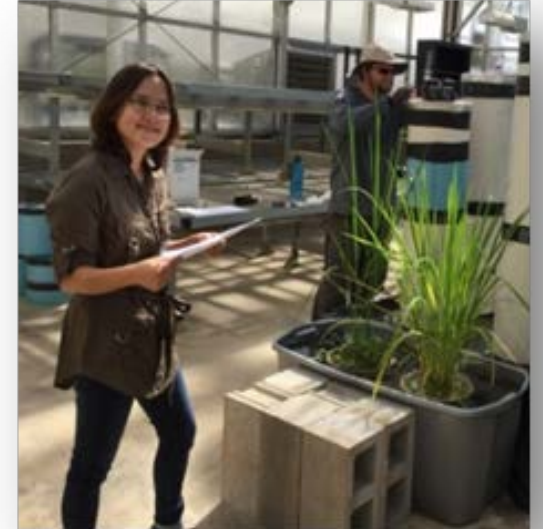


# The Role of Rice Genotypes in Mitigation of Methane Emissions



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Stuttgart, AR

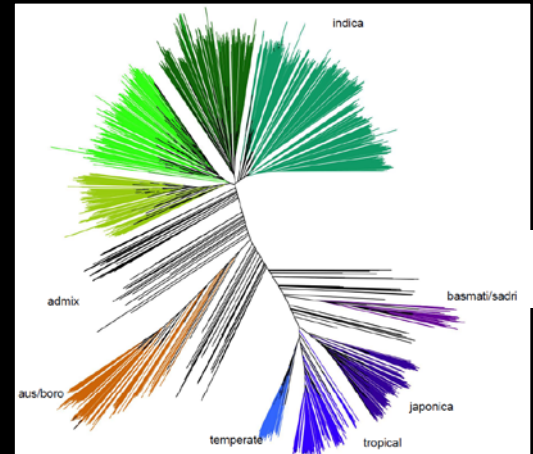


# The Mission of the DBNRRC

- Explore global genetic diversity
- Understand Trait-Gene relationships
- New breeding tools and varieties



