

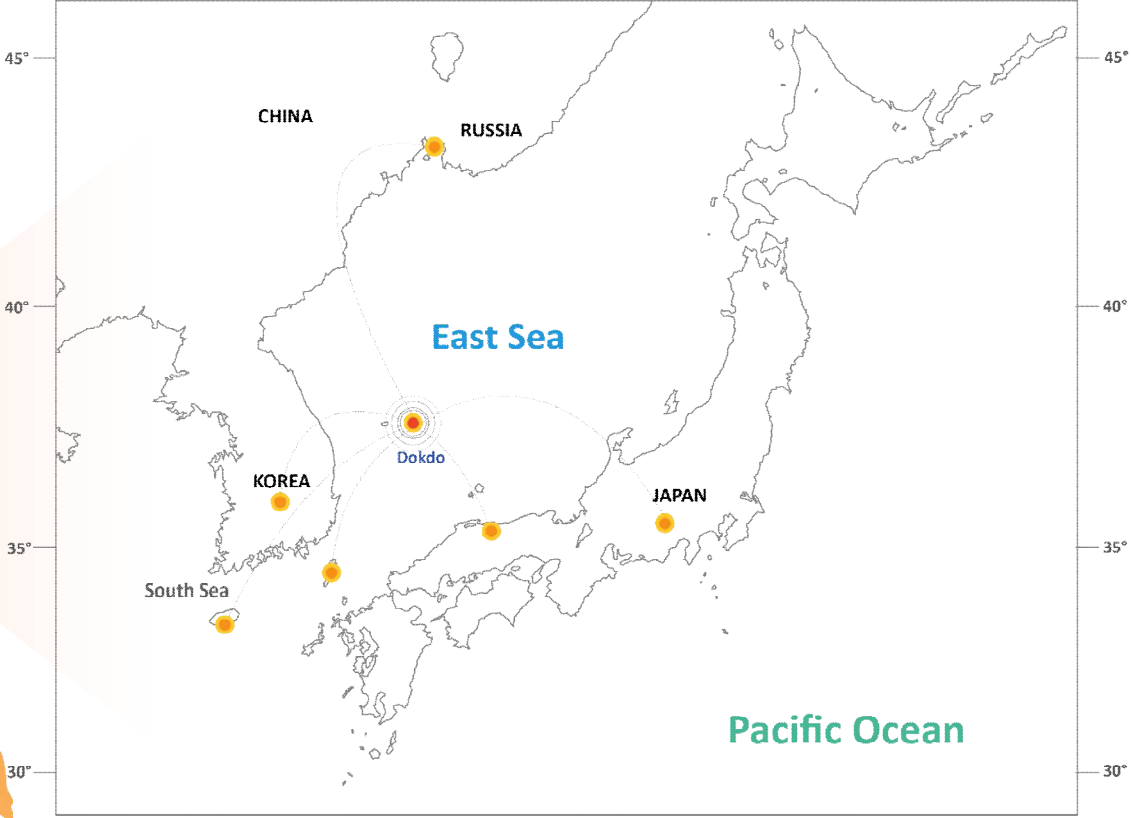
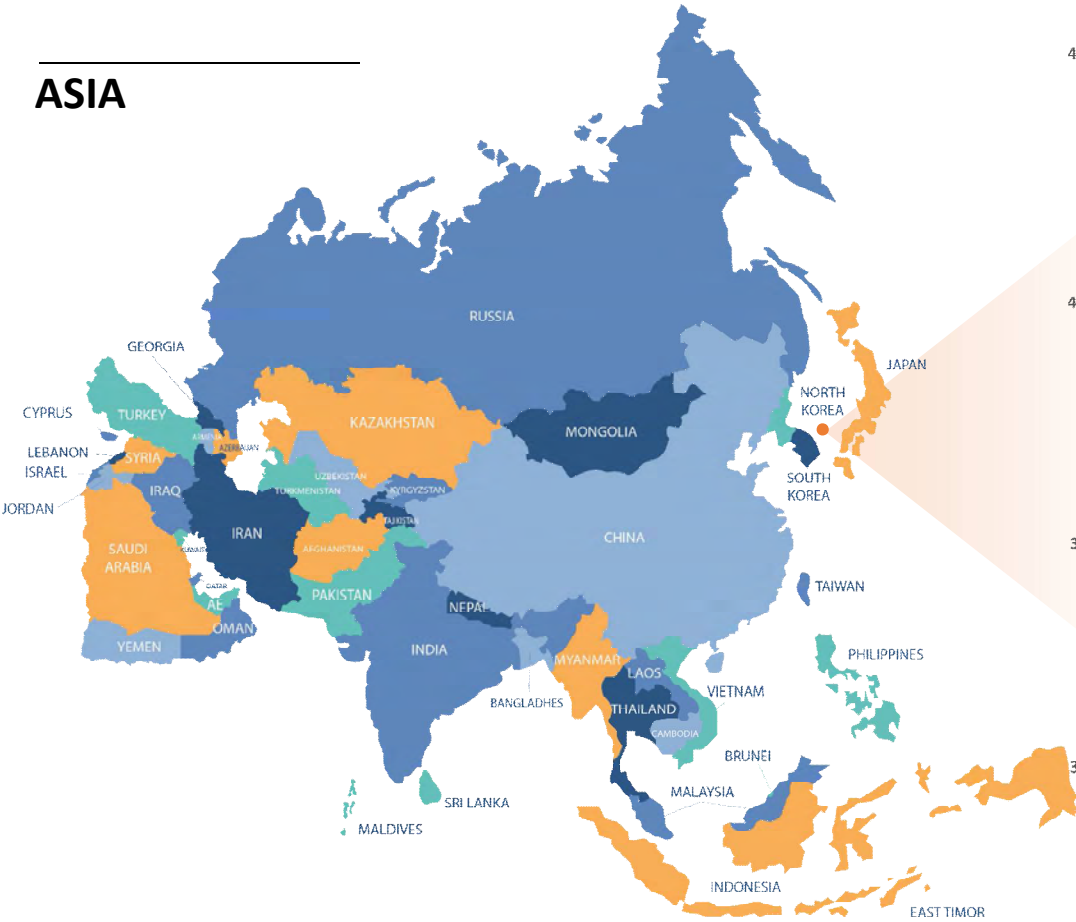
Phylogeography of marine invertebrates in the pan-East Sea Rim and genome-based arthropod phylogeny

Professor / Director
Ui Wook Hwang

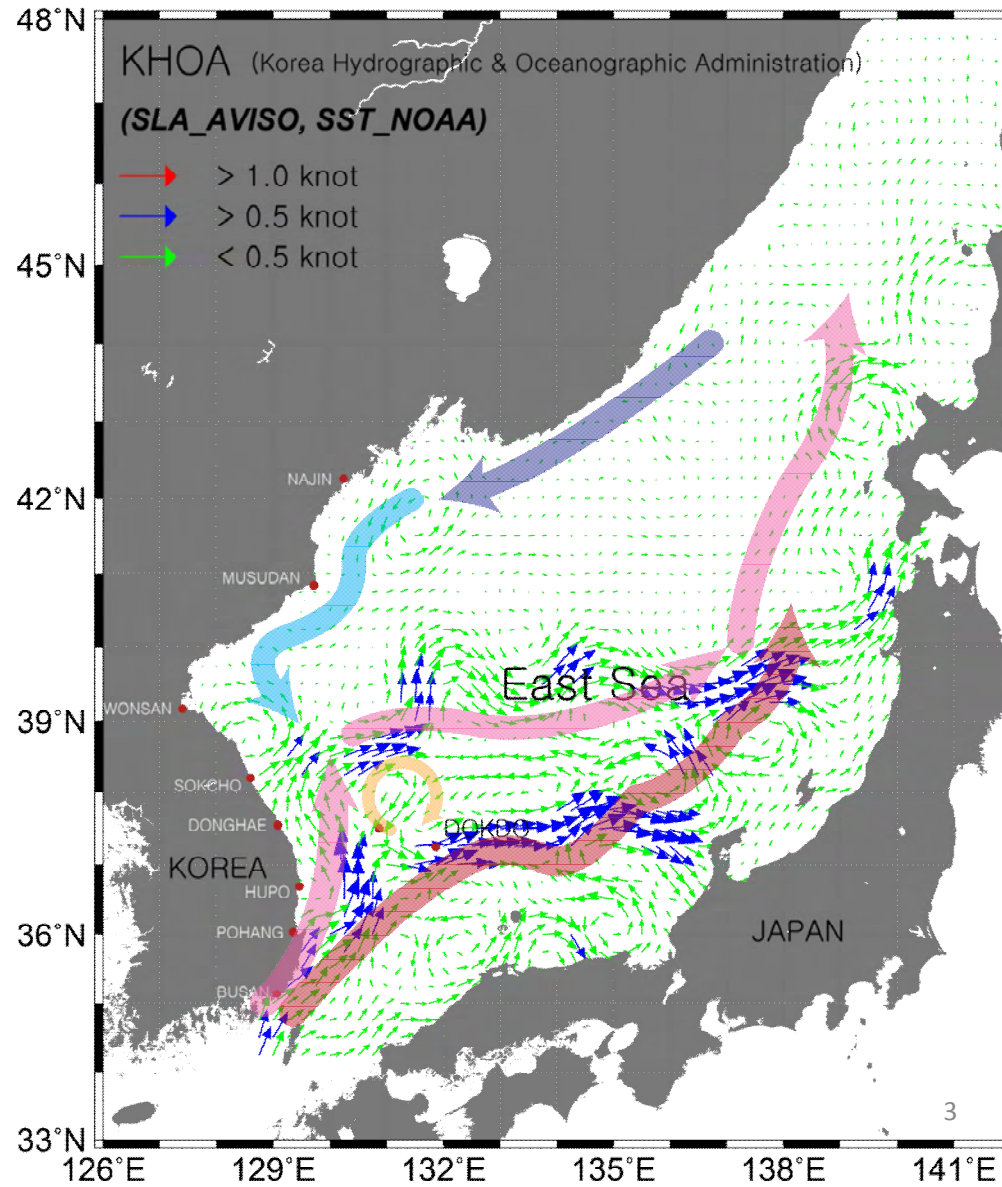
Department of Biology Education, Teachers College & Institute for Phylogenomics and Evolution,
Kyungpook National University, Republic of Korea

The pan-East Sea Rim

ASIA



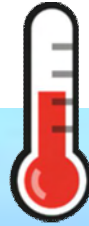
East Sea surface currents



Dokdo is located in the center of the Pan-East Sea Rim.



