EPIPLANT 2022

22-24 June 2022, Banyuls-sur-mer, France

I hereby certify that JENNY JOHANA GALLO has participated in the above mentioned international conference.

Perpignan, September 1, 2022

Guillaume MOISSIARD
For the Local Scientific Committee

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Whole-genome DNA methylation patterns of *Oryza sativa* (L.) and *Oryza glumaepatula* (Steud) genotypes associated with aluminum response

Jenny Johana Gallo-Franco, Thaura Ghneim-Herrera, Fabián Tobar-Tosse,
Miguel Ángel Romero, Juliana Chaura & Mauricio Alberto Quimbaya

EpiPlant 2022

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ómicas

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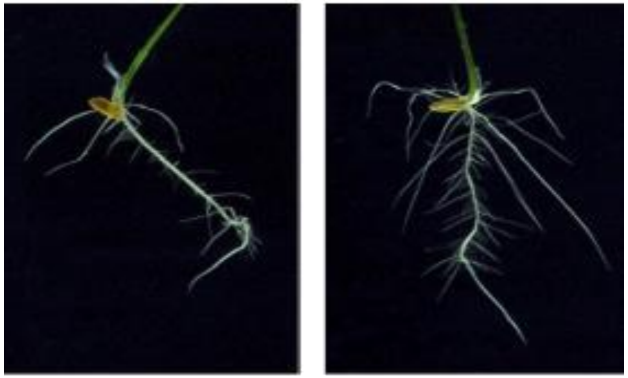
¿ Why study aluminum toxicity ?

- Aluminum (Al) is the third **most common** element in the world (~ 7%)

- When the **pH of the soil** is below 5, it becomes its most toxic form Al^{3+}

- Most of the **cereals** around the world such as corn, wheat and rice, grow in acid soils and are exposed to the Al^{3+} toxicity, which **inhibits** the **plants development.**

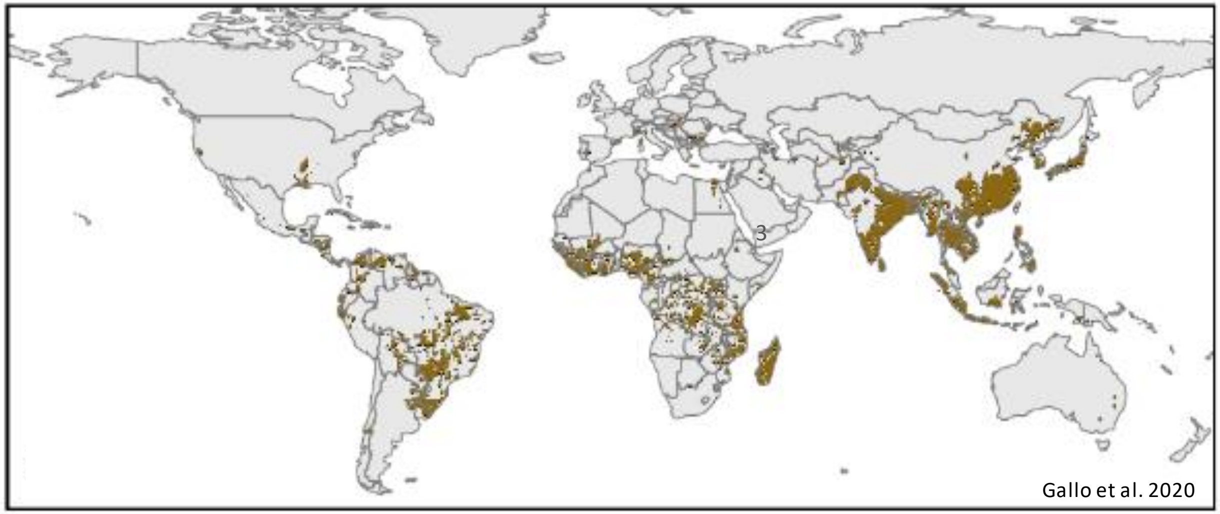


Famoso et al. 2010

¿ Why study the methylome of rice crops?

Rice is an important crop that represents the **food security** of more than half of the world's population.

Class: *Monocotyledoneae*
Order: *Poales*
Family: *Poaceae*
Tribe: *Oryzeae*
Gender: *Oryza*



Gallo et al. 2020

¿ Why study the methylome of rice crops?

Model organism for evolutionary and molecular studies in cereals and monocotyledonous plants.

Oryza sativa is the most Al tolerant crop.