Germplasm



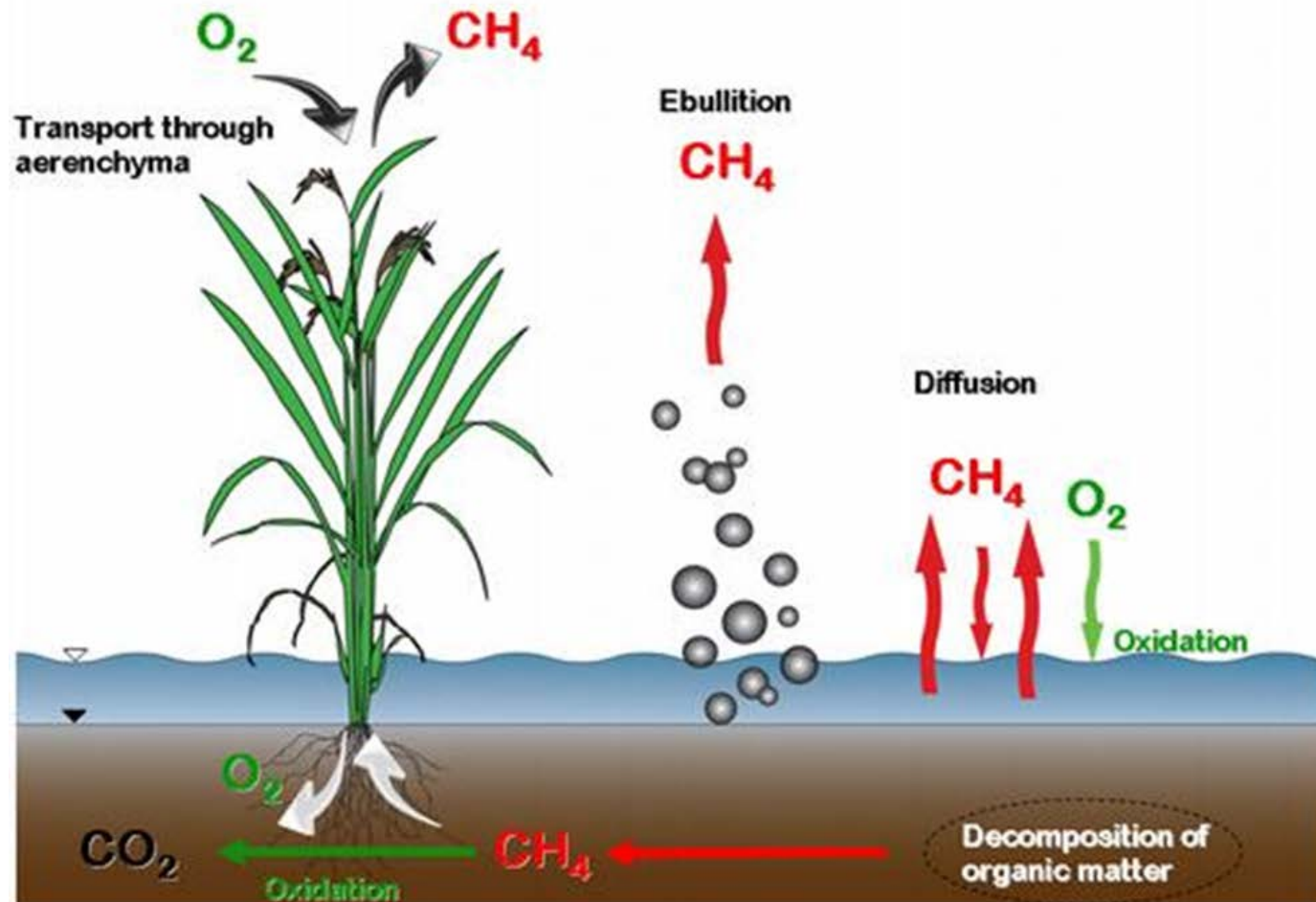
Genomics



Traits



How does rice genetics contribute to this process as well as serve as a means of mitigation?



