

5th International Workshop on Regulatory Approaches for Agricultural Applications of Animal Biotechnologies



近畿大学
KINDAI UNIVERSITY



京都大学
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Application of genome editing technology in marine fish aquaculture in Japan



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Genome-edited food products for which notification has been completed in Japan

No.	Name	Date of Notification	Notifiers	Market launch date
1	Tomatoes with partially modified glutamic acid decarboxylase gene to increase GABA content	December 11, 2020	Sanatech Seed Co.,Ltd.	September 1, 2021
2	Increased edible portion red sea bream	September 17, 2021	Regional Fish Institute, Ltd.	October 1, 2021
	Additin of strains	December 5, 2022	Regional Fish Institute, Ltd.	January 1, 2023
3	High-growth tiger puffer	October 29, 2021	Regional Fish Institute, Ltd.	November 1, 2021
	Additin of strains	December 5, 2022	Regional Fish Institute, Ltd.	January 1, 2023
4	PH1V69 CRISPR-Cas9 waxy corn	March 20, 2023	Corteva Japan Ltd.	undecided
5	Tomatoes with partially modified glutamic acid decarboxylase gene to increase GABA content	July 27, 2023	Sanatech Seed Co.,Ltd.	undecided
6	High-growth Japanese flounder	October 24, 2023	Regional Fish Institute, Ltd.	undecided

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Disruption of *mstn* in Red sea bream

Target Fish :

Red sea bream
(*Pagrus major*)

Target gene :

myostatin gene
(*mstn*)

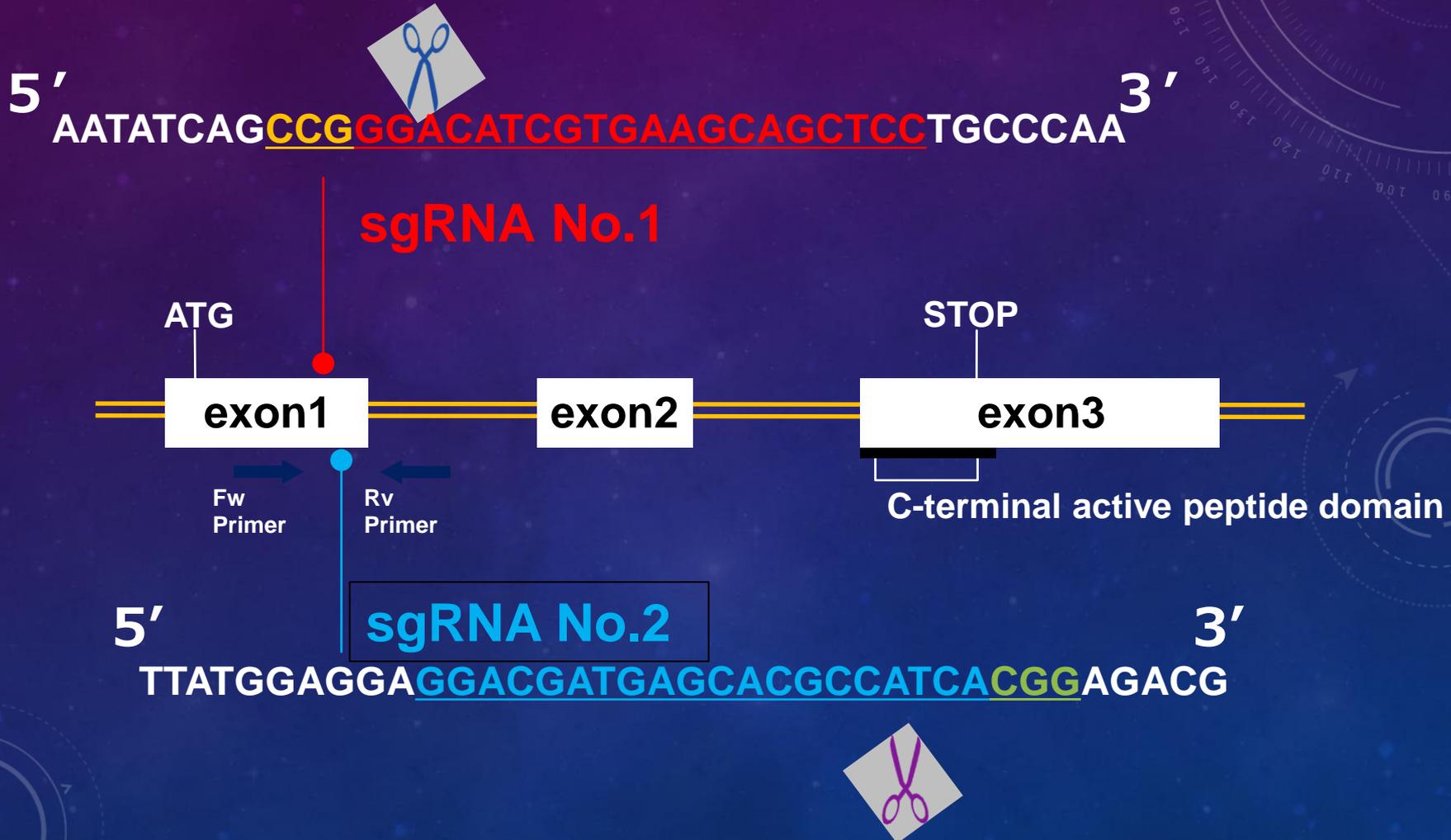
Genome editing tool :

