

The 12th Korea-China-Japan Bioinformatic Training Course & Symposium

Ocean Suites Hotel, Jeju, South Korea

June 18 – 20, 2014

KCJ Bioinformatics Training Course 2014

”How to analyze Big Data: Marine Metagenomics and the Diversity of Microorganisms”

Ocean Suites Hotel,
June 20, 2014

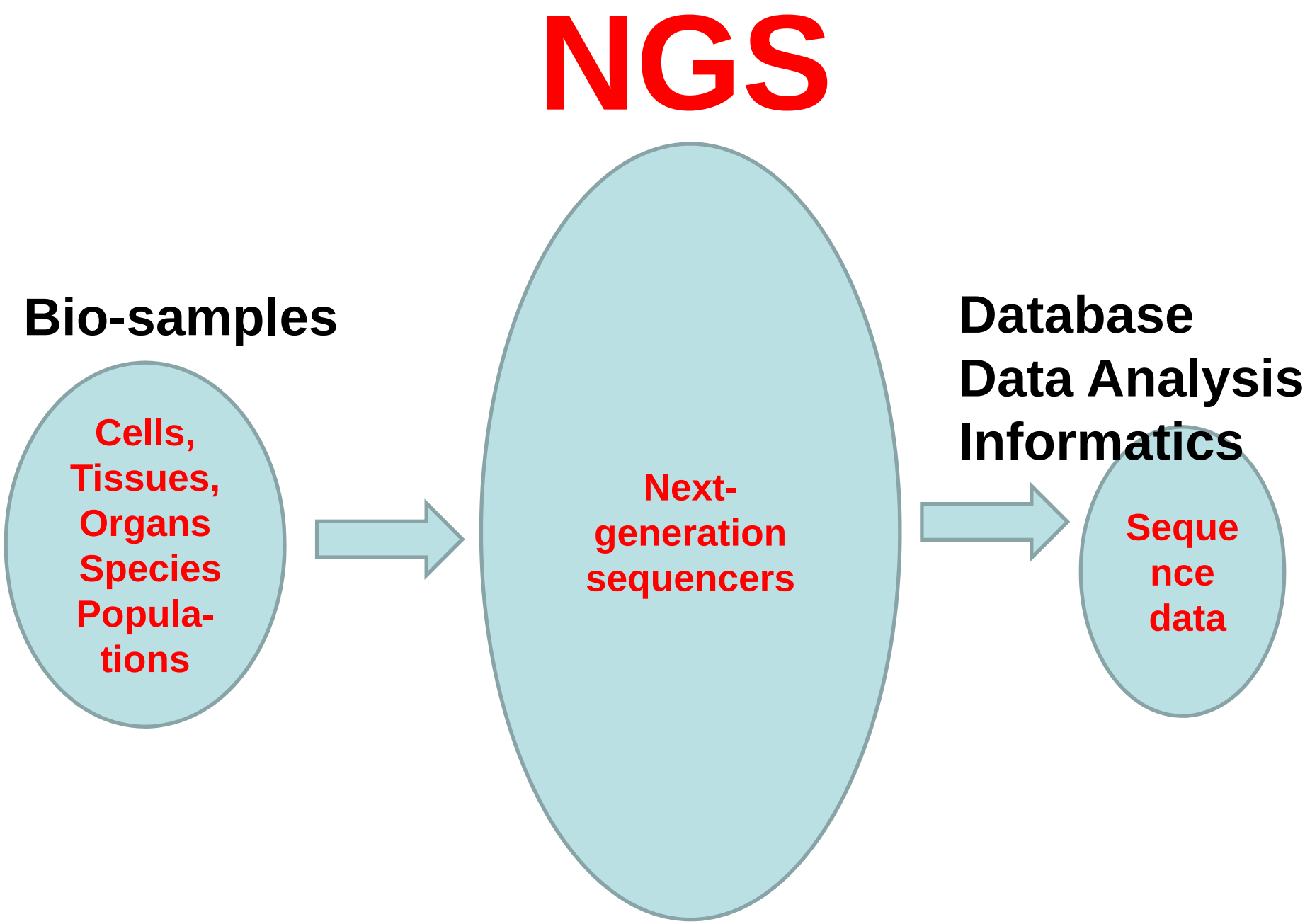
Takashi Gojobori

KAUST (King Abdullah University of Science and Technology), KSA and
NIG (National Institute of Genetics), Japan

How to analyze Big Data (1)!

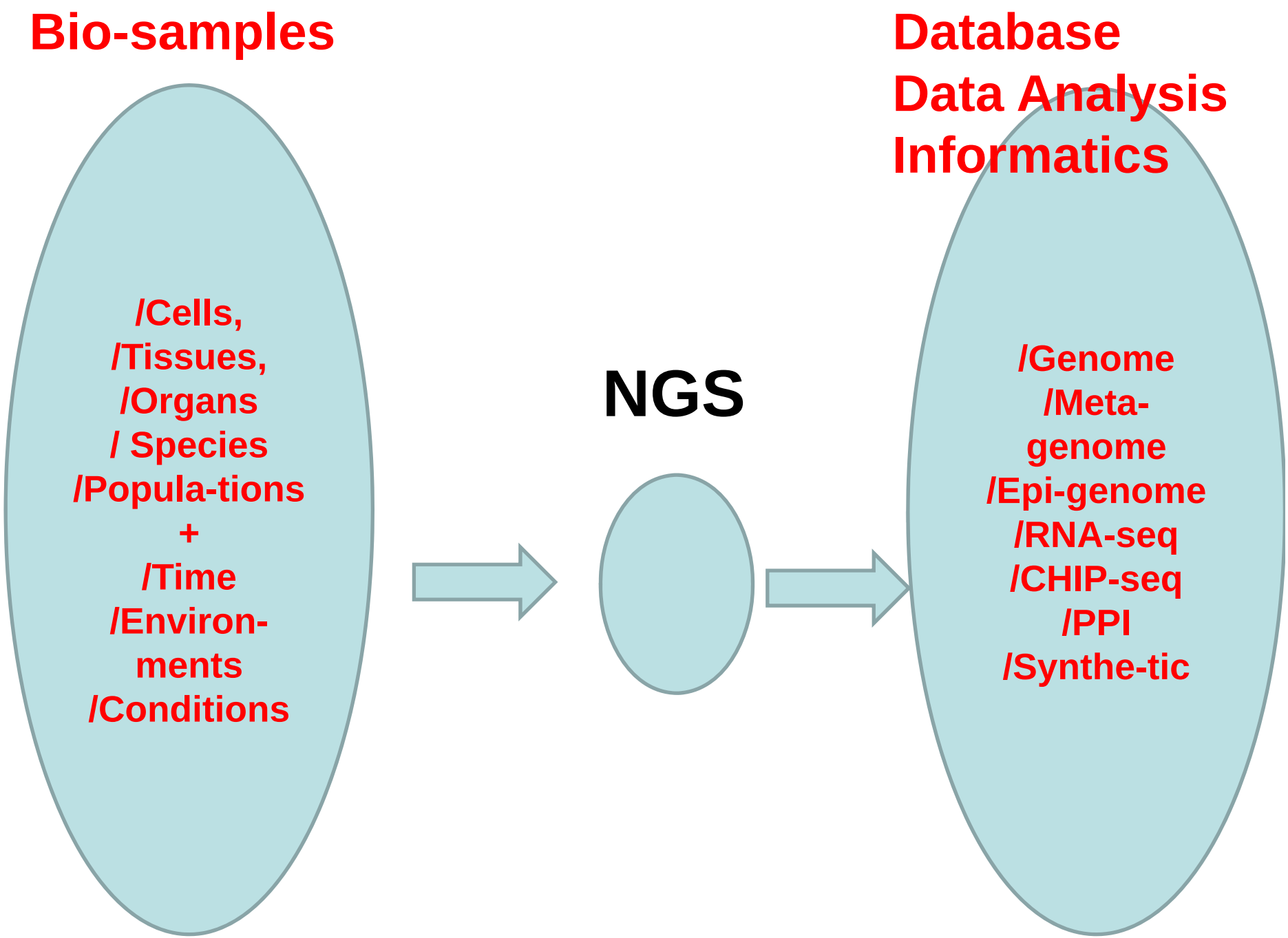
Genome analysis is a tool,

but not purpose!


NGS
Bio-samples
Cells,
Tissues,
Organs
Species
Popula-
tions
Next-
generation
sequencers
Database
Data Analysis
Informatics
Seque
nce
data

Item	Description
Read Length and Speed	512 nanopores x 15bp/sec => ~7500 bp/sec
Read Accuracy	99.8%
6 Hours Life Time	150 x 106bp
Applied Currency /Blockage	60 picoamps to anywhere from 20-40 picoamps
No. of nanopore	2,000 nanopores / cartridge. Will become available in early 2013 containing over 8,000 nanopores. →Delivers a complete human genome in 15 minutes.
Sample Preparation	Any user-derived sample preparation resulting in double stranded DNA (dsDNA) in solution is compatible with the system.
Amplification	No sample amplification.
Cost	$900
Commercialization	Oxford Nanopore intends directly to customers withi

Nano Pore Oxford (2012)