Sources of methane emissions from flooded rice fields



Weather



Irrigation



Fertilizer and  
Soil Chemistry



Soil  
Microbiome



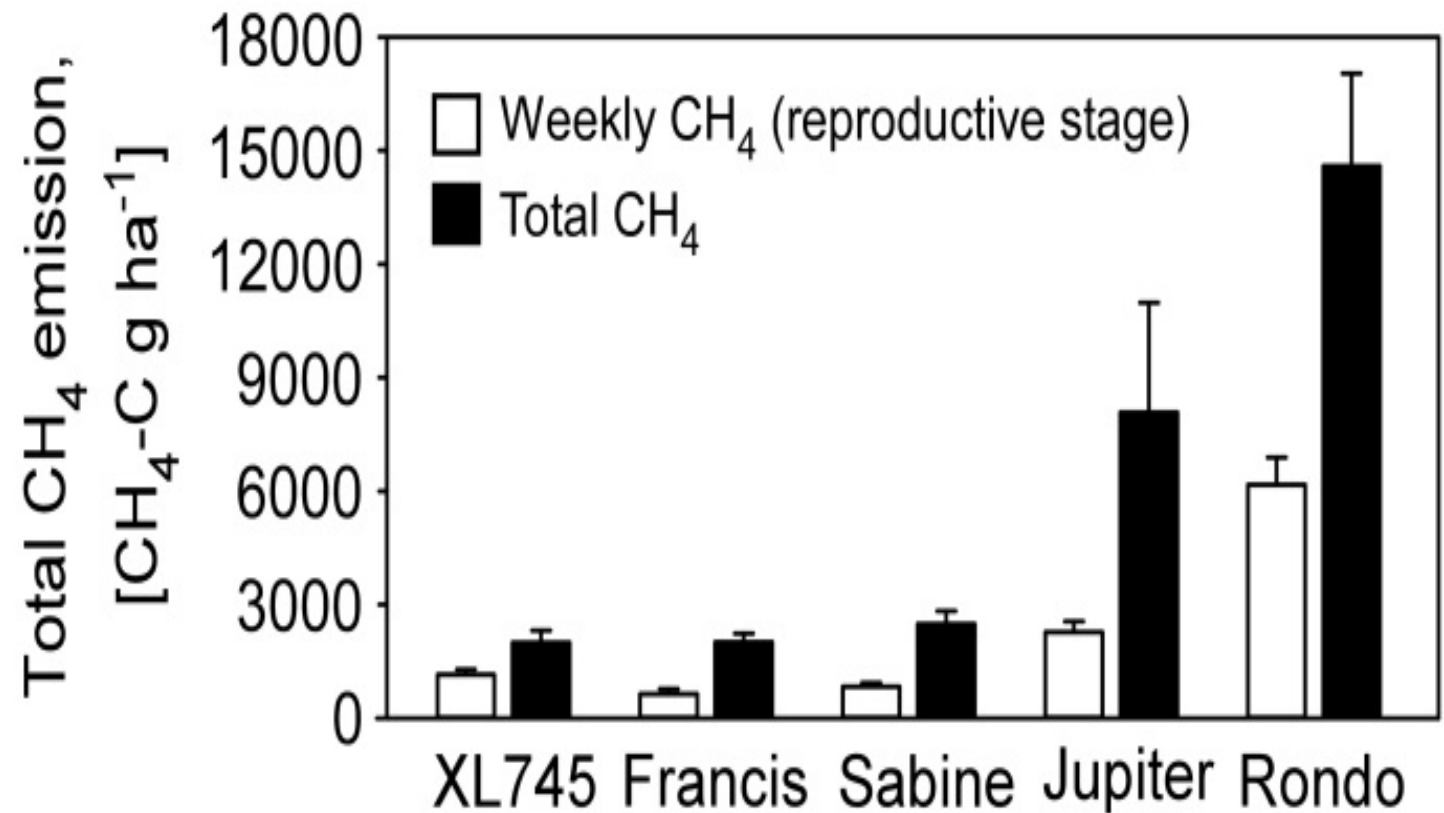
Cultivar	Seasonal CH <sub>4</sub>	Seasonal N <sub>2</sub> O	Seasonal GWP <sup>†</sup>	Seasonal GWP <sub>y</sub> <sup>‡</sup>
	kg CH <sub>4</sub> -C ha <sup>-1</sup>	kg N <sub>2</sub> O-N ha <sup>-1</sup>	kg CO <sub>2</sub> eq ha <sup>-1</sup>	kg CO <sub>2</sub> eq <sup>-1</sup> Mg <sup>-1</sup> CA-1§
Calmati-202	58 (2.9)a¶	0.05 (0.021)a	1988 (90)a	277 (19)a
L206	60 (12)a	0.06 (0.004)a	2074 (399)a	218 (29)a
M206	69 (9.6)a	0.06 (0.018)a	2370 (319)a	225 (30)a
				CA-2
Calmati-202	6.7 (0.9)b	-0.15 (0.016)a	83 (31)b	10 (3.6)b
CLXL745	11 (3.1)ab	-0.19 (0.025)a	309‡ (99)ab	29# (12)ab
CLXP4534	11 (0.4)ab	-0.16 (0.037)a	229 (40)ab	22 (2.6)ab
L206	14 (2.2)a	-0.13 (0.016)a	353 (62)a	33 (6.1)a
M206	11 (1.1)ab	-0.11 (0.028)a	277 (61)ab	23 (6.1)ab
				AR-1††
CLXP4534	25	0.17	981	140
Francis	43	0.10	1526	282
Jupiter	15	0.08	573	83
Sabine	55	0.10	1936	384
				AR-2
CLXL745	56 (9.2)b	0.02 (0.047)a	1899 (344)b	232 (44)b
Francis	77 (14)a	0.10 (0.052)a	2677 (459)a	381 (81)a
Jupiter	72 (16)ab	-0.01 (0.022)a	2397 (534)ab	345 (59)ab
Sabine	75 (7.5)ab	0.11 (0.114)a	2623 (154)a	397 (30)a

