

YCAM InterLab Camp vol.3

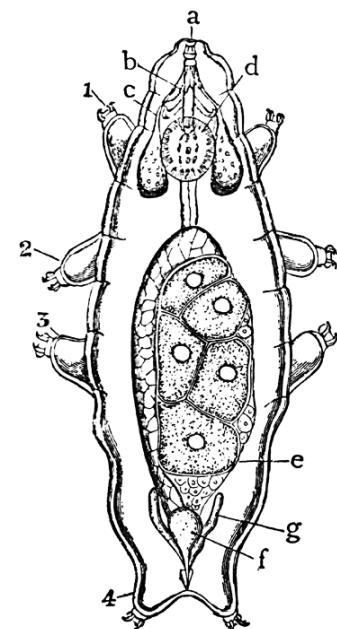
# クマムシゲノムプロジェクト

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片山俊明

ライフサイエンス統合データベースセンター

[ktym@dbcls.jp](mailto:ktym@dbcls.jp)



# クマムシ



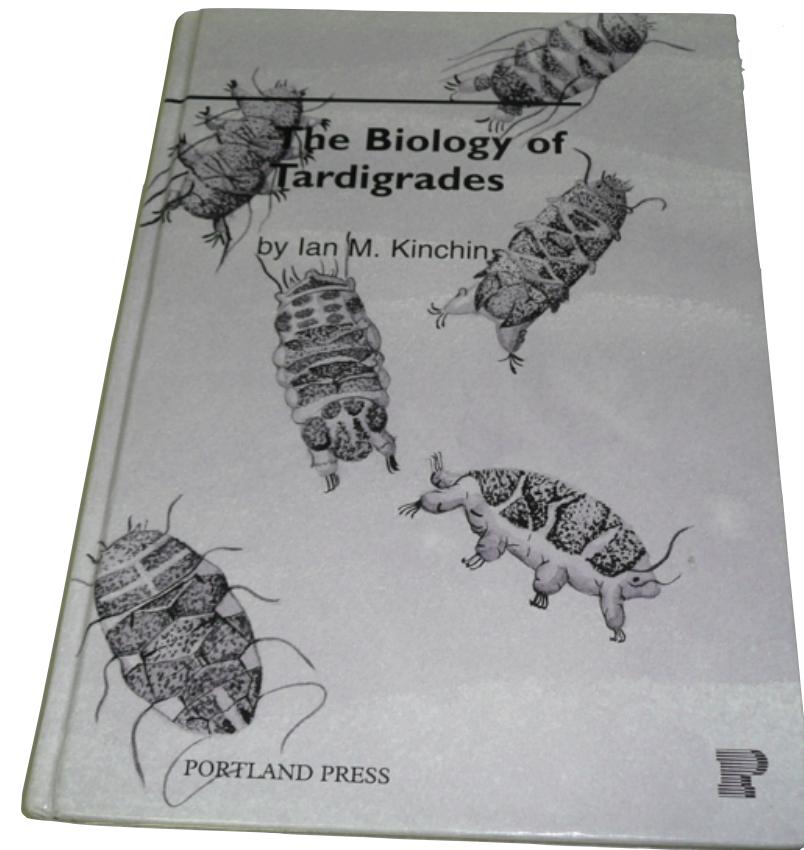
- 緩歩動物門 - 線虫と昆虫の間くらいに位置する1mm以下のかわいい動物
  - その辺のコケから深海や南極まで、地球上どこにでもいる！
- 乾燥すると究極の極限環境耐性
  - 高温 : +151°C (ラーム, 1921)
  - 低温 : -273°C (ベクレル, 1950)
  - 高圧 : 7.5GPa (750,000mの水圧)
  - 低圧 :  $5 \times 10^{-4}$ Pa (ほぼ真空)
  - 放射線 : X線 100,000 Gy  
(ヒト致死量の1,000倍)  
ガンマ線 7,000Gy  
Heイオン 8,000Gy
  - 化学物質 : アルコール (消毒剤)  
臭化メチル (防虫剤)



# クマムシの歴史

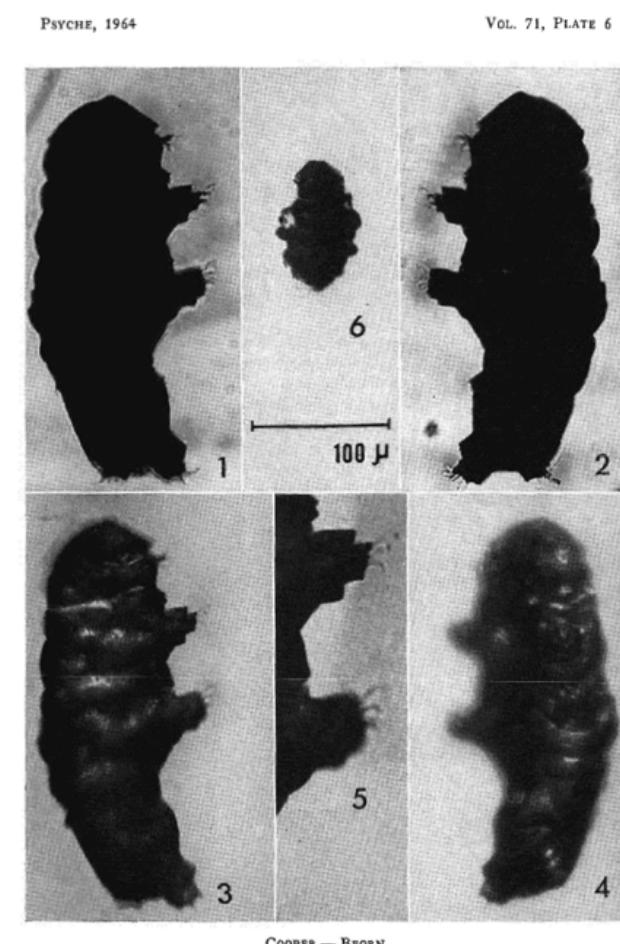
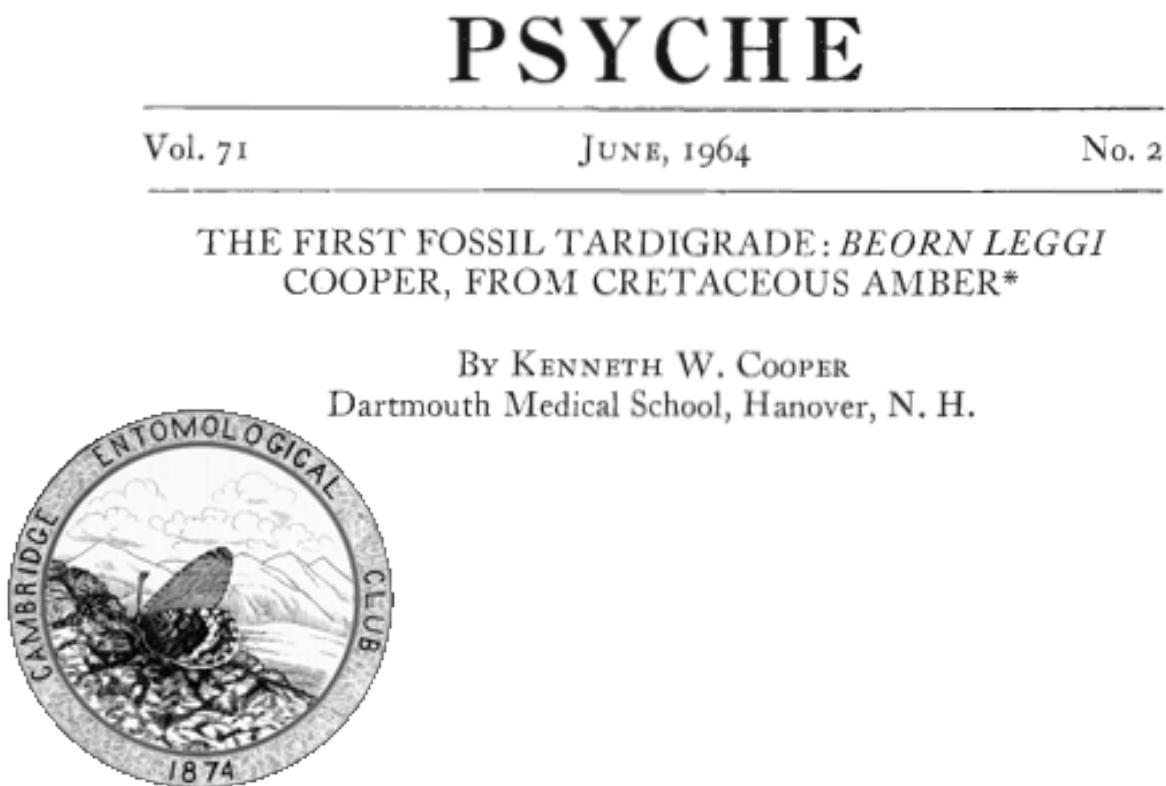
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- 1674 Leeuwenhoek が顕微鏡で微生物の存在を発見
- 1767 クマムシ最初の記載 (Eichhorn)
- 1790 リンネが *Systema Naturae* にクマムシを追加
- 1849 最初の海産クマムシの記載 (Boulengey)
- 1921 高温耐性 (151°C) の記載 (Rahm)
- 1929 節足動物門に真クマムシと異クマムシ (Marcus)
- 1950 低温耐性 (-273°C) の記載 (Becquerel)
- 1962 クマムシ「緩歩動物門」に独立 (Ramazzotti)
- 1964 X線耐性 (100,00Gy) の記載 (May)
- 1964 クマムシの化石を発見 (Cooper)
- 1968 クマムシの電子顕微鏡観察 (Rosati)
- 1974 第1回国際クマムシ学会
- 2005 γ線耐性 (6,000Gy) の記載 (Jönsson)
- 2006 α線耐性 (7,000Gy) の記載 (Horikawa)
- 2008 低圧耐性の記載 (Jönsson)
- 2008 高圧耐性 (7.5GPa) の記載 (Ono)
- 2008 ヨコヅナクマムシのゲノムプロジェクト開始
- 2009 第11回国際クマムシ学会



# 化石から見つかったクマムシ

- 共に白亜紀(約>6000万年前)のコハクから発見(Cooper, 1964)
  - 真クマムシ(eutardigrada) Beorn leggi
  - 異クマムシ(heterotardigrada) 無名



<http://psyche.entclub.org/71/71-041.html>

<http://www.hindawi.com/journals/psyche/1964/048418.abs.html>

# 皇居から見つかったクマムシ

## 4. 皇居のクマムシ類（緩歩動物）

阿部 渉（北大院・理・生物科学）・武田正倫  
(国立科博・動物)

