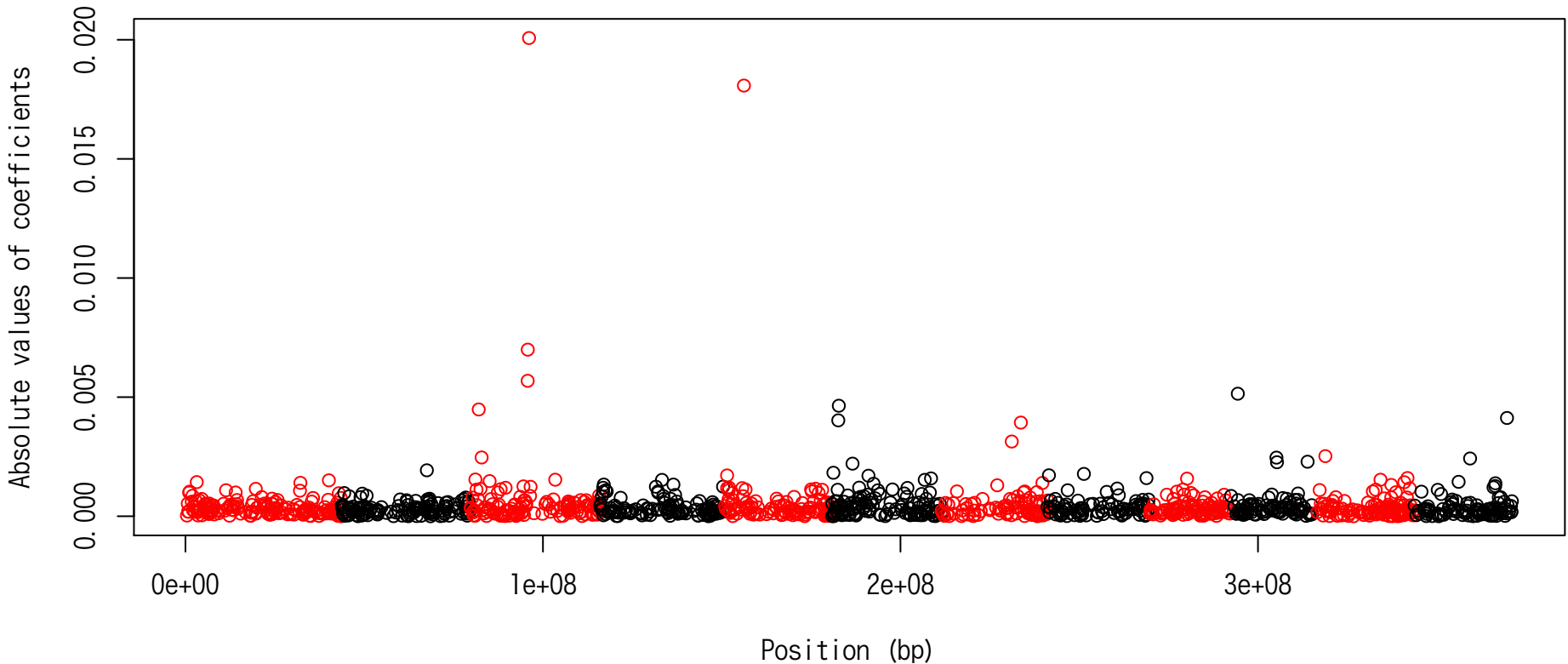


2017専門実習 課題

種子の縦横比・粒長・粒幅のGWASの結果について、
原因 遺伝子を探索を行い、
その遺伝子の役割について考察してください。

チュートリアルであつかったGWAS 縦横比

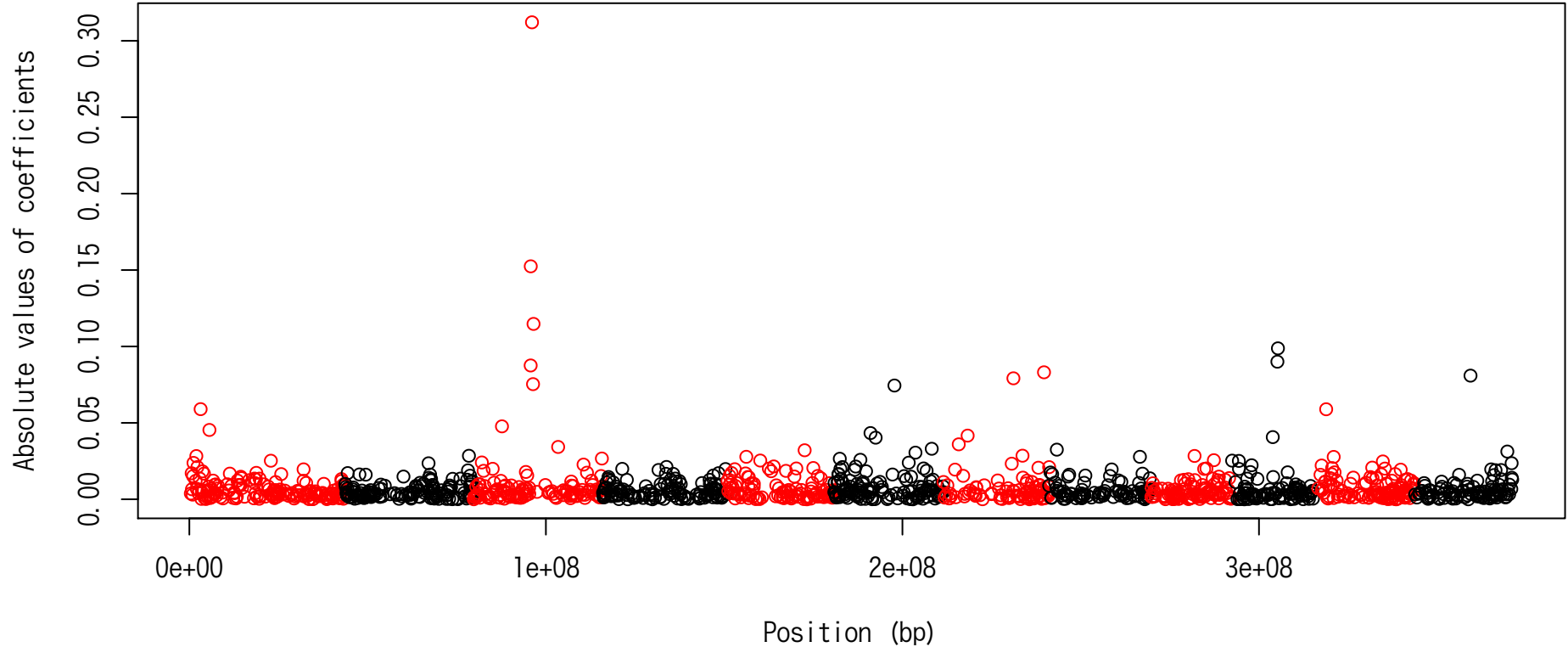
GWAS - BayesB - Seed. width/Seed. length



| marker | chr | pos | abs.fmBB.ETA.MRK.b. |
|------------|-----|------------|---------------------|
| id3008333 | 3 | 16,621,452 | 0.020073506 |
| id5002699 | 5 | 5,273,692 | 0.0180782 |
| id3008139 | 3 | 16,272,206 | 0.006993685 |
| id3008127 | 3 | 16,247,306 | 0.005685386 |
| id10000498 | 10 | 2,043,939 | 0.00514448 |
| id6001632 | 6 | 2,160,757 | 0.004639277 |