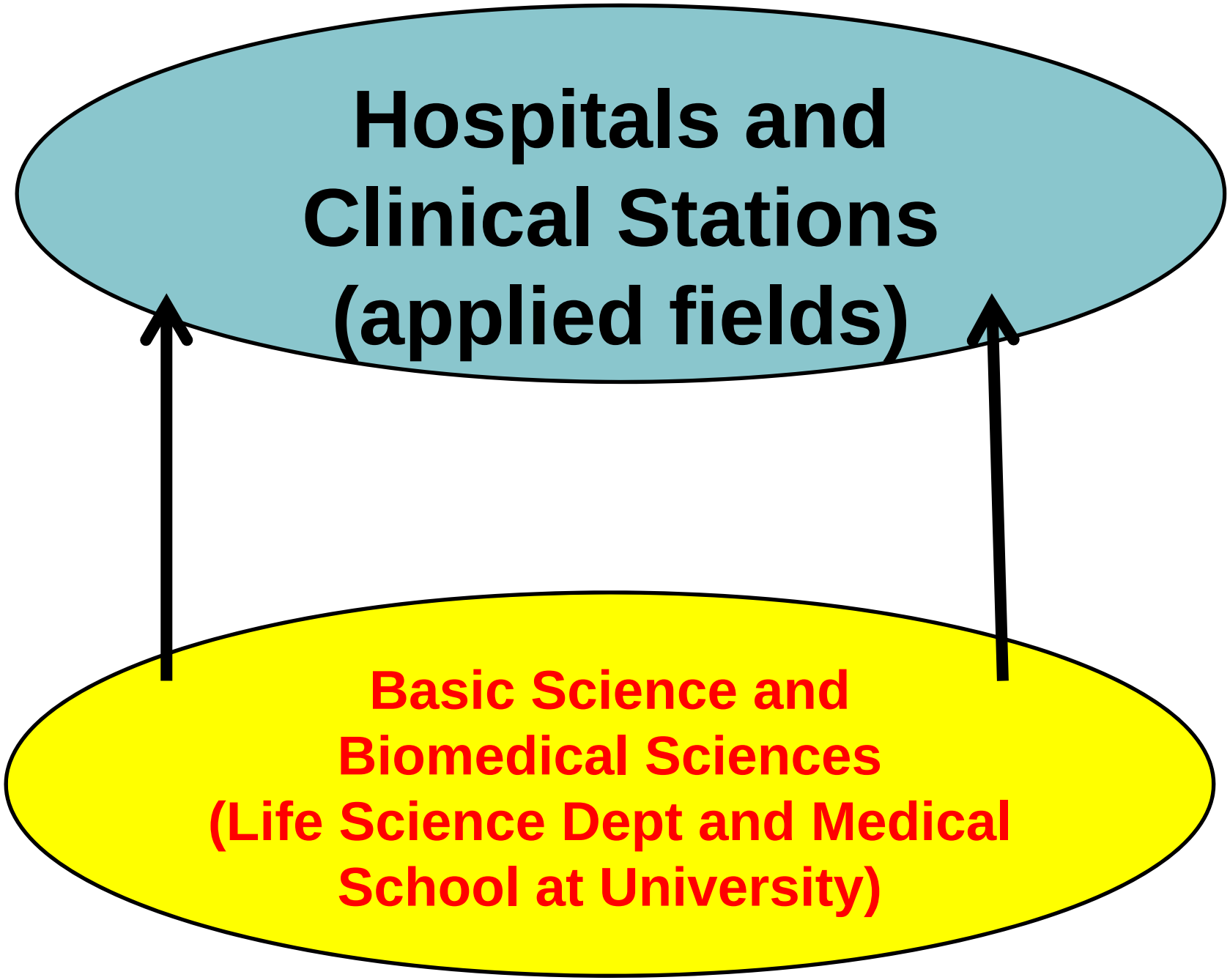

Bio-samples
/Cells,
/Tissues,
/Organs
/ Species
/Popula-tions
+
/Time
/Environ-
ments
/Conditions
NGS
Database
Data Analysis
Informatics
/Genome
/Meta-
genome
/Epi-genome
/RNA-seq
/CHIP-seq
/PPI
/Synthe-tic

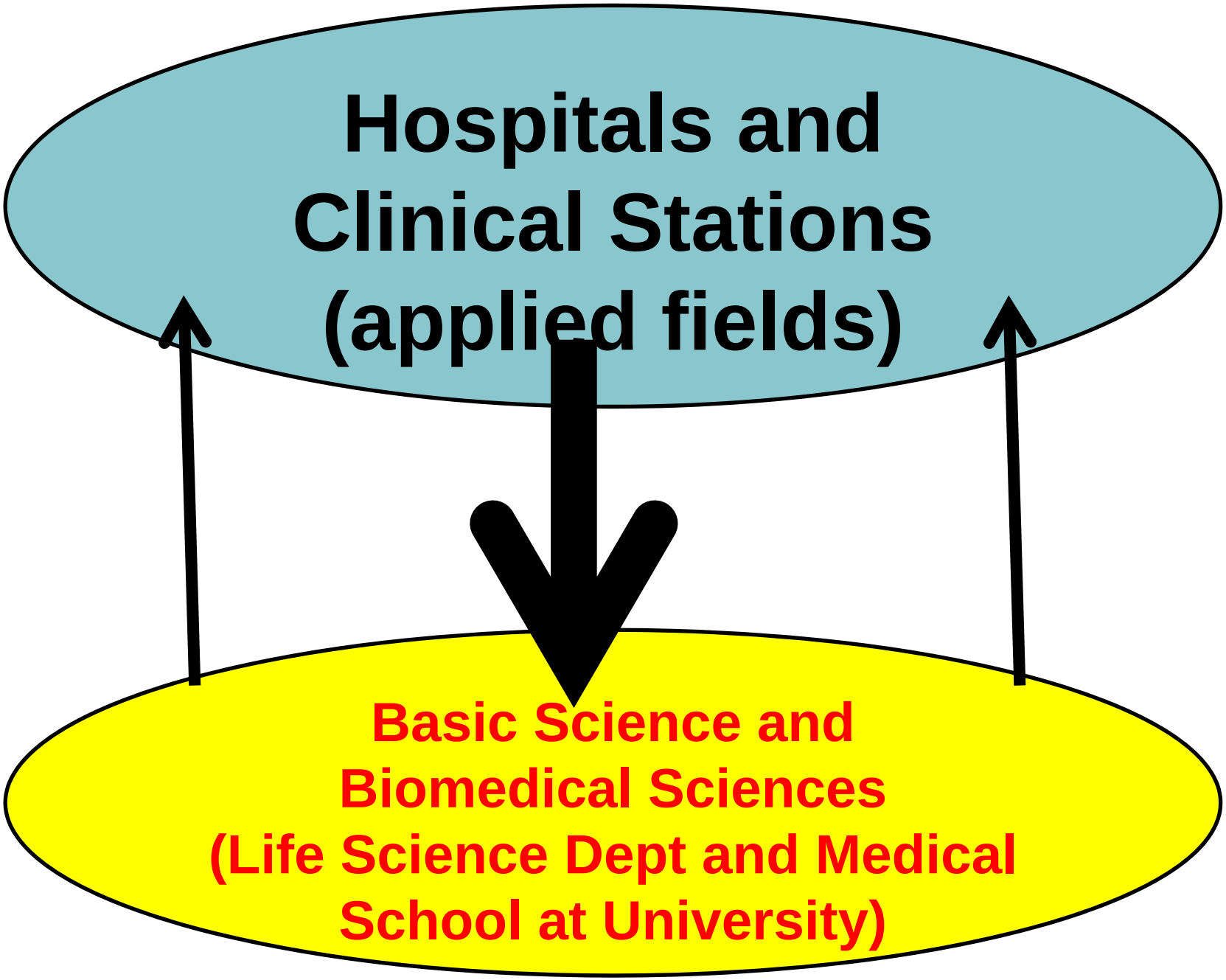
How to analyze Big Data (2)!

Biosamples are

a Key!

Large or rare


Hospitals and
Clinical Stations
(applied fields)
Basic Science and
Biomedical Sciences
(Life Science Dept and Medical
School at University)

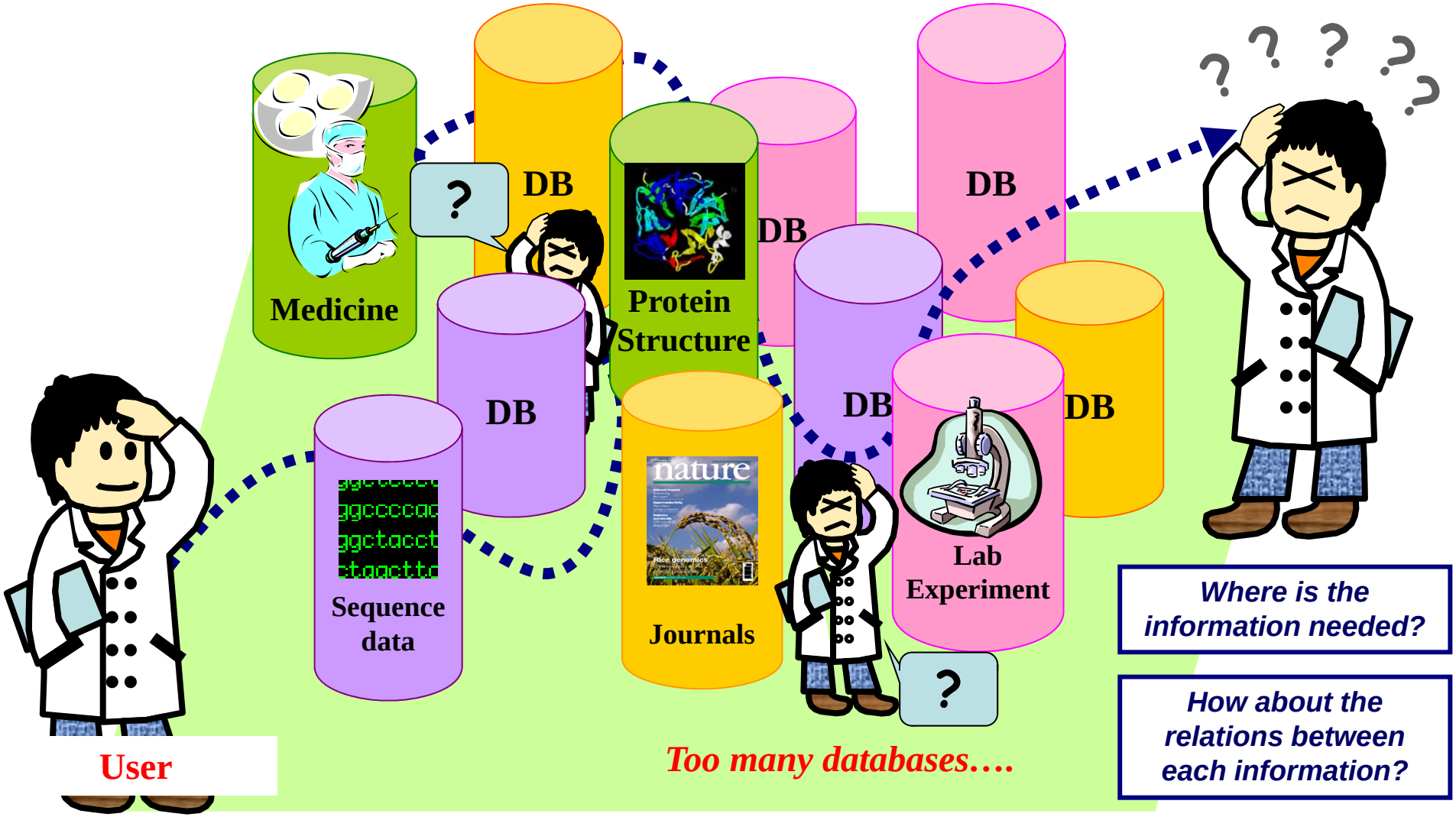

Hospitals and
Clinical Stations
(applied fields)
Basic Science and
Biomedical Sciences
(Life Science Dept and Medical
School at University)

How to analyze Big Data (3)!