国立科学博物館による皇居の生物調査の一環として、1996年から1999年にかけて陸生および淡水生のクマムシ類の調査を行った。蘚苔類・地衣類・藻類・リターなど多様な生息環境を調査した結果、13種の未確定種を含む2綱3目4科9属22種のクマムシ類を確認した。このうち、淡水産種はオオヅメクマムシ属の1種*Dactylobiotus* sp.のみであった。チョウメイムシ科のミカドチョウメイムシ *Calcarobiotus imperialis*は本調査の過程で Abe & Takeda (2000) により新種として記載された種である。ミカドチョウメイムシ属 *Calcarobiotus*は南アフリカ産の2種しか知られていなかった極めて稀な属である。

ZOOLOGICAL SCIENCE 17: 259–263 (2000)

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## A New *Calcarobiotus* (Tardigrada: Macrobiotidae) from the Imperial Palace of Japan

Wataru Abe<sup>1,2\*</sup> and Masatsune Takeda<sup>2</sup>

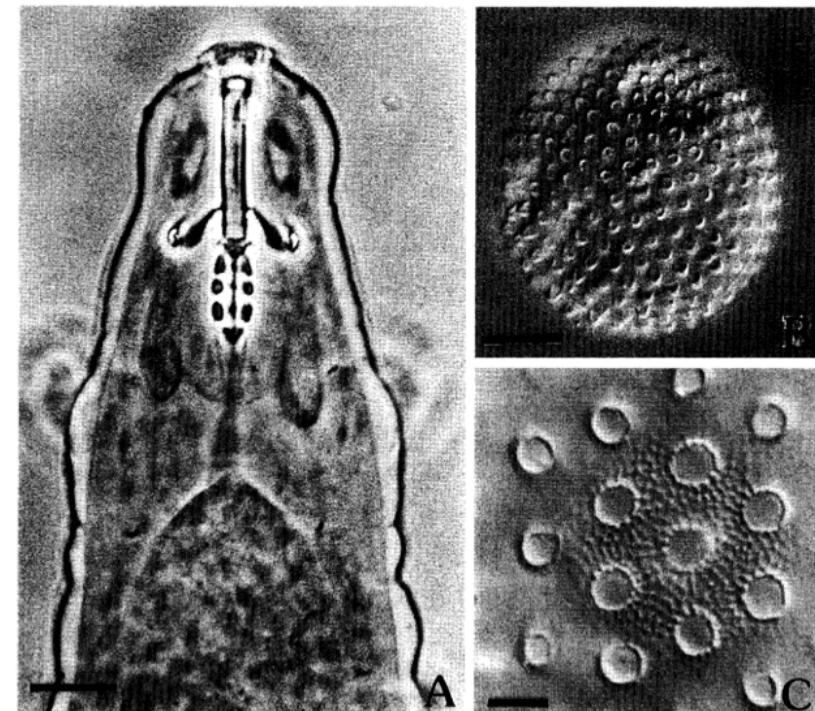


Fig. 2. *Calcarobiotus imperialis*, new species. A, Holotype (NSMT Tg-45); B, C, Paratype (NSMT Tg-50). (A) Anterior body. (B) Egg sculpture (computer-enhanced). (C) Detail of egg shell surface. Scales: A, B=20 μm; C=5 μm.

# カタツムリのウンから見つかったクマムシ

421

*ECHINISCUS MOLLUSCORUM* Fox and Garcia-Moll, 1962 (Fig. 229).

Length 185-196 $\mu$ , color orange or red, eye spots present or absent. The sculpture is a dense and strong granulation and the individual granules are larger and prominent in the central zone of the various plates, and especially on the terminal.

The lateral cirri A are very short (about 19 $\mu$ ) and its length is always less than double that of the buccal cirri (internal buccal cirri about 11 $\mu$ , external 14 $\mu$ ). There are no other lateral appendices; dorsally exists minuscule spicules B<sup>d</sup> on the scapular plate, visible with much difficulty; in dorsolateral position, on the first paired plate, are present spicules C', just as minuscule.

Median plate 3 is probably absent, because we can not perceive its lateral limits: however the space between the second paired plate and the terminal is strongly sculptured. The terminal plate is not faceted and the usual two notches are present, even if not always very evident. Fourth pair of legs with papilla and dentate collar, composed of teeth of irregular shape: the claws of this pair of legs are 14 to 19 $\mu$  long and all four have at the bases a spur, which may however be lacking. The larvae of two claws measure about 98 $\mu$ .

*E. molluscorum* was at first observed in the feces of the terrestrial gastropod *Bulimulus exilis*, collected in different localities in San Juan (Puerto Rico, U.S.A.). Over 886 snails examined, coming from 18 different localities, the author observed tardigrades in the feces of 2.1% of them.

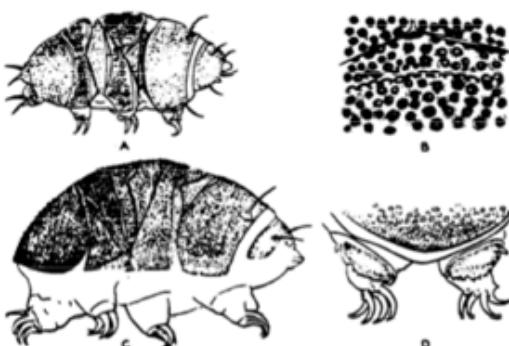


Fig. 229 - *E. molluscorum* Fox & Garcia-Moll. A, larva in dorsal view; B, cuticle between the second dorsal plate and the terminal plate; C, adult in lateral view; D, detail of the 4th pair of legs (from Fox and Garcia-Moll).

at the bases a spur, which may however be lacking. The claws of two claws measure about 98 $\mu$ .

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# 宇宙旅行に行ったクマムシ

Tardigrades In Space (TARDIS) is the first research project to evaluate the ability of tardigrades to survive under open space conditions. TARDIS is one of the projects within the Biopan-6 research platform provided by European Space Agency (ESA), and will be sent into space with the russian FOTON-M3 mission.

## What is the aim of TARDIS?

Why should we send dry aquatic invertebrates into space, an environment that certainly is not normal for these animals? There are many answers to this question. One would be: to see if these animals, as the first ever, are able to cope with the extremely dry conditions of deep vacuum and the harmful solar and galactic radiation up there. In the past, several biologists have suggested that tardigrades may be one of the few animals that have a chance to come back alive after a trip in real space. Finally we will be able to find out if this is true.

At a more mechanistic biological level, exposure of organisms to space conditions will reveal how living cells react to the potentially very stressful impact of space parameters. And organisms that can handle the damaging space parameters will be important sources of knowledge for how to generate the space ecosystems that will be necessary for the more permanent human establishments in space that is envisaged today.

The TARDIS experiment consists of two sets of samples: one set exposed to both space vacuum and solar radiation, and another set exposed to space vacuum only. All tardigrade specimens included in the study are in a dry, anhydrobiotic state. Species included are: Richtersius coronifer, Milnesium tardigradum, Echiniscus testudo, Ramazzottius oberhaeuseri. These are all known to be very tolerant to desiccation.

Once on the ground again, these samples will be analysed for survival and reproductive potential, and for damage on DNA.

FRIDAY, JANUARY 9, 2009

**Tardigrades No. 1 at Wired Science!**

The space tardigrades have been listed Number 1 on "Top 10 Things Launched Into Space in 2008" at Wired Science <http://blog.wired.com/wiredscience/2009/01/top-10-things-1.html>. The tiny tardigrades left behind such big things as the Jules Verne Automated Transfer Vehicle (with a size of a double-decker bus), and the *Fermi Gamma Ray Space Telescope*.



**Current Biology**  
**Vol 18 No 17**  
**pR729 (2008)**

**Tardigrades  
survive exposure  
to space in low  
Earth orbit**

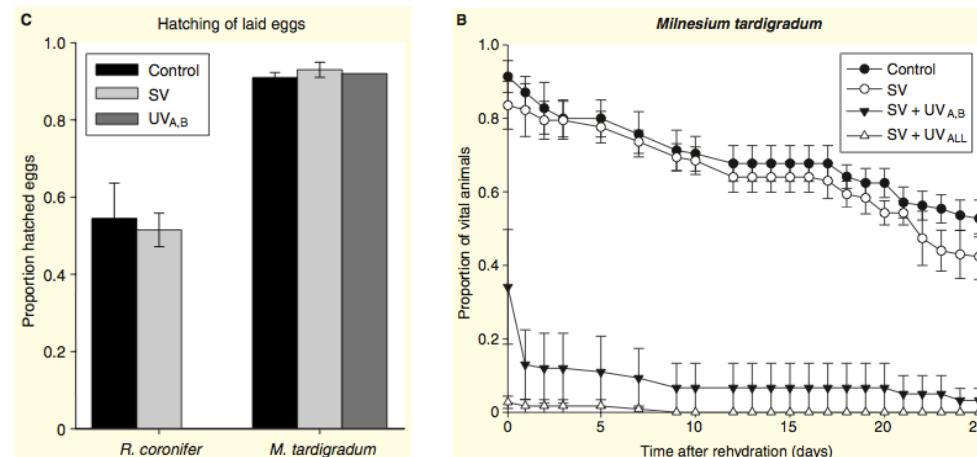
**K. Ingemar Jönsson<sup>1,\*</sup>,  
Elke Rabbow<sup>2</sup>, Ralph O. Schill<sup>3</sup>,  
Mats Harms-Ringdahl<sup>4</sup> and  
Petra Rettberg<sup>2</sup>**

# ミッション概要と宇宙環境暴露後の生存率

- 2007年9月 European Space Agency
  - 人工衛星の外側にクマムシを暴露（高度 258~281km）
- 乾燥したカザリヅメチョウメイムシとオニクマムシの2種
  - Richtersius coronifer** カザリヅメチョウメイムシ
  - Milnesium tardigradum** オニクマムシ
- 条件は3種
  - 宇宙真空と通常の宇宙線への暴露 → 余裕
  - + UV-A と UV-B にも暴露 (280~400nm) → 産卵（オニ）
  - + 全ての UV もフィルタせず暴露 (116.5~400nm) → 厳しい