GWAS Seed length

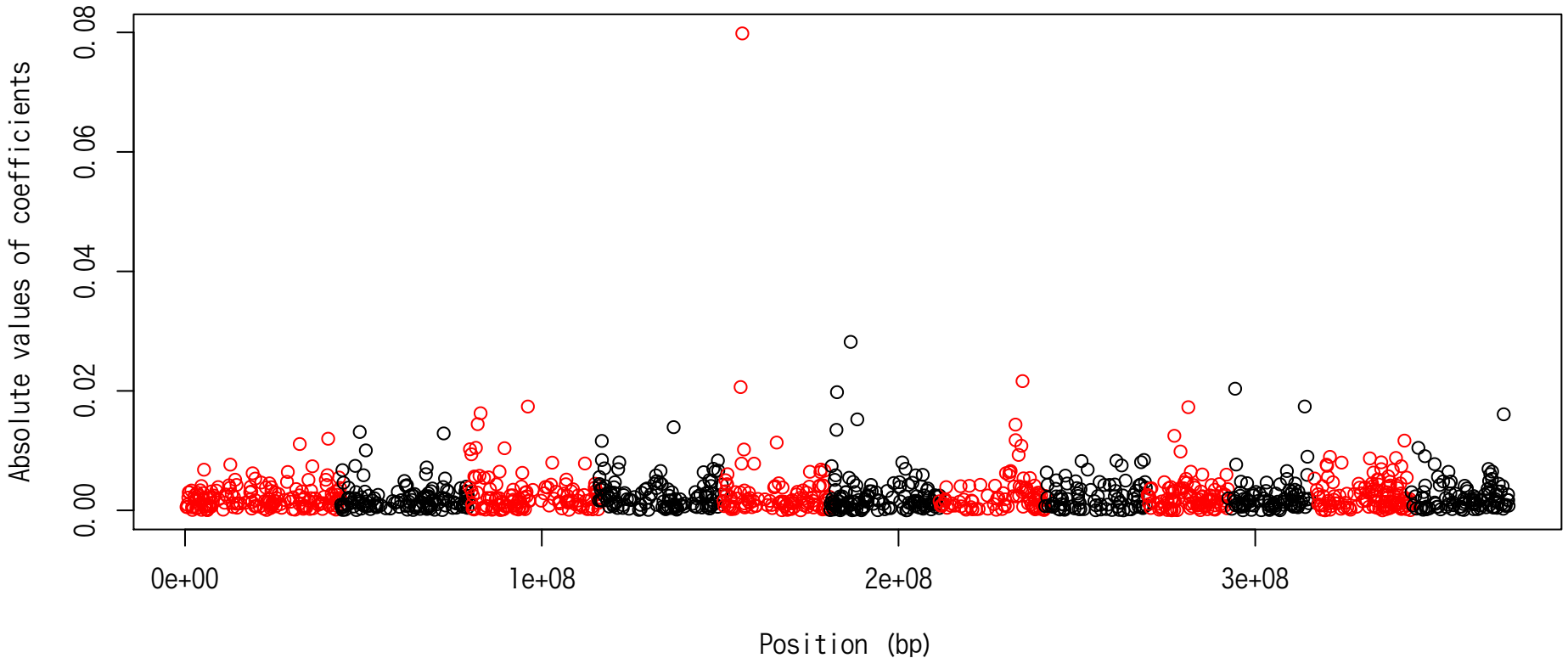
GWAS – BayesB – Seed. length



| marker | chr | pos | abs.fmBB.ETA.MRK.b. |
|------------|-----|------------|---------------------|
| id3008333 | 3 | 16,621,452 | 0.31211751 |
| id3008139 | 3 | 16,272,206 | 0.15244834 |
| id3008459 | 3 | 17,047,630 | 0.11475756 |
| id10003501 | 10 | 13,008,071 | 0.09877811 |
| id10003462 | 10 | 12,850,534 | 0.09005561 |
| id3008127 | 3 | 16,247,306 | 0.08758173 |

GWAS Seed width

GWAS – BayesB – Seed. width



| marker | chr | pos | abs.fmBB.ETA.MRK.b. |
|------------|-----|------------|---------------------|
| id5002699 | 5 | 5,273,692 | 0.07983603 |
| id6003829 | 6 | 5,994,007 | 0.02820405 |
| id7004106 | 7 | 23,250,996 | 0.02163568 |
| id5002528 | 5 | 4,797,494 | 0.02064282 |
| id10000498 | 10 | 2,043,939 | 0.02036695 |
| id6001632 | 6 | 2,160,757 | 0.01978717 |