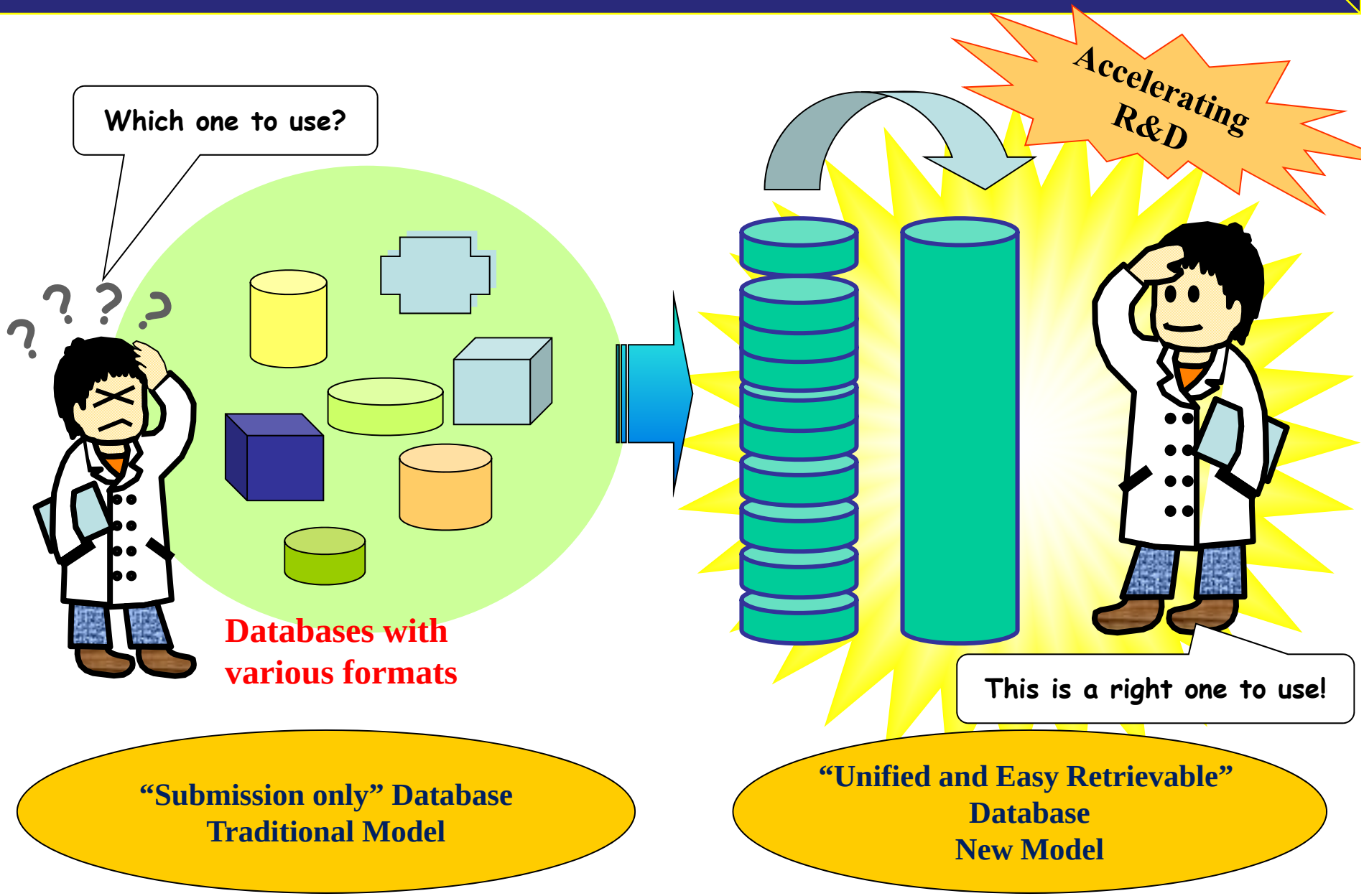
Database Construction is a Key!

Issues on retrieving the necessary information

(The Gist) **Lack of the standard format without unified information often hinders research and development seriously**



Be Unified and Easily Retrievable Format from Sporadic Information !



D. Howe, M. Costanzo, P. Fey, T. Gojobori,
L. Hannick, W. Hide, D. Hill, R. Kania, M. Schaeffer,
S. St Pierre, S. Tweigger, and S. Rhee

Nature (2008) 455: 47-50

How to analyze Big Data (4)!

A gene for the genome is a Key!

Nakamura et al. *PNAS* (2013)

Evolutionary changes of multiple visual pigment genes in the complete genome of Pacific bluefin tuna

Yoji Nakamura[a,1], Kazuki Mori[b], Kenji Saitoh[a], Kenshiro Oshima[c], Miyuki Mekuchi[a], Takuma Sugaya[a], Yuya Shigenobu[a], Nobuhiko Ojima[a], Shigeru Muta[b], Atushi Fujiwara[a], Motoshige Yasuike[a], Ichiro Oohara[a], Hideki Hirakawa[d], Vishwajit Sur Chowdhury[e], Takanori Kobayashi[f], Kazuhiro Nakajima[g], Motohiko Sano[e], Tokio Wada[f], Kousuke Tashiro[b], Kazuho Ikeo[h], Masahira Hattori[c], Satoru Kuhara[b], Takashi Gojobori[a,1], and Kiyoshi Inouye[g]

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Edited[a] by Tomoko Ohta, National Institute of Genetics, Mishima, Japan, and approved May 20, 2013 (received for review February 2, 2013)

Tunas are migratory fishes in offshore habitats and top predators with unique features. Despite their ecological importance and high market values, the open-ocean lifestyle of tuna, in which effective sensing systems such as color vision are required for capture of prey, has been poorly understood. To elucidate the genetic and evolutionary basis of optic adaptation of tuna, we determined the genome sequence of the Pacific bluefin tuna (*Thunnus orientalis*), using next-generation sequencing technology. A total of 26,433 protein-coding genes were predicted from 16,802 assembled scaffolds. From these, we identified five common fish visual pigment genes: red-sensitive (middle/long-wavelength sensitive; M/LWS), UV-sensitive (short-wavelength sensitive 1; SWS1), blue-sensitive (SWS2), rhodopsin (RH1), and green-sensitive (RH2) opsin genes. Sequence comparison revealed that tuna's RH1 gene has an amino acid substitution that causes a short-wave shift in the absorption spectrum (i.e., blue shift). Pacific bluefin tuna has at least five RH2 paralogs, the most among studied fishes; four of the proteins encoded may be tuned to blue light at the amino acid level. Moreover, phylogenetic analysis suggested that gene conversions have occurred in each of the SWS2 and RH2 loci in a short period. Thus, Pacific bluefin tuna has undergone evolutionary changes in three genes (RH1, RH2, and SWS2), which may have contributed to detecting blue-green contrast and measuring the distance to prey in the blue-pelagic ocean. These findings provide basic information on behavioral traits of predatory fish and, thereby, could help to improve the technology to culture such fish in captivity for resource management.

tuna genome

Tunas are considered "the ultimate fish," because they are top predators in ocean ecosystems, in addition to their unique

duplication occurred and each copy has been maintained for a long time. Previous studies have accumulated molecular information on opsins, focusing on the residues surrounding the retinal-binding pocket (10–12).

Many physiological studies have been conducted on fish visual system underwater (13, 14). As for tuna, spectrophotometric analyses have demonstrated several wavelengths of maximal absorbance (λ_{max}) in the visual pigments of yellowfin tuna (*Thunnus albacares*) (15) and Pacific bluefin tuna (*Thunnus orientalis*) (16), respectively. However, little is known about the genetic basis and evolutionary history of tuna's optic adaptation to an open-ocean predatory lifestyle. In this study, we have sequenced the draft genome of Pacific bluefin tuna and analyzed the opsin genes in a phylogenetic framework to look for evidence of optic adaptation at the molecular level. The origins of tuna's opsin paralogs were dated by genome-wide comparison among the teleosts for which genomic information is available, and the relationship between the evolutionary pathway of opsin genes and adaptation to ocean environment is discussed.

Results

Genome Sequencing and Gene Prediction. The diploid genome of a wild-caught male Pacific bluefin tuna (*T. orientalis*) was sequenced. A whole-genome shotgun sequencing and assembling strategy with a combination of Roche 454 FLX Titanium (Roche Diagnostics) and Illumina GaIIx platforms provided 192,169 contigs (>500 bp) and 16,802 scaffolds (>2 kb) totaling 740.3 Mb, corresponding to 92.5% of the estimated genome size (~800 Mb) (ref. 17; Table 1). The scaffolds were obtained by assembling 31.9 million 454 reads, including 4.9 million paired ends (11.9-fold coverage) and 229.7 million Illumina paired-end reads (43-fold coverage) (Tables S1 and S2 and Fig. S1). Sequence

How to analyze Big Data (5)!

Comparative (medical, evolutionary) genome is a Key!

OPEN ACCESS Freely available online

Nakamura *et al. PLoS One* (2013)

PLOS ONE

The First Symbiont-Free Genome Sequence of Marine Red Alga, Susabi-nori (*Pyropia yezoensis*)

Yoji Nakamura[1]*, Naobumi Sasaki[2], Masahiro Kobayashi[3], Nobuhiko Ojima[1], Motoshige Yasuike[1], Yuya Shigenobu[1], Masataka Satomi[1], Yoshiya Fukuma[4], Koji Shiwaku[4], Atsumi Tsujimoto[5], Takanori Kobayashi[6], Ichiro Nakayama[7], Fuminari Ito[8], Kazuhiro Nakajima[9], Motohiko Sano[1], Tokio Wada[6], Satoru Kuhara[10], Kiyoshi Inouye[6], Takashi Gojobori[2]*, Kazuho Ikeo[2]

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Abstract

Nori, a marine red alga, is one of the most profitable mariculture crops in the world. However, the biological properties of this macroalga are poorly understood at the molecular level. In this study, we determined the draft genome sequence of susabi-nori (*Pyropia yezoensis*) using next-generation sequencing platforms. For sequencing, thalli of *P. yezoensis* were washed to remove bacteria attached on the cell surface and enzymatically prepared as purified protoplasts. The assembled contig size of the *P. yezoensis* nuclear genome was approximately 43 megabases (Mb), which is an order of magnitude smaller than the previously estimated genome size. A total of 10,327 gene models were predicted and about 60% of the genes validated lack introns and the other genes have shorter introns compared to large-genome algae, which is consistent with the compact size of the *P. yezoensis* genome. A sequence homology search showed that 3,611 genes (35%) are functionally unknown and only 2,069 gene groups are in common with those of the unicellular red alga, *Cyanidioschyzon merolae*. As color trait determinants of red algae, light-harvesting genes involved in the phycobilisome were predicted from the *P. yezoensis* nuclear genome. In particular, we found a second homolog of phycobilisome-degradation gene, which is usually chloroplast-encoded, possibly providing a novel target for color fading of susabi-nori in aquaculture. These findings shed light on unexplained features of macroalgal genes and genomes, and suggest that the genome of *P. yezoensis* is a promising model genome of marine red algae.