カザリヅメ  
チョウメイムシ  
オニクマムシ

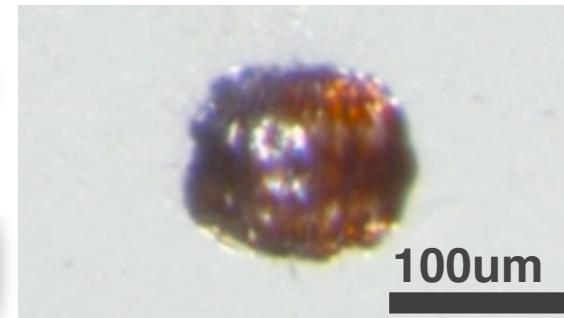


宇宙真空	○	
+ UV <sub>A,B</sub>	1匹	68% (30min)
+ UV <sub>ALL</sub>	×	3匹

# クマムシの乾燥耐性と極限環境耐性



活動状態

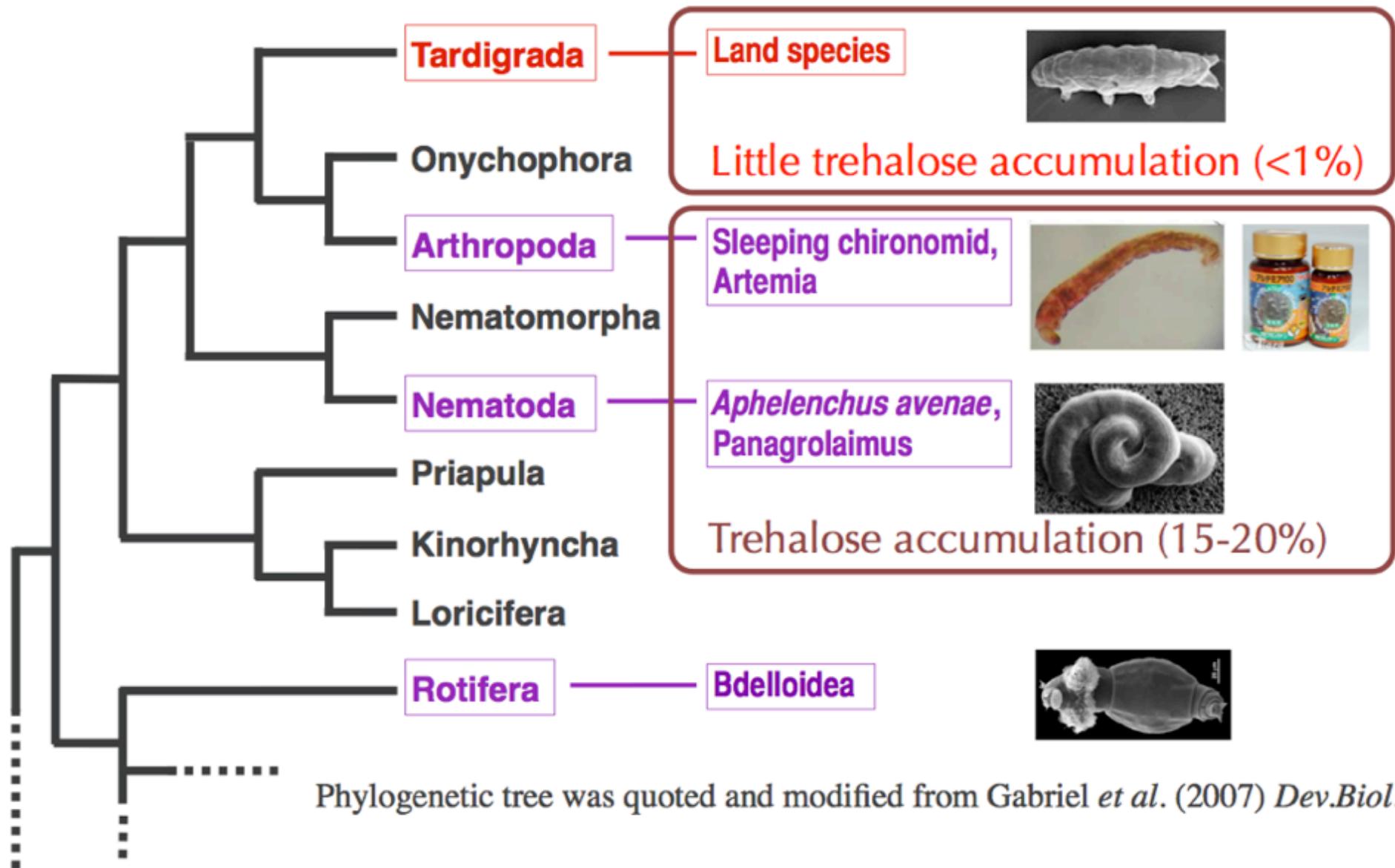


乾眠状態

約80%	水分量	数%
あり	代謝活性	なし
放射線		放射線 高温・低温 超高压・真空
ヒトの致死量の 1000倍以上でもOK	極限環境耐性	

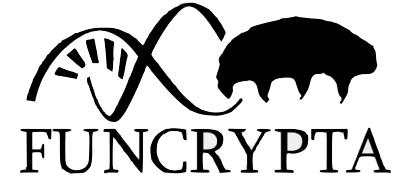
高温		+151°C	野菜の天ぷらを揚げる油温に近い温度
低温		-273°C	ほぼ絶対零度
高圧		7.5GPa	水深約 750km の水圧
低圧		30μPa	国際宇宙ステーションの外と同程度の真空
X線		5,000Gy	人間の致死量の 1,000 倍

# クマムシの系統関係

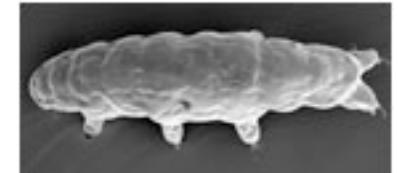


# クマムシ研究の海外における状況

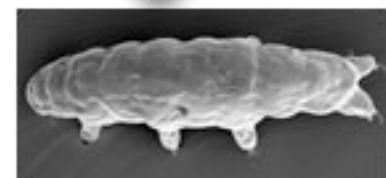
- Schill ら (ドイツ) <http://www.funcrypta.de/>
  - 2006年度から
  - ドイツ連邦教育研究省のグラント 3年で150万ユーロ (2.5億円)
  - チョウメイムシ (乾燥耐性は弱い) ゲノムサイズ >300MB
- MIT (Broad Institute)
  - 2007年度から
  - ヤマクマムシ (乾燥耐性が無い) ゲノムサイズ 70MB
  - 5x coverage のドラフト, EST 10万ペアリード



- 乾燥耐性のあるヨコヅナクマムシを日本で!
  - 2008年度から
  - 比較ゲノム解析
  - メタボローム解析

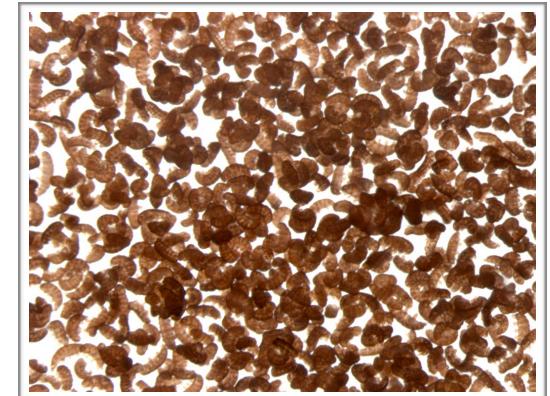


# 横綱クマムシ



# クマムシゲノム解析の分担とスケジュール

- ・ 平成20年度 (2008年)
  - ・ 國枝：ヨコヅナクマムシの培養、遺伝子解析
    - ・ 目標：2万匹
  - ・ 豊田：クローンライブラリ、Fosmidライブラリの作成
    - ・  $4\mu\text{g}$ のゲノムDNA
- ・ 平成21年度 (2009年)
  - ・ 特定領域「ゲノム」支援班
    - ・ 全ゲノムのショットガン配列解読
    - ・ 次世代シーケンサーによるトランスクリプトーム解読
  - ・ 片山：バイオインフォマティクス解析, データベース化
  - ・ 荒川：メタボローム解析



<http://kumamushi.org/>

# クマムシゲノムプロジェクト

Kumamushi Genome Project

http://kumamushi.org/

Google

## Kumamushi Genome Project

home database contact

### Genome sequence of an extreme animal

Kumamushi is the tardigrades (water bears) in Japanese. This organism is scientifically interesting from a phylogenetic view point that water bears are believed to sit between worms and arthropods on the tree of life. Besides, this tiny animal is famous as they can survive the following extreme environments when dehydrated.

- High (151°C)<sup>[1]</sup> and low (-273°C)<sup>[2]</sup> temperatures.
- High (7.5GPa)<sup>[3]</sup> and low (open space vacuum)<sup>[4]</sup> pressures.
- X-rays (10000Gy)<sup>[5]</sup>, Gamma-rays (6000Gy)<sup>[6,7]</sup>, and Helium ion beam (7000Gy)<sup>[7]</sup> radiations.

Our goal is to reveal the molecular basis of tolerance to those enormous stresses by decoding the genome sequence of this creature.

### YOKOZUNA-1

We developed the efficient rearing system<sup>[8]</sup> of [the extremotolerant tardigrade \*Ramazzottius varieomatus\*](#), one of the desiccation tolerant water bears. We isolated a strain named "YOKOZUNA-1" from an egg and established a culture for our genome project.

### References

1. Rahm P.G. (1921) Biologische und physiologische Beiträge zur Kenntnis der Moosfauna. Z. allgem. Physiol. 20, 1-35.
2. Becquerel P. (1950) La suspension de la vie au dessous de 1/20 K

### About

We have started the genome sequencing project of the tardigrada in 2008, which is supported by KAKENHI (Grant-in-Aid for Scientific Research) on Priority Areas "Comparative Genomics" from the Ministry of Education, Culture, Sports, Science and Technology of Japan.

[Read more ...](#)

### Recent Updates

- [Mini Genome Hiroba](#) public forum 20 Dec 09
- [Press release](#) (photo news 1, 2) at jiji.com 10 Dec 09
- [MBSJ2009 presentation](#) 10 Dec 09
- Short reads of genome and mRNA-seq 23 Nov 09
- 3rd sanger assembly build 11 Sep 09
- [ISEPEP3](#) presentation 24-28 Aug 09
- 2nd sanger assembly build 20 Aug 09
- [11th Tardigrada Symposium](#) 7 Aug 09
- 1st sanger assembly build 9 Apr 09
- [Genome Hiroba](#) public forum 25-26 Oct 08
- Project started 1 Apr 08

### Community Site

There is a community site for general information on tardigrades in Japanese language ([クマムシゲノムプロジェクト](#)).



# 次世代 DNA シーケンサー

<b>ABI 3730</b>	700b x 48 / hour	700-1100bp	800Kb / day	2002-
<b>ABI 3730XL</b>	700b x 96 / hour	700-1100bp	1.6Mb / day	2002-
Roche <b>454</b> GS20	20Mb / 5 hours	100bp	100Mb / day	2005-
Roche <b>454</b> FLX	100Mb / 7.5 hours	200-500bp	300Mb / day	2006-
Illumina <b>Solexa</b>	1.5Gb / 2.5 days	50bp	600Mb / day	2006-
ABI <b>SOLiD</b>	4Gb / 8 days	35bp	500Mb / day	2007-
<b>Helicos</b>	2Gb / day	150bp	2Gb / day	2008-
<b>PacBio</b> SMRT	100Gb / hour	-25000bp	2.4Tb / day	2010?