Direct seeded, flood,  
CA and AR

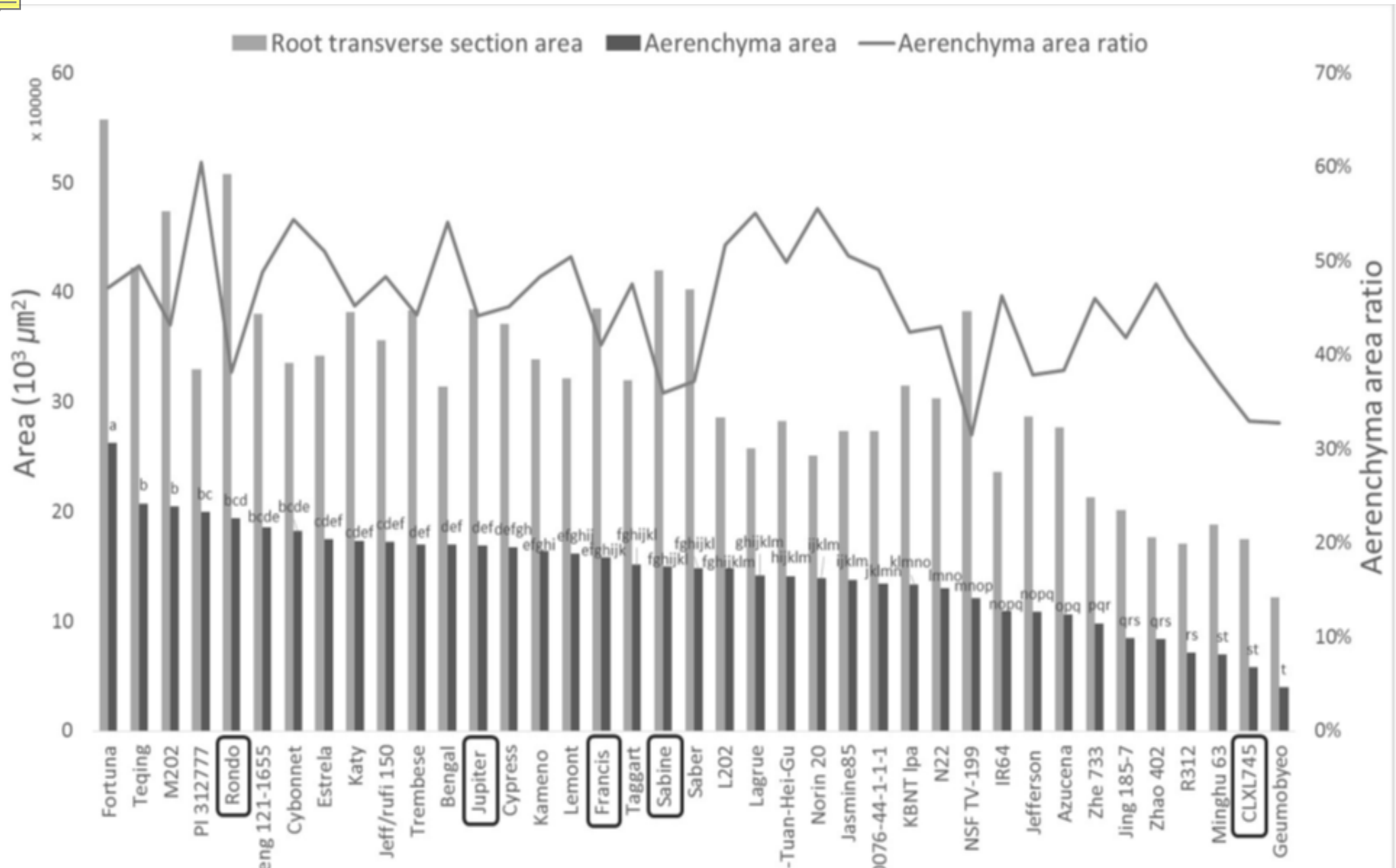
Environmental  
Variability  
Cultivar Differences,  
Unstable  
N2O of little effect

Simmonds, 2015. *Journal of  
Environmental Quality*, 44(1),  
pp.103-114.

2016 Conducted greenhouse study comparing five cultivars – three US tropical japonica cultivars from the previous field study, a hybrid, and a high yielding indica cultivar.



What is the genetic basis for these differences?