CRISPR-Cas9 system

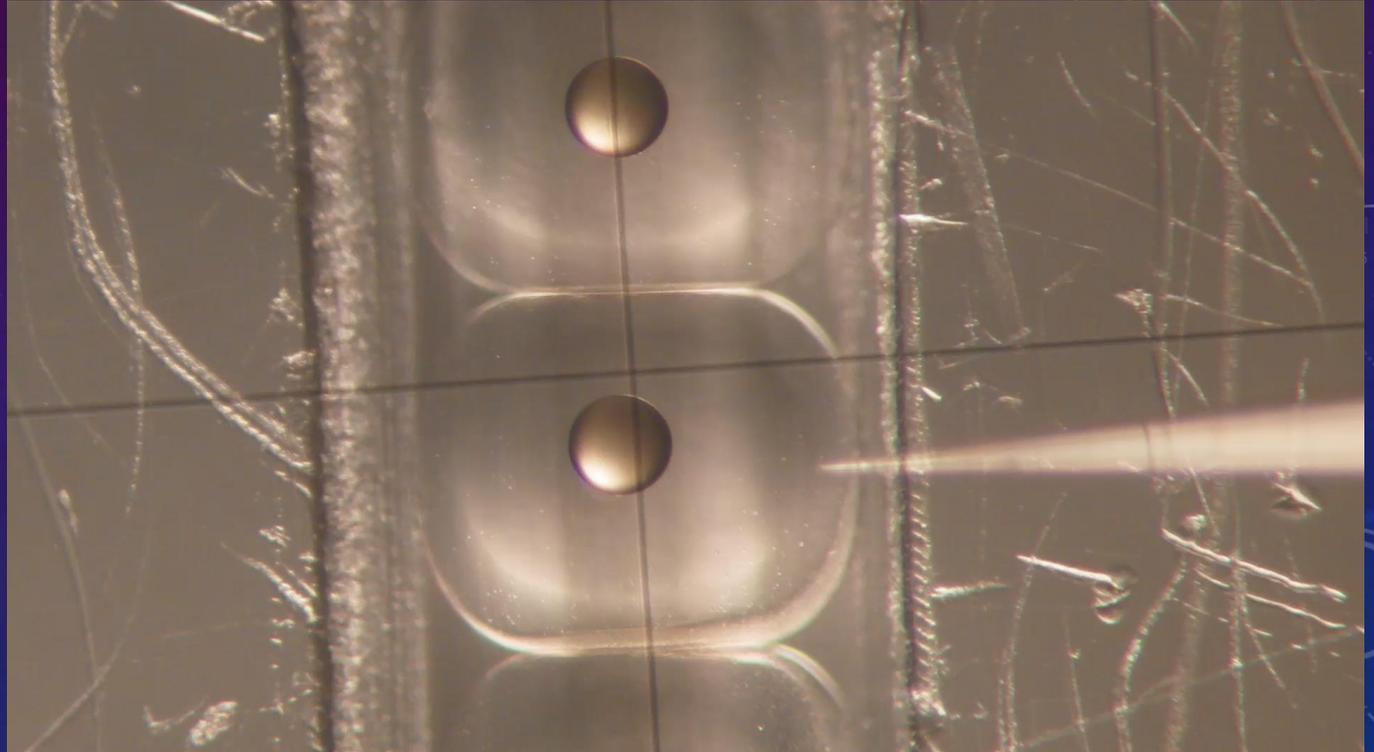
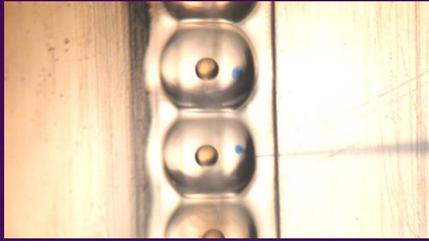


Design CRISPR-Cas9 (sgRNA)