3730XL



454 Life Sciences



Solexa



SOLiD



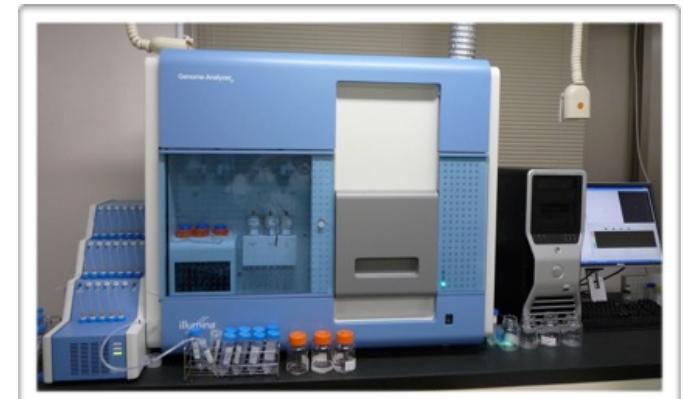
HeliScope

# ゲノム解読の状況

- ・ 全ゲノム解析 (ABI 3730xl) : read長は約1000塩基
  - ・ 772,854 reads (951Mb)
  - ・ 42,592 fosmids (55Mb)
    - ・ 合計、約1,006Mb (16x coverage)
  - ・ 4,191 contigs (58.3Mb)
  - ・ 3,002 supercontigs (58.8Mb)
    - ・ ゲノムサイズ 60Mb の 98% を解読完了

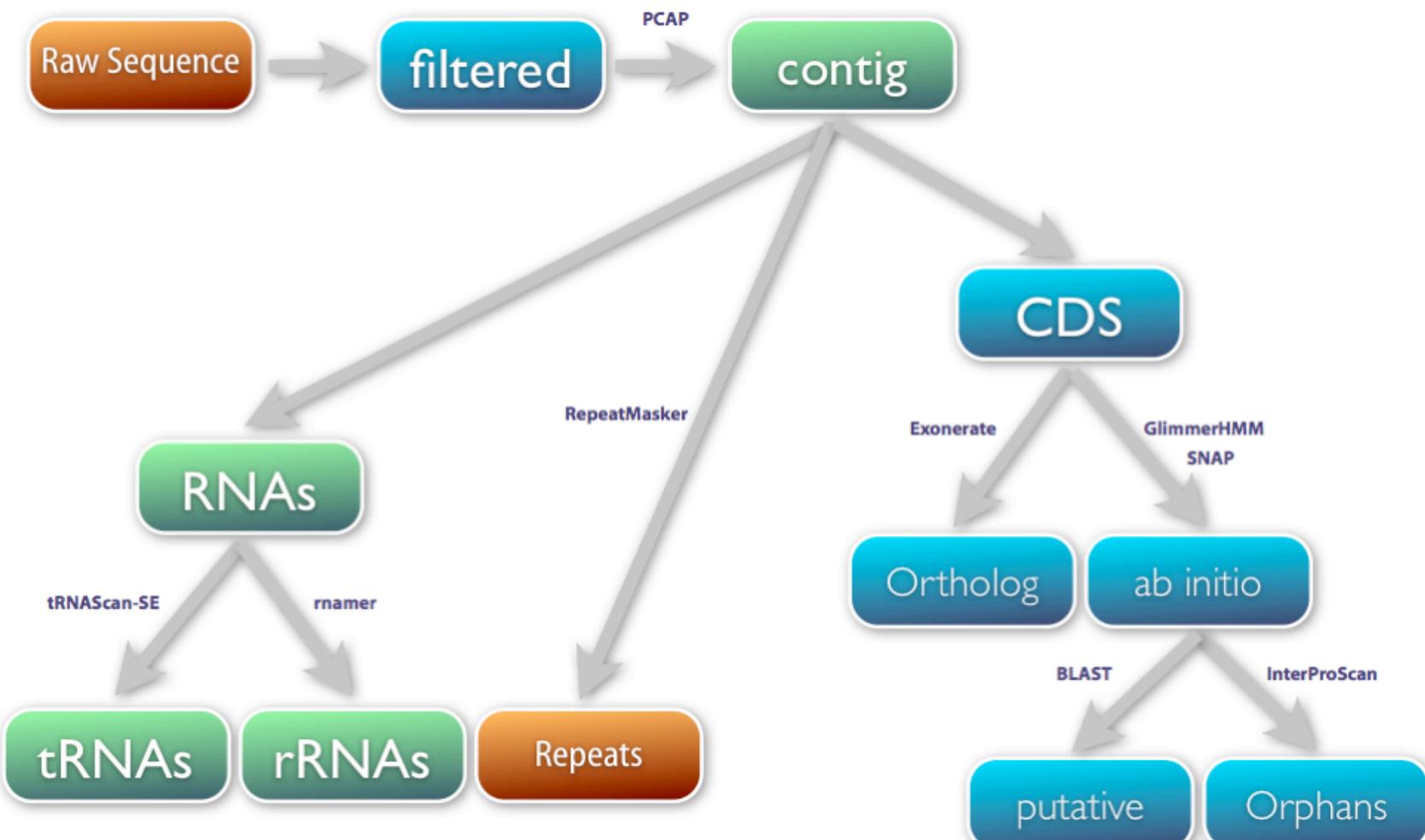


- ・ トランスクリプトーム解析 (Illumina Solexa) : read長は75塩基
  - ・ ゲノム
    - ・ 1億2000万 reads (9Gb)
    - ・ 通常～乾燥～復帰まで4状態での発現遺伝子
      - ・ 4000万 reads × 4 = 1億6000万 (12Gb)



# ゲノム解読の実際

約100万本の配列



RNA遺伝子予測

リピート解析

タンパク質配列解析



# 既知遺伝子との 相同性検索



*D. melanogaster*  
14023 genes



*C. elegans*  
20185 genes

1760 genes  
(12.6%)

1427 genes  
(7.0%)



## SwissProt

Percent identity > 50  
20293 entries hit  
1052 unique locus  
4.47 introns / gene ( $\pm 3.75$ )

Percent identity > 30  
82489 entries hit  
2222 unique locus

## UniRef50

Percent identity > 50  
6451 entries hit  
2237 unique locus

Percent identity > 30  
54990 entries hit  
4865 unique locus

## GlimmerHMM 3.0.1

(Majoros WH et al., Bioinformatics 2004)



Machine learning  
from *D. melanogaster*  
gene models

28666 predicted genes



Machine learning  
from *C. elegans*  
gene models

32545 predicted genes

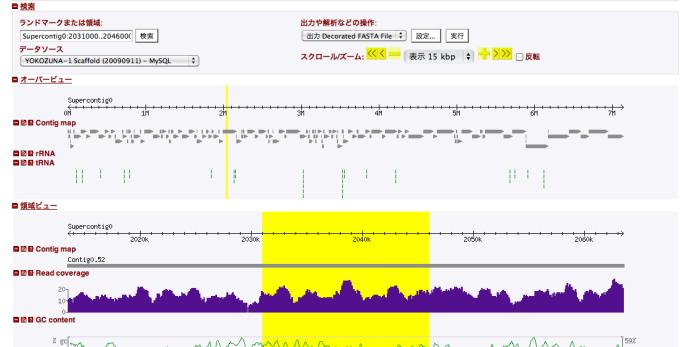
## SNAP

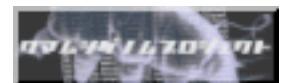
(Korf I, BMC Bioinformatics 2004)