イネの粒長、粒重、形に関する遺伝子

| Locus / Gene | RAP ID | Chr | start | end | reference |
|------------------------|--------------|-------|------------|------------|---|
| DWARF61 / OsBRI1 | Os01g0718300 | chr01 | 29,927,587 | 29,931,452 | Zhao et al 2013 Plant Science |
| GW2 | Os02g0244100 | chr02 | 8,115,223 | 8,121,651 | Song et al 2007 Nat Gen |
| GS2 | Os02g0701300 | chr02 | 28,863,274 | 28,866,997 | Zhang et al 2013 Crop Journal |
| PGL2 | Os02g0747900 | chr02 | 31,423,973 | 31,424,983 | Heang and Sassa 2012 Breeding Sci |
| smg1 / OsMKK4 | Os02g0787300 | chr02 | 33,442,070 | 33,443,948 | Duan et al 2014 Plant J |
| PGL1 | Os03g0171300 | chr03 | 3,814,378 | 3,823,216 | Heang and Sassa 2012 PLoS One |
| GS3 | Os03g0407400 | chr03 | 16,729,501 | 16,735,109 | Fan et al 2006 TAG; Mao et al 2010 PNAS |
| qGL3 / OsPPKL1 | Os03g0646900 | chr03 | 25,042,427 | 25,045,410 | Hu et al 2012 JIPB |
| GIF1 | Os04g0413500 | chr04 | 20,422,171 | 20,426,921 | Wang et al 2008 Nat Gen |
| DWARF11 | Os04g0469800 | chr04 | 23,467,167 | 23,471,592 | Tanabe et al 2005 Plant Cell |
| APG | Os05g0139100 | chr05 | 2,246,835 | 2,248,876 | Heang and Sassa 2012 PLoS One |
| SGL / SRS3 | Os05g0154700 | chr05 | 3,207,517 | 3,210,183 | Wu et al 2014 Plant Cell Rep |
| GS5 | Os05g0158500 | chr05 | 3,439,304 | 3,443,769 | Li et al 2011 Nat Genet |
| GW5 | Os05g0187500 | chr05 | 5,365,121 | 5,366,701 | Shomura et al 2008 Nat Genet |
| D1 / RGA1 | Os05g0333200 | chr05 | 15,609,569 | 15,613,588 | Ashikari et al 1999 PNAS |
| BU1 | Os06g0226500 | chr06 | 6,556,697 | 6,557,748 | Tanaka et al 2009 Plant Phys |
| GW6/OsGLHAT1/ GW6a | Os06g0650300 | chr06 | 26,591,905 | 26,593,464 | Song et al 2015 PNAS |
| GL7 / GW7 / qSS7 / GS7 | Os07g0603300 | chr07 | 24,664,328 | 24,669,321 | Shao et al 2012 TAG; Wang Y et al 2015 Nat Gen; Wang S et al 2015 Nat Gen |
| SRS1/DEP2 | Os07g0616000 | chr07 | 25,381,698 | 25,389,532 | Abe et al 2010 Genes Genet Syst |
| OsFIE1 | Os08g0137250 | chr08 | 2,095,644 | 2,100,604 | Folsom et al 2014 Plant Phys |
| GW8 / OsSPL16 | Os08g0531600 | chr08 | 26,501,167 | 26,506,198 | Wang et al 2012 Nat Gen |
| DEP1 | Os09g0441900 | chr09 | 16,411,151 | 16,415,851 | Huang et al 2009 Nat Gen |
| SG1 | Os09g0459200 | chr09 | 17,350,940 | 17,352,413 | Nakagawa 2012 Plant Phys |
| SRS5 | Os11g0247300 | chr11 | 7,960,531 | 7,963,375 | Segami et al 2012 Rice |

GW5について調べる

<https://shigen.nig.ac.jp/rice/oryzabase/gene/advanced/search>

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検索 | リスト | ダウンロード | trait classification | ヘルプ

検索 - 遺伝子

キーワード検索

キーワード

詳細検索

| | | |
|---------------|----------------------------------|-----------------------------|
| CGSNL 遺伝子シンボル | <input type="text"/> | (例 : AATP6) |
| CGSNL 遺伝子名 | <input type="text"/> | (例 : A-ATPASE SUBUNIT 6) |
| タンパク質名 | <input type="text"/> | |
| 染色体 | <input type="text" value="All"/> | |
| 対立遺伝子 | <input type="text"/> | (例 : cle1-1) |
| RAP ID | <input type="text"/> | (例 : Os09g0457100,Os01*) |
| 解説 | <input type="text"/> | (例 : ADP-glucose synthase) |