Citation: Nakamura Y, Sasaki N, Kobayashi M, Ojima N, Yasuike M, et al. (2013) The First Symbiont-Free Genome Sequence of Marine Red Alga, Susabi-nori (*Pyropia yezoensis*). PLoS ONE 8(3): e57122. doi:10.1371/journal.pone.0057122

Editor: Juergen Kroymann, French National Centre for Scientific Research, Université Paris-Sud, France

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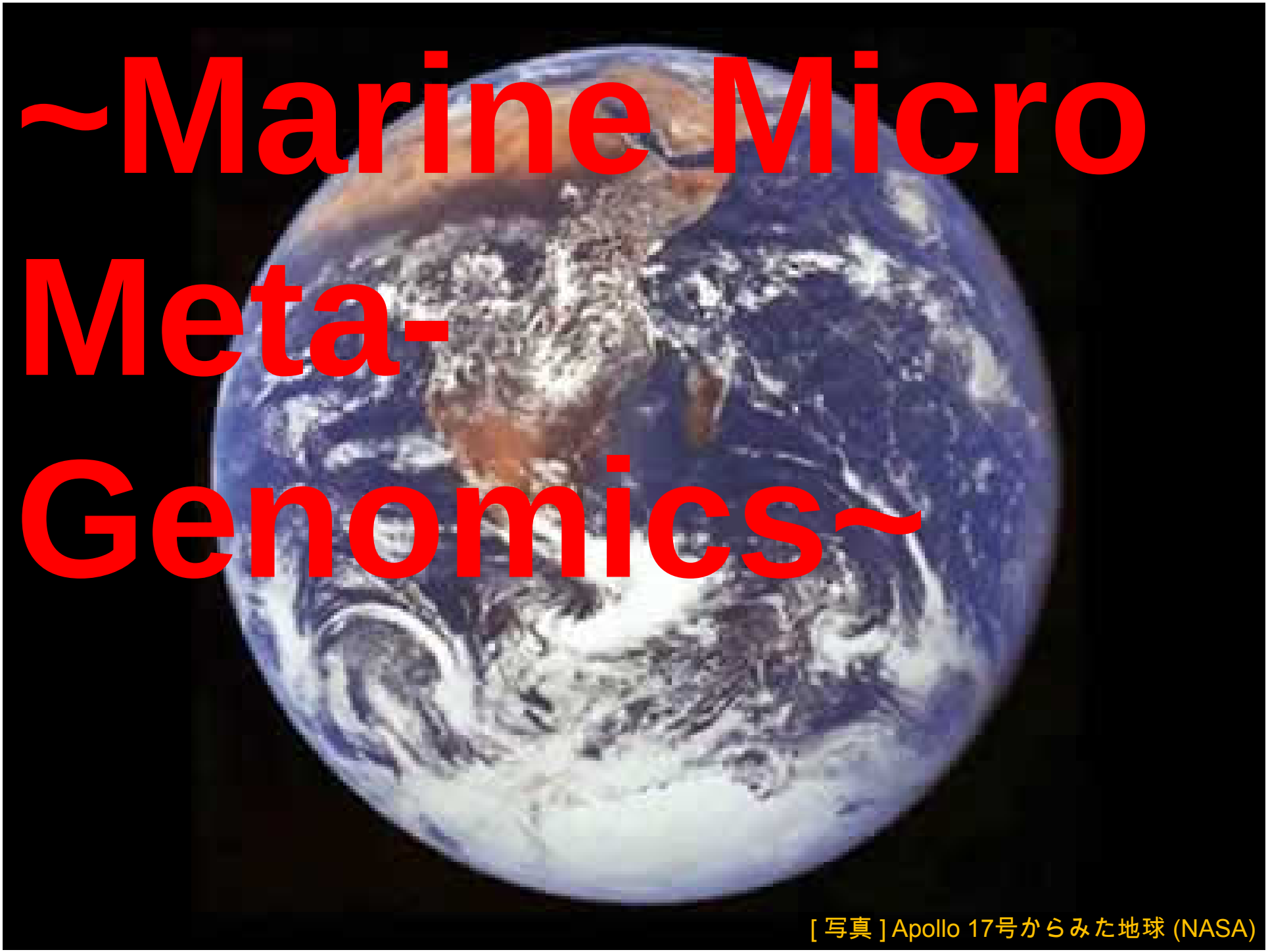
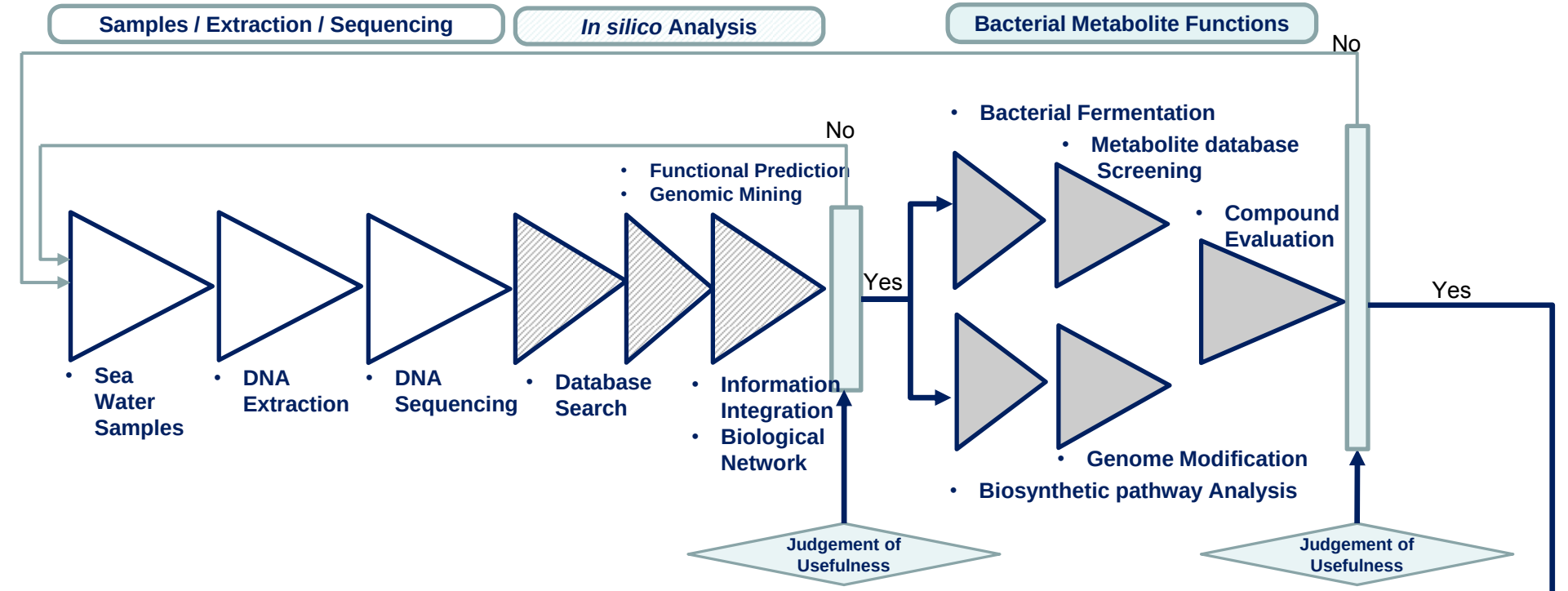
~Marine Micro Meta-Genomics~

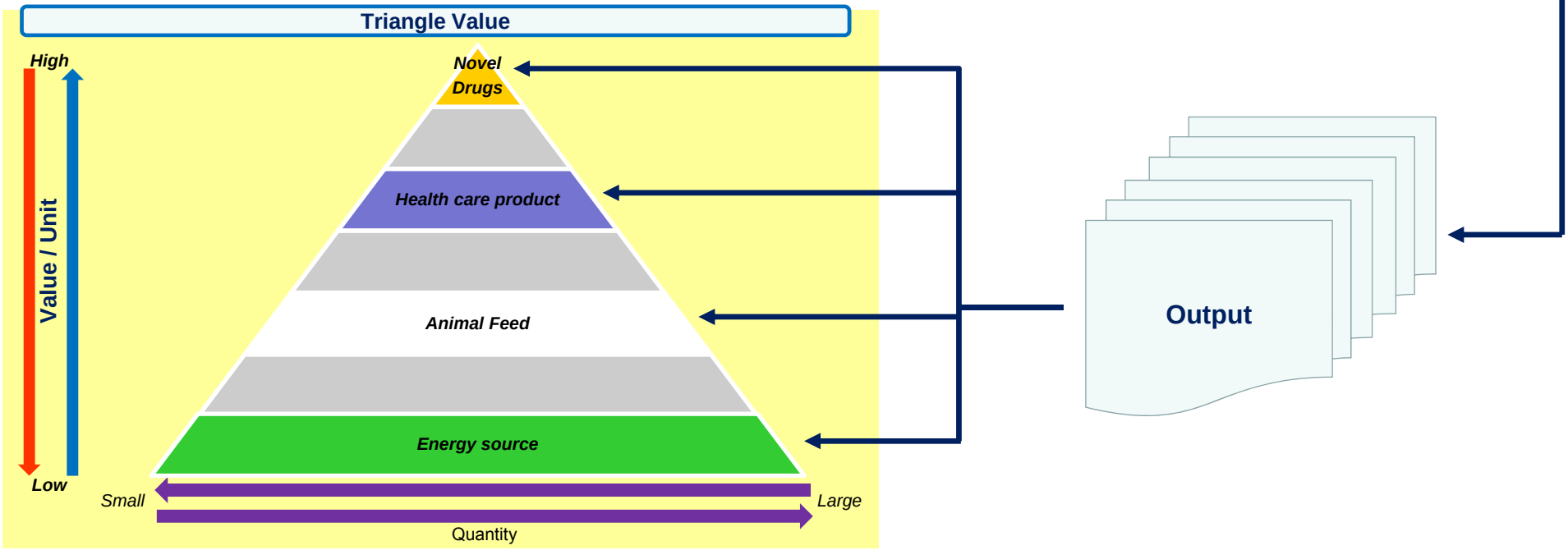


[写真] Apollo 17号からみた地球 (NASA)

How to analyze Big Data (6)!