## SNAP

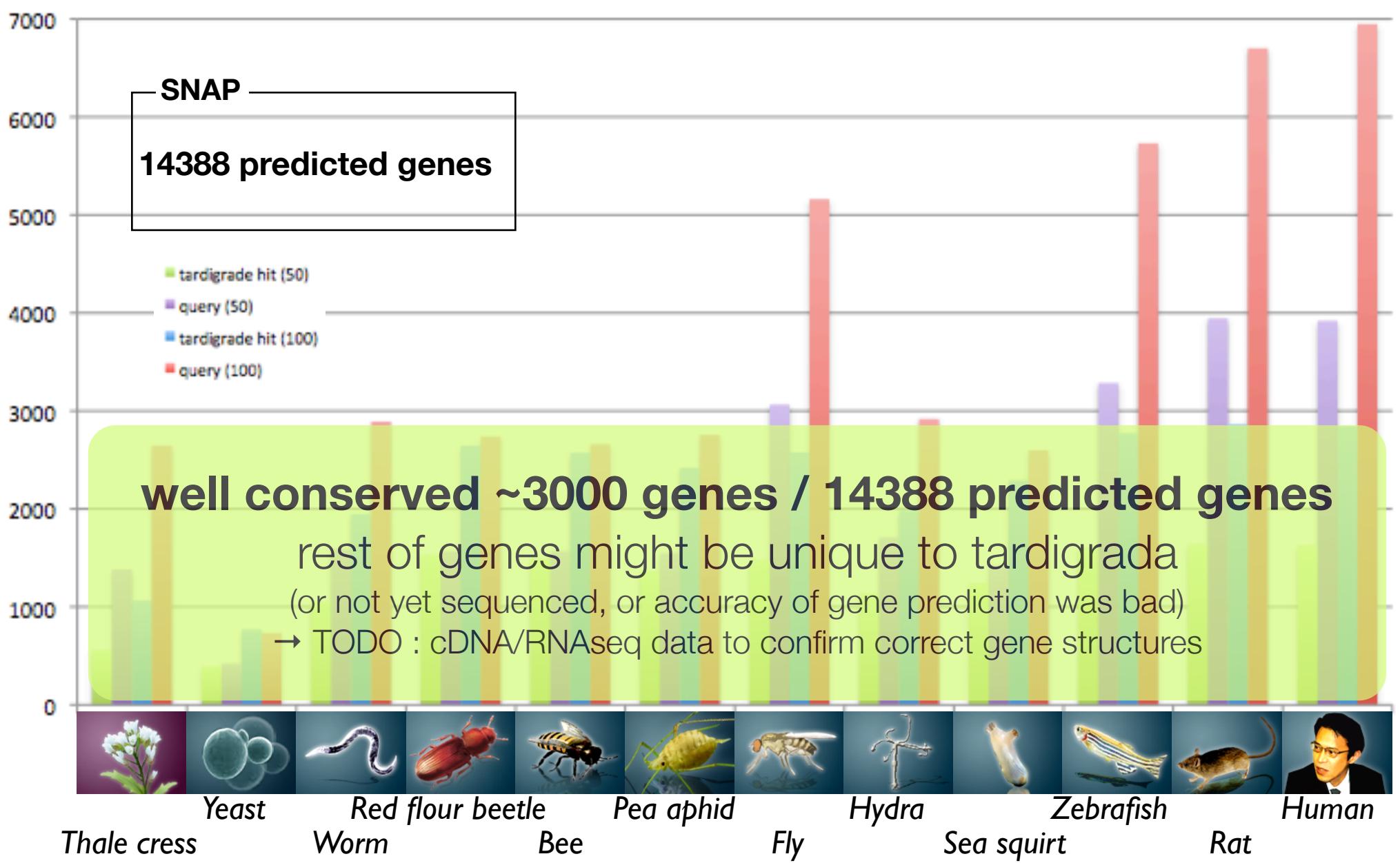
14388 predicted genes

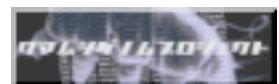
# 遺伝子の予測





# Mutual seq similarity with model organisms





# tRNA : tRNAscan-SE 1.21 (Lowe TM and Eddy SR, NAR 1997)

first	second				third
	T	C	A	G	
T	TTT F 2	TCT S 2	TAT Y i3	TGT C 2	T
	TTC F 3	TCC S	TAC Y i1	TGC C 2	C
	TTA L 1i1	TCA S i1	TAA / 0	TGA / 0	A
	TTG L i2	TCG S 1i1	TAG / 0	TGG W 2	G
C	CTT L 2	CCT P 2	CAT H	CGT R 3	T
	CTC L	CCC P	CAC H 2	CGC R	C
	CTA L 1	CCA P 3	CAA Q 2	CGA R 2	A
	CTG L 1i1	CCG P 1	CAG Q 2	CGG R 1	G
A	ATT I 3	ACT T 3	AAT N	AGT S	T
	ATC I	ACC T	AAC N 3	AGC S 2	C
	ATA I i1	ACA T 1(2)	AAA K 2	AGA R 1	A
	ATG M 3	ACG T 1	AAG K 3	AGG R 1	G
G	GTT V 3	GCT A 2	GAT D	GGT G	T
	GTC V	GCC A	GAC D 1	GGC G 4	C
	GTA V 1	GCA A 2(1)	GAA E 3	GGA G 2	A
	GTG V 1	GCG A 1	GAG E 3	GGG G 1	G

yellow minus charge

red plus charge

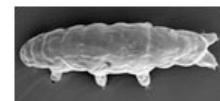
blue noncharge

green nonpolar

Number of tRNA coding genes  
 i = incomplete (fragmented/pseudo)  
 () = tRNAs with introns

## YOKOZUNA-1

91 tRNAs



8 incomplete genes  
 3 tRNAs with introns

## D. melanogaster (fly)

304 tRNAs



4 predicted pseudogenes  
 15 tRNAs with introns

## C. elegans (worm)

820 tRNAs



211 predicted pseudo genes  
 31 tRNAs with introns



rRNA : RNAmmer 1.2 (Lagesen K, et al. NAR 2007)

#	seqname	source	feature	start	end	score	+/-	frame	attribute
	Supercontig2	RNAHammer-1.2	rRNA	2426207	2426321	84.4	-	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	1651157	1651271	82.0	+	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	1851030	1851147	59.1	-	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	2160902	2161016	80.1	-	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	2481469	2481583	84.4	-	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	2594270	2594384	79.3	+	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	2601766	2601880	82.3	+	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	2656333	2656447	82.3	+	.	8s_rRNA
	Supercontig4	RNAHammer-1.2	rRNA	3100252	3100372	27.1	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	960792	960906	85.5	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2013470	2013584	84.4	-	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2126016	2126130	82.9	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2353291	2353405	84.4	-	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2496470	2496584	84.4	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2502639	2502753	84.4	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2710676	2710790	84.4	-	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2784306	2784420	81.7	+	.	8s_rRNA
	Supercontig5	RNAHammer-1.2	rRNA	2838691	2838805	46.3	-	.	8s_rRNA
	Supercontig6	RNAHammer-1.2	rRNA	3414023	3414140	78.2	-	.	8s_rRNA
	Supercontig11	RNAHammer-1.2	rRNA	421645	421759	75.3	-	.	8s_rRNA
	Supercontig11	RNAHammer-1.2	rRNA	959473	959587	83.2	-	.	8s_rRNA
	Supercontig11	RNAHammer-1.2	rRNA	1067823	1067937	84.4	-	.	8s_rRNA
	Supercontig60	RNAHammer-1.2	rRNA	2315	4203	1098.9	+	.	18s_rRNA
	Supercontig314	RNAHammer-1.2	rRNA	2	1196	150.8	-	.	18s_rRNA
	Supercontig362	RNAHammer-1.2	rRNA	102	1171	48.5	+	.	18s_rRNA
	Supercontig379	RNAHammer-1.2	rRNA	2	1258	476.1	-	.	18s_rRNA
	Supercontig403	RNAHammer-1.2	rRNA	126	1150	60.5	+	.	18s_rRNA
	Supercontig410	RNAHammer-1.2	rRNA	2	2564	125.7	-	.	18s_rRNA
	Supercontig606	RNAHammer-1.2	rRNA	29	1068	51.0	-	.	18s_rRNA
	Supercontig832	RNAHammer-1.2	rRNA	84	1206	70.6	+	.	18s_rRNA
	Supercontig943	RNAHammer-1.2	rRNA	1	1225	205.9	+	.	18s_rRNA
	Supercontig973	RNAHammer-1.2	rRNA	38	1104	59.6	+	.	18s_rRNA
	Supercontig1243	RNAHammer-1.2	rRNA	1	1238	224.7	-	.	18s_rRNA
	Supercontig1327	RNAHammer-1.2	rRNA	34	1156	69.3	+	.	18s_rRNA
	Supercontig1357	RNAHammer-1.2	rRNA	1	1150	111.5	-	.	18s_rRNA
	Supercontig1426	RNAHammer-1.2	rRNA	1	1152	90.8	+	.	18s_rRNA
	Supercontig1428	RNAHammer-1.2	rRNA	38	1121	168.8	+	.	18s_rRNA
	Supercontig1429	RNAHammer-1.2	rRNA	1	1138	69.3	+	.	18s_rRNA
	Supercontig1477	RNAHammer-1.2	rRNA	42	1145	221.5	+	.	18s_rRNA
	Supercontig1818	RNAHammer-1.2	rRNA	46	1163	112.1	+	.	18s_rRNA
	Supercontig1869	RNAHammer-1.2	rRNA	161	1152	21.9	+	.	18s_rRNA
	Supercontig1930	RNAHammer-1.2	rRNA	41	1224	257.0	+	.	18s_rRNA
	Supercontig2094	RNAHammer-1.2	rRNA	28	1125	193.3	+	.	18s_rRNA
	Supercontig2704	RNAHammer-1.2	rRNA	2	1280	274.1	+	.	18s_rRNA
	Supercontig2729	RNAHammer-1.2	rRNA	1	1171	147.1	+	.	18s_rRNA
	Supercontig2742	RNAHammer-1.2	rRNA	1	1147	38.5	+	.	18s_rRNA
	Supercontig2745	RNAHammer-1.2	rRNA	250	1287	53.7	+	.	18s_rRNA
	Supercontig2836	RNAHammer-1.2	rRNA	1	1155	136.6	-	.	18s_rRNA
	Supercontig3226	RNAHammer-1.2	rRNA	1	1135	457.3	-	.	18s_rRNA
	Supercontig164	RNAHammer-1.2	rRNA	2	1178	36.4	+	.	28s_rRNA
	Supercontig295	RNAHammer-1.2	rRNA	2	1294	220.9	+	.	28s_rRNA
	Supercontig1094	RNAHammer-1.2	rRNA	3	1250	118.8	+	.	28s_rRNA
	Supercontig1396	RNAHammer-1.2	rRNA	1	1173	80.3	-	.	28s_rRNA
	Supercontig1402	RNAHammer-1.2	rRNA	2	1175	31.8	+	.	28s_rRNA
	Supercontig1509	RNAHammer-1.2	rRNA	1	1212	44.1	+	.	28s_rRNA
	Supercontig2491	RNAHammer-1.2	rRNA	1	1167	54.1	-	.	28s_rRNA



# Genome browser (GMOD/GBrowse)

**Kumamushi Genome Project**

home database contact

6,001 kbp の範囲を Supercontig177 から表示、塩基番号 4,200 から 10,200

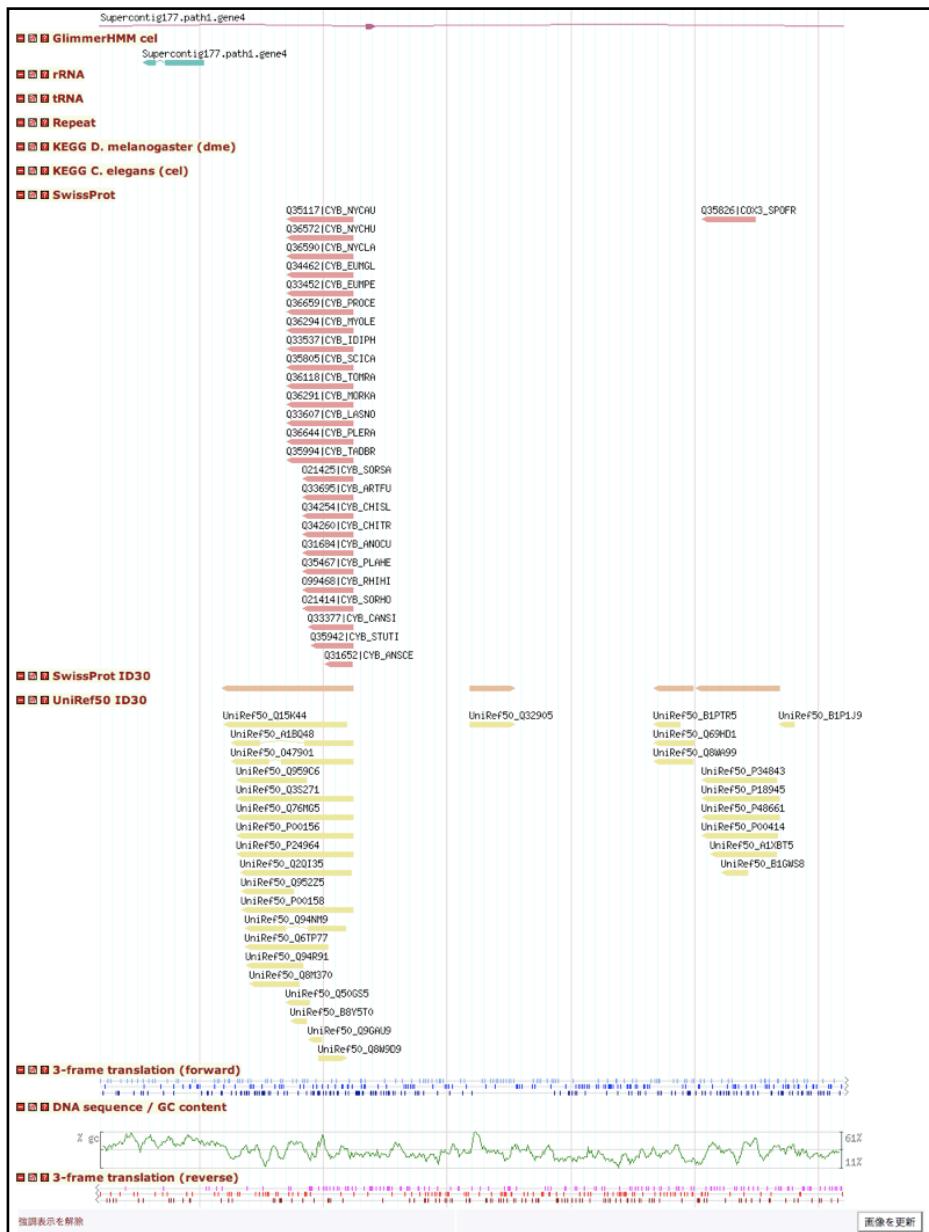
■ 説明  
配列の名前、遺伝子名、ゲノム上の位置、その他のランドマークなどを使って検索します。ワイルドカード文字として\*を使うことができます。ルーラー上でクリックした位置が中心になります。スクロールとズームボタンを使って拡大率と位置を変更します。