Precipitation (강수량)
Annual average 1,240mm



Temperature (기온)
Annual average 12°C



Volcanic island (화산섬)
Basalt (현무암) 및 Trachyte (조면암)



Height 168.5m
Circumference 2.6km

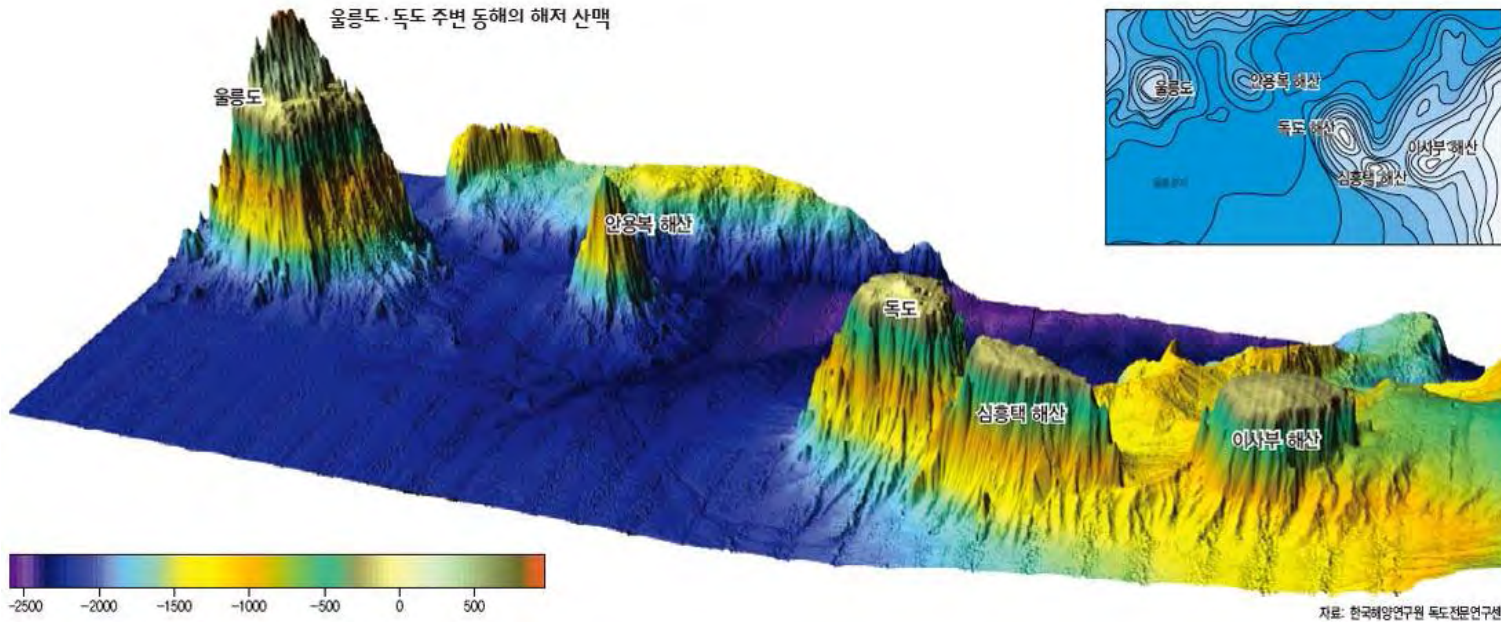
Height 98.6m
Circumference 2.8km

Seodo
37° 14' 30.6" N
131° 51' 54.6" E
Area 88.740m²

Dongdo
37° 14' 26.8" N
131° 52' 10.4" E
Area 73.297m²

Dokdo: the best place for island biogeography researches

The Korean Galapagos and oceanic island that has never been connected with continents



A key marine invertebrates for our researches

군부(Chiton)
Liolophura japonica
Lischke, 1873



갯강구(slater)
Ligia exotica



**검은큰따개비
(acorn barnacles)**
Tetraclita japonica
(Pilsbry, 1916)

**바위게
(lined seashore crab)**
Pachygrapsus crassipes
Randall, 1840

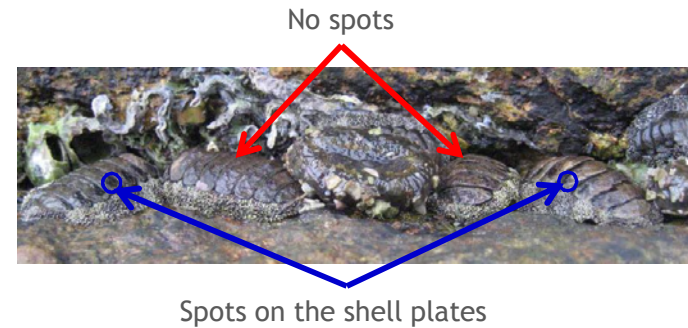


**거북손
(Japanese goose barnacle)**
Capitulum mitella
(Linnaeus, 1758)

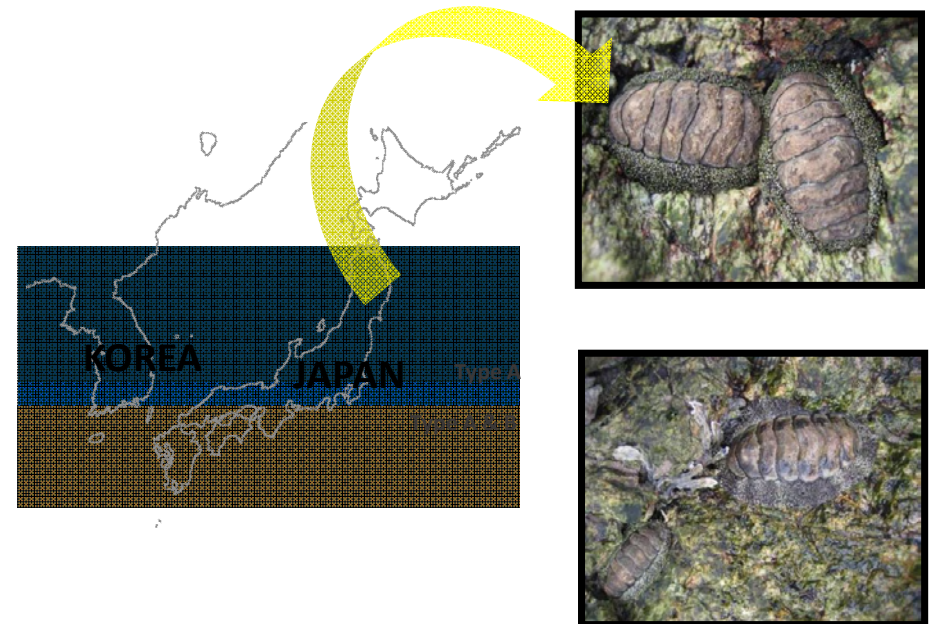


Examples of marine invertebrate researches in the pan-East Sea Rim

A chiton Liolophura japonica



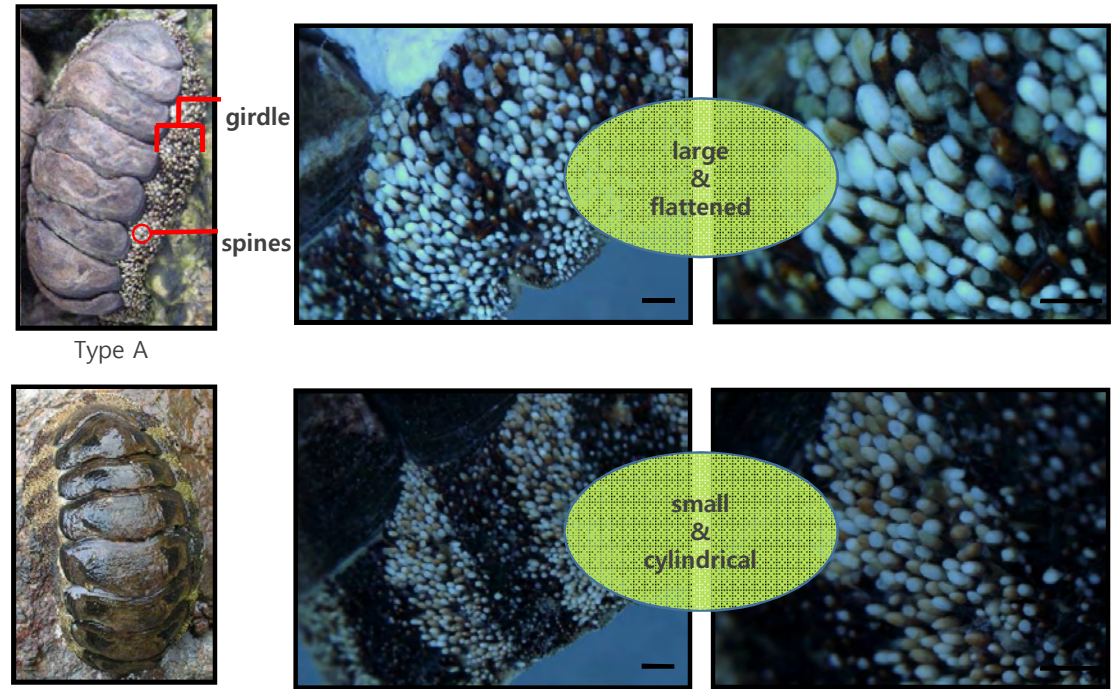
- (synonym) *Acanthopleura japonica*
- (분포) 전 세계적으로 일본, 대만, 홍콩, 태국 등지에 분포. 우리나라의 경우, 제주도, 전남, 경남 연안 및 강원 중북부 연안에 서식
- (특이사항) 일본 내에 서식하는 군부 집단에서 잠재적 자매종(cryptic species)이 존재함을 보고(Okoshi & Hamaguchi 2006)
- (선행연구) 국내 서식하는 군부는 2개의 유전적 타입이 존재하는 것을 확인
- (개체확보) 분포 기록을 참조하여 한국, 일본을 중심으로 9개 지점 이상에서 70개체 이상의 샘플을 확보
- (분석마커) *COX1*, *16S rRNA*