Class: *Monocotyledoneae*
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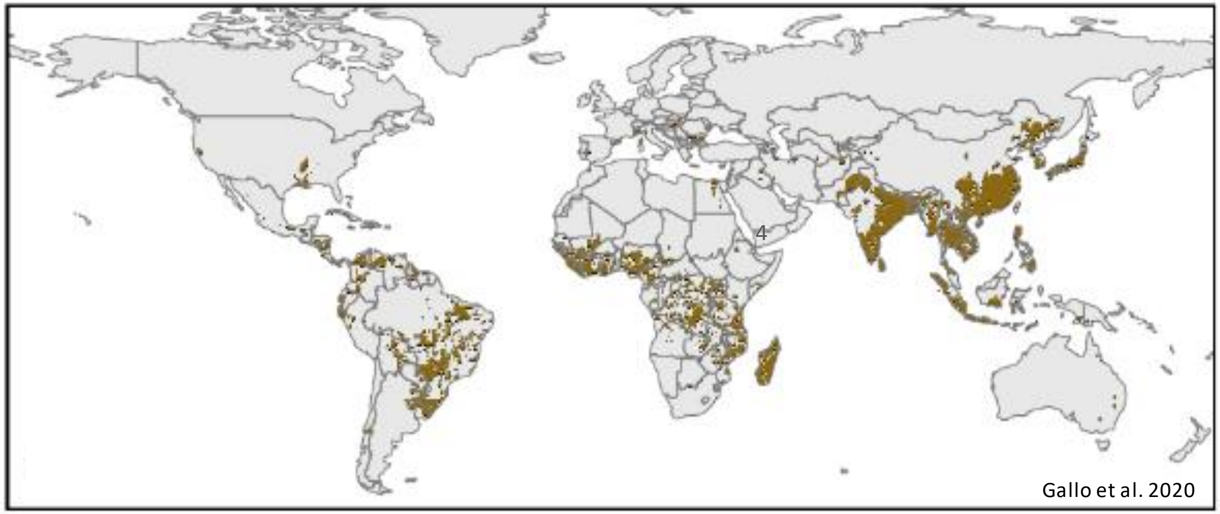
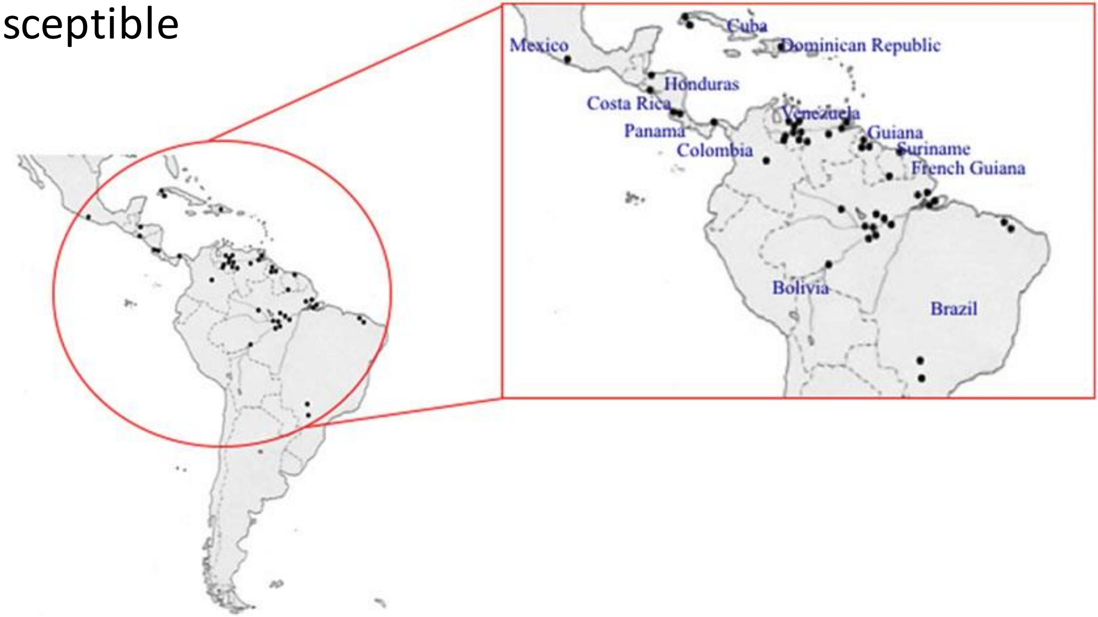


Gallo et al. 2020

¿Why *Oryza glumaepatula?*

Potential source of Al^{3+} tolerant varieties

- Wild type rice species
- Endemic from Center and South America
- Unknown tolerance mechanisms to Al^{3+}
- Biological collection in the Icesi University (Cali-Colombia)
- 65 accessions of tolerant and susceptible *O. glumepatula* genotypes