例: Supercontig0, Supercontig1, Supercontig2, Supercontig176.

[この表示をブックマーク] [独自アノテーションをアップロード] [バーを隠す] [これらの項目を共有] [この画像へのリンク] [高品質SVG画像] [ヘルプ] [リセット]

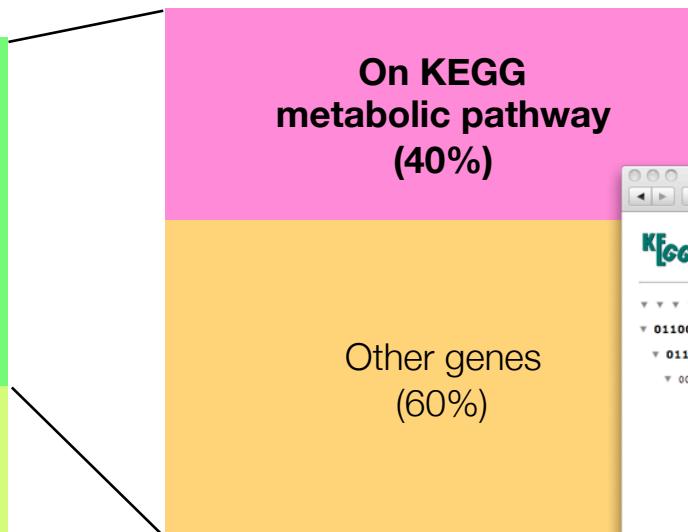
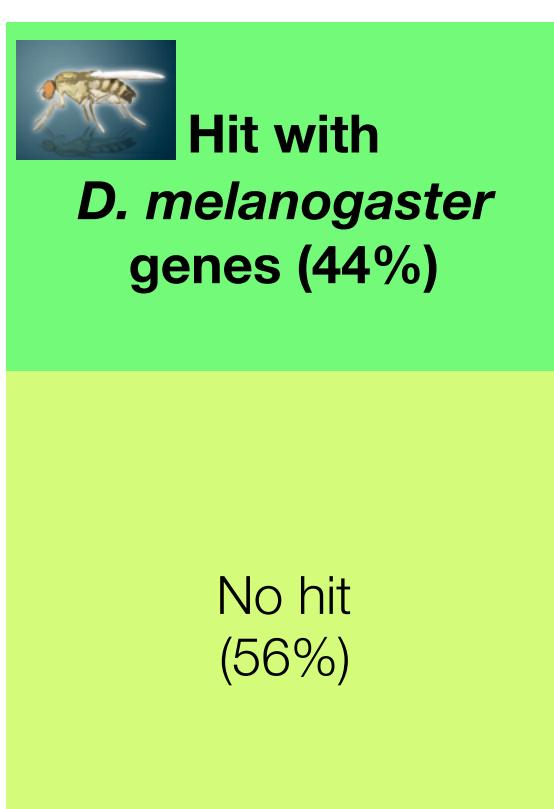
■ 検索  
ランドマークまたは領域:  
Supercontig177:4200..10200 検索  
データソース  
YOKOZUNA-1 Scaffold (20090409) - MySQL dev  
スクリール/ズーム: << << 表示 6,001 kbp >> >> 反転

■ オーバービュー  
Contig map  
rRNA  
tRNA  
領域ビュー  
Contig map  
Read coverage  
GC content  
詳細ビュー  
Kumamushi scaffolds  
Kumamushi contigs  
Kumamushi contigs (gap)  
Kumamushi reads  
GlimmerHMM dme  
GlimmerHMM cel  
rRNA  
tRNA



# 予測遺伝子のパスウェイ解析

14,388予測遺伝子のうち



6362 / 14388 (44%) *D. melanogaster* (1e-5)  
5835 / 14388 (41%) *C. elegans* (1e-5)  
5555 / 14388 (39%) *D. melanogaster* (1e-10)  
4884 / 14388 (34%) *C. elegans* (1e-10)

KEGG Orthology (KO)