Differences in microhabitat preference



Differences of morphological characters

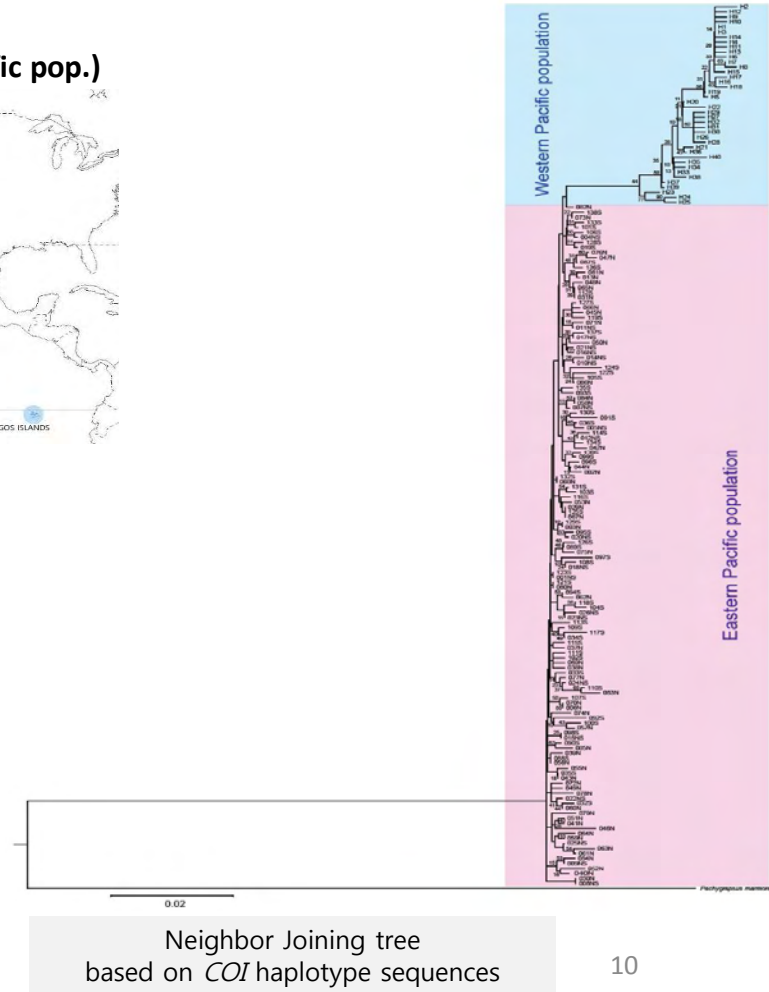


Scale bar = 0.1mm

A lined shore crab *Pachygrapsus crassipes*



- **(분류)** Arthropoda 절지동물문 > Crustacea 갑각아문 > Malacostraca 연갑강 > Decapoda 십각목 > Grapsidae 바위게과
- **(synonym)** *Grapsus eydouxi* H. Milne Edwards, 1853, *Leptograpsus gonagrus* H. Milne Edwards, 1853
- **(분포)** 한국(동해의 삼척이남, 대한해협, 제주도, 황해 남부), 일본(하코다테-큐슈), 하와이, 갈라파고스 군도, 미국 서해안(캘리포니아 이남), 칠레
- **(특이사항)** 북아메리카가 원산지로 알려져 있으며 서태평양 지역에서 발견되는 바위게는 1890년대 일본에서의 기록이 최초. 선박의 밸러스트 워터(ballast water)를 통해 조에아 유생 시기에 옮겨진 것으로 추측하고 있으며 한국에는 19세기 말 일본을 거쳐 오는 선박에 의해 유입된 것으로 알려짐
- **(선행연구)** 국내 서식하는 바위게는 3개의 유전적 타입이 존재하는 것을 확인
- **(개체확보)** 분포 기록을 참조하여 한국, 일본을 중심으로 7개 지점 이상에서 70개체 이상의 샘플을 확보, 북미 서식 개체군의 유전정보와 비교 분석
- **(분석마커)** *COX1*, *16S rRNA*



Neighbor Joining tree based on *COI* haplotype sequences

A sea slater *Ligia exotica*



Taxonomy

- ▶ Kingdom Animalia
- ▶ Phylum Arthropoda
- ▶ Class Crustacea
- ▶ Order Isopoda
- ▶ Family Ligiidae
- ▶ Genus *Ligia*

1 Strictly a coastal, not a marine animal

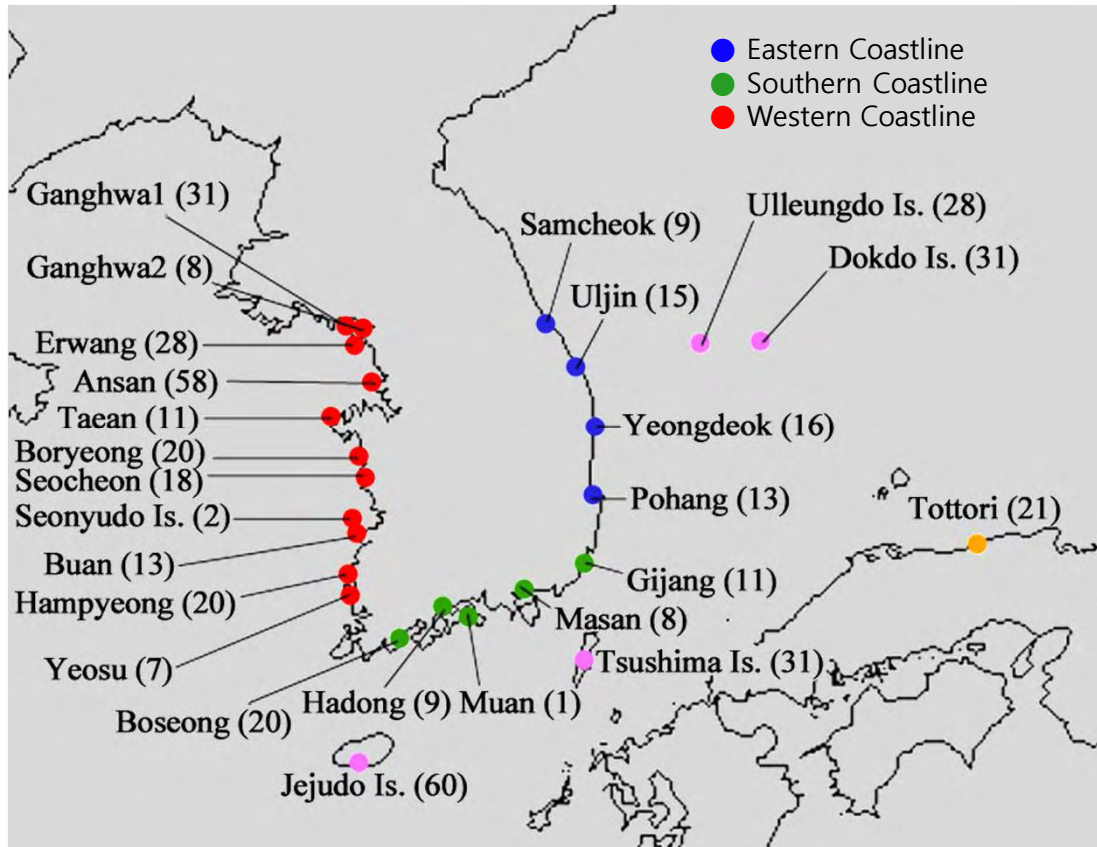
2 37 species in the genus *Ligia*

3 In South Korea, only one species

4 Only two reports related with *L. exotica* genetic lineages in South Korea (Jung, 2004 & 2008)

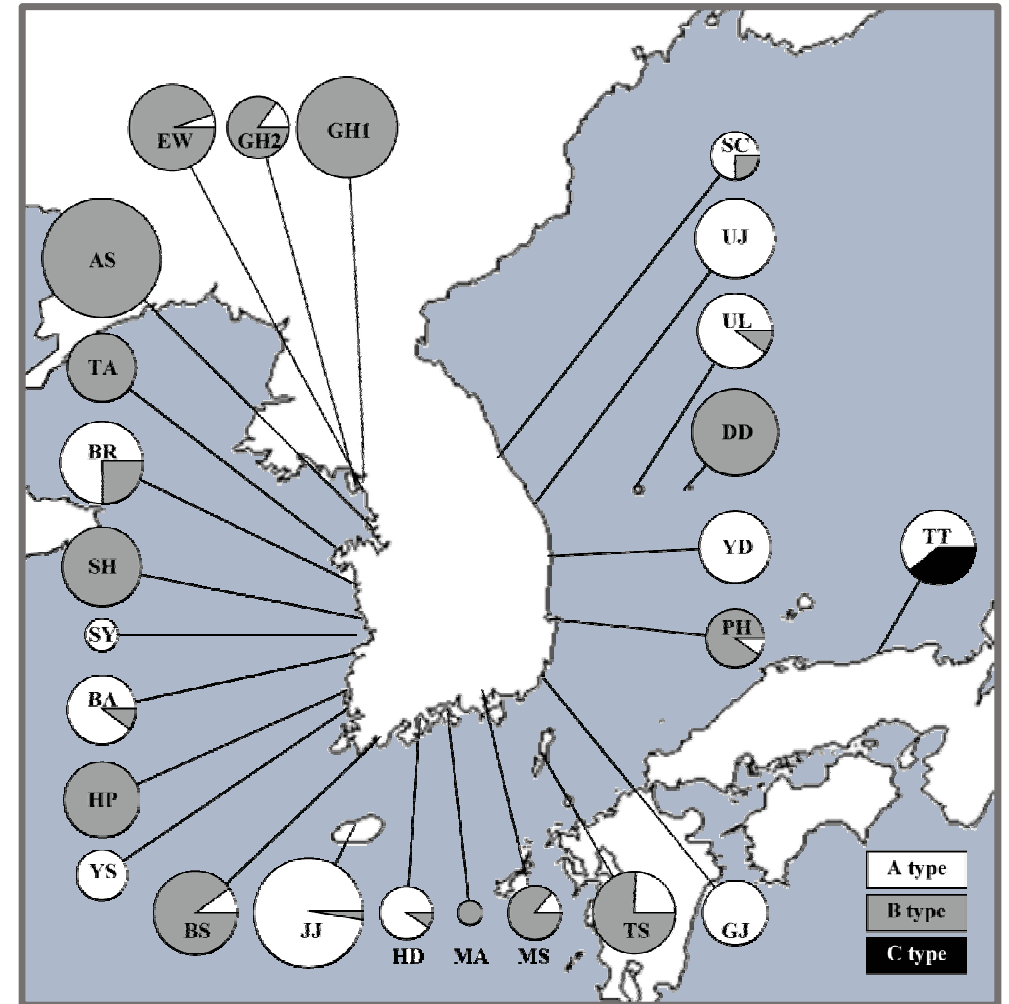
Collection site and number of individuals

