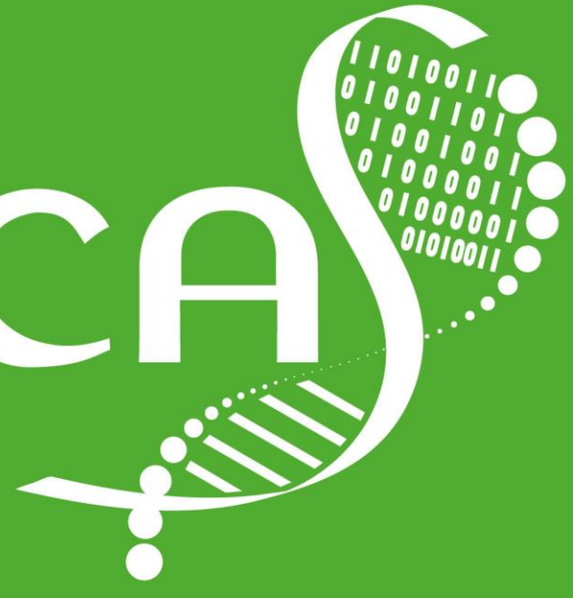
ÓMICAS



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Week report

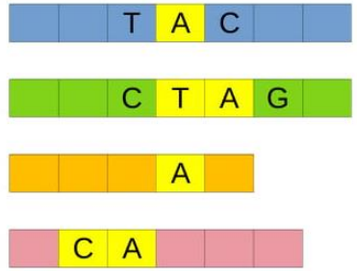
Camila Riccio Rengifo

September 18th, 2020

QUERY GENOME MAPPING

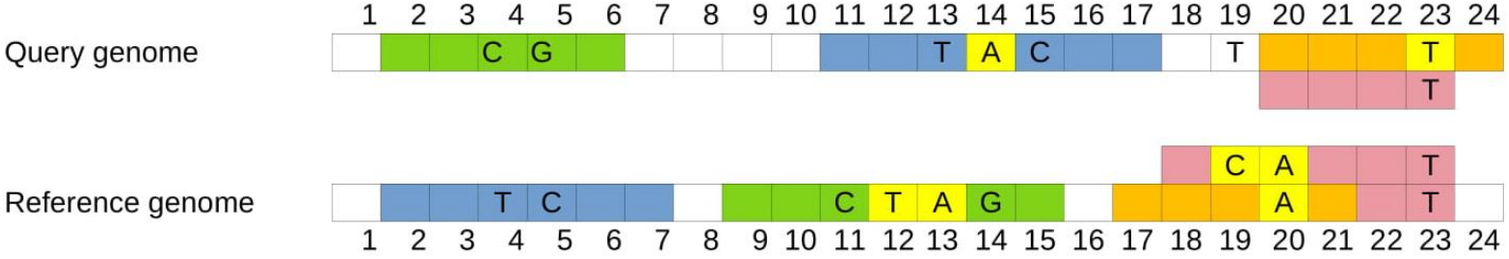
COORDS

	Sr	Er	Sq	Eq	len_r	len_q	%IDY
0	2	7	11	17	6	7	99.3
1	9	15	2	6	7	5	98.6
2	17	21	20	24	5	5	99.5
3	18	21	50	55	4	6	99.3



VARIANTS

	rpos	ref	query
0	4	T	TA
1	11	CTA	C
2	20	A	T



rpos	rbase	qpos	qbase	snp	var	inv	idt
1	C	-	-	0	0	0	-
2		11		0	0	0	1
3		12		0	0	0	1
4	T	13	T	0	-1	0	1
5	C	15	C	0	0	0	1
6		16		0	0	0	1
7		17		0	0	0	1
8	-	-	-	0	0	0	-
9		3		0	0	0	1
10		4		0	0	0	1
11	C	5	C	0	2	0	1
12	T	-	-	0	0	0	-
13	A	-	-	0	0	0	-
14	G	6	G	0	0	0	1
15		7		0	0	0	1
16	-	-	-	0	0	0	-
17		20		0	0	0	1
18		21		0	0	0	1
19		22		0	0	0	1
20	A	23	T	1	0	0	0
21		24		0	0	0	1
22		22		0	0	0	1
23	T	23	T	0	0	0	1