01100 Metabolism

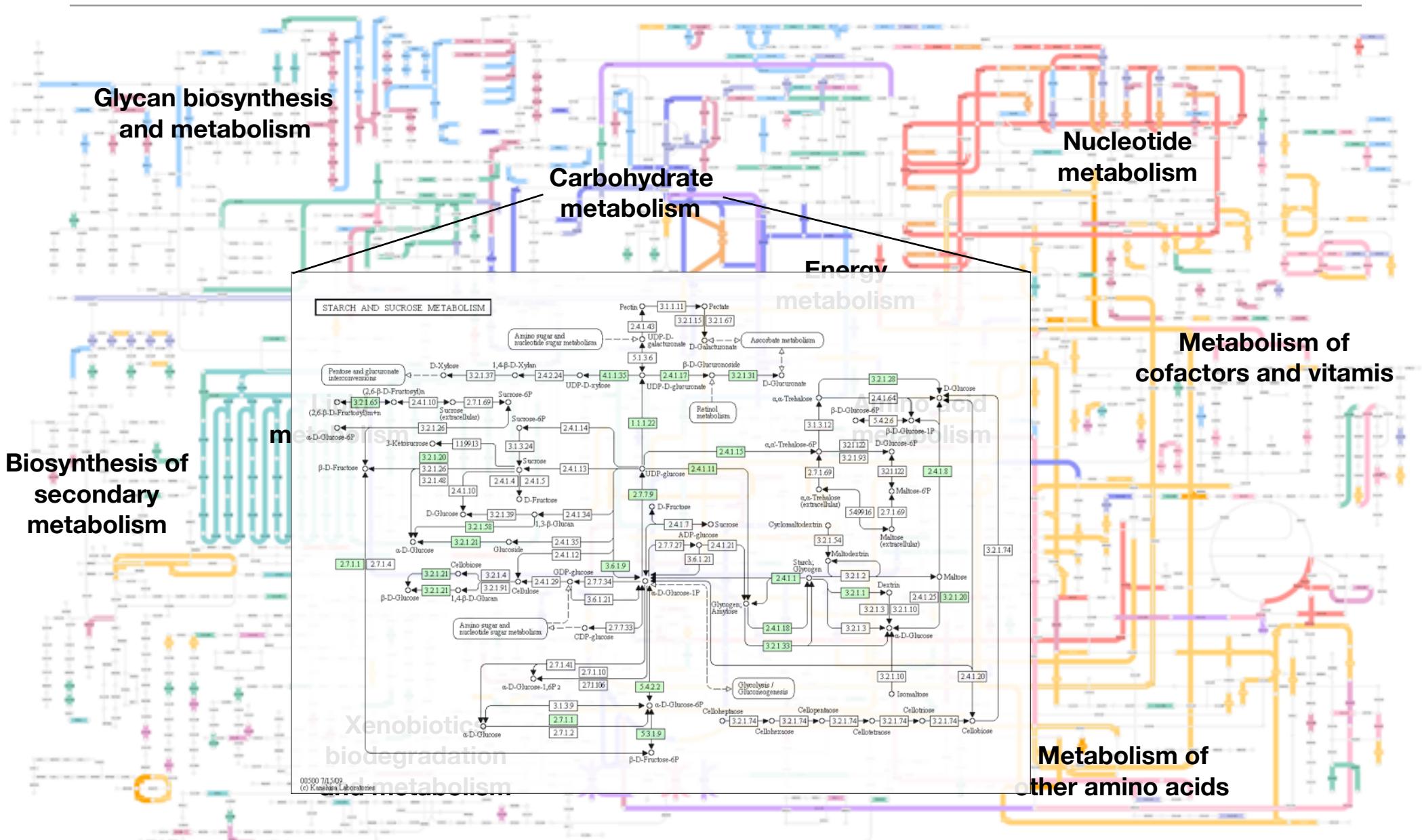
01101 Carbohydrate Metabolism

00010 Glycolysis / Gluconeogenesis [PATH:ko00010]

Supercontig9.74; KO0844 HK; hexokinase  
Supercontig9.17; KO0850 HK; hexokinase  
Supercontig3.177; KO0850 FTK; pkx; 6-P  
Supercontig45.63; KO3841 FBP; fbp; fructose-1,6-bisphosphatase  
Supercontig21.92; KO1623 ALDO; fbaB; fructose-bisphosphate aldolase  
Supercontig17.133; KO1803 TP1; tp1; triosephosphate isomerase  
Supercontig0.25; KO0134 GAPDH; gapA; glyceraldehyde-3-phosphate dehydrogenase  
Supercontig2.152; KO0927 PGK; pgk; phosphoglycerate kinase  
Supercontig14.86; KO1834 PGAM; pgm; phosphoglycerate mutase  
Supercontig11.99; KO0134 ENO; eno1; enolase [EC4.1.2.1]  
Supercontig45.1; KO1689 ENO; eno1; enolase [EC4.1.2.1]  
Supercontig28.12; KO0161 PDHA; pdha1; pyruvate dehydrogenase complex subunit alpha  
Supercontig69.41; KO0873 PK; pyk; pyruvate kinase  
Supercontig28.12; KO0161 PDHA; pdha1; pyruvate dehydrogenase complex subunit alpha  
Supercontig19.24; KO0627 DLAT; acetF; pdhc1; pyruvate dehydrogenase complex subunit epsilon  
Supercontig104.7; KO0382 DLD; lpd; pdhd; dihydrolipoyl dehydrogenase  
Supercontig7.123; KO0016 LDH; ldhA; L-lactate dehydrogenase  
Supercontig12.1; KO0160 E1.1.1.1; aldA; alcohol dehydrogenase  
Supercontig10.169; KO0128 E1.2.1.3; aldehyde dehydrogenase  
Supercontig74.19; KO0128 E1.2.1.3; aldehyde dehydrogenase  
Supercontig74.44; KO0128 E1.2.1.3; aldehyde dehydrogenase  
Supercontig9.135; KO1895 ACSS; acm; acetyl-CoA synthase  
Supercontig106.40; KO1835 E5.4.2.2; pgm; phosphoglucomutase  
Supercontig129.11; KO1835 E5.4.2.2; pgm; phosphoglucomutase  
Supercontig9.177; KO1596 E4.1.1.32; pckA; PEPCK; phosphoenolpyruvate carboxykinase (PEPCK)  
00020 Citrate cycle (TCA cycle) [PATH:ko00020]  
Supercontig9.182; KO1647 CS; gltA; citrate synthase  
Supercontig42.21; KO1644 ACLY; ATP citrate lyase (pro-S)  
Supercontig81.1; KO1681 ACO; acmA; aconitase hydratase  
Supercontig102.34; KO1681 ACO; acmA; aconitase hydratase  
Supercontig13.171; KO0039 IDH3; isocitrate dehydrogenase  
Supercontig10.22; KO0030 IDH3; isocitrate dehydrogenase  
Supercontig0.386; KO01644 OGDH; suca; 2-oxoglutarate dehydrogenase complex subunit  
Supercontig104.7; KO0382 DLD; lpd; pdhd; dihydrolipoyl dehydrogenase  
Supercontig11.56; KO1900 LSC2; succinyl-CoA synthetase  
Supercontig17.78; KO0239 sdhA; succinate dehydrogenase  
Supercontig17.78; KO0239 sdhA; succinate dehydrogenase  
:

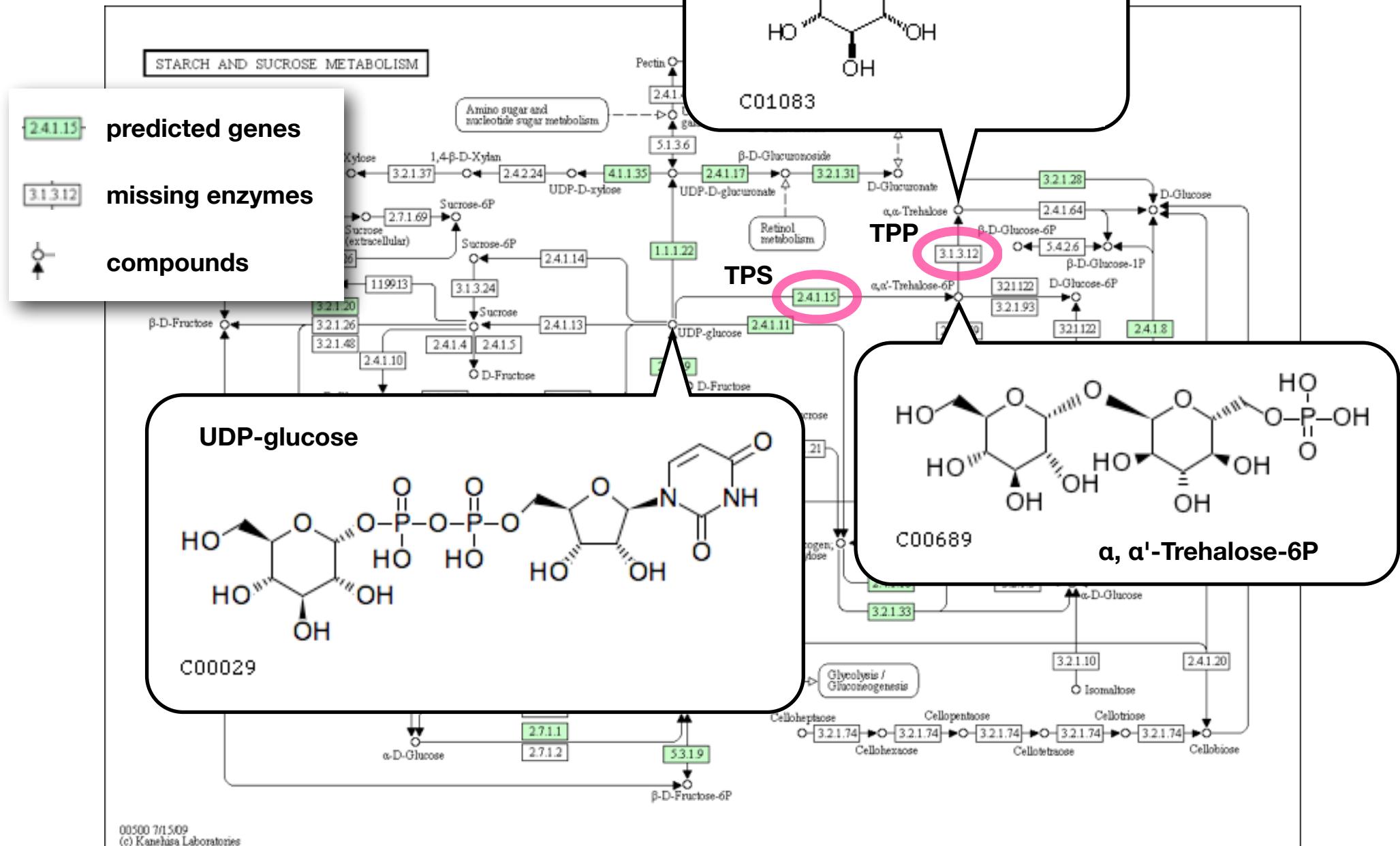


# Pathway reconstruction





# Trehalose metabolism



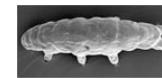


# TPS (trehalose-6-phosphate syntase) / TPP (trehalose phosphatase)

Query= Supercontig4.256  
(1153 letters)

Sequences producing significant alignments:

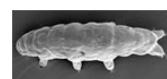
		Score	E	
		(bits)	Value	
dme:Dmel(CG4104	Tps1; Trehalose-6-phosphate syntase 1 (EC:2.4....	369	e-102	TPS
dme:Dmel(CG5177	CG5177 gene product from transcript CG5177-RA (...	56	1e-07	TPP
dme:Dmel(CG5171	CG5171 gene product from transcript CG5171-RC (...	53	7e-07	
dme:Dmel(CG13280	CG13280 gene product from transcript CG13280-R...	52	1e-06	
dme:Dmel(CG3609	CG3609 gene product from transcript CG3609-RA	52	2e-06	
dme:Dmel(CG3597	CG3597 gene product from transcript CG3597-RA	47	5e-05	