Plants can respond and adapt to environmental conditions

Abiotic stress

Biotic stress

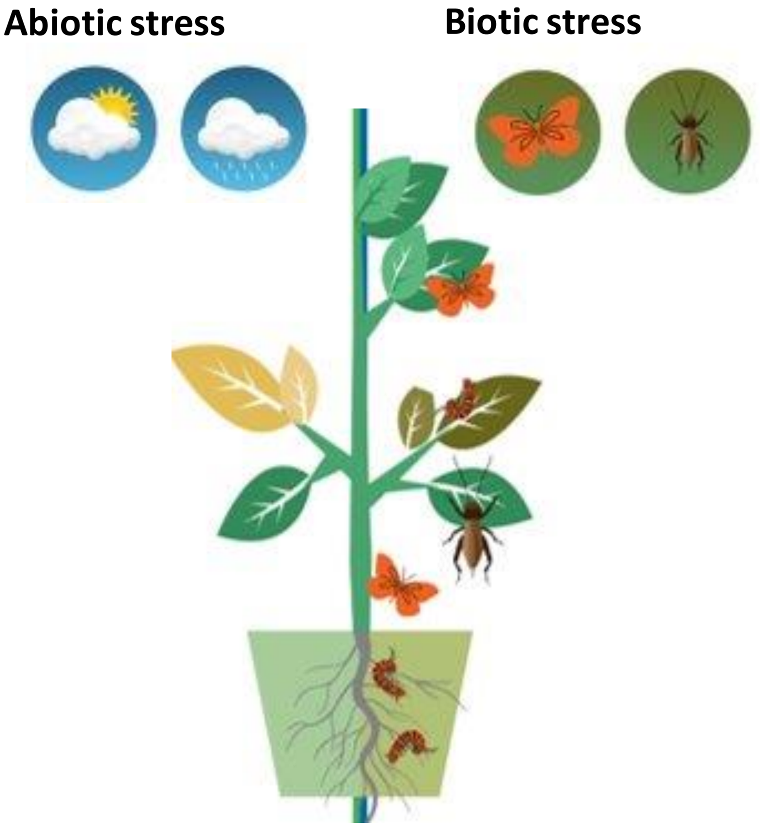
Introduction

Plants can respond and adapt to environmental conditions

Are there differences in methylation patterns between **cultivated and rice wild species?**

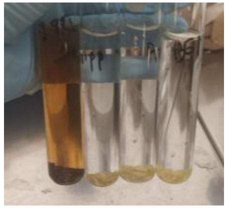
Are there pre-established methylation patterns associated with the **aluminum stress** response in tolerant and susceptible rice genotypes?

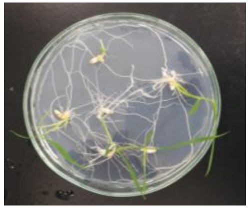
Are they different **between rice species**?

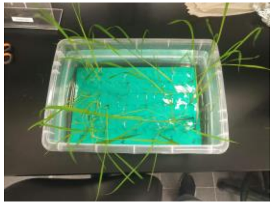


Materials and Methods

Experimental design



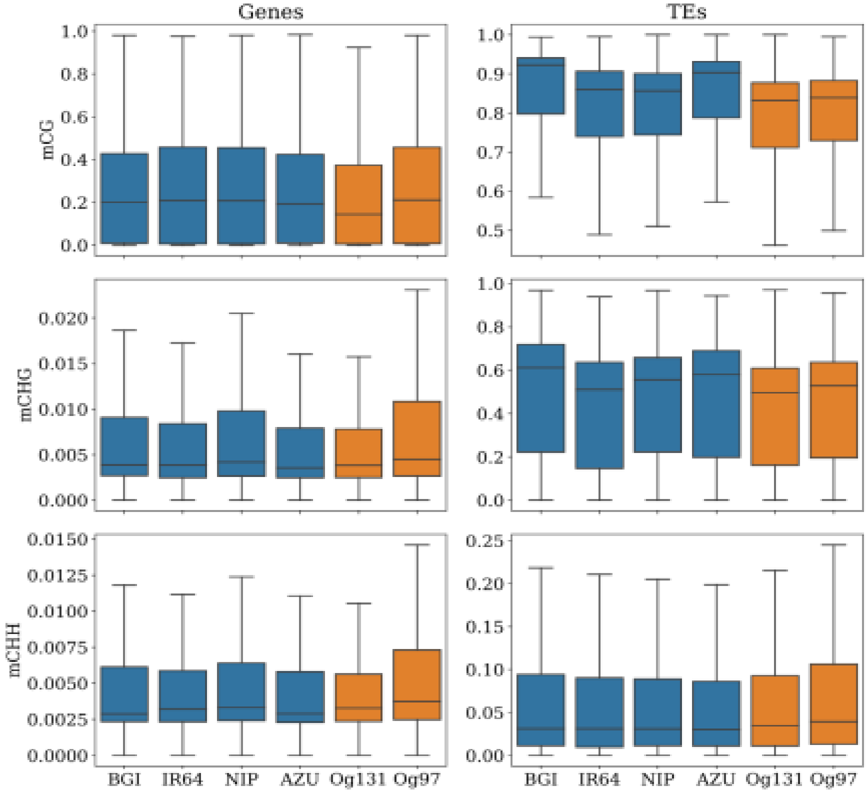




Seeds selection and desinfection → Germination → **Hydroponic culture Kimura B 3 weeks** → Roots collect → DNA Extraction → Whole genome bisulfite sequencing Illumina