: 25 populations, 489 individuals



Distribution of *L. exotica* on collecting sites

: three genetic types

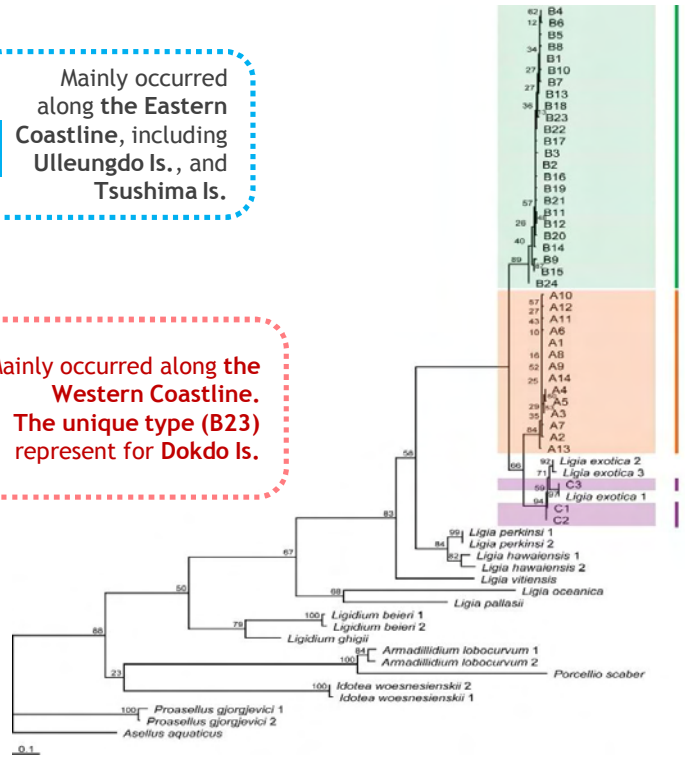




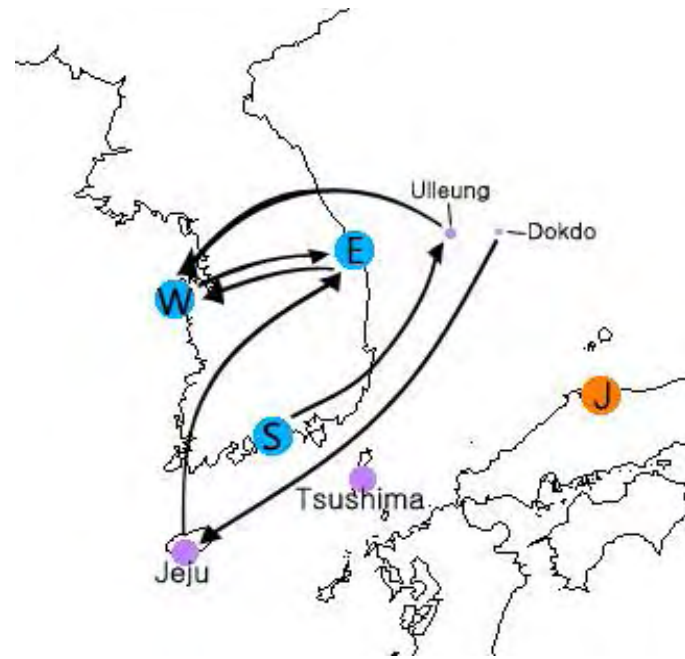
A type
Mainly occurred along the Eastern Coastline, including Ulleungdo Is., and Tsushima Is.

B type
Mainly occurred along the Western Coastline. The unique type (B23) represent for Dokdo Is.

C type
NOT occurred in Korean Coastline, but only in Tottori, Japan.



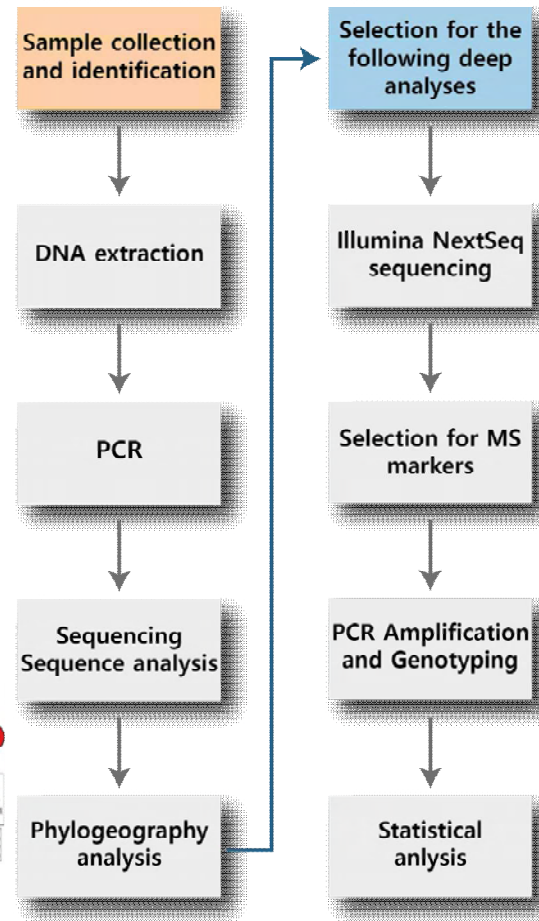
Maximum likelihood tree based on 16S rDNA haplotype sequences (GTR+I+G, 1000 reps)



Possible migration paths of sea slaters in Korea and Japan
(W: Western coastline, S: Southern coastline, E: East coastline, J: Japan)

갯강구는 확연히 구별되는 세 개의 유전적 type이 관찰되었고, B type만이 존재하는 독도 개체군은 일본 집단과는 유전적으로 다른 기원이며, 일본과는 이주 및 전입이 일어나지 않았을 것으로 확인됨

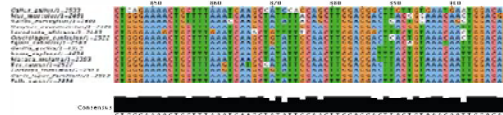
Methods for phylogeographic and population genetic researches



QIAGEN DNeasy Blood & Tissue kits
BIOANALYZER DNA QC

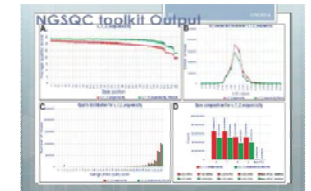


MARKER COX1, 16S rRNA



ABI 3730xl ABI PRIM BIC Dye termination system
BIOEDIT Biological sequence Alignment Editor
CLUSTAL X Multiple Sequence Alignment program

TCS Phylogenetic Network Estimation using Statostocal Parsimony
DNASP DNA sequence Polymorphism Analysis
NETWORK Phylogenetic Network Software
MEGA, RAxML, MrBayes Phylogenetic analysis
ARLEQUIN Performed hierarchical analysis of population subdivision
BEAST Bayesian Skyline Plot analysis
MITRATE Estimation of effective population sizes and gene flow using the coalescent
GEODIS Statistically test the associations between the genetic and geographical distances

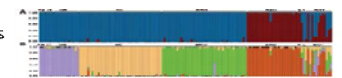


- Construction of the NGS library and quality control (QC)
- Running NGS and analysis of the output data
- Calidity confirmation of the de novo sequencing data
- Producing contig based on multiple sequence alignment

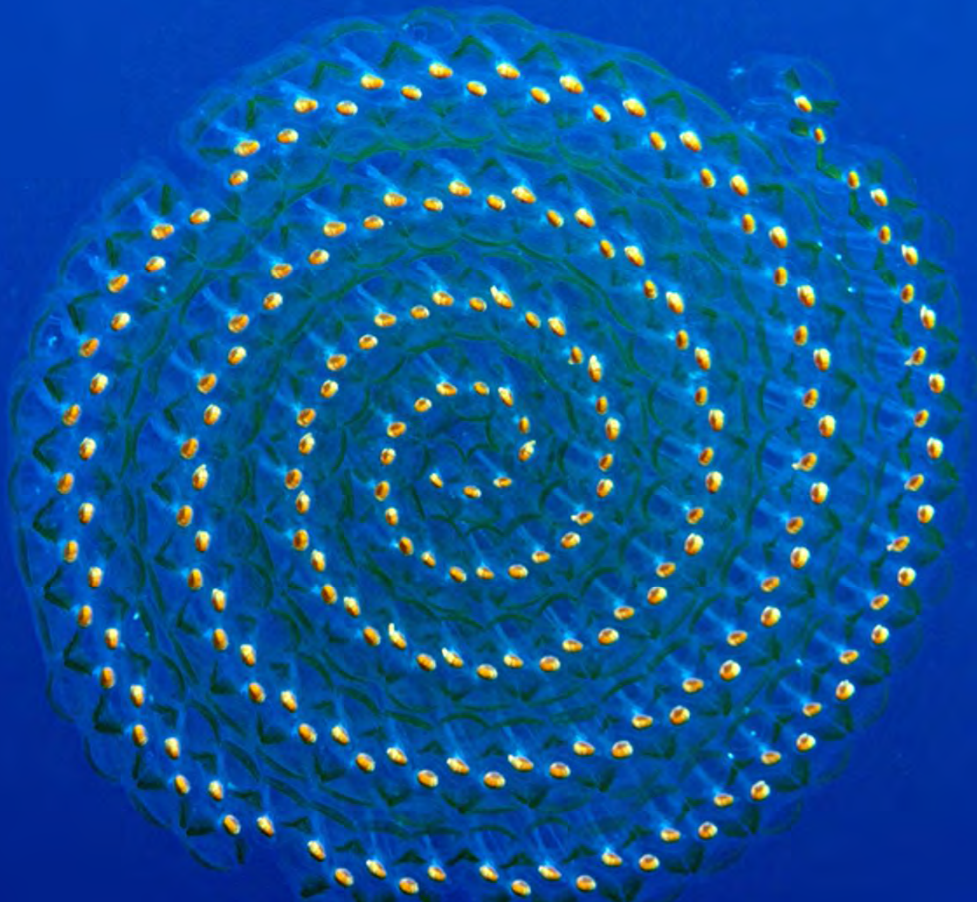
- Masking of the repetitive sequence
- Selection of the hotspot using length of the repeated motif and number of the contig
- With microsatellite markers, identification of the mutation site after sequence screening

- Confirmation with the PCR for analyzing the fragment
- Genotyping of the microsatellite using genetic analyzer
- Size typing of the allele with the Genemapper

ALREQUIN Observed Heterozygosity and Expected Heterozygosity
ALREQUIN F_s , Pairwise F_{ST} and R_{ST}
GENEPOP HWE (Hardy-Weinberg equilibrium) p-value
GENALEX number of allele and gene flow
GENODIVE Mantel test and AMOVA test
STRUCTURE Population structure
PCoA Principal coordinates analysis
BARRIER Detection of barrier



Genome-based arthropod phylogeny



Post genomic era for the phylogenomics of arthropods : Omics


High resolution sequencing

NGS technology

Next Generation Sequencing

2nd generation sequencing method

- Re-sequencing (extance of the reference genome of transcriptome)