Red sea bream *myostatin* gene



Microinjection



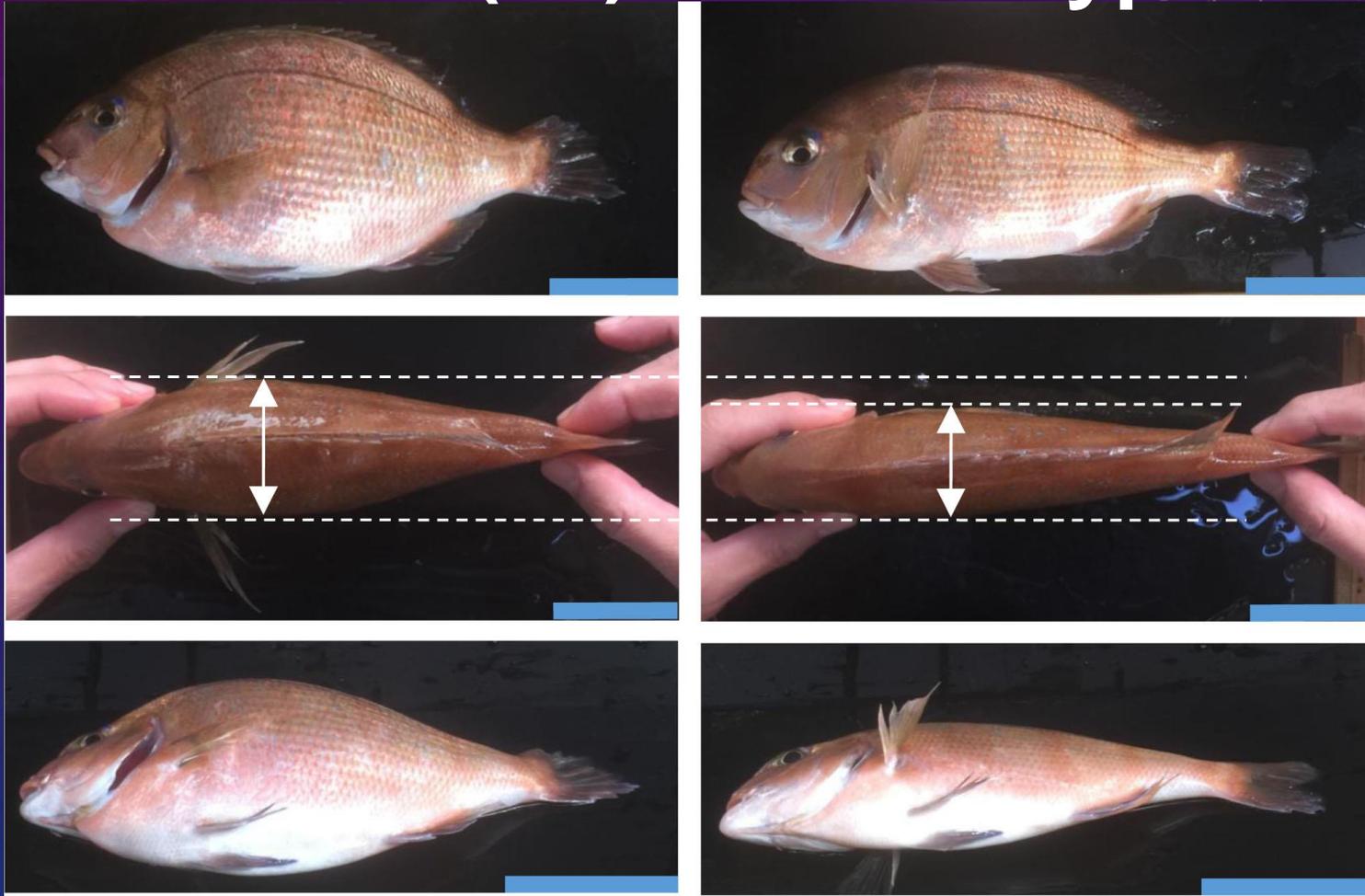
sgRNA : 25ng/ul
Cas9 RNA: 100ng/ul

1,000-3,000 eggs / person / day

Increased muscle mass in 2nd generation

mstn KO (F2)

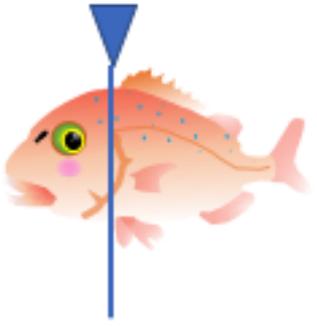
Wildtype



329-days old

Kishimoto et al. (2018) *Aquaculture* 495, 415–427

Increased muscle mass in 2nd generation



1 year old

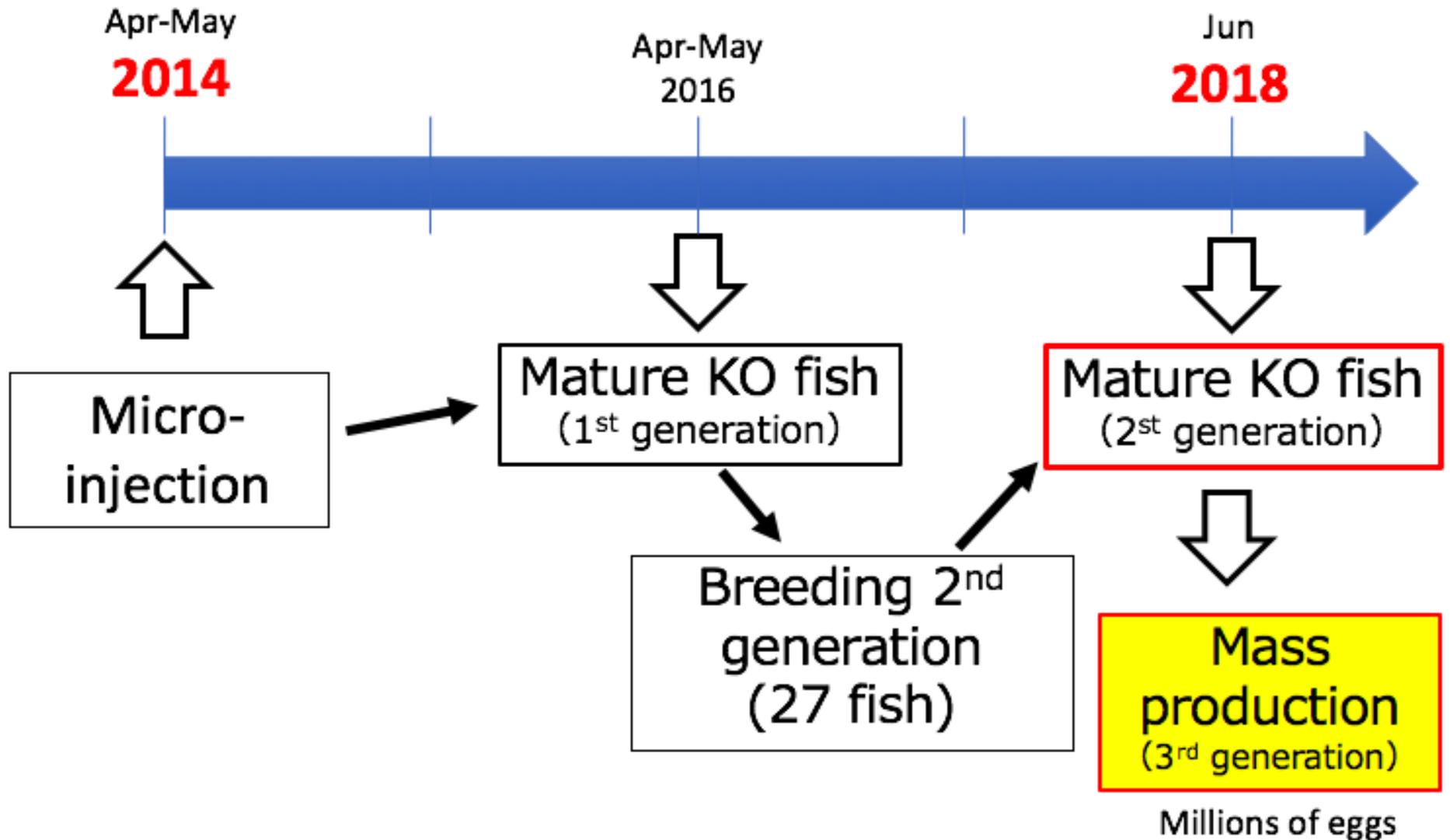
mstn KO (F2)