Species	**Genotype**	**Response to Al3+**
O. sativa	Azucena	Tolerant
O. sativa	Nipponbare	Tolerant
O. sativa	BGI	Susceptible
O. sativa	IR64	Intermidiate
O. glumaepatula	Og97	Tolerant
O. glumaepatula	Og131	Susceptible

Genome-wide DNA methylation patterns in cultivated and wild rice

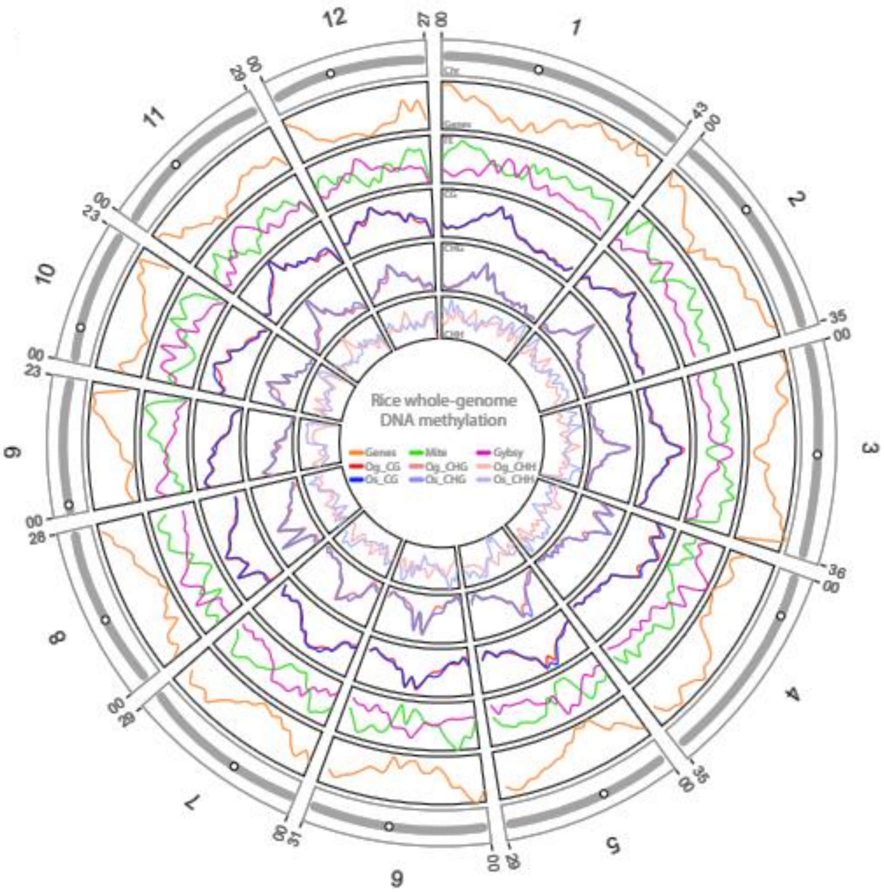


Methylation patterns associated with genes and TEs for both rice species are conserved.

Results

DNA methylation profiles of genes and TEs in rice

	Genes	Mite	Gypsy	Os_CG	Og_CG	Os_CHG	Og_CHG	Os_CHH	Og_CHH
Genes	1.00	0.51	-0.59	-0.85	-0.82	-0.81	-0.76	0.54	-0.16
Mite	0.51	1.00	-0.49	-0.60	-0.57	-0.64	-0.60	0.56	0.07
Gypsy	-0.59	-0.49	1.00	0.69	0.67	0.72	0.68	-0.40	0.21
Os_CG	-0.85	-0.60	0.69	1.00	0.95	0.92	0.85	-0.63	0.13
Og_CG	-0.82	-0.57	0.67	0.95	1.00	0.88	0.90	-0.59	0.20
Os_CHG	-0.81	-0.64	0.72	0.92	0.88	1.00	0.93	-0.51	0.26
Og_CHG	-0.76	-0.60	0.68	0.85	0.90	0.93	1.00	-0.46	0.34
Os_CHH	0.54	0.56	-0.40	-0.63	-0.59	-0.51	-0.46	1.00	0.38
Og_CHH	-0.16	0.07	0.21	0.13	0.20	0.26	0.34	0.38	1.00