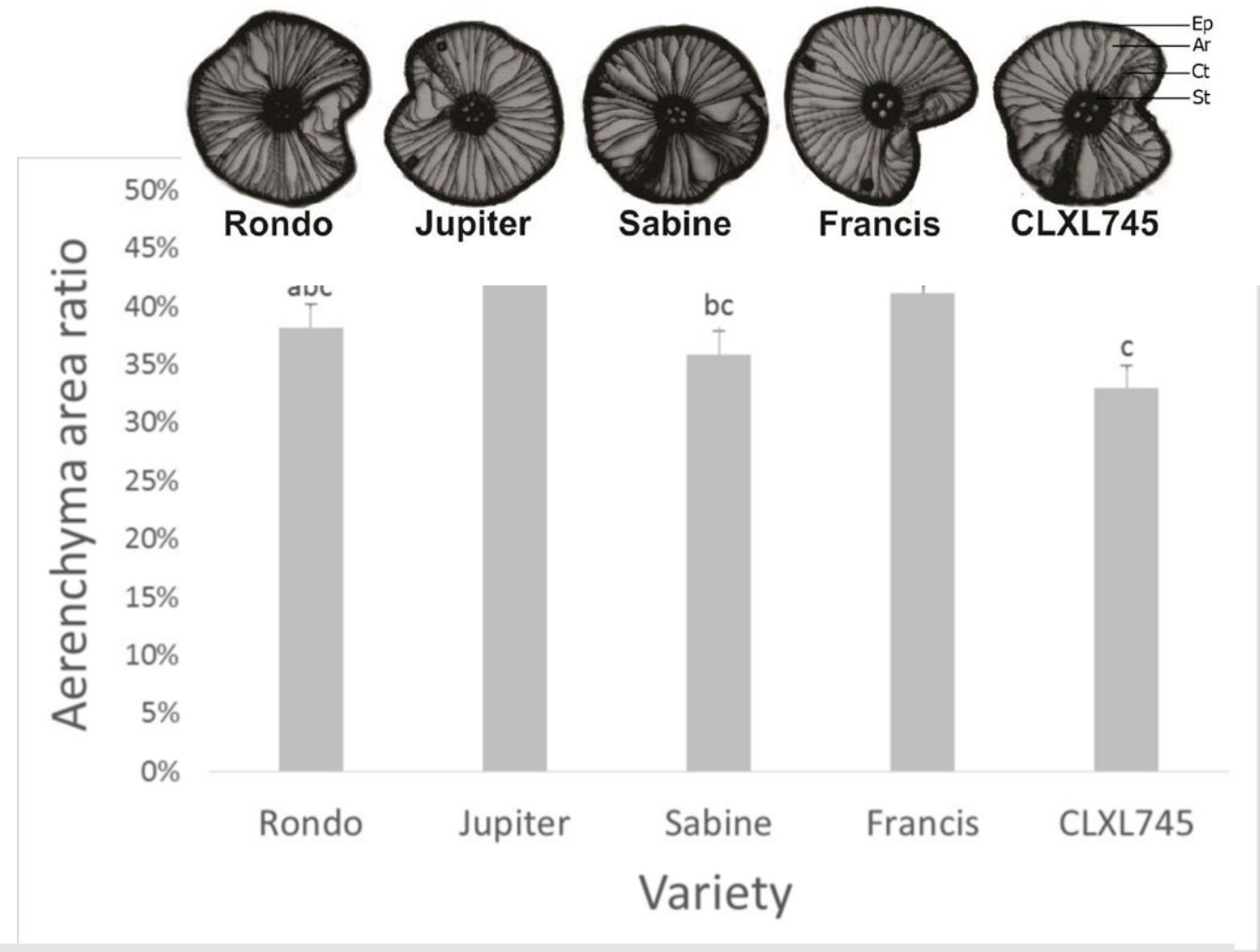


A survey of 39 global varieties grown under flooded field conditions was performed to determine genetic variability for root size and aerenchyma traits.



Cultivars differing in CH<sub>4</sub> emissions showed moderate positive correlations with root size parameters but not % aerenchyma.

Root size (RTS)  $r = 0.61$   
Aerenchyma area  
 $r = 0.57$



CH<sub>4</sub> Emissions: Very High   Mod. High   Low   Low   Low

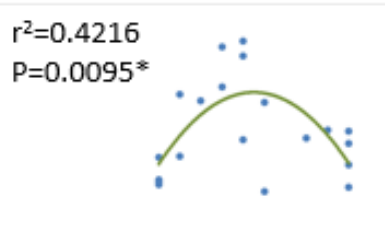
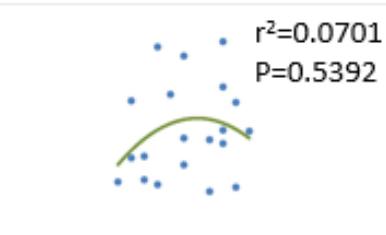
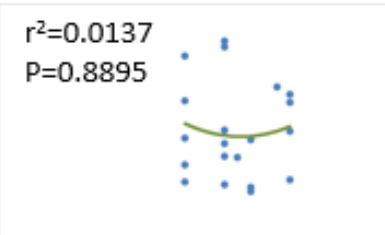
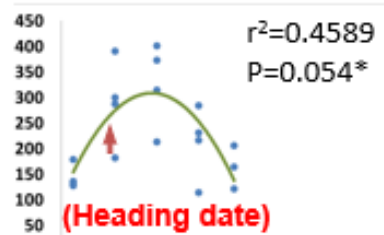
Kim, 2018.