QUERY GENOME MAPPING

COORDS (5.208 contigs)

	Sr	Er	Sq	Eq	len_r	len_q	%IDY
0	8701	184119	1	175451	175419	175451	99.88
1	184133	193002	176105	184984	8870	8880	98.93
2	193099	218454	184979	210400	25356	25422	98.49
3	218635	246229	225148	252840	27595	27693	98.36
4	247275	249168	252834	254721	1894	1888	98.94

VARIANTS (450.980)

	#CHROM	POS	ID	REF	ALT	QUAL	FILTER
0	chr01	8714	.	T	TA	30	PASS
1	chr01	8735	.	CTA	C	30	PASS
2	chr01	8738	.	A	C	30	PASS
3	chr01	8739	.	A	T	30	PASS
4	chr01	8744	.	TACA	T	30	PASS

Reference genome:
IR64

Query genome:
AZUCENA

Mapping (44.350.042 bp)

	rpos	rbase	qpos	qbase	inversion	snp	variant	identical
8711	8712	C	11	C	False	0	0	1
8712	8713	C	12	C	False	0	0	1
8713	8714	T	13	T	False	0	-1	1
8714	8715	A	15	A	False	0	0	1
8715	8716	A	16	A	False	0	0	1
⋮								
8733	8734	C	34	C	False	0	0	1
8734	8735	C	35	C	False	0	2	1
8735	8736	T	0	-	False	0	0	0
8736	8737	A	0	-	False	0	0	0
8737	8738	A	36	C	False	1	0	0
8738	8739	A	37	T	False	1	0	0
8739	8740	A	38	A	False	0	0	1
8740	8741	C	39	C	False	0	0	1
8741	8742	C	40	C	False	0	0	1
8742	8743	C	41	C	False	0	0	1

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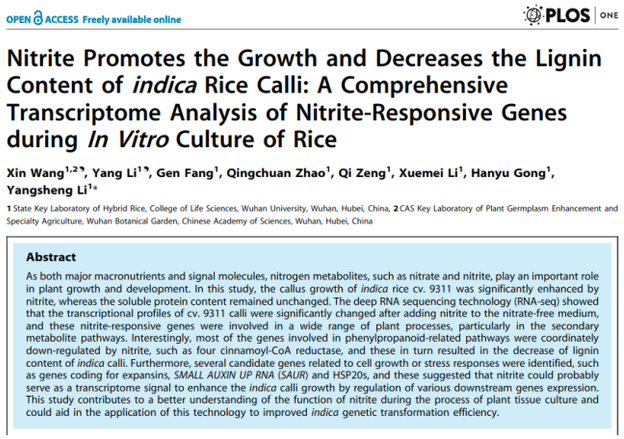
Gene nomenclature conversion

TU
13101.t01104

→

LOC
LOC_Os01g12420

Supplementary data



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PLOS ONE

Nitrite Promotes the Growth and Decreases the Lignin Content of *indica* Rice Calli: A Comprehensive Transcriptome Analysis of Nitrite-Responsive Genes during *In Vitro* Culture of Rice