Illumina SOLEXA **ABI SOLID**

- de novo* sequencing

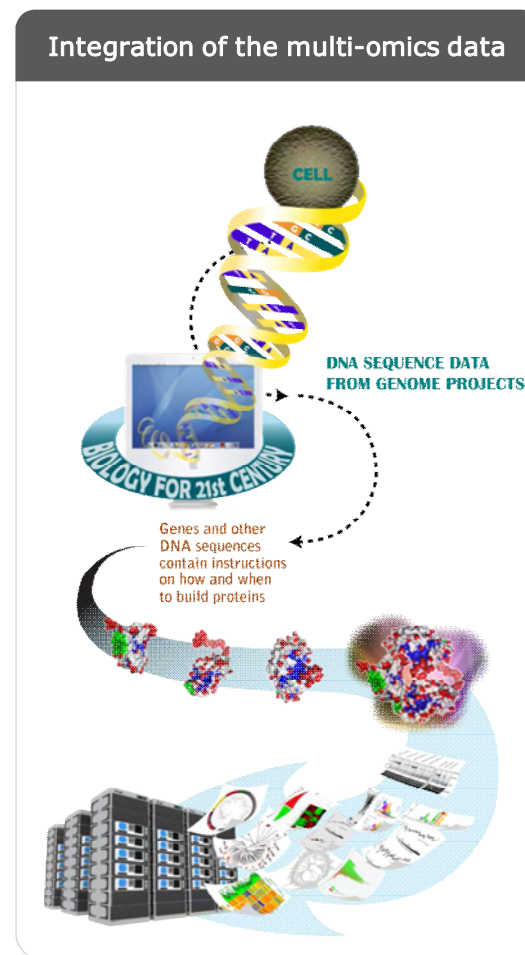
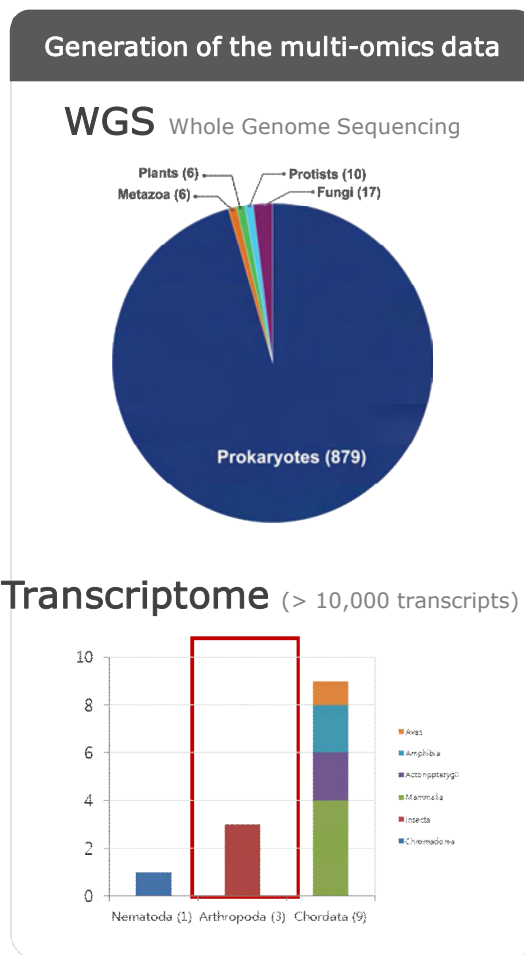
Roche 454 pyrosequencing



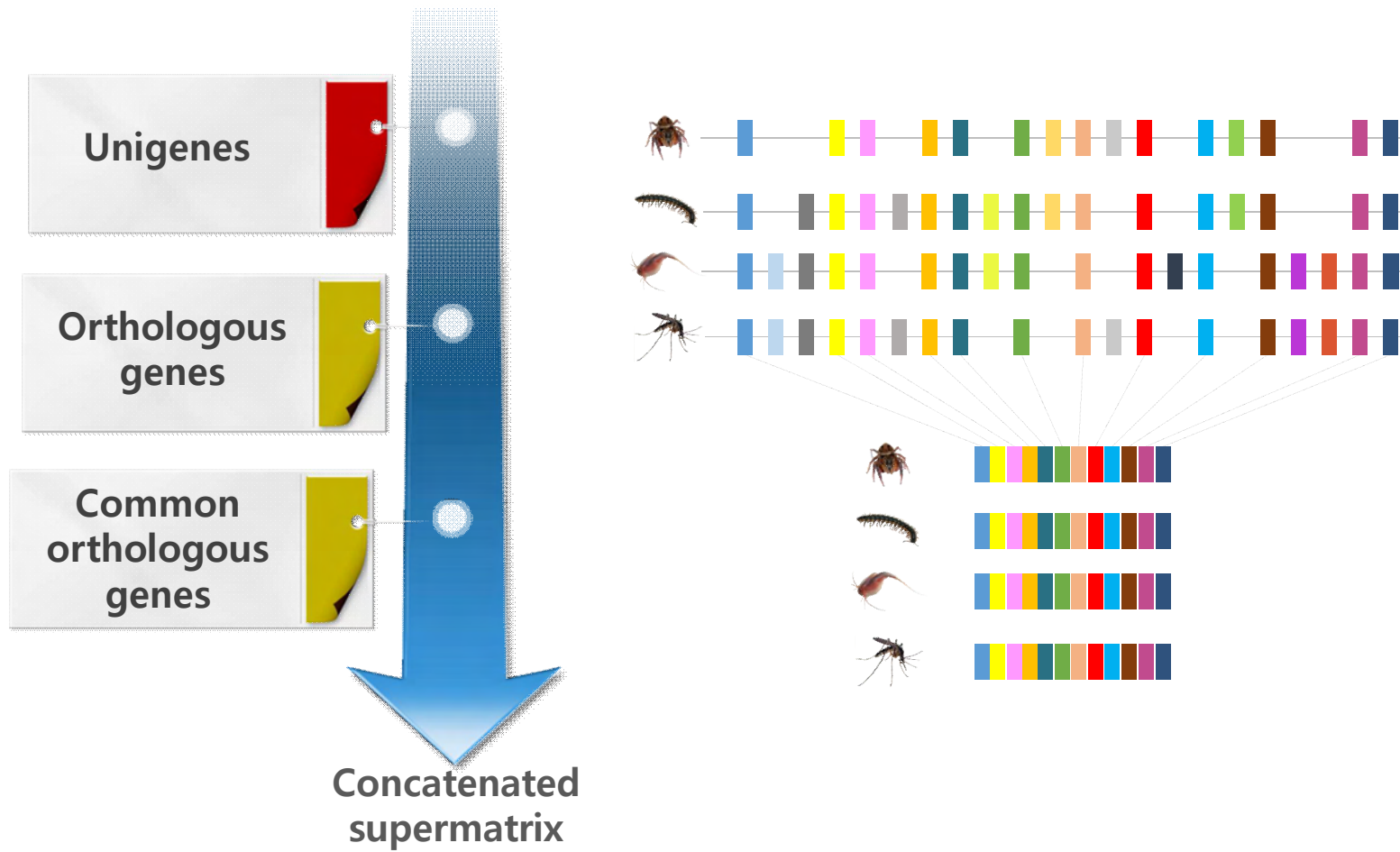
2.5 generation sequencing method

- RNA-seq (transcriptome studies)
- Chip-seq (DNA-proteins interaction)
- Dnase-seq (identification of most active regulatory regions)
- CNV-seq (copy number variation)
- Methyl-seq (genome wide profiling of epigenetic marks)

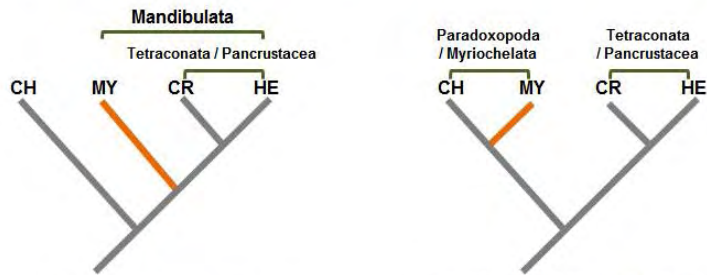
Illumina HiSeq 2000

Construction of supermatrix (conserved genes) based on the omics data

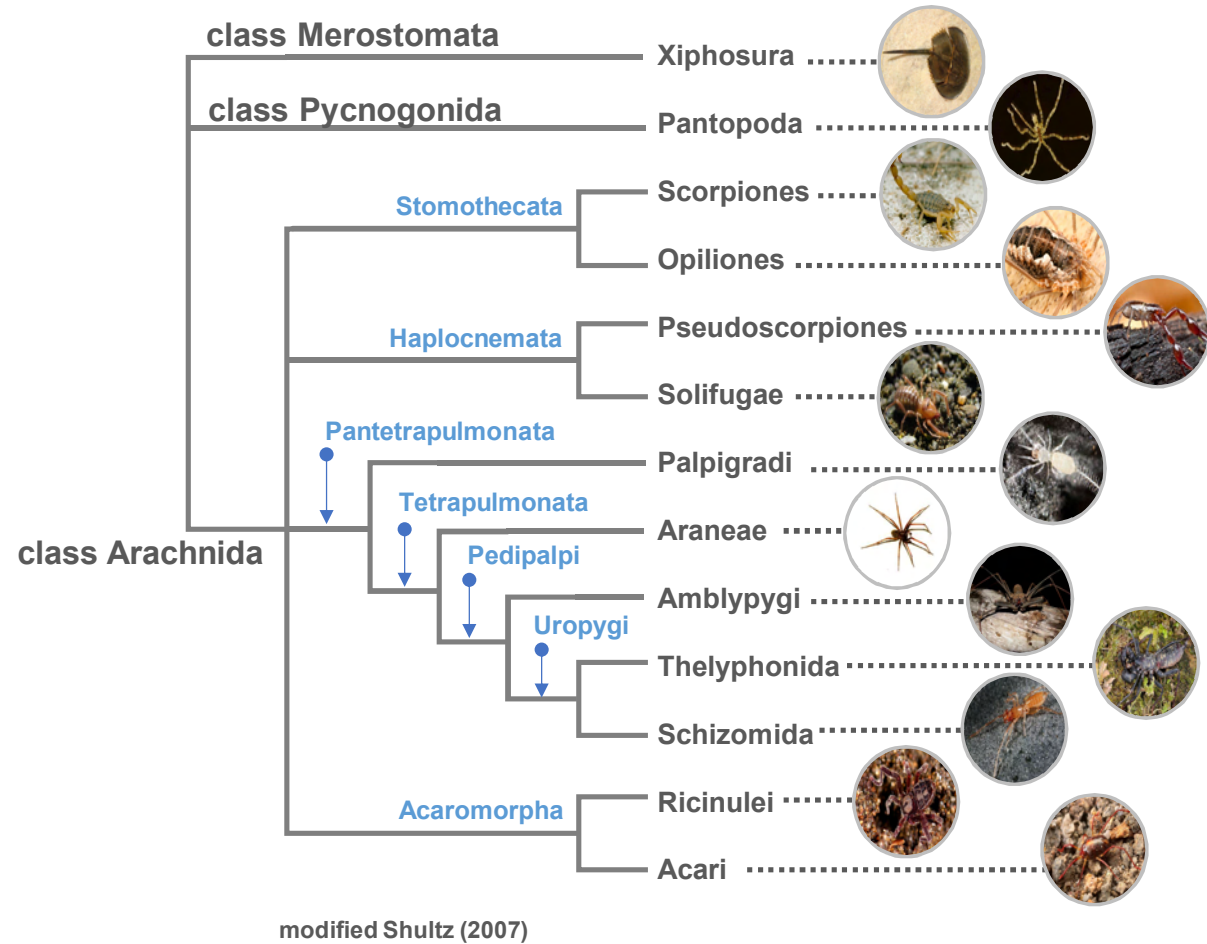


Arthropod phylogeny



• Giribet et al. (2001, *Nature*, 6 genetic loci), Regier et al. (2005, *Proc R Soc B*, 3 genetic loci), Regier et al. (2010, *Nature*, EST)

• Hiwang et al. (2001, *Nature*, mitogenomes), Pisani (2004, *Syst. Biol.*, mitogenomes), Cook et al. (2001, *Curr Biol.*, *hox* gene), Mallatt et al. (2004, *Mol Phylogenet Evol.*, 18S+28S rDNA), Park et al. (2007, *BMC Genomics*, mitogenomes), Boxshall, (2007, *Zootaxa*, fossils)



A variety of arthropods



Achelia bituberculata



Carcinoscorpius tridentatus



Tachypleus tridentatus



Mesobuthus martensii



Heterometrus longimanus



Liocheles australasiae



Thelyponidae sp.