Wildtype



20% increase in edible portion !

4 years to establish new breed



4 years to establish new breed

Apr-May



Apr-May



Jun

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n)

gs

Toward distribution of genome-edited fish

Estimated Food Safety Risks for Genome-Edited Red Sea Bream

1. Residual genome editing tool (Cas9, sgRNA)
2. Effects of off-target mutations
3. Biosynthesis of new proteins due to partial deletion of target genes
4. Changes in metabolite composition due to loss of function of the target gene

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Detection of Cas9 and sgRNA, and the DNA sequences used in their synthesis



Genome size of red sea bream:
about 800Mb

Analysis of about 30 Gb of the genome of
genome-edited fish
(About 40 times as many bases as the
genome of the sea bream)

NextSeq 550

**16.25-120Gb
Output range**

↓
No Cas9, sgRNA, etc. detected

↓
No genome editing tools remain

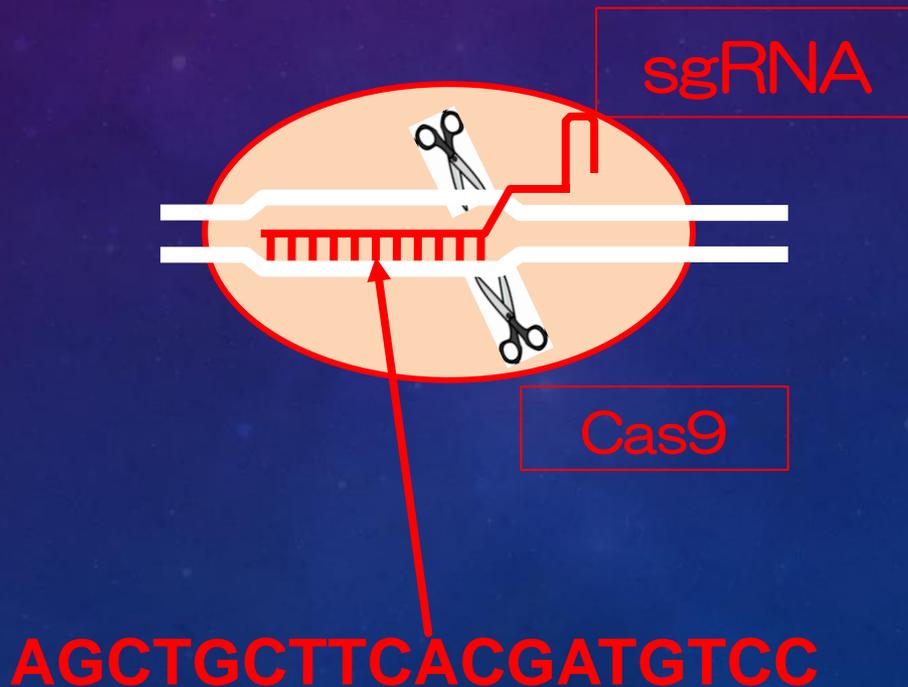
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2. Effects of off-target mutations

In the case of the CRISPR-Cas9 system, it recognizes and cleaves one part (18 bases) of the target gene, but it is possible that it may incorrectly cleave a similar sequence.



Example of off-target analysis

Targeted DNA sequence	Number of mismatched bases from the original sequence	Changes due to genome editing
AGCTGCTTCACGATGTCC	Original sequence	-
AG G TGCTTCACG C TGTCC	2	Not detected
AGCTGCTTCAG G ATGT C A	2	Not detected
A A CTG G TTCACGATGTCC	2	Not detected
AGCTGCTTCAT T GATG A CC	2	Not detected
A T CTG C TCACGATGTCC	2	Not detected
AGC - GCTTCACG G TGTCC	2	Not detected
AGCTGC - TCA A GATGTCC	2	Not detected
A T CTGCTTCACG - TGTCC	2	Not detected
AGC A GCTTCACGATG T C -	2	Not detected
AGCTGCTTCA - G - TGTCC	2	Not detected
AGC -- CTTCACGATGTCC	2	Not detected
AGCTGCTTCAC - A - GTCC	2	Not detected
AGCTGCTTTT C AC - GATGTCC	2	Not detected
AGCTGCT G TCACGA - GTCC	2	Not detected

Toward distribution of genome-edited fish

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Allergen analysis of genome-edited fish 14 base deleted individuals (-14)