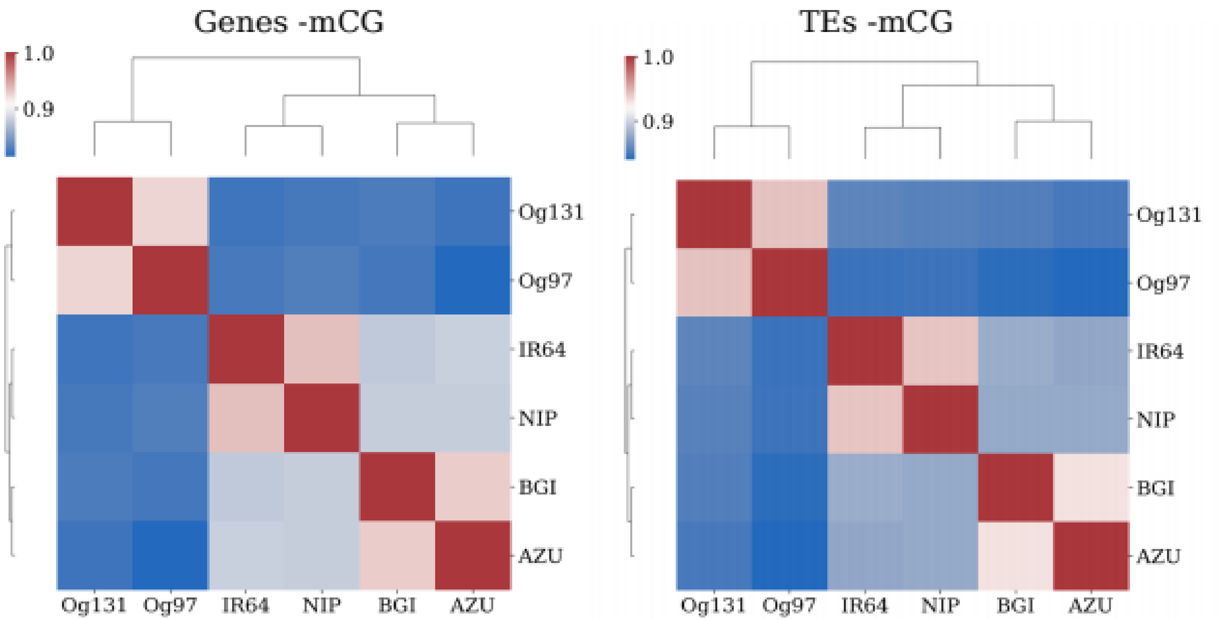


Positive correlation between the methylation level and density of Gypsy TEs.

Negative correlation between the methylation level and density of Mite TEs and genes.