Ideobisium sp.



Leiobunum japonicum japonicum



Oligolophus tienmusanensis



Nephila clavata



Lithobius forficatus



Bothriopolys sp.



Antrokoreana gracilipes



Argyroneta aquatica



Phidippus gassneri



Chasmodon convexus



Protactia brevitarsis seulensis



Lethocerus deyrollei



Triops longicaudatus



Capitulum mitella



Uca lactea lactea



Chiromantes dehaani

letters to nature

- 28. Harry, D. L. & Sawyer, D. S. A dynamic model of extension in the Baltimore Canyon Trough region. *Tectonics* **11**, 420–436 (1992).
- 29. Louden, K. E. & Chian, D. in *Response of the Earth's Lithosphere to Extension* (eds White, R. S., Hardman, R. F. P., Watts, A. B. & Whitmarsh, R. B.) 767–799 (Phil. Trans. R. Soc. Ser. A, Royal Society, London, 1999).
- 30. Taylor, R., Goodliffe, A. M. & Martinez, F. How continents break up: Insights from Papua New Guinea. *J. Geophys. Res.* **104**, 7497–7512 (1999).



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R.B.W.

eny joins

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The animal phylum Arthropoda is very useful for the study of body plan evolution given its abundance of morphologically diverse species and our profound understanding of *Drosophila* development¹. However, there is a lack of consistently resolved phylogenetic relationships between the four extant arthropod subphyla, Hexapoda, Myriapoda, Chelicerata and Crustacea. Recent molecular studies^{2–4} have strongly supported a sister group relationship between Hexapoda and Crustacea, but have not resolved the phylogenetic position of Chelicerata and Myriapoda. Here we sequence the mitochondrial genome of the centipede species *Lithobius forficatus* and investigate its phylogenetic information content. Molecular phylogenetic analysis of conserved regions from the arthropod mitochondrial proteome yields highly resolved and congruent trees. We also find that a sister group relationship between Myriapoda and Chelicerata is strongly supported. We propose a model to explain the apparently parallel evolution of similar head morphologies in insects and myriapods.

The basal diversification of arthropod lineages, which date back into the late Cambrian period is still unclear. Morphological analyses^{5,6} all suggest a monophyletic Arthropoda within which insects and myriapods are most closely related. Controversy, however, continued over whether insects, myriapods and crustaceans form a second major subclade, Mandibulata, on the basis of the shared derived possession of mandibles⁵ or whether crustaceans are a sister group to chelicerates on the basis of the occurrence of biramous appendages in representatives of both groups⁶. Several independent molecular studies provided strong support for arthropod monophyly, a monophyletic Hexapoda, Myriapoda and Chelicerata, and, most significantly, a sister group relationship between insects and crustaceans (Pancrustacea) (for a review see ref. 7). Although they ruled out the possibility of insect/myriapod or crustacean/chelicerate sister clades, previous molecular studies did not resolve relationships between myriapods, chelicerates and

Pancrustacea^{2–4}. Mitochondrial gene order rearrangements were initially interpreted to support a monophyletic Mandibulata⁸, but were later re-interpreted to further corroborate the Pancrustacea clade².

Complete mitochondrial genome sequences can be informative at deep phylogenetic levels⁹. We therefore investigated their potential use for arthropod phylogeny. As examples of mitochondrial genomes are known from all arthropod subphyla except myriapods, we determined the complete mitochondrial genome sequence of the centipede *Lithobius forficatus*. The *Lithobius* mitochondrial genome is 15,437 base pairs (bp) (details will be given elsewhere). Gene content and arrangement correspond to that of conservatively evolving arthropod mitochondrial genomes with two exceptions. Most crustacean and insect mitochondrial genomes differ from *Lithobius* with regard to the position of the transfer RNA^{Leu(UUR)} gene, which in crustaceans is located between the COXI and COXII genes and in *Lithobius* between the tRNA^{Leu(CUN)} and ND1 genes. This is consistent with the previous demonstration that the COXI/tRNA^{Leu(UUR)}/COXII arrangement is a synapomorphy of the Pancrustacea².

Another difference concerns the position of the tRNA^{Gln} gene, which in most arthropods resides between tRNA^{Trp} and tRNA^{Tyr} (Fig. 1), but in *Lithobius* it lies within the non-coding region of the

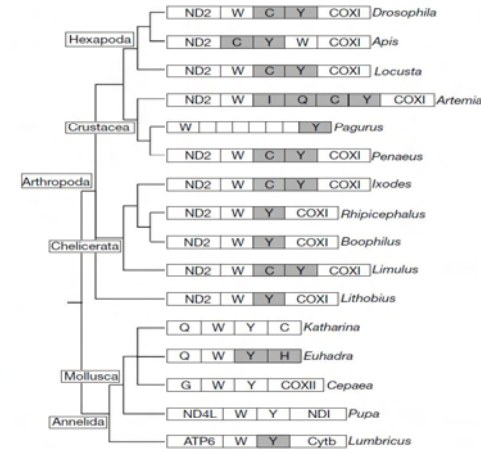
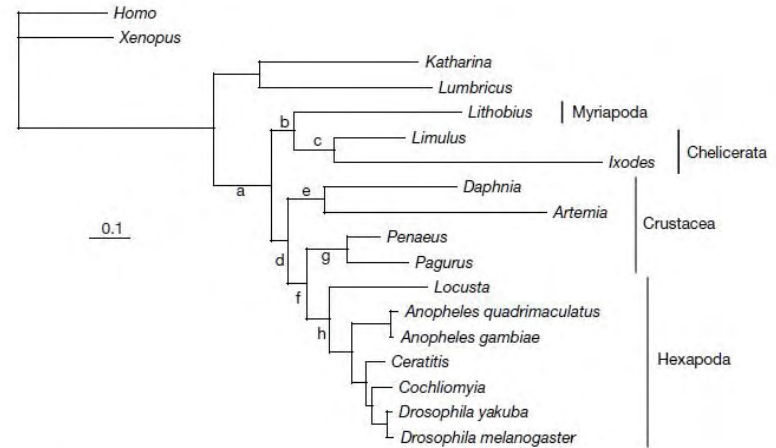


Figure 1 Phylogenetic distribution of tRNA^{Gln} arrangements in arthropod mitochondrial genomes. The relative location of tRNA^{Trp} (W), tRNA^{Gln} (C) and tRNA^{Tyr} (Y) is shown for representative arthropod and outgroup species with similar arrangements. Multiple coding units separating tRNA^{Trp} and tRNA^{Tyr} in *Pagurus* are indicated by boxes. Transcription units in clear boxes code from left to right, those in shaded boxes code from right to left. The mollusc *Euhadra heriklotzi* is the only non-arthropod species known so far in which tRNA^{Trp} and tRNA^{Tyr} are neighbours in opposite coding orientation, as in *Lithobius*. In a few non-arthropod species tRNA^{Trp} and tRNA^{Tyr} are next to each other, although in the same coding orientation. Re-examining non-annotated regions in published mitochondrial genome sequences, we found that the annelid species *Lumbricus terrestris* has coding probability for a second tRNA^{Tyr}, which could result in a *Lithobius*-like tRNA^{Trp} and tRNA^{Tyr} arrangement (J.W.H., unpublished observation). This possibility, however, awaits confirmation by tRNA transcript analysis.

Hwang et al. (2001)
 Nature 413, 154-157



	a	b	c	d	e	f	g	h
MP	100/97	83/84	65/54	40 ¹ /92	70/92	57/38 ⁴	100/100	91/98
NJ	100/100	100/96	100/81	17 ² /88	99/86	100/97	100/100	100/100
QP	91/94	99/99	100/99	46 ³ /57	99/97	95/84	100/97	99/96

Figure 3 Phylogram of best maximum-likelihood tree with 18P2560 alignment (ln(likelihood) = -42925.32). Bar represents 0.1 substitutions per site. Branches with letters have branch support values (BP) given below the tree for maximum parsimony (MP), neighbour-joining (NJ) and the maximum-likelihood-based quartet puzzling method (QP)²⁸. Left numbers refer to 18P2560 alignment, right numbers to 18P1528 alignment.

Superscript numbers indicate branches that are not included in bootstrap majority rule consensus trees: 1, Branchiopoda placed at the base of arthropods with BP = 57; 2, Branchiopoda placed at the base of the arthropods with BP = 82; 3, Branchiopoda placed at the base of the arthropods with BP = 53; 4, monophyletic Crustacea supported with BP = 53.

Park et al. (2007)
BMC Genomics 8, 343



BMC Genomics

Research article
The complete mitochondrial genome of the sea spider *Achelia bituberculata* (Pycnogonida, Ammotheidae): arthropod ground pattern of gene arrangement
Shin-Ju Park, Yong-Seok Lee and Uli Wook Hwang*

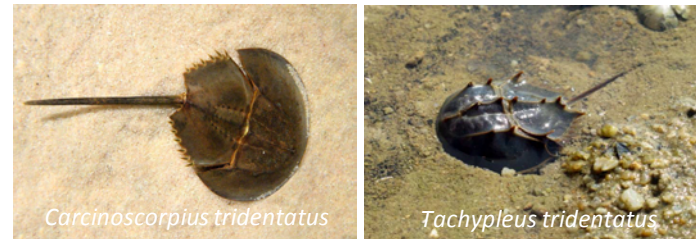
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Back et al. (2014)
Int. J. Biol. Sci. 10, 479-489



Int. J. Biol. Sci. 2014, Vol. 10

International Journal of Biological Sciences
2014, 10(7): 479-489, doi:10.7554/ijbs.1279

Research Paper
Complete Mitochondrial Genomes of *Carcinoscorpium rotundicauda* and *Tachylepus tridentatus* (Xiphosura, Arthropoda) and Implications for Chelicerate Phylogenetic Studies