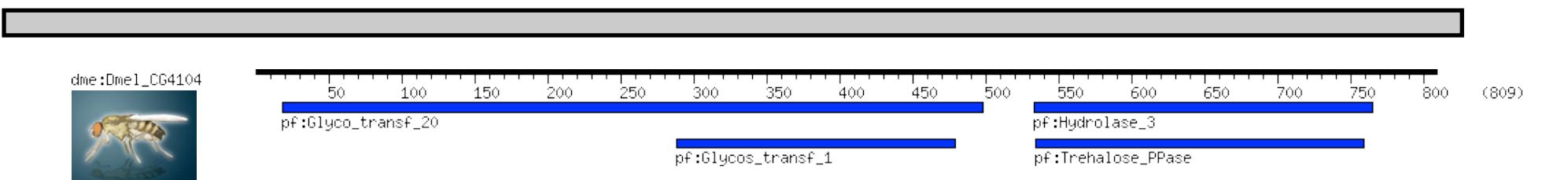
**SNAP predicted gene**



**D. melanogaster proteins**



**TPS1 : 1153aa (Supercontig4.256)**



**TPS1 : 809aa**



**TPP : 276aa**



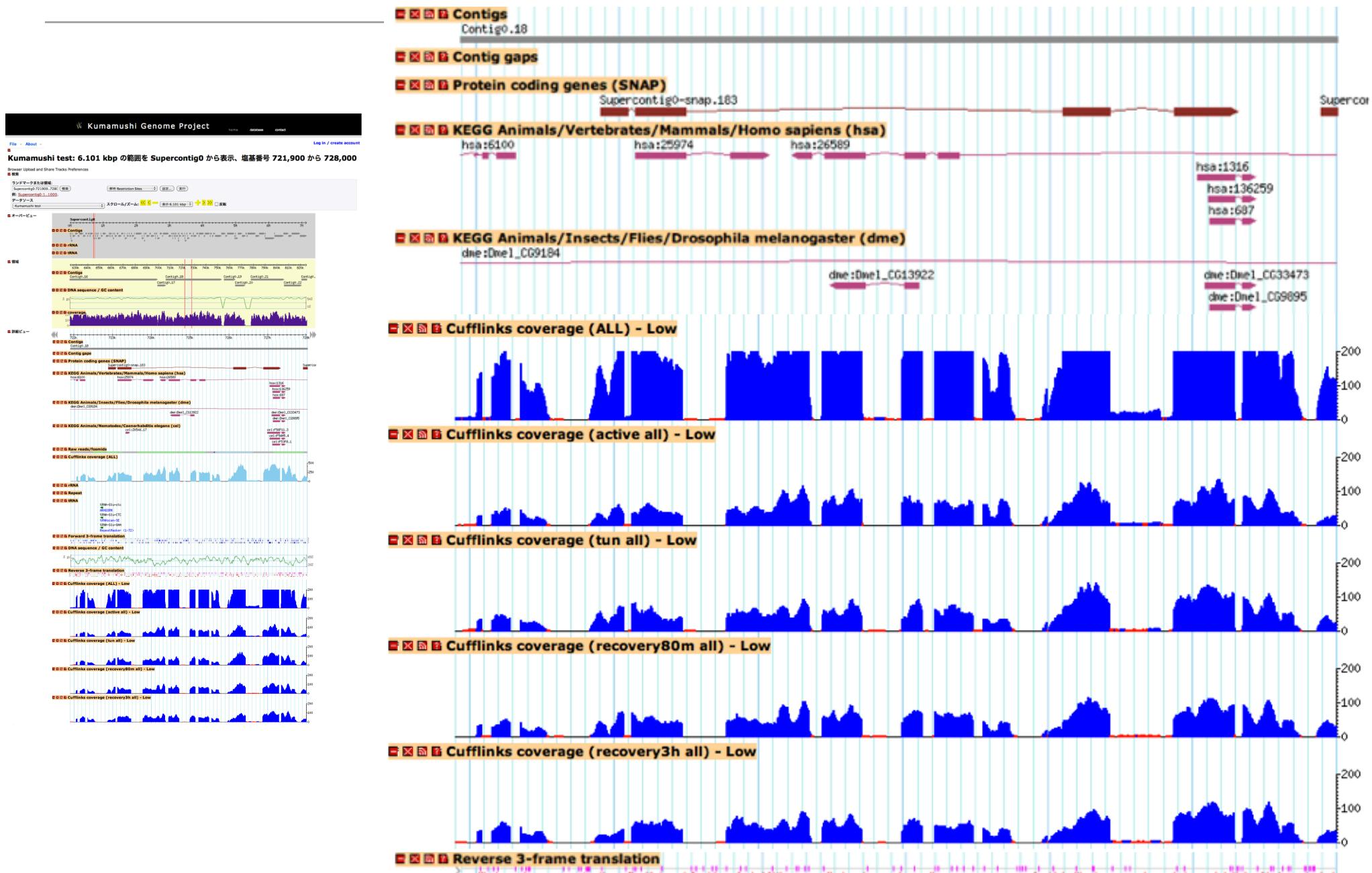
**TPP : 273aa**

# トランスクリプトームの発現変動解析

# ショートリードのマッピング



# Genome browser (GMOD/GBrowse2)



## ARTICLE

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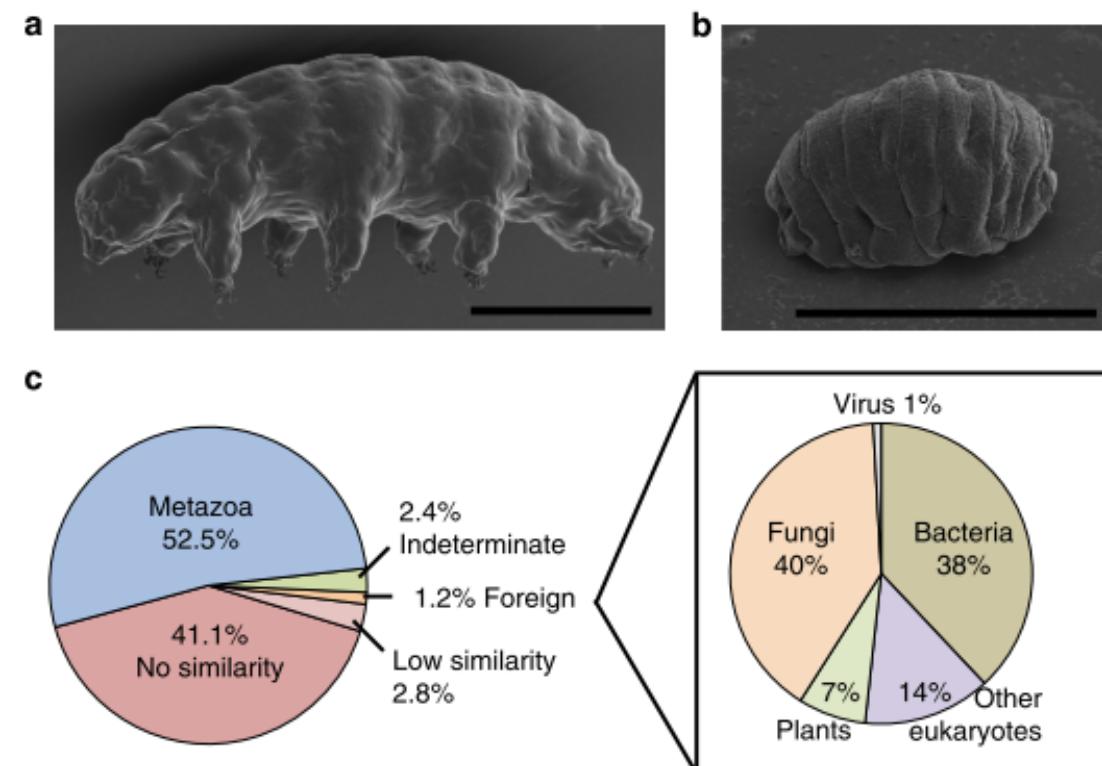
OPEN

# Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein

Takuma Hashimoto<sup>1,\*</sup>, Daiki D. Horikawa<sup>1,2,3,\*</sup>, Yuki Saito<sup>1</sup>, Hirokazu Kuwahara<sup>1,4</sup>, Hiroko Kozuka-Hata<sup>5</sup>, Tadasu Shin-I<sup>6</sup>, Yohei Minakuchi<sup>7</sup>, Kazuko Ohishi<sup>6</sup>, Ayuko Motoyama<sup>7</sup>, Tomoyuki Aizu<sup>7</sup>, Atsushi Enomoto<sup>8</sup>, Koyuki Kondo<sup>1</sup>, Sae Tanaka<sup>1</sup>, Yuichiro Hara<sup>9</sup>, Shigeyuki Koshikawa<sup>10,11</sup>, Hiroshi Sagara<sup>5</sup>, Toru Miura<sup>10</sup>, Shin-ichi Yokobori<sup>12</sup>, Kiyoshi Miyagawa<sup>8</sup>, Yutaka Suzuki<sup>13</sup>, Takeo Kubo<sup>1</sup>, Masaaki Oyama<sup>5</sup>, Yuji Kohara<sup>6</sup>, Asao Fujiyama<sup>7,14</sup>, Kazuharu Arakawa<sup>3</sup>, Toshiaki Katayama<sup>15</sup>, Atsushi Toyoda<sup>7</sup> & Takekazu Kunieda<sup>1</sup>

Tardigrades, also known as water bears, are small aquatic animals. Some tardigrade species tolerate almost complete dehydration and exhibit extraordinary tolerance to various physical extremes in the dehydrated state. Here we determine a high-quality genome sequence of *Ramazzottius varieornatus*, one of the most stress-tolerant tardigrade species. Precise gene repertoire analyses reveal the presence of a small proportion (1.2% or less) of putative foreign genes, loss of gene pathways that promote stress damage, expansion of gene families related to ameliorating damage, and evolution and high expression of novel tardigrade-unique proteins. Minor changes in the gene expression profiles during dehydration and rehydration suggest constitutive expression of tolerance-related genes. Using human cultured cells, we demonstrate that a tardigrade-unique DNA-associating protein suppresses X-ray-induced DNA damage by ~40% and improves radiotolerance. These findings indicate the relevance of tardigrade-unique proteins to tolerability and tardigrades could be a bountiful source of new protection genes and mechanisms.

<sup>1</sup>Department of Biological Sciences, Graduate School of Science, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan. <sup>2</sup>Institute of Environmental Earth Science, Hokkaido University, Kita 8, Nishi 5, Kita-ku, Sapporo, Hokkaido 060-0810, Japan. <sup>3</sup>Institute of Keio University, Mizukami 246-2, Kakuganji, Tsuruoka, Yamagata 997-0052, Japan. <sup>4</sup>Department of Biological Sciences, Graduate School of Biotechnology, Tokyo Institute of Technology, 2-12-1 Ookayama, Meguro-ku, Tokyo 152-8550, Japan. <sup>5</sup>Medical Proteomics Laboratory, National Institute of Technology, Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan. <sup>6</sup>Genome Biology Laboratory, National Institute of Genetics, 1111 Yata, Mishima, Shizuoka 411-8540, Japan. <sup>7</sup>Comparative Genomics Laboratory, National Institute of Genetics, 1111 Yata, Mishima, Shizuoka 411-8540, Japan. <sup>8</sup>Laboratory of Molecular Radiobiology, Graduate School of Medicine, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan. <sup>9</sup>Phyloinformatics Unit, RIKEN Center for Life Science Technologies, 2-2-3 Minatojima-minami, Chuo-ku, Kobe, Hyogo 650-0037, Japan. <sup>10</sup>Ecological Genetics, Graduate School of Environmental Science, Hokkaido University, Kita 8, Nishi 5, Kita-ku, Sapporo, Hokkaido 060-0810, Japan. <sup>11</sup>The Hakubi Center for Advanced Research and Graduate School of Science, Kyoto University, Kitashirakawa-oiwake-cho, Sakyo-ku, Kyoto 606-8501, Japan. <sup>12</sup>Laboratory of Extremophiles, Department of Applied Life Sciences, School of Life Sciences, Tokyo University of Pharmacy and Molecular Sciences, 1432-1 Horinouchi, Hachioji, Tokyo 192-0392, Japan. <sup>13</sup>Department of Computational Biology and Medical Science, Graduate School of Frontier Sciences, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan. <sup>14</sup>Department of Genetics, SOKENDAI (The Graduate University for Advanced Studies), 1111 Yata, Mishima, Shizuoka 411-8540, Japan. <sup>15</sup>Database Center for Life Science, 178-4-4 Wakashiba, Kashiwa, Chiba 277-0052, Japan. \*Authors contributed equally to this work. Correspondence and requests for materials should be addressed to T.K. (email: kunitada@nig.ac.jp).



ゲノムひろば 2008 特別付録

## クマムシを探してみよう

Presented by クマムシゲノムプロジェクト  
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採集用のビニール袋を持ってお散歩にいこうね



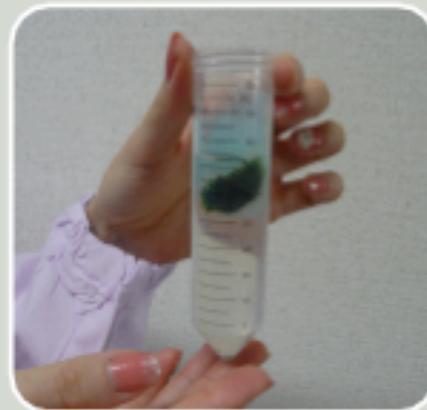
晴れた日にコケを取ってきます  
意外と、よく乾いたコケが狙い目です。



採集袋にいれて持って帰りましょう  
コケを取った場所と日付を書いておこう。



メッシュに包んで水に戻します  
試験管などの間に水を入れて浸します。



数時間くらい放置します  
クマムシがコケから落ちて底に溜まるよ。



庭の水をスポットで吸って顕微鏡で見よう  
理科の先生に実体顕微鏡を借りて見てね。



いた！トグクマムシ！かっこいいー  
ほかにも線虫やワムシが見つかるよ。



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---

- Material preparation
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  - T. Shin-I (NIG)
  - K. Ohishi (NIG)
  - A. Motoyama (NIG)
  - T. Aizu (NIG)
  - Y. Kohara (NIG)
  - A. Fujiyama (NIG)
- Genome analysis
  - K. Arakawa (Keio U.)
  - Y. Hasebe (Keio U.)
  - N. Kido (Keio U.)
  - M. Kanehisa (Kyoto U.)



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