50

WT: MHPSQIVLYL SLLIVLGPVV LSDQETQQQQ QQQQQQQPSA TSPEDTEQCA

-14: MHPSQIVLYL SLLIVLGPVV LSDQETQQQQ QQQQQQQPSA TSPEDTEQCA

WT: TCEVRQQIKT MRLNAIKSQI LSKLRMKEAP NISRDIVKQL LPKAPPLQQI₁₀₀

-14: TCEVRQQIKT MRLNAIKSQI LSKLRMKEAP NISRDIVKQL LPKAPPLQQI

WT: LDQYDVLGDD NRDVVMEEDD EHAITETIMM MATEPESVVQ VDGEPRCCFF

-14: LDQYDVLGDD NRDVVMEEDD EHDYDDGH

128

150

WT: SFTQKIQANR IVRAQLWVHL RASDEATTVF LQISRLMPVT DGNGHIHIRS

LKIDVNAGVG SWQSIDVKQV LSVWLRQPET NWGIQINAFD SRGNDLAVTS

AEPGEDGLQP FMEVKIŞEGP KRVRRDSGLD CDENSPE SRC CRYPLTVDFE

DFGWDWIIAP KRYKANYCSG ECEYMHLQKY PHTHLVNKAN PRGSAGPCCT

PTKMSPINML YFNRKEQIIY GKIPSMVVDR CGCS

388

Allergen Prediction Results for Genome-Edited red sea bream

Table 1. Full-length sequence comparison (wild type retrieved up to 150 amino acids)

	-14 (1-128 a.a.)	WT (1-150 a.a.)
FAO/WHO (>35% in 80 a.a)	VL(1)GPVVLS(1)D QE(1)TQQQQQQQ QQQQP (gliadin)	VL(1)GPVVLS(1)D QE(1)TQQQQQQQ QQQQP (gliadin)

Table 2. Comparison of the new amino acid sequence and its upstream 10 amino acids as a query

	-14 (10+new a.a.)	WT
FAO/WHO (6 a.a exact match)	No	-
Motif-based(ADFS)	No	-
Epitope search (ADFS)	No	-

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Transcriptome and metabolome analysis

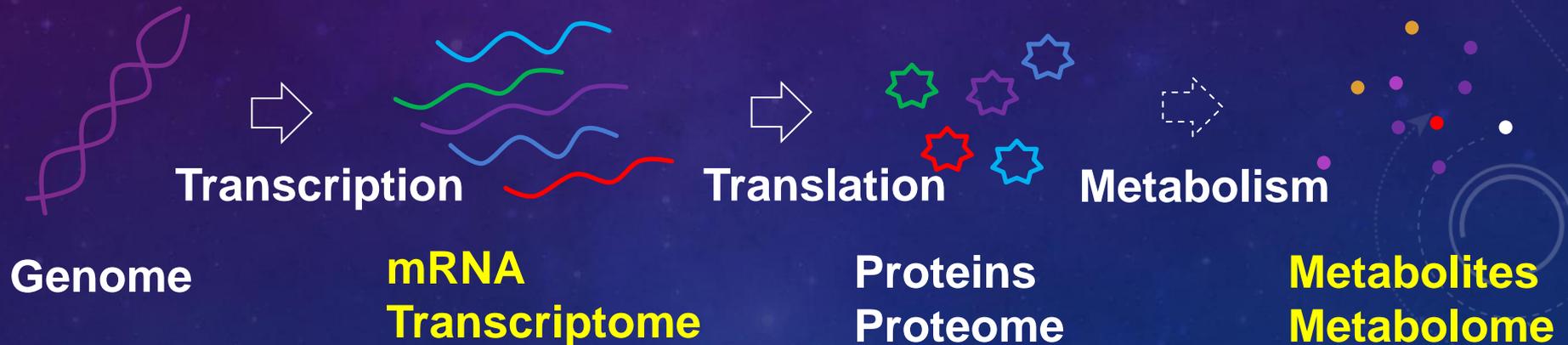
① Transcriptome analysis of skeletal muscle

(3 mutant fish, 3 WT fish)

② Metabolome analysis of skeletal muscle

(6 mutant fish, 3 WT fish)

Proteins
Nucleic acids
Sugars
Lipids, etc.