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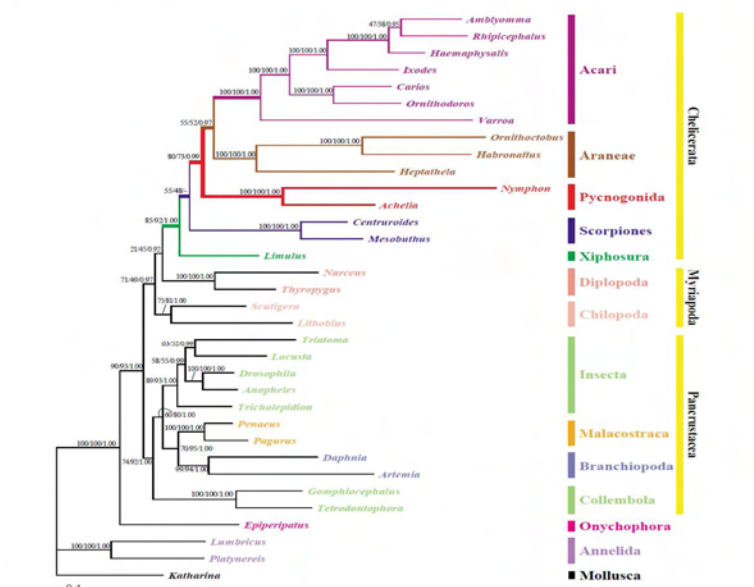
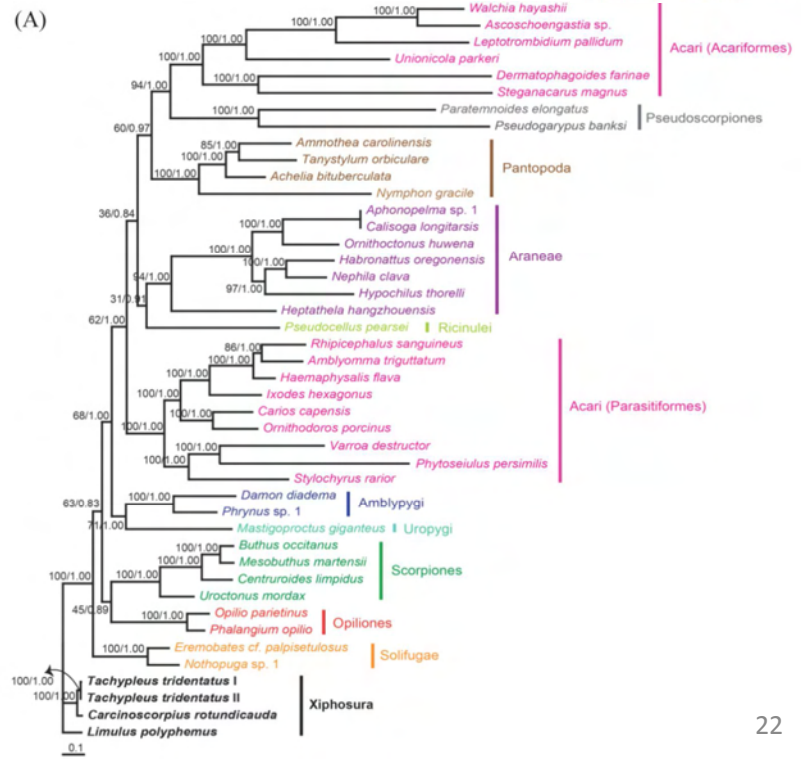


Figure 6
Maximum likelihood tree inferred from amino acid residues deduced from 12 mitochondrial protein-coding genes of 30 arthropods and 4 non-arthropods. The pycnogonids *Achelia bituberculata* and *Nymphon gracile* appear within the monophyletic Chelicerata with high node confidence values. Scorpiones are placed as the basal arachnid group. The inclusion of Pycnogonida within Arachnida (Arachnida plus Hexapoda) and Myriochelata or Paradoxopoda (Myriapoda and Chelicerata) are strongly supported. The numbers above/below the branches indicate the node confidence values: BP_{ML} (bootstrap proportion in the maximum likelihood analysis), BP_{BI} (bootstrap proportion in Bayesian inference) and BPP (Bayesian posterior probability) in order. The tree was obtained from a final alignment 2232 aa sites in length (refer to Materials and Methods for more detailed information). The log likelihood value of the best tree is -72575.641555. For more detail information about the taxon, refer to Table 1.



Choi et al. (2007)
DNA Seq. 18: 461-473



DNA Sequence, December 2007; 18(6): 461-473

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FULL LENGTH RESEARCH PAPER

Complete mitochondrial genome of a Chinese scorpion *Mesobuthus martensii* (Chelicerata, Scorpiones, Buthidae)

EUN HWA CHOI, SHIN JU PARK, KEUM HEE JANG, & WOOK HWANG

Department of Biology, Teachers College, Kyungpook National University, Daegu 702-701, South Korea

(Received 9 November 2006)

Lim and Hwang (2006)
Mol. Cells 22, 314-322



Mol. Cells, Vol. 22, No. 3, pp. 314-322

Molecules
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Cells
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The Complete Mitochondrial Genome of *Pollicipes mitella* (Crustacea, Maxillopoda, Cirripedia): Non-Monophylies of Maxillopoda and Crustacea

Jong Tae Lim and Ui Wook Hwang*

Department of Biology, Teachers College, Kyungpook National University, Daegu 702-701, Korea.

(Received August 23, 2006; Accepted October 10, 2006)

Woo et al. (2007)
Mol. Cells 23, 182-191



Mol. Cells, Vol. 23, No. 2, pp. 182-191

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and
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Complete Mitochondrial Genome of a Troglobite Millipede *Antrokoreana gracilipes* (Diplopoda, Juliformia, Julida), and Juliformian Phylogeny

Hyung-Jik Woo, Yong-Seok Lee, Shin-Ju Park, Jong-Tae Lim, Keum-Hee Jang, Eun-Hwa Choi, Yong-Gun Choi¹, and Ui Wook Hwang*

Department of Biology, Teachers College, Kyungpook National University, Daegu 702-701, Korea;

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(Received November 21, 2006; Accepted January 6, 2007)

Park et al. (2016)
Mitochondrial DNA Part A 27, 2268-2269



Mitochondrial
DNA

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ISSN: 2470-1334 (print); 2470-1408 (electronic)
Mitochondrial DNA Part A, 2016; 27(3): 2268-2269
© 2014 Informa UK Ltd. DOI: 10.3109/19401736.2014.984174

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of a centipede *Bothropolys* sp. (Chilopoda, Lithobiomorpha, Lithobiidae)

Sin Ju Park¹*, Eun Hwa Choi²*, Jae Sam Hwang¹, and Ui Wook Hwang^{1,2}

¹Department of Biology Education, Teachers College, Kyungpook National University, Daegu, South Korea, ²Institute for Phylogenomics and Evolution, Kyungpook National University, Daegu, South Korea, and ³Department of Agricultural Biology, Rural Development Administration, Jeonju, South Korea

DB construction for the arthropod omics data

Lee et al. (2008)
Nucleic Acids Research 36, D938-D942

MITOME 미토콘드리아 유전체 DB 운영

*D938–D942 Nucleic Acids Research, 2008, Vol. 36, Database issue
doi:10.1093/nar/gkm763* Published online 16 October 2007

Mitome: dynamic and interactive database for comparative mitochondrial genomics in metazoan animals

Yong Seok Lee^{1,2}, Jeongsu Oh², Young Uk Kim², Namchul Kim², Sungjin Yang² and Ui Wook Hwang^{1,*}

The screenshot displays the Mitome database interface with four main tabs: **Contents Tab** (showing a list of mitochondrial genomes), **Tree Tab** (showing a phylogenetic tree), **Conserved regions Tab** (showing a list of conserved regions), and **Plot analyses Tab** (showing two plots: 'New Plot' and 'Cluster Plot').

The screenshot shows a file explorer window with a list of mitochondrial genome files, including: *Acariella_ssp_120804_1*, *Acariella_ssp_120804_1.1*, *Acariella_ssp_120804_1.2*, *Acariella_ssp_120804_1.3*, *Acariella_ssp_120804_1.4*, *Acariella_ssp_120804_1.5*, *Acariella_ssp_120804_1.6*, *Acariella_ssp_120804_1.7*, *Acariella_ssp_120804_1.8*, *Acariella_ssp_120804_1.9*, *Acariella_ssp_120804_1.10*, *Acariella_ssp_120804_1.11*, *Acariella_ssp_120804_1.12*, *Acariella_ssp_120804_1.13*, *Acariella_ssp_120804_1.14*, *Acariella_ssp_120804_1.15*, *Acariella_ssp_120804_1.16*, *Acariella_ssp_120804_1.17*, *Acariella_ssp_120804_1.18*, *Acariella_ssp_120804_1.19*, *Acariella_ssp_120804_1.20*, *Acariella_ssp_120804_1.21*, *Acariella_ssp_120804_1.22*, *Acariella_ssp_120804_1.23*, *Acariella_ssp_120804_1.24*, *Acariella_ssp_120804_1.25*, *Acariella_ssp_120804_1.26*, *Acariella_ssp_120804_1.27*, *Acariella_ssp_120804_1.28*, *Acariella_ssp_120804_1.29*, *Acariella_ssp_120804_1.30*, *Acariella_ssp_120804_1.31*, *Acariella_ssp_120804_1.32*, *Acariella_ssp_120804_1.33*, *Acariella_ssp_120804_1.34*, *Acariella_ssp_120804_1.35*, *Acariella_ssp_120804_1.36*, *Acariella_ssp_120804_1.37*, *Acariella_ssp_120804_1.38*, *Acariella_ssp_120804_1.39*, *Acariella_ssp_120804_1.40*, *Acariella_ssp_120804_1.41*, *Acariella_ssp_120804_1.42*, *Acariella_ssp_120804_1.43*, *Acariella_ssp_120804_1.44*, *Acariella_ssp_120804_1.45*, *Acariella_ssp_120804_1.46*, *Acariella_ssp_120804_1.47*, *Acariella_ssp_120804_1.48*, *Acariella_ssp_120804_1.49*, *Acariella_ssp_120804_1.50*, *Acariella_ssp_120804_1.51*, *Acariella_ssp_120804_1.52*, *Acariella_ssp_120804_1.53*, *Acariella_ssp_120804_1.54*, *Acariella_ssp_120804_1.55*, *Acariella_ssp_120804_1.56*, *Acariella_ssp_120804_1.57*, *Acariella_ssp_120804_1.58*, *Acariella_ssp_120804_1.59*, *Acariella_ssp_120804_1.60*, *Acariella_ssp_120804_1.61*, *Acariella_ssp_120804_1.62*, *Acariella_ssp_120804_1.63*, *Acariella_ssp_120804_1.64*, *Acariella_ssp_120804_1.65*, *Acariella_ssp_120804_1.66*, *Acariella_ssp_120804_1.67*, *Acariella_ssp_120804_1.68*, *Acariella_ssp_120804_1.69*, *Acariella_ssp_120804_1.70*, *Acariella_ssp_120804_1.71*, *Acariella_ssp_120804_1.72*, *Acariella_ssp_120804_1.73*, *Acariella_ssp_120804_1.74*, *Acariella_ssp_120804_1.75*, *Acariella_ssp_120804_1.76*, *Acariella_ssp_120804_1.77*, *Acariella_ssp_120804_1.78*, *Acariella_ssp_120804_1.79*, *Acariella_ssp_120804_1.80*, *Acariella_ssp_120804_1.81*, *Acariella_ssp_120804_1.82*, *Acariella_ssp_120804_1.83*, *Acariella_ssp_120804_1.84*, *Acariella_ssp_120804_1.85*, *Acariella_ssp_120804_1.86*, *Acariella_ssp_120804_1.87*, *Acariella_ssp_120804_1.88*, *Acariella_ssp_120804_1.89*, *Acariella_ssp_120804_1.90*, *Acariella_ssp_120804_1.91*, *Acariella_ssp_120804_1.92*, *Acariella_ssp_120804_1.93*, *Acariella_ssp_120804_1.94*, *Acariella_ssp_120804_1.95*, *Acariella_ssp_120804_1.96*, *Acariella_ssp_120804_1.97*, *Acariella_ssp_120804_1.98*, *Acariella_ssp_120804_1.99*, *Acariella_ssp_120804_1.100*.