A pipeline is a Key!

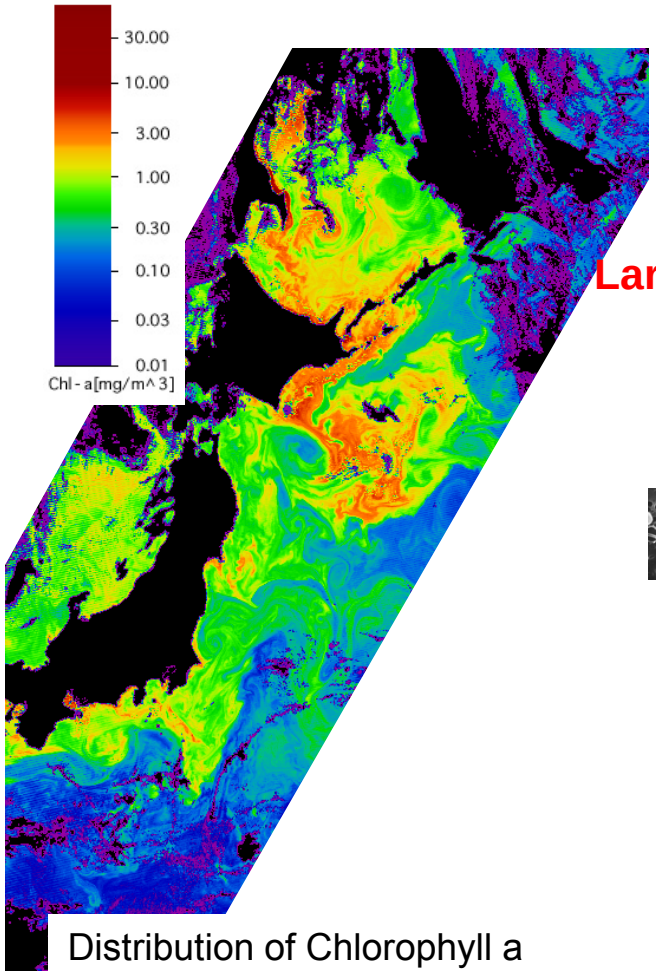

Samples / Extraction / Sequencing
In silico Analysis
Bacterial Metabolite Functions
No
No
Yes
Yes
• Sea Water Samples
• DNA Extraction
• DNA Sequencing
• Database Search
• Functional Prediction
• Genomic Mining
• Information Integration
• Biological Network
Judgement of Usefulness
• Bacterial Fermentation
• Metabolite database Screening
• Compound Evaluation
• Genome Modification
• Biosynthetic pathway Analysis
Judgement of Usefulness


Triangle Value
High
Low
Value / Unit
Novel Drugs
Health care product
Animal Feed
Energy source
Small
Large
Quantity
Output

How to analyze Big Data (7)!

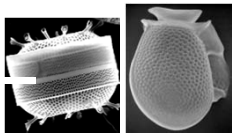
“Science is gamble, then need to win” is a Key!

—A View of marine micro-organism ecosystem—



Distribution of Chlorophyll a
In Tohoku sea coast

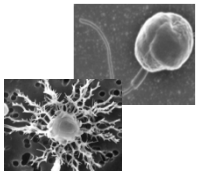
Tohoku sea coast → One of species-richest spots



Foods chain

Large plant planktons → **Animal planktons** → **Fish**

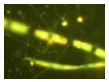
Micro plant planktons



Soluble organiucs

Protozoa

Micro-organism loop



Bacteria

Understanding of Marine Microorganism Diversity by use of the Digital DNA chip system through Metagenomics

～Subjects and Division of Roles～

	Subjects	Role
1	Data Analysis of Metagenomics and Project Management	NIG
2	Construction of Marine Metagenomics Database and Developments of the Digital DNA Chip System	NIG/JSM
3	NGS Sequencing of Metagenomic data	Tokyo U/ NIG
4	Isolation of DNAs from sea water samples/ Sampling machine developments	Kyushu U
5	Sea Water Sampling and Measurements of Physical Conditions	NMRC
6	Analysis of Plant Pico-Planktons by Flow Cytometry	NIE