CH<sub>4</sub>

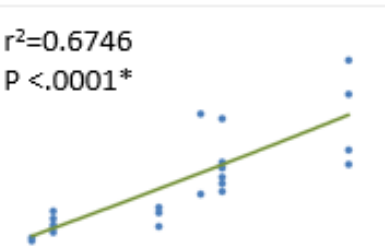
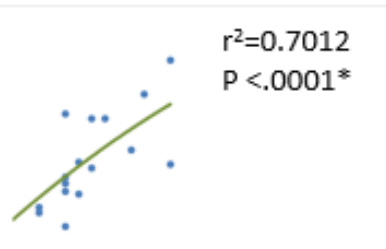
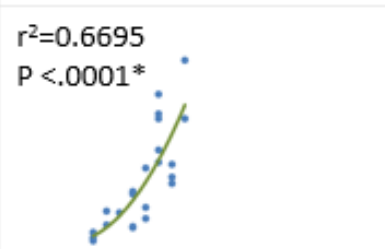
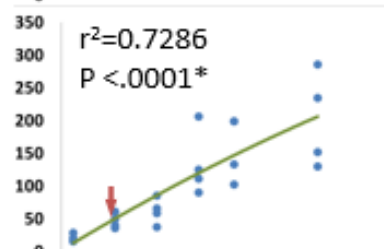
Low

CLXL745



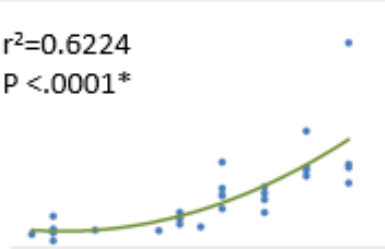
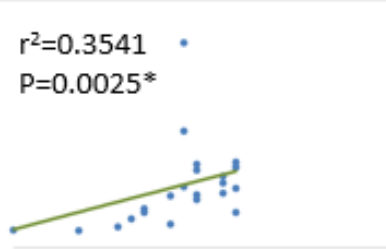
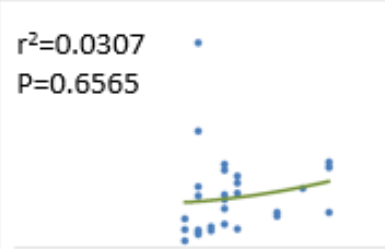
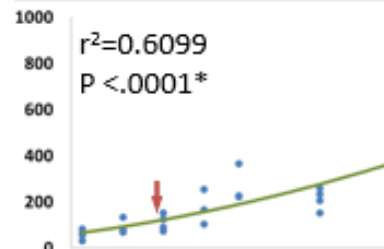
Low

Francis



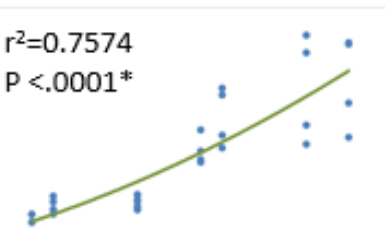
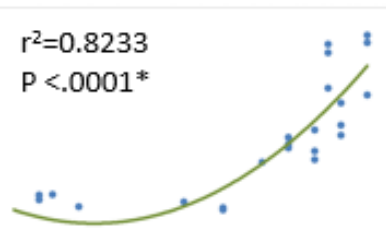
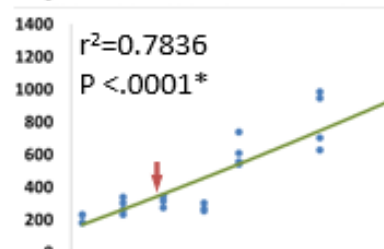
Mod. High

Jupiter



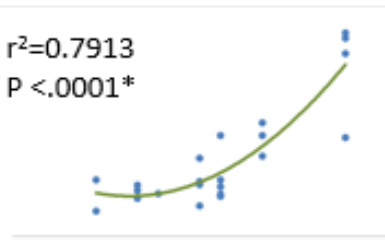
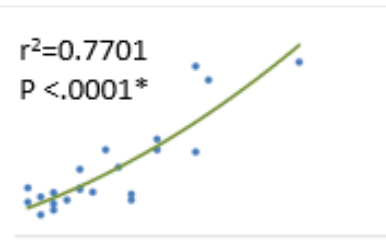
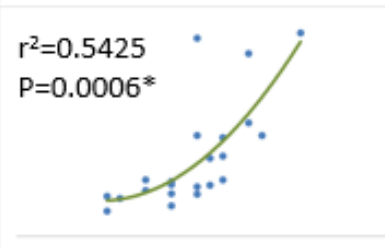