The screenshot displays the Mitome database interface with three main tabs: **Arrangement view Tab** (showing a detailed view of a mitochondrial genome arrangement), **ATV applet** (showing a phylogenetic tree), and **Arrangement search Tab** (showing a search interface for mitochondrial genomes).



IPE

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- Good work environment

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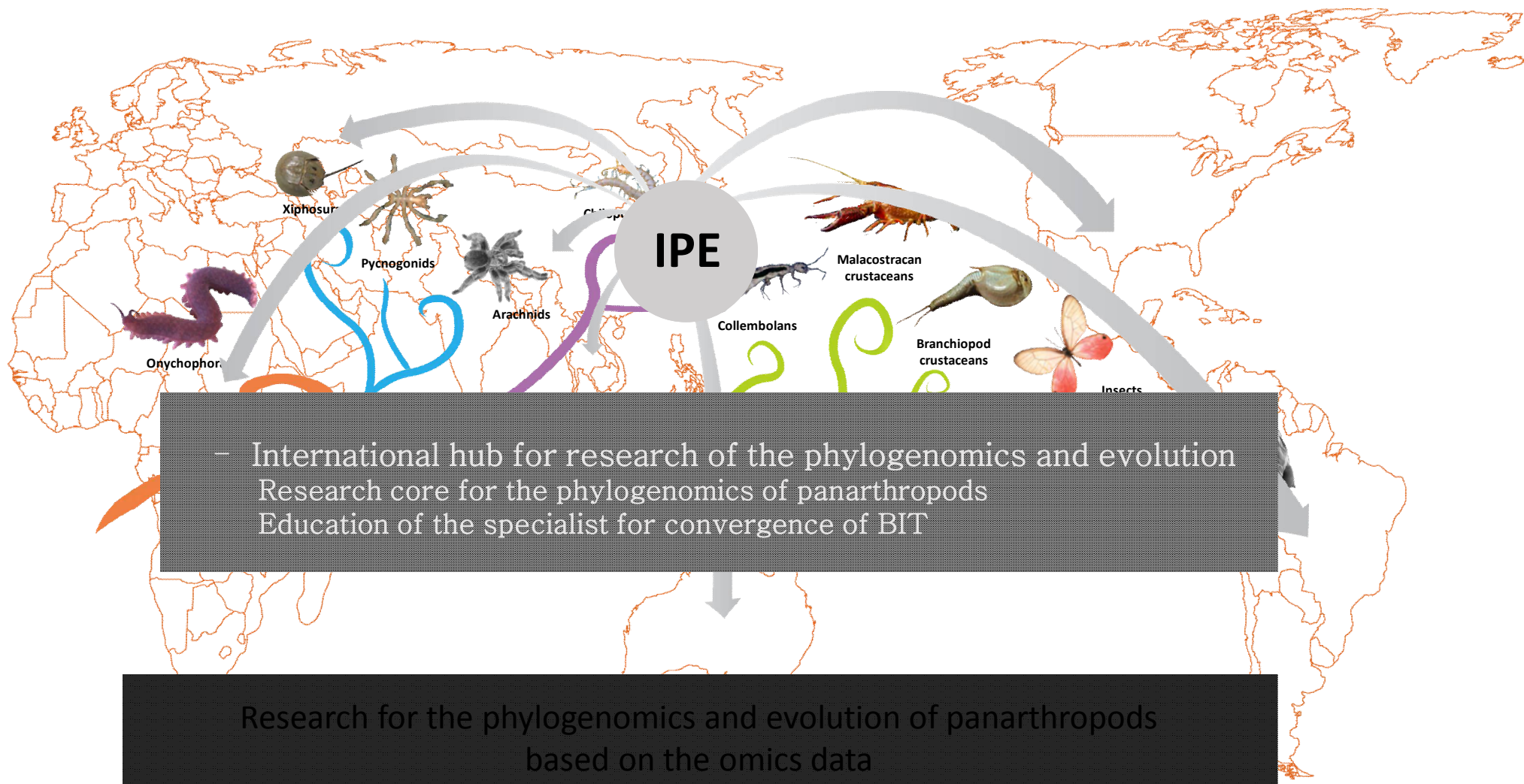
- 3 Research professors
- 2 Post-docs
- 6 Masters
- 8 Research assistants

Excellent research management system

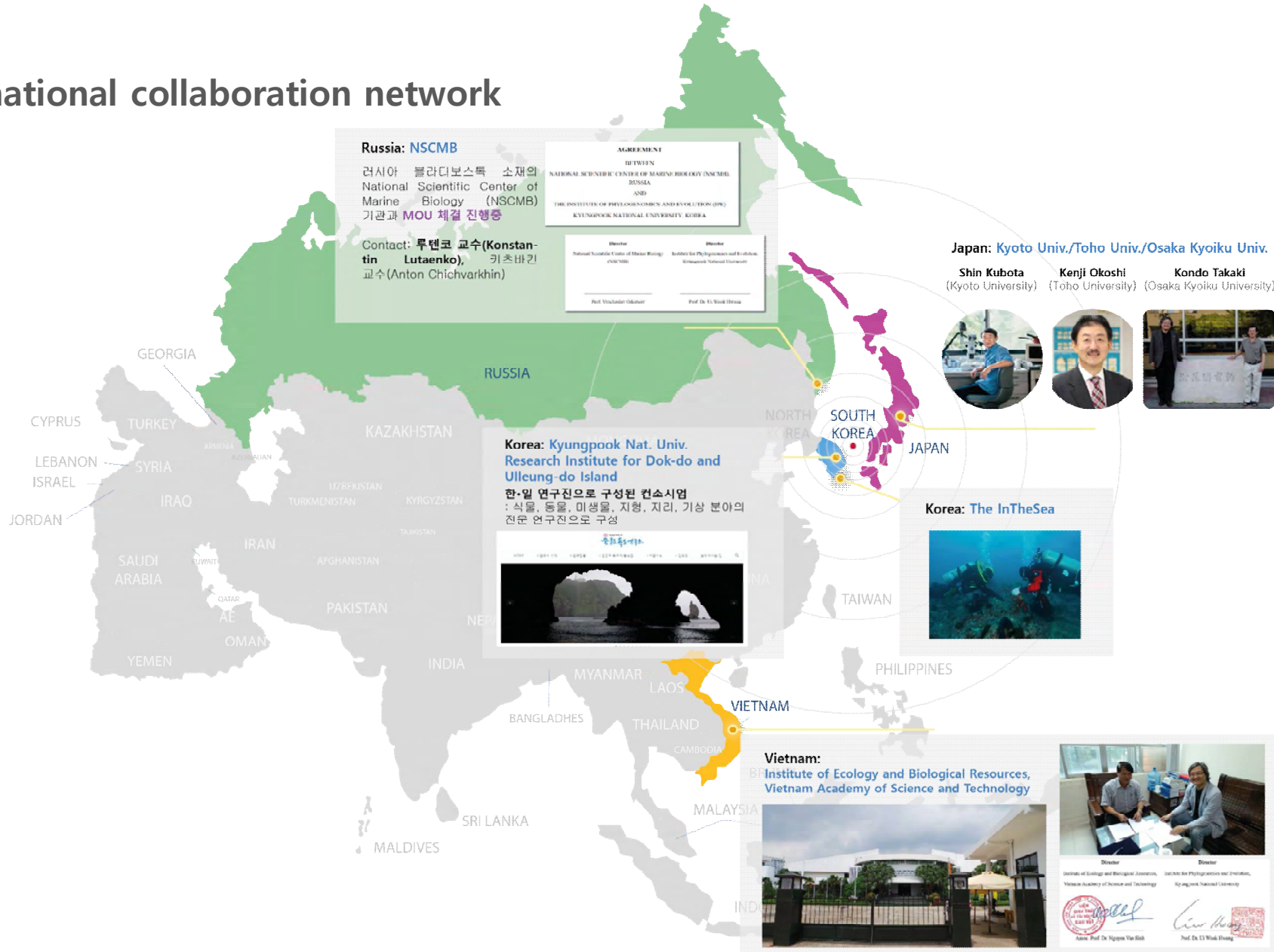
- Main: 22
- Collaboration: 15

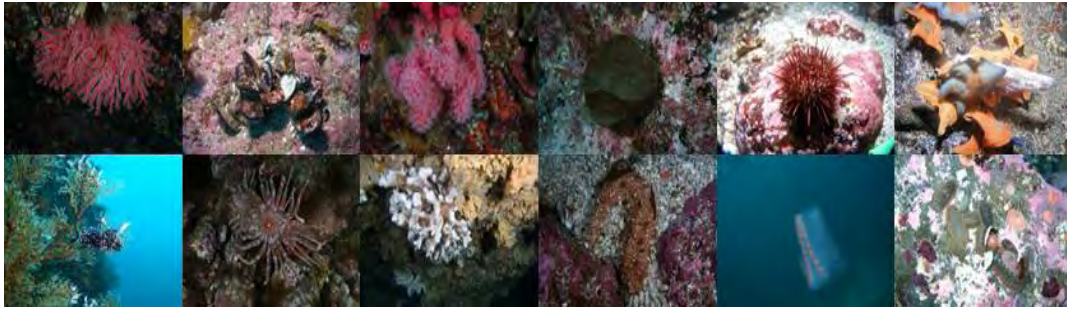
International collaboration networks

- Genome institutes and Bio-resources institutes in Asia



International collaboration network





11-1462762-001(250-01)

독도의 생물다양성

(육상식물, 곤충, 조류)

국립생물자원관

This section contains eight detailed pages of biological information:

- 1. 육상식물 (Terrestrial Plants):**
 - 1.1. 육상식물 (Terrestrial Plants) - Overview
 - 1.2. 육상식물 (Terrestrial Plants) - Detailed list
- 2. 곤충 (Insects):**
 - 2.1. 곤충 (Insects) - Overview
 - 2.2. 곤충 (Insects) - Detailed list
- 3. 조류 (Birds):**
 - 3.1. 조류 (Birds) - Overview
 - 3.2. 조류 (Birds) - Detailed list

독도의 생물다양성

육상식물 | 곤충 | 조류 | 해양생물

독도의 생물다양성

육상식물 | 곤충 | 조류 | 해양생물

This section features a comprehensive grid of marine life species:

- 해양생물 (Marine Life):**
 - 1. 해양생물 (Marine Life) - Overview
 - 2. 해양생물 (Marine Life) - Detailed list

At the bottom, there are two tables with detailed species lists and their characteristics.



Thank you for your attention!