Results

Differential methylation patterns between cultivated and wild rice

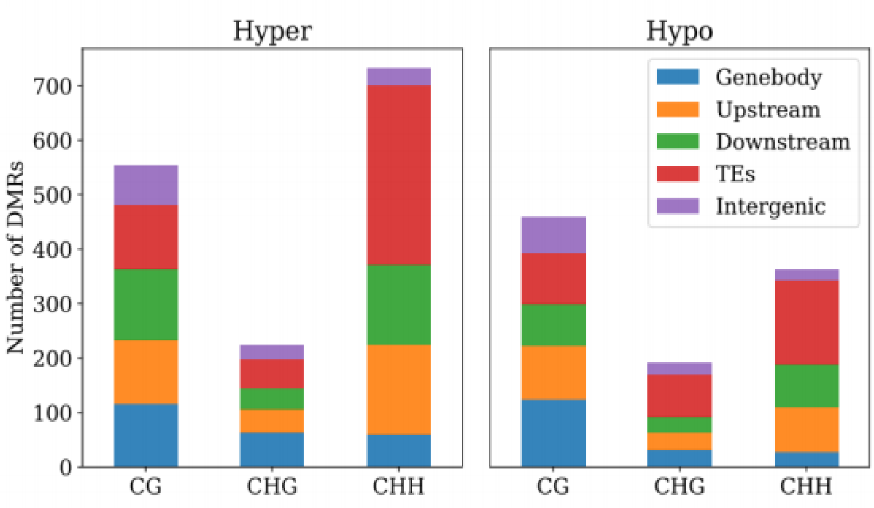


There is a differentiation of the methylome according to the rice species

Results

Differential methylation patterns between cultivated and wild rice

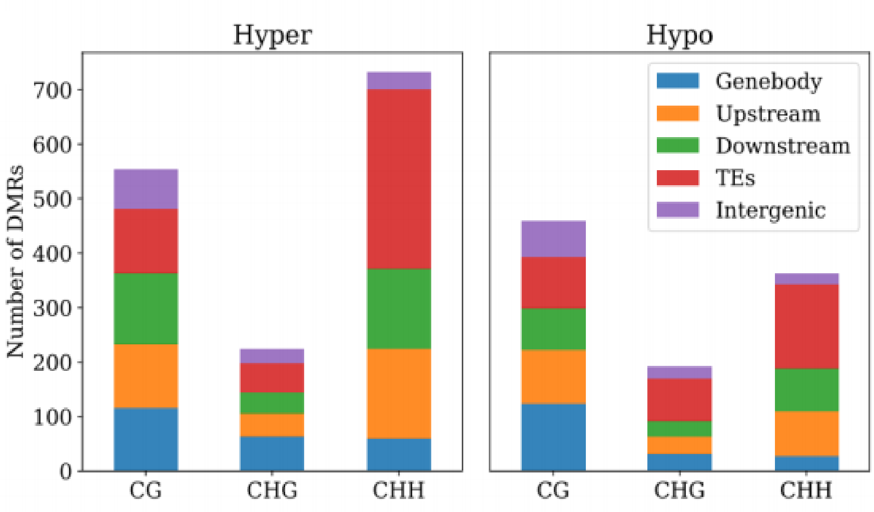
There are several genomic regions with species-specific methylation patterns, reflecting the own evolutionary histories of *O. sativa* and *O. glumaepatula*

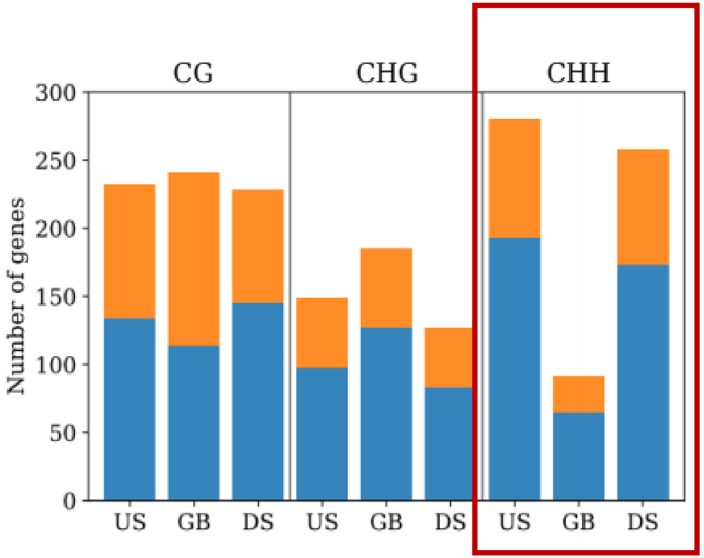


We found two genes related to domestication processes in rice: FRIZZI PANICLE-FZP and SCENTED KERNEL-SK2

Differential methylation patterns between cultivated and wild rice

There are several genomic regions with species-specific methylation patterns, reflecting the own evolutionary histories of *O. sativa* and *O. glumaepatula*