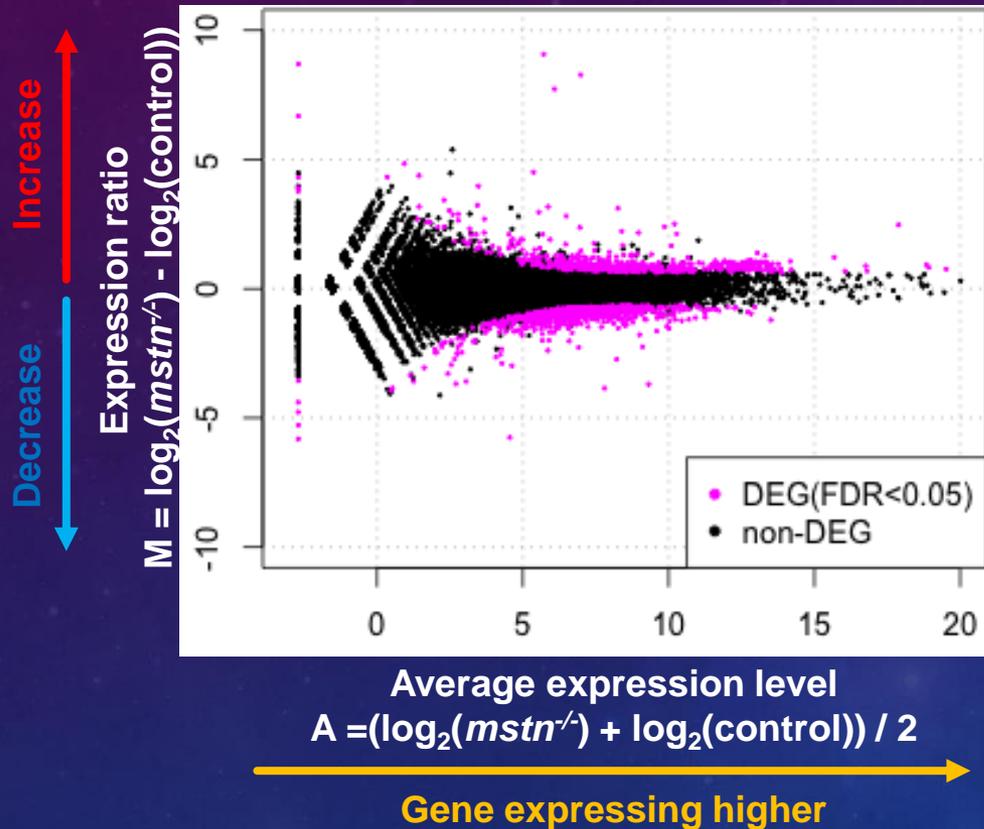
Sample

Left side dorsal muscle: Transcriptome 50mg, Metabolome 1 g

Transcriptome analysis

— Comparison between WT and Mutant fish —

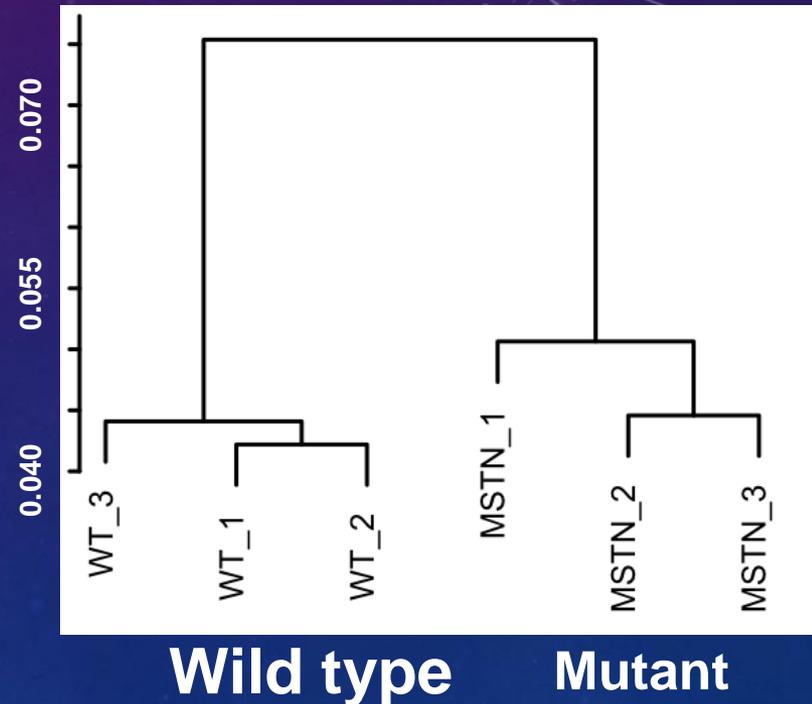
MA plot



※ DEG : Differentially Expressed Gene
FDR < 0.05 ; 1159
FDR < 0.1 ; 1718
total genes ; 22878

Hierarchical clustering

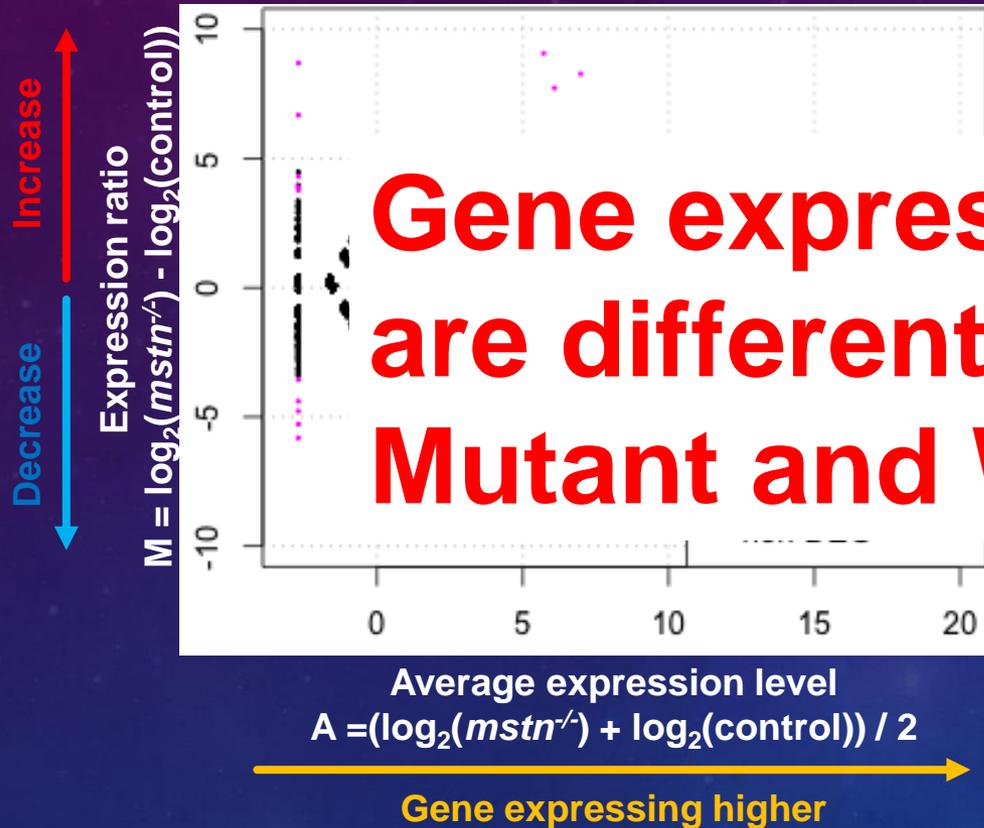
Using R; Spearman's rank correlation coefficient and ward's method