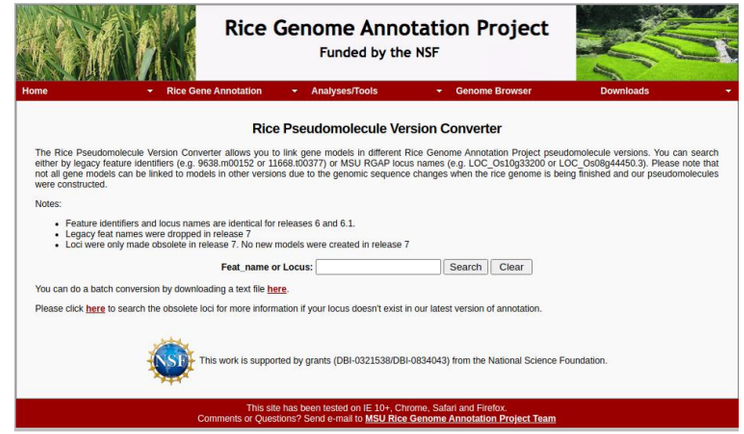
Xin Wang[1,2], Yang Li[1], Gen Fang[1], Qingchuan Zhao[1], Qi Zeng[1], Xuemei Li[1], Hanyu Gong[1], Yangsheng Li[1]*

1 State Key Laboratory of Hybrid Rice, College of Life Sciences, Wuhan University, Wuhan, Hubei, China, **2** CAS Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, Hubei, China

Abstract

As both major macronutrients and signal molecules, nitrogen metabolites, such as nitrate and nitrite, play an important role in plant growth and development. In this study, the callus growth of *indica* rice cv. 9311 was significantly enhanced by nitrite, whereas the soluble protein content remained unchanged. The deep RNA sequencing technology (RNA-seq) showed that the transcriptional profiles of cv. 9311 calli were significantly changed after adding nitrite to the nitrate-free medium, and these nitrite-responsive genes were involved in a wide range of plant processes, particularly in the secondary metabolite pathways. Interestingly, most of the genes involved in phenylpropanoid-related pathways were coordinately down-regulated by nitrite, such as four cinnamoyl-CoA reductase, and these in turn resulted in the decrease of lignin content of *indica* calli. Furthermore, several candidate genes related to cell growth or stress responses were identified, such as genes coding for expansins, *SMALL AUXIN UP RNA* (*SAUR*) and HSP20s, and these suggested that nitrite could probably serve as a transcriptome signal to enhance the *indica* calli growth by regulation of various downstream genes expression. This study contributes to a better understanding of the function of nitrite during the process of plant tissue culture and could aid in the application of this technology to improved *indica* genetic transformation efficiency.

Web Scraping



Rice Genome Annotation Project

Funded by the NSF

Home | Rice Gene Annotation | Analyses/Tools | Genome Browser | Downloads

Rice Pseudomolecule Version Converter

The Rice Pseudomolecule Version Converter allows you to link gene models in different Rice Genome Annotation Project pseudomolecule versions. You can search either by legacy feature identifiers (e.g. 9638.m00152 or 11668.t00377) or MSU RGAP locus names (e.g. LOC_Os10g33200 or LOC_Os08g44450.3). Please note that not all gene models can be linked to models in other versions due to the genomic sequence changes when the rice genome is being finished and our pseudomolecules were constructed.

Notes:

- Feature identifiers and locus names are identical for releases 6 and 6.1.
- Legacy feat names were dropped in release 7
- Loci were only made obsolete in release 7. No new models were created in release 7

Feat_name or Locus: Search Clear

You can do a batch conversion by downloading a text file here.

Please click here to search the obsolete loci for more information if your locus doesn't exist in our latest version of annotation.

This work is supported by grants (DBI-0321538/DBI-0834043) from the National Science Foundation.

This site has been tested on IE 10+, Chrome, Safari and Firefox.
Comments or Questions? Send e-mail to MSU Rice Genome Annotation Project Team

4594 genes
51%

4335 genes
49%

In-silico

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AUTOMATIZACION S.A.

Caltech

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東京大学
THE UNIVERSITY OF TOKYO

ILLINOIS

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IES Ancla

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Universidad de Ibagué

UNILLANOS
UNIVERSIDAD DE LOS LLANOS

Universidad de los Andes
Colombia

UNIVERSIDAD ICESI

Pontificia Universidad JAVERIANA Bogotá

[VIGILADA MINEDUCACIÓN Res. 12220 de 2016]

Apoyan

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