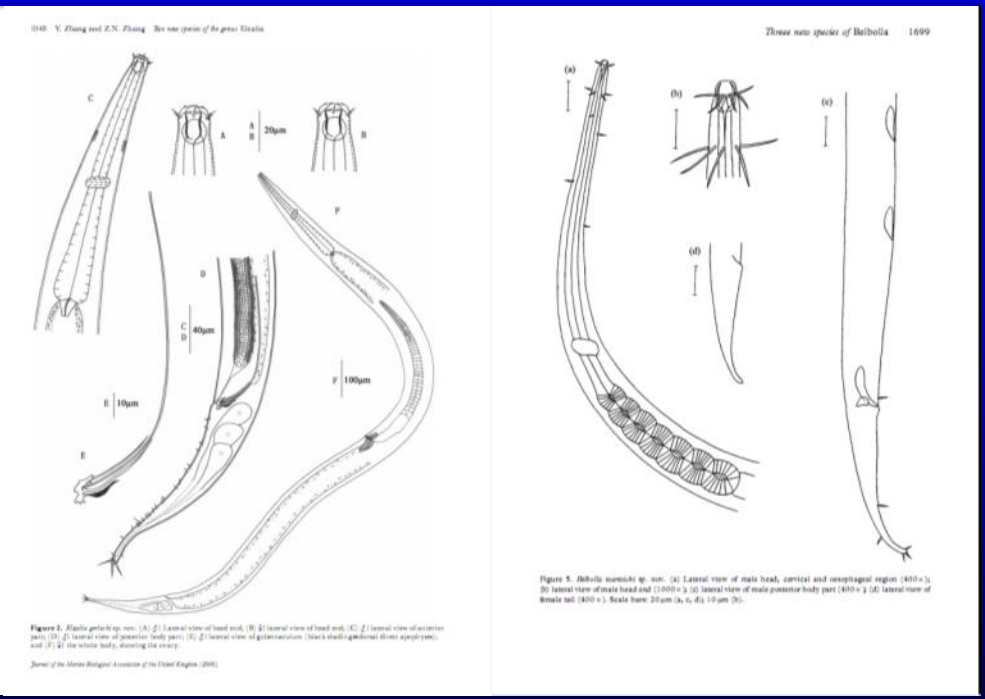
Field Sampling for Benthos



CLUSTER of macrofaunal community



N-J tree of 18S sequences for the 15 phytal nematodes



New species of marine nematodes

cooperation partner

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