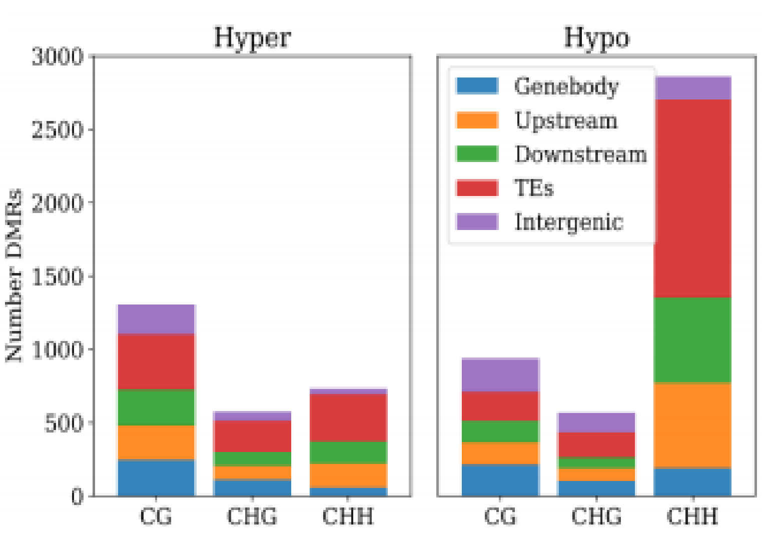




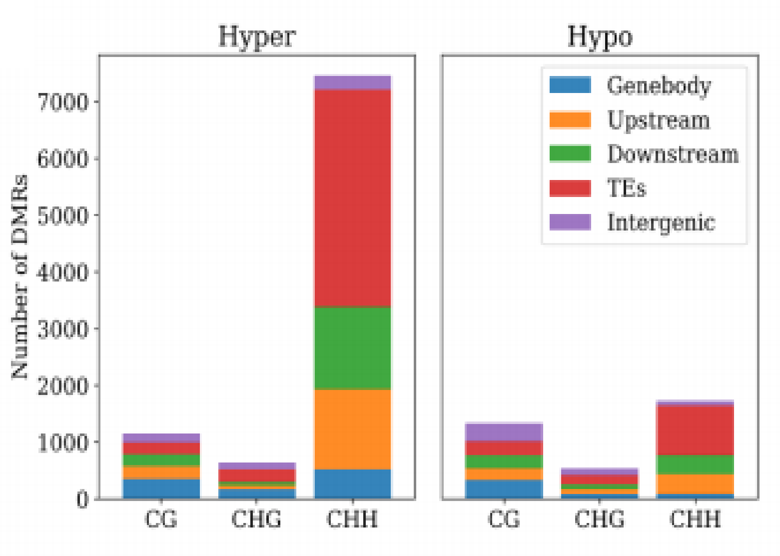
We found two genes related to domestication processes in rice: FRIZZI PANICLE-FZP and SCENTED KERNEL-SK2

Differential methylation patterns associated with Al-tolerance: a comparison between wild and cultivated rice

O. sativa

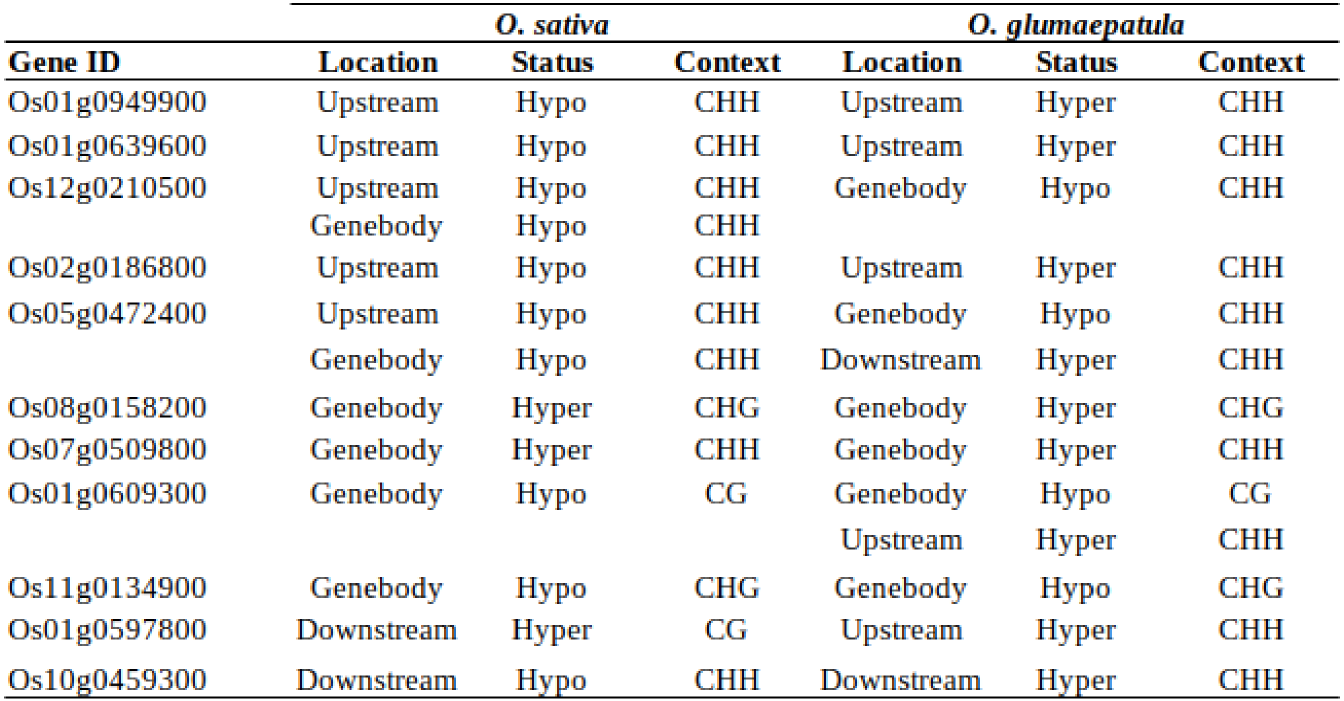


O. glumaepatula



Several DMRs are related to genes involved in Al-tolerance in rice according to Arbelaez *et al*., (2017) and Arenhart *et al*., (2014).