GW5と入力する

GW5の情報が表示される

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遺伝子 - 詳細

検索 | リスト | ダウンロード | trait classification

詳細 - 遺伝子

| Basic Information | |
|--------------------|---|
| CGSNL 遺伝子シンボル | GW5 |
| 遺伝子シンボルシノニム | qSW5/GW5, GSE5 |
| CGSNL 遺伝子名 | GRAIN WIDTH 5 |
| 遺伝子名シノニム | GRAIN SIZE ON CHROMOSOME 5 |
| タンパク質名 | |
| 対立遺伝子 | gse5-cr |
| 染色体番号 | 5 |
| 解説 | LOC_Os05g09520. a Plasma Membrane-Associated Protein with IQ Domains. |
| 形質クラス | 種子 - 形態学的な特色 - 粒形 QTLの特性 - 収穫と生産性 |
| 発現 | |
| Sequence/Locus | |
| cDNA Accession No. | - |

RAP-DBでもGW5について調べる

<http://rapdb.dna.affrc.go.jp/index.html>

rap-db
The Rice Annotation Project Database

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The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa* ssp. *japonica* cv. Nipponbare genome sequencing by the **International Rice Genome Sequencing Project** with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation.

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★★★★★

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Execute NCBI BLAST against rice genome or genes
★★★★★

BLAT
Align your sequence with rice genome
★★★★★

ID Converter
Convert IDs between RAP and MSU
★★★★★

Keyword search
Keywords
Search Advanced

Batch Retrieval
★★★★★

What's New

16/Nov/2017 **NEW**
We've just started Twitter. Please follow @rapdb.

15/Nov/2017 **NEW**

- Genotype data (SNPs/InDels called against the Nipponbare IRGSP-1.0 reference genome) for 333 rice varieties are available in the TASUKE multiple genome browser. User can access to the TASUKE from script
- We have updated CGSNL annotation and manual curation data (see [update_2017-08-04.txt](#)).
- miRNA data from miRBase and FST data of the Taiwan Rice Insertional Mutant (TRIM) have

More

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Os05t0187500-01の詳細を調べる

Os05t0187500-01



Locus

Os05g0187500

Description

IQ calmodulin-binding motif family protein, Positive regulator of brassinosteroid signalling, Regulates root growth and weight

RAP-DB Gene Symbol Synonym(s)

GW5, qSW5/GW5

RAP-DB Gene Name Synonym(s)

GRAIN WIDTH 5

Literature
PMID: 28394310

GW5の文献情報を入手

PubMed

Format: Abstract ▾

Full text links

nature
plants

Nat Plants. 2017 Apr 10;3:17043. doi: 10.1038/nplants.2017.43.

GW5 acts in the brassinosteroid signalling pathway to regulate grain width and weight in rice.

Liu J¹, Chen J¹, Zheng X¹, Wu F¹, Lin Q¹, Heng Y¹, Tian P¹, Cheng Z¹, Yu X², Zhou K², Zhang X¹, Guo X¹, Wang J¹, Wang H¹, Wan J^{1,2}.

Author information

Abstract

Grain size is a major determinant of grain yield in cereal crops. qSW5/GW5, which exerts the greatest effect on rice grain width and weight, was fine-mapped to a 2,263-bp/21-kb genomic region containing a 1,212-bp deletion, respectively. Here, we show that a gene encoding a calmodulin binding protein, located -5 kb downstream of the 1,212-bp deletion, corresponds to qSW5/GW5. GW5 is expressed in various rice organs, with highest expression level detected in young panicles. We provide evidence that the 1,212-bp deletion affects grain width most likely through influencing the expression levels of GW5. GW5 protein is localized to the plasma membrane and can physically interact with and repress the kinase activity of rice GSK3.

文献検索の方法

- PubMed

<https://www.ncbi.nlm.nih.gov/pubmed>

TOGO TV

PMC (PubMedCentral) の使い方 2017

<http://togotv.dbcls.jp/20171209.html>

- Google Scholar

<https://scholar.google.co.jp>

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<http://togotv.dbcls.jp/20170605.html>