第五大海丸

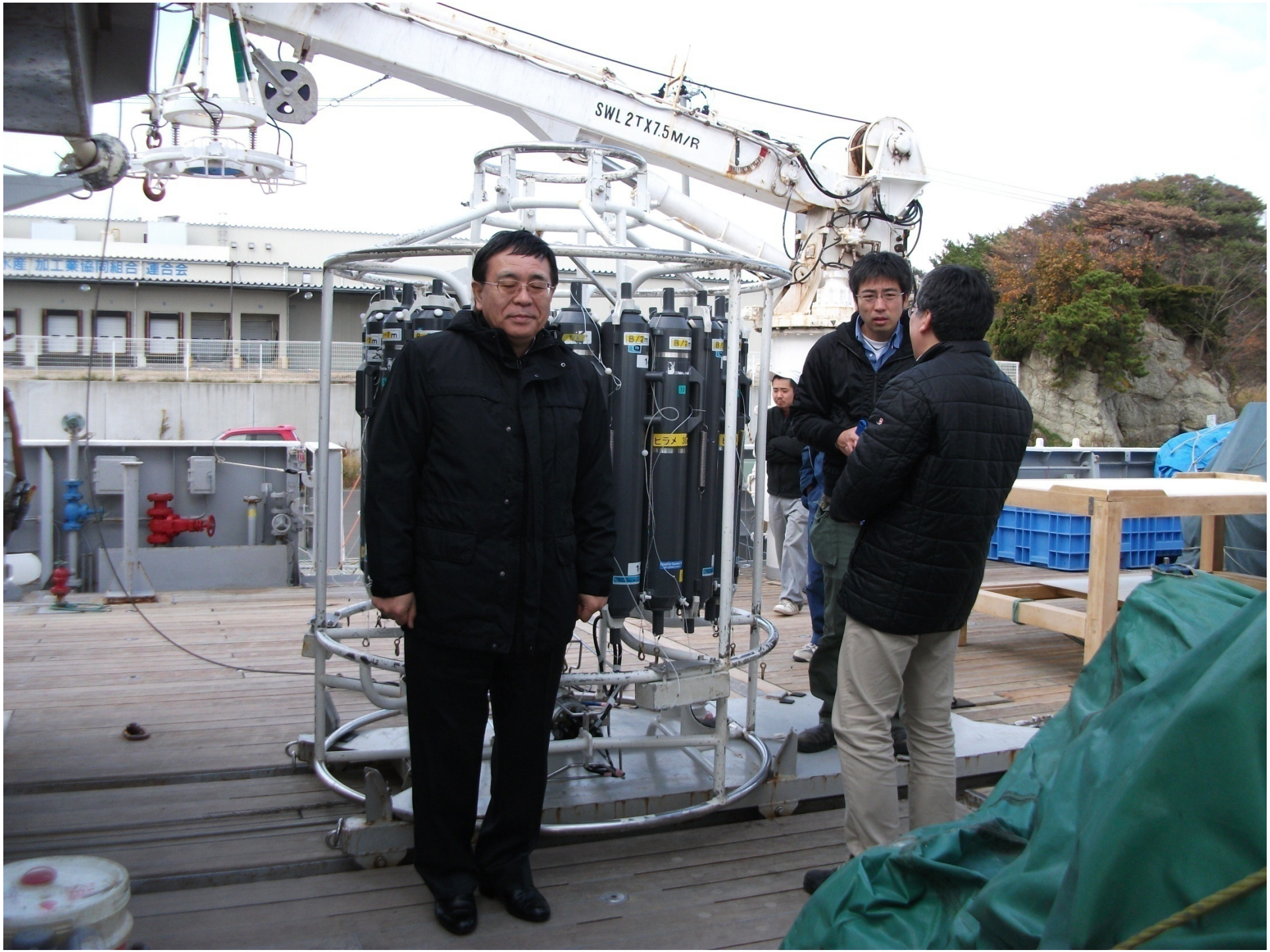

-1936


若鷹丸
WAKATAKA MARU


丸 鷲 若
WAKATAKA MARU

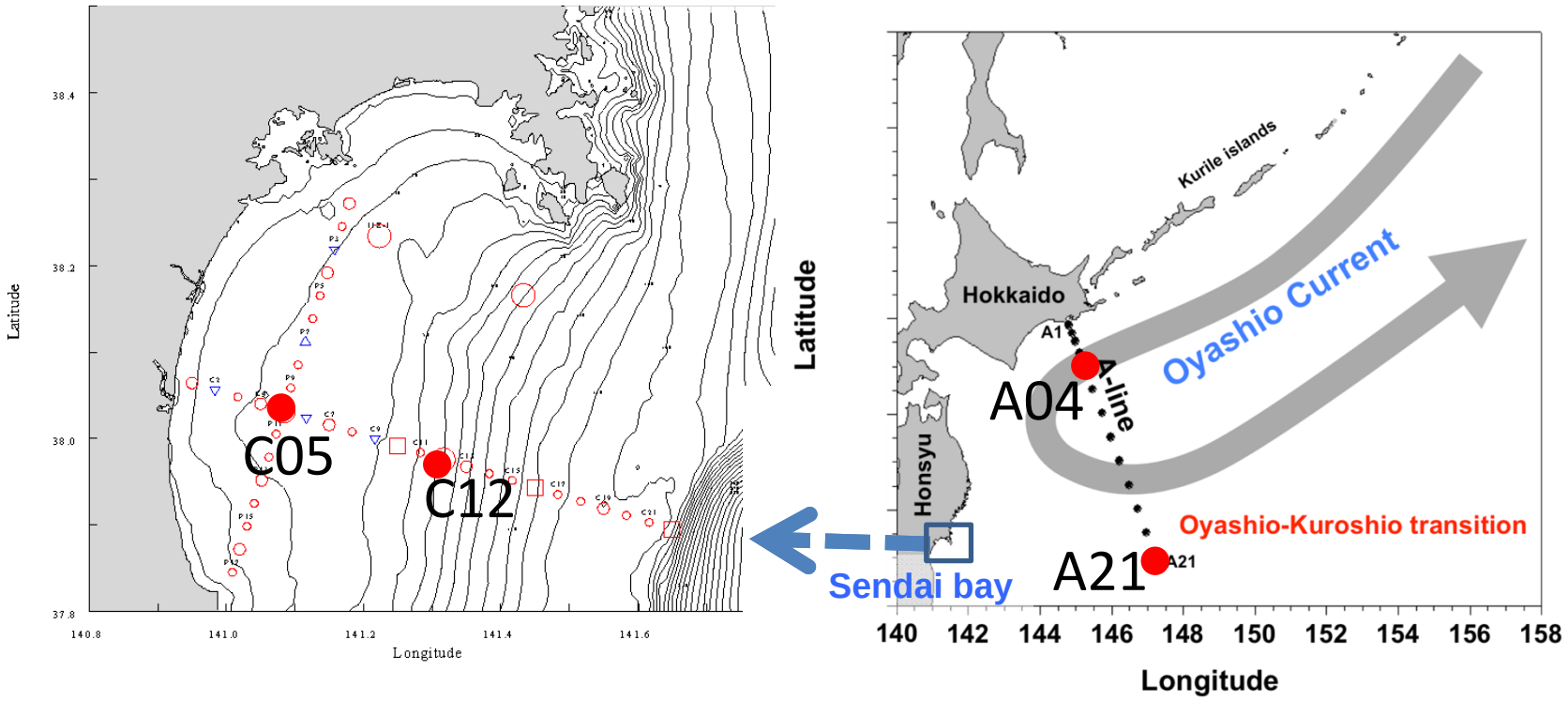

B-7m
B-7m
B-7m
20
19
17


30m
30m
10m
10m
6
4
2
10m


SWL 2TX7.5M/R


0.2μ

Observation Points at the Sendai Bay and Nemuro Sea as a Control



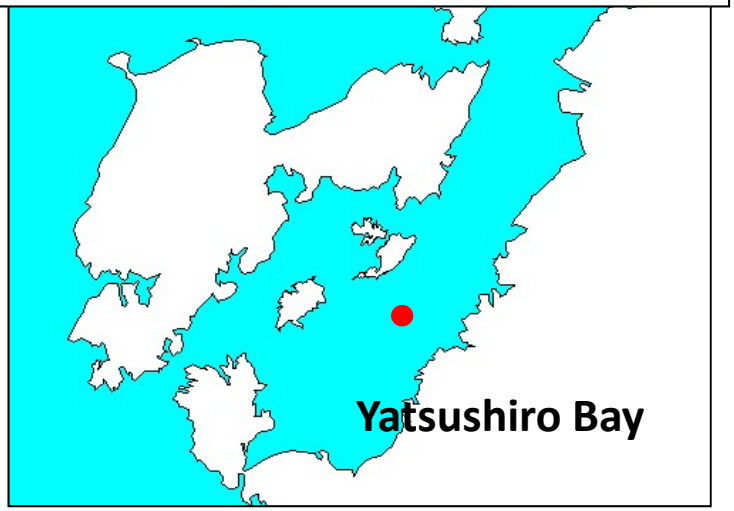
Observation Points （Sendai Bay）

A-line（Near Sea）

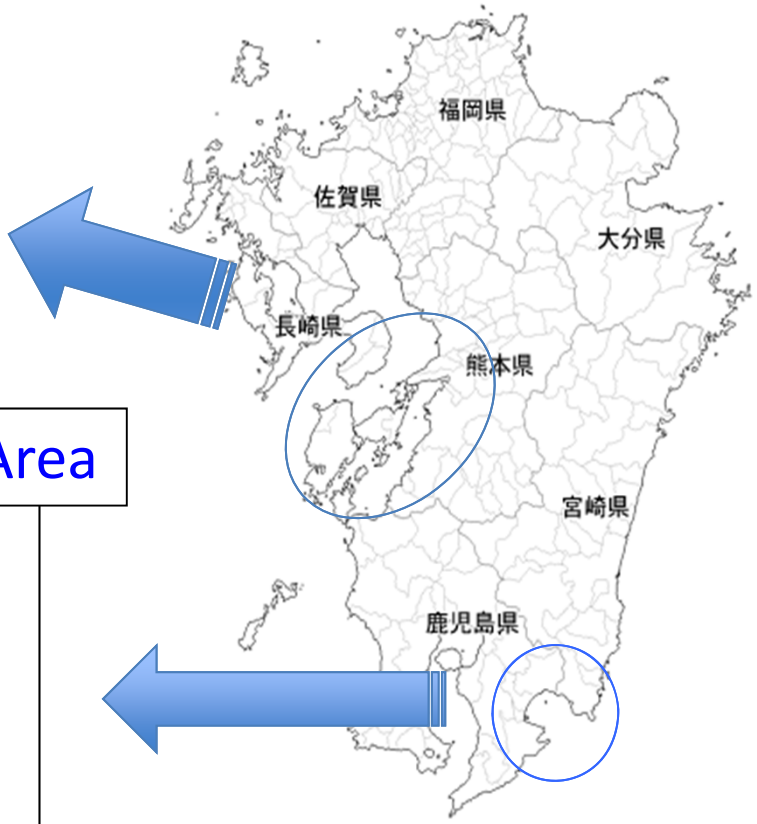
Sea Water Sampling Points in Kyushu for “Red Tide” Monitoring

Comparative Metagenomics for Detecting any changes in marine microorganism diversity

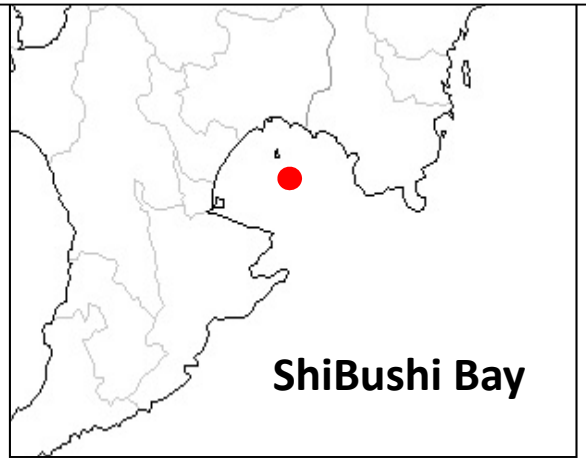
Red Tide Occurrence Sea Area



Periodical Sampling



Red Tide Non-Occurrence Sea Area

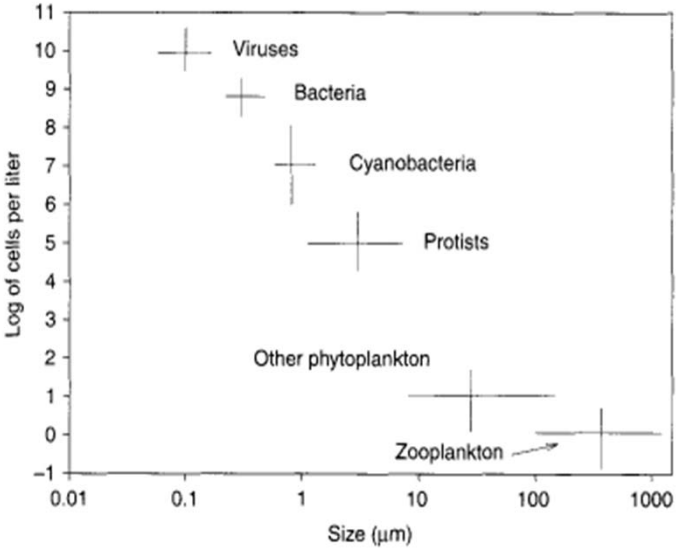


Sampling of Sea Waters at Observation Points in Sendai Bay and Nemuro Sea

Sails	Dates	Sea points	Depth (m)	Sea Volume(Kg)
WK1203	2012.3.5	A04	10	22.8
WK1203	2012.3.5	A04	30	20.6
WK1203	2012.3.11	A21	10	20.0
WK1203	2012.3.11	A21	10	20.0
WK1203	2012.3.13	P10(C5)	1	7.0
WK1203	2012.3.13	C12	1	21.0
Rent1204	2012.4.16	P10(C5)	1	15.1
Rent1204	2012.4.16	P10(C5)	18	6.8
Rent1204	2012.4.16	C12	1	4.5
Rent1204	2012.4.16	C12	10	7.2
WK1205	2012.5.10	A04	10	17.1
WK1205	2012.5.10	A04	20	15.1
WK1205	2012.5.15	A21	10	6.8
WK1205	2012.5.15	A21	40	9.0
WK1205	2012.5.16	P10(C5)	1	9.2
WK1205	2012.5.16	P10(C5)	15	9.3
WK1205	2012.5.17	C12	1	9.4
WK1205	2012.5.17	C12	20	8.6
WK1206D	2012.6.17	F3	5	8.5
WK1206D	2012.6.17	F3	20	8.0
WK1206D	2012.6.18	P10(C5)	5	9.0
WK1206D	2012.6.18	P10(C5)	20	9.0
WK1207	2012.7.14	C5(P10)	2	8.0
WK1207	2012.7.14	C5(P10)	10	8.5
WK1207	2012.7.16	C12	2	9.0
WK1207	2012.7.16	C12	30	9.5

Isolation of DNAs (Kyushu U.)