DMR-associated genes related to Al-tolerance shared between rice species



	O. sativa			*O. glumaepatula*		
Gene ID	**Location**	**Status**	**Context**	**Location**	**Status**	**Context**
Os01g0949900	Upstream	Hypo	CHH	Upstream	Hyper	CHH
Os01g0639600	Upstream	Hypo	CHH	Upstream	Hyper	CHH
Os12g0210500	Upstream	Hypo	CHH	Genebody	Hypo	CHH
	Genebody	Hypo	CHH			
Os02g0186800	Upstream	Hypo	CHH	Upstream	Hyper	CHH
Os05g0472400	Upstream	Hypo	CHH	Genebody	Hypo	CHH
	Genebody	Hypo	CHH	Downstream	Hyper	CHH
Os08g0158200	Genebody	Hyper	CHG	Genebody	Hyper	CHG
Os07g0509800	Genebody	Hyper	CHH	Genebody	Hyper	CHH
Os01g0609300	Genebody	Hypo	CG	Genebody	Hypo	CG
				Upstream	Hyper	CHH
Os11g0134900	Genebody	Hypo	CHG	Genebody	Hypo	CHG
Os01g0597800	Downstream	Hyper	CG	Upstream	Hyper	CHH
Os10g0459300	Downstream	Hypo	CHH	Downstream	Hyper	CHH

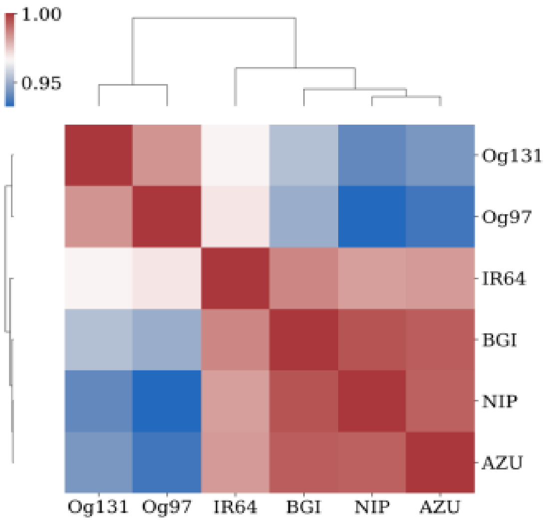
Common DMR-associated genes for *O. sativa* and *O. glumaepatula* according to Arbelaez *et al*., (2017) and Arenhart *et al*., (2014).

Results

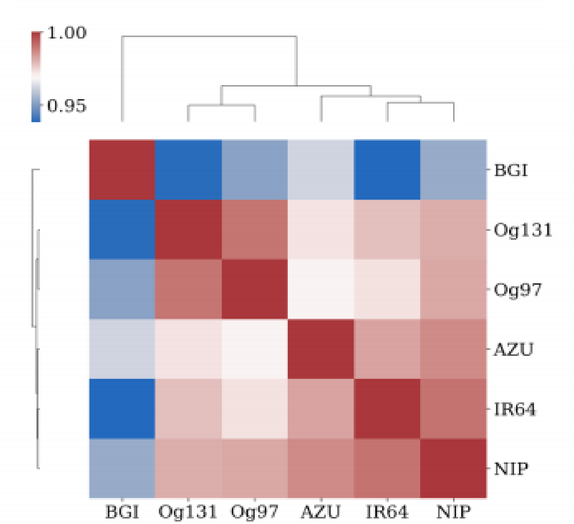
Methylation patterns of TEs close to Al-response genes

79 TEs were associated with a DMRs in *O. glumaepatula* and
70 TEs in *O. sativa.*

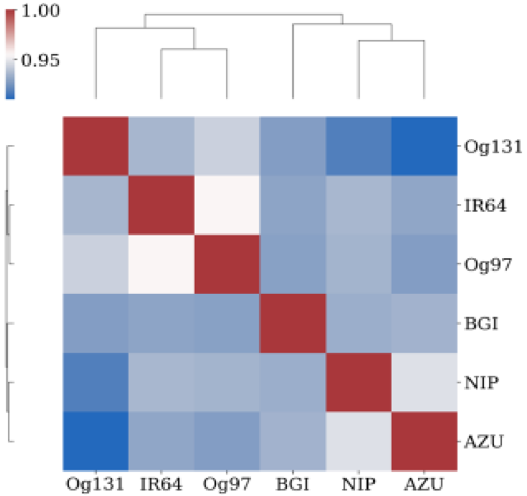
CG



CHG



CHH



Conclusions

- The methylation patterns associated with genes and TEs for both rice species are conserved.
- There is a positive correlation between the methylation level and the density of Gypsy TEs. But a negative correlation was found between the methylation level and the density of Mite TEs and genes.
- There exist several genomic regions with species-specific methylation patterns, reflecting the own evolutionary histories of *O. sativa* and *O. glumaepatula*.
- There are several regions potentially regulated through epigenetics that are related to Al-tolerance in rice.

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Thanks !

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