Transcriptome analysis

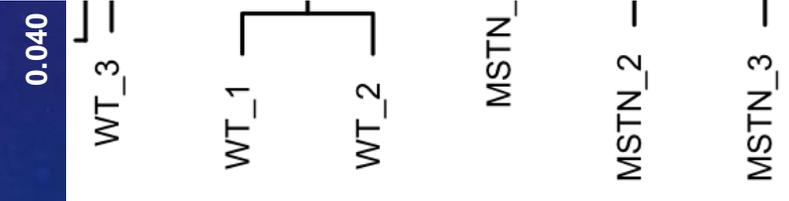
— Comparison between WT and Mutant fish —

MA plot



Hierarchical clustering

Using R; Spearman's rank correlation coefficient and ward's method



Wild type

Mutant

Gene expression patterns are different between Mutant and WT fish.

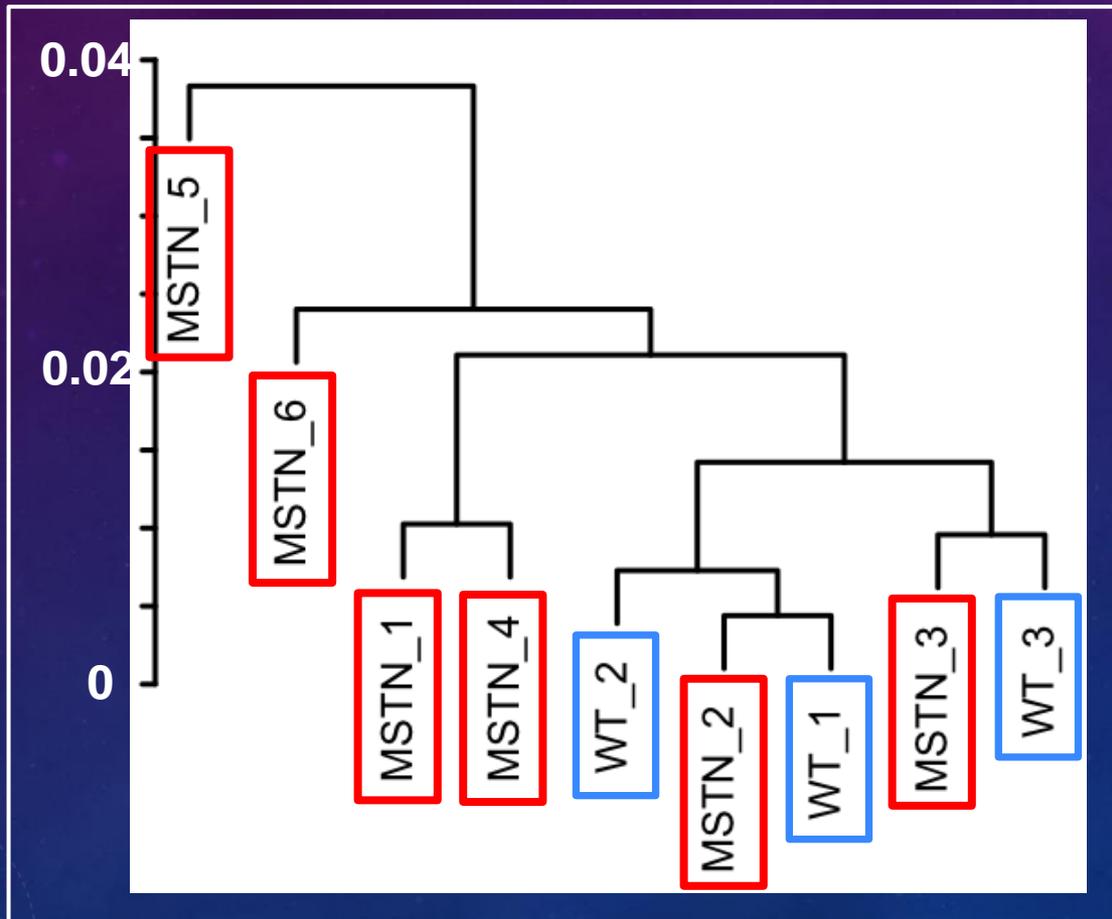
※ DEG : Differentially Expressed Gene
FDR < 0.05 ; 1159
FDR < 0.1 ; 1718
total genes ; 22878

Metabolome analysis

— Comparison between WT and Mutant fish —

Hierarchical clustering

Using R; Spearman's rank correlation coefficient and ward's method



MSTN 1-3: -14/-14

MSTN 4-6: -14/-8

WT and mutant
fish not separated



**There is no
clear
difference
between them.**



JP | EN



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Genome Editing

– from “the Unexpected” to “the Expected”

Genome editing is a core technology to realize high-speed breeding. The technology enables us to fast forward the current breeding process by promoting natural changes on DNA.