Sails	Dates	Points	Depth (m)	Volume (Kg)
WK1203	2012.3.5	A04	10	22.8
WK1203	2012.3.5	A04	30	20.6
WK1203	2012.3.11	A21	10	20.0
WK1203	2012.3.11	A21	10	20.0
WK1203	2012.3.13	P10(C5)	1	7.0
WK1203	2012.3.13	C12	1	21.0
Rent1204	2012.4.16	P10(C5)	1	15.1
Rent1204	2012.4.16	P10(C5)	18	6.8
Rent1204	2012.4.16	C12	1	4.5
Rent1204	2012.4.16	C12	10	7.2
WK1205	2012.5.10	A04	10	17.1
WK1205	2012.5.10	A04	20	15.1
WK1205	2012.5.15	A21	10	6.8
WK1205	2012.5.15	A21	40	9.0
WK1205	2012.5.16	P10(C5)	1	9.2
WK1205	2012.5.16	P10(C5)	15	9.3
WK1205	2012.5.17	C12	1	9.4
WK1205	2012.5.17	C12	20	8.6
WK1206D	2012.6.17	F3	5	8.5
WK1206D	2012.6.17	F3	20	8.0
WK1206D	2012.6.18	P10(C5)	5	9.0
WK1206D	2012.6.18	P10(C5)	20	9.0
WK1207	2012.7.14	C5(P10)	2	8.0
WK1207	2012.7.14	C5(P10)	10	8.5
WK1207	2012.7.16	C12	2	9.0
WK1207	2012.7.16	C12	30	9.5



Sea water samples

5 µm pore size filter → **DNA Isolation (Protists)**

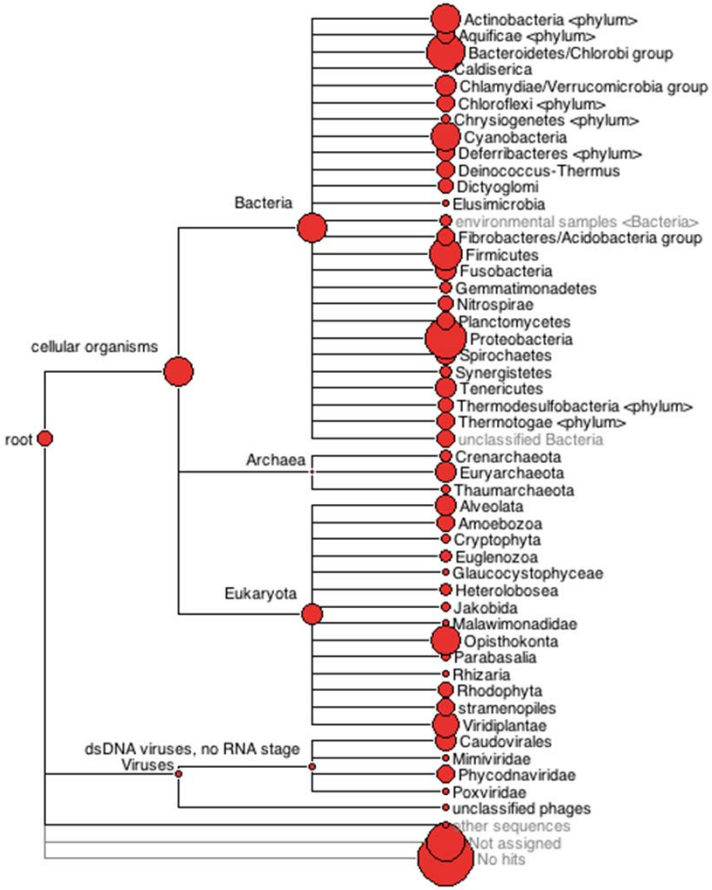
0.8 µm pore size filter → **DNA Isolation (Cyanobacteria)**

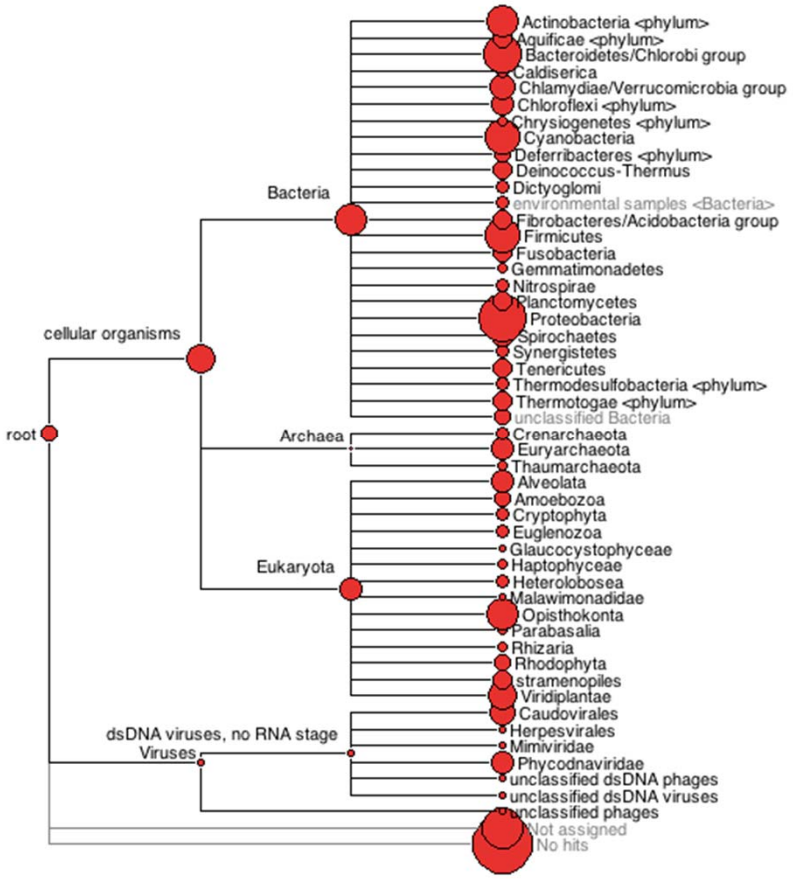
0.2 µm pore size filter → **DNA Isolation (Bacteria)**

Metagenomic Data Analysis -1- (NIG)

Buzen-1	
Total reads:	2899428
Assigned reads:	102789
Unassigned reads:	18583
Reads with no hits:	2778056

Buzen-2	
Total reads:	4340338
Assigned reads:	168021
Unassigned reads:	26405
Reads with no hits:	4145912





Conclusion and Summary

Summary

1. **We constructed pipelines for understanding dynamics of marine bacteria in Sendai area using metagenomic data analysis**

2. **Proteobacteria was major bacteria in spring and winter while cyanobacteria was increased in August and October in Sendai area**

3. **Bacterial communities at surface were similar to those at 20m below surface in spring and winter, while bacterial communities at surface in summer and autumn were different from those at 20m below surface**

4. **Metagenomics showed that 26 metabolic pathways were present in the Sendai area and genes associated with photosynthesis pathway were increased in August and October**

Conclusion

“Metagenomics is a powerful method for understanding dynamics of marine bacteria in ocean ecosystem”

How to analyze Big Data (8)!

Monitoring (time and space)
is
a Key!

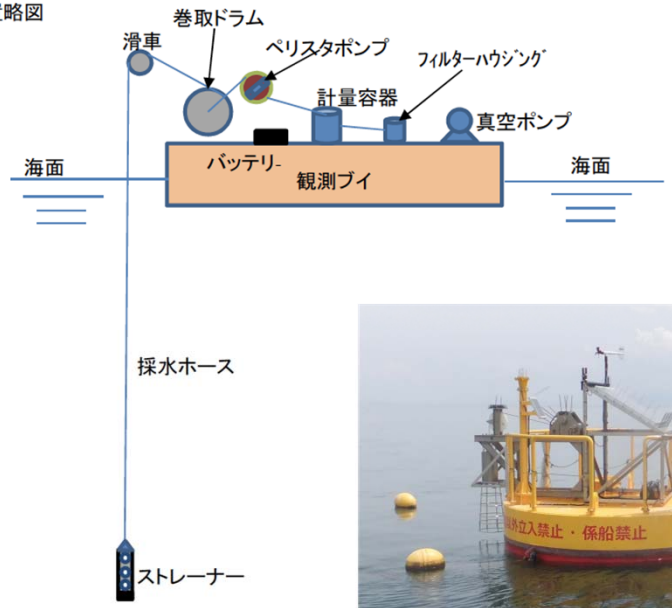
Sampling device with a monitoring system（Kyushu U.）

自立式海洋微生物DNA採取装置

装置製作条件

表層から10mまでの柱状サンプル(2.5L程度)を1日に1回採取し、既定のフィルターでろ過を行う。
これを1週間行った後、サンプルとしてフィルター(7個)を回収する。
電源に関しては、今回は太陽電池等を用いないため動作に必要な電源を、鉛蓄電池で確保する。

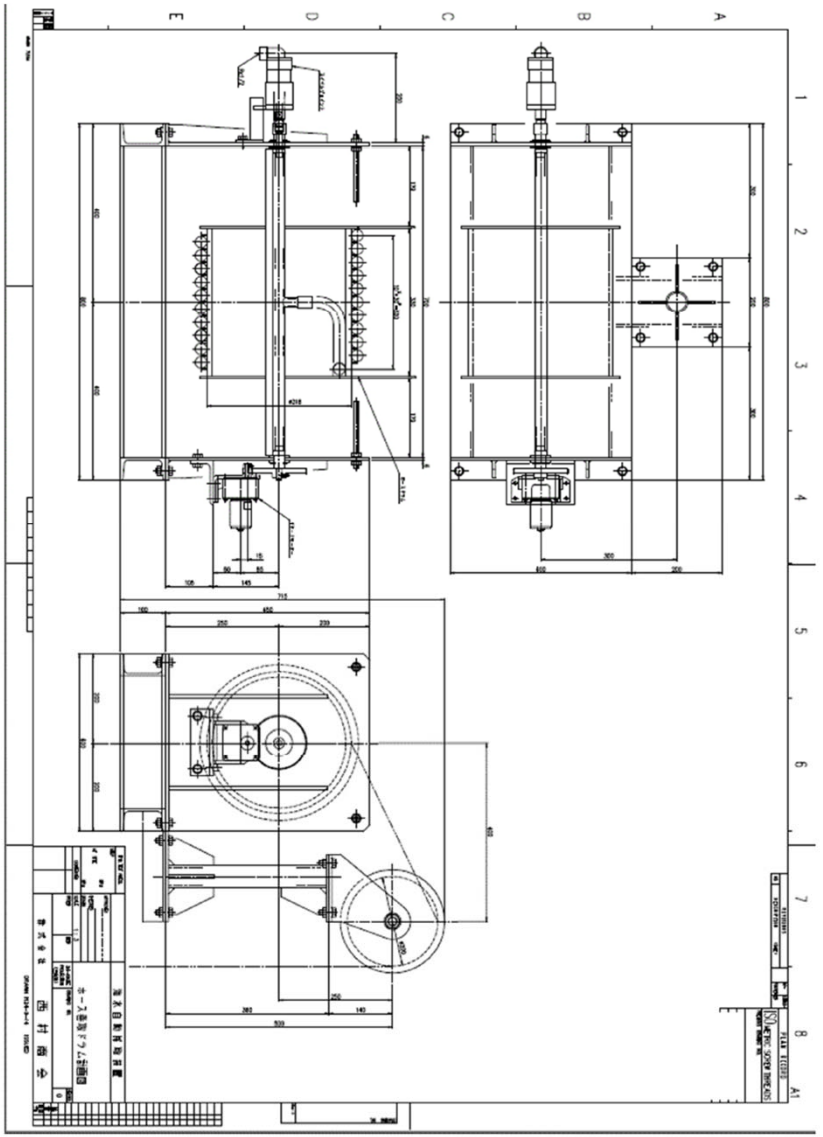
採取装置略図



巻取ドラム仕様

駆動部	ギヤドモータ(DC12V)	
	減速比	1/180
	回転数	30.8rpm
	トルク	35kgf・cm
	さらに平歯車で1/6減速	
	ドラムの回転数	5.13rpm
	トルク	2.1kgf・m
	ホースの移動速度	92mm/s