Toward distribution of genome-edited fish

Rules for the Use of Genome-Edited Foods and Relevant Ministries and Agencies

1. Whether or not the organism is genetically modified (the Ministry of the Environment)
2. Characteristics of the organism and how to cultivate it (the Ministry of Agriculture, Forestry and Fisheries)
3. Safety as food (the Ministry of Health, Labour and Welfare)
4. Labeling (the Consumer Affairs Agency)

Toward distribution of genome-edited fish

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Whether or not the organism is genetically modified (Ministry of the Environment, 2019)

Is the organism introduced with extracellularly processed nucleic acids (DNA and RNA)?

YES

Is the organism confirmed to have no residual transferred nucleic acid or its replicates?

NO

Genetically modified organism
(Subject to regulation)

YES

Not a genetically modified organism
(Not subject to regulation)

NO

Toward distribution of genome-edited fish

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- 4. Labeling (the Consumer Affairs Agency)**

Prior consultation and notification to the Ministry of Agriculture, Forestry and Fisheries (2021)

- Characteristics of the organism or not
- Genetically modified organisms
- Production methods and its process
- Rearing facilities and methods
- Use as a material for feed

Hearing from academic experts

Submit additional information if needed

Verify additional information

Determined to be applicable for notification

Submission of information form and report of when to start shipping the product (notification)

Toward distribution of genome-edited fish

Rules for the Use of Genome-Edited Foods and Relevant Ministries and Agencies

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- 4. Labeling (the Consumer Affairs Agency)**

Prior consultation and notification to the Ministry of Health, Labour and Welfare (2019)

- Production methods and its process
- Genetically modified organisms or not
- Presence of off-target mutations
- Presence of allergens
- Effect on metabolism

Expert Committee on Genetically Modified Foods, etc.

If necessary, the Food Safety Commission discuss the matter

Determined to be applicable for notification

Submission of information form and report of when to start shipping the product (notification)

Toward distribution of genome-edited fish

Rules for the Use of Genome-Edited Foods and Relevant Ministries and Agencies

1. Whether or not the organism is genetically modified (the Ministry of the Environment)
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4. Labeling (the Consumer Affairs Agency)

Labeling (Consumer Affairs Agency, 2019)

The items notified to the Ministry of Health, Labour and Welfare are those for which the business operator provides information on labeling, etc. to the consumer.

(obligation to make effort)

Not subject to labeling under the Food Labeling Standard at this stage

(No obligation to label)

ゲノム編集で品種改良 身の量1.2倍のマダイ 販売開始へ 京都

2021年9月17日 18時41分

遺伝子を自在に操作できる「ゲノム編集」の技術を使って品種改良し、身の量を増やしたマダイについて、京都市のベンチャー企業が流通の際に求められる「ゲノム編集食品」としての届け出を厚生労働省に行いました。

会社では試験販売の受け付けを始めたということで「ゲノム編集食品」の販売は国内で2例目です。



届け出が行われたのは、ゲノム編集の技術を使って、身の量を通常よりおよそ1.2倍に増やしたマダイで、京都市のベンチャー企業「リージョナルフィッシュ」が京都大学や近畿大学と共同で開発しました。

•Press Conference on Completion of Notification (17 Sep 2021)

•This was the first case in the world where a government authorized the distribution of genome-edited fish.

世界初！ゲノム編集技術を利用して開発された「22世紀鯛」を多くの人に届けたい！

リージョナルフィッシュ株式会社

フード・飲食店

京都府

コロナサポートプログラム対象



リージョナルフィッシュ株式会社は、ゲノム編集技術を利用した品種改良法「ナノジーン育種」によって、日本の水産業の再興・世界のタンパク質不足の解決に挑んでいます！この度私たちが開発した、日本の水産業を救う可能性を秘めた可食部増量マダイ「22世紀鯛」を、食卓で味わってみませんか？

シェア ツイート LINEで送る URLコピー QRコード 埋め込み

¥ 現在の支援総額

3,205,500円

320%

目標金額は1,000,000円

支援者数

231人

募集終了まで残り

終了

このプロジェクト
31人の支援により
9-30に募集を終了

Online store

Regional Fish Online

HOME 目指す未来 当社の技術 ブランドライン ふるさと納税 お問い合わせ



22世紀鯛

詳細はこちら

商品一覧

- ・送料は全国一律で1,500円です。
- ・配送日のご指定は、カートページにてご指定いただけます。
- ・領収書の発行をご希望の方は、[お問い合わせフォーム](#)よりお問い合わせください。



【新登場】22世紀ふくx下鴨茶寮 黄沢セット



22世紀ふく てっちりセット ¥3,290.1円から



22世紀鯛 昆布締めセット【京都料亭コラボ】

Contributors

Kindai University : Yohei WASHIO

Kyoto University : Masato KINOSHITA

**Regional fish institute: Mitsuki Ohama
Kenta KISHIMOTO
Tadanori UMEKAWA**

National Institute of Genetics : Atsushi TOYODA

**Japan Fisheries Research
and Education Agency : Yasutoshi YOSHIURA**

**All stuffs and students involved in the selective breeding
and genome editing of red sea bream in Kindai University**

A close-up photograph of a fish's head, focusing on its eye and scales. The scales are a mix of light brown and grey, with a prominent vertical line running down the side of the head. The eye is large and dark, with a visible iris and pupil. The background is a soft, out-of-focus blue, suggesting an underwater environment. The image is framed by a dark blue border with faint white circular patterns and a scale-like graphic in the top right corner.

Thank you for your attention!