ウインチ装置部参考図面




関係者以外立入禁止

The Outline of KAUST (King Abdullah University of Science and Technology)

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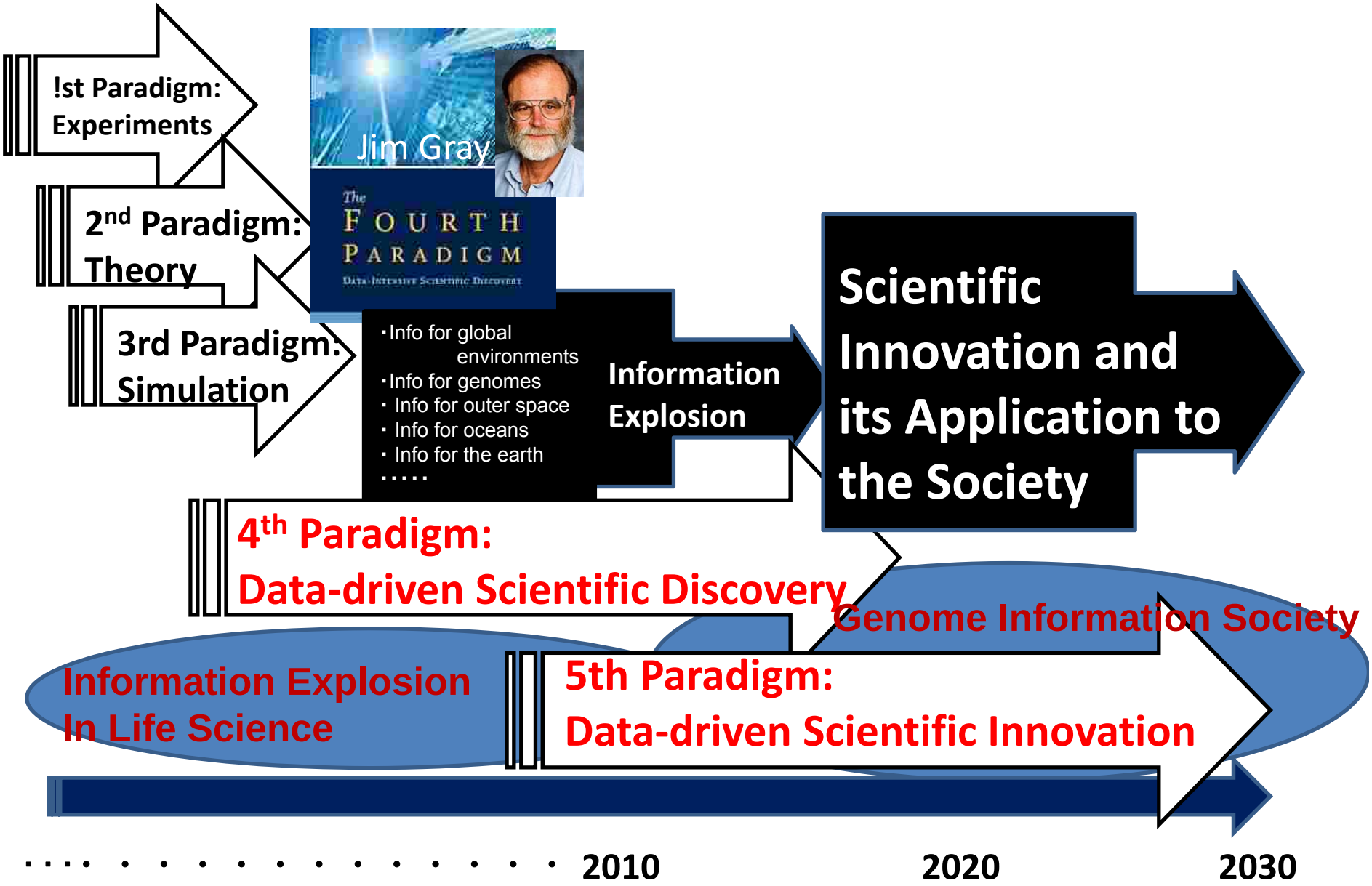
Thuwal 23955-6900
Saudi Arabia

KAUST is located along the Red Sea.

Overlooking the sea, the KAUST campus incorporates a distinctive blend of traditional architecture and modern styles.

Beyond the 4th Paradigm proposed by Jim Gray

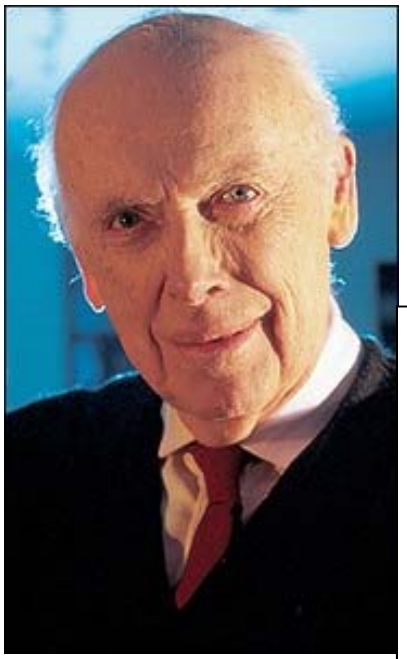


How to analyze Big Data (9)!

“Data-driven needs working hypothesis” is a Key!

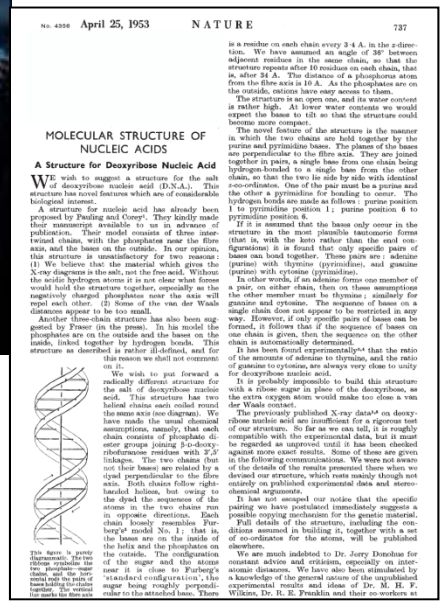
特別講演　11月24日（日）14時00分～15時00分

60 years of DNA



James D. Watson
(CSHL, The Nobel Prize in Physiology or Medicine 1962)

1962年度　ノーベル生理学・医学賞



No. 4356 April 25, 1953 NATURE 737

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three inter-twined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate di-ester groups joining β-D-deoxyribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate–sugar chains, and the joining material the pairs of bases. The vertical line marks the fibre axis.

略　歴

1968年～1993年　ニューヨークのコールド・スプリング・ハーバー研究所の所長
1993年～2007年　同研究所会長
1989年～1992年　NIH（国立衛生研究所）の国立ヒトゲノム研究センター初代所長

- 全米科学アカデミー会員
- イギリス王立協会（ロイヤルソサイエティ）会員
- 大統領自由勲章
- 全米科学界の栄誉とされるアメリカ国家科学賞を受ける
- 海洋研究においては、ウッズホール海洋生物学研究所に在籍


国際水圏メタゲノムシンポジウム
水圏メタゲノミクスの展開と水圏生物多様性研究の展望
International Symposium on Aquatic Metagenomics
Development of Aquatic Metagenomics and Perspective of the Studies on Aquatic Biodiversity
Special Lecture
60 years of DNA
James D. Watson


Special Lecture
60 years of DNA
James D. Watson
Receiver Channels
Ch.1 日本語
Ch.2 English
Speaker


Special Lecture
60 years of DNA
James D. Watson
Speaker
日本語
English


国際水圏メタゲノムシンポジウム
水圏メタゲノミクスの展開と水圏生物多様性研究の展望
International Symposium on Aquatic Metagenomics
Development of Aquatic Metagenomics and Perspective of the Studies on Aquatic Biodiversity
After reading the physicist Erwin Schrödinger's new book What is Life early in 1946, I began auditing the University of Chicago's great geneticist Sewell Wright's spring 1946 lectures on "physiological genetics" (how do genes affect the physiology of the cell), soon finding that what the gene was at the chemical level more exciting to study than how birds migrate over great distances.
E. ERWIN SCHRÖDINGER
WHAT IS LIFE ?
Speaker

How to analyze Big Data (10)!

“Dr. Jim Watson’s Ten Commands” I call is a Key!

Collaborators

- Kazuo Ikeo (NIG)
- Takahisa Mori (NIG)
- Naobumi Sasaki (NIG)
- FRA (Fishery Research Agency)
- Ishino's group (Kyushu University)

- Shiho Hayakawa (British Colombia)
- Shang Hwang (Malyasia)
- Katsuhiko Mineta (now, KAUST)
- Walter Gehring
  (Basel, deceased on May 29, 2014)

Acknowledgements

Main work

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Atsushi Ogura (NIG)
Yasuharu Takaku (NIG)
Naobumi Sasaki (NIG)
Masahiro Mori (NIG)
Masakazu Ishikawa (NIG)
Masa-aki Yoshida (NIG)
Sonoko Kinjo (NIG)

Walter Gehring (Basel)
Hiroshi Suga (formerly Basel)

Planarian, Hydra, & Acidian

Kiyokazu Agata (Kyoto)
Hiroshi Shimizu (NIG)
Toshitaka Fujisawa (NIG)
Hiroaki Yamamoto (Nagaoka Bio U)

Marine Metagenomics

FRA
Kyushu University
Tokyo University
Kitasato University
Tokai University
AIST
CREST Project

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- Katsuhiko Mineta (CBRC/KAUST)

- Vlad Bajic (CBRC, KAUST)
- John Archer (CBRC, KAUST)
- --------
- Shugo Watabe (Kitasato University, Japan)
- Kakehhiko Ogata (Kitasato University, Japan)

- Pei-Yuan Qian (HKUST, Hong Kong)
- Yoshizumi Ishino (Kyushu University, Japan)

DNA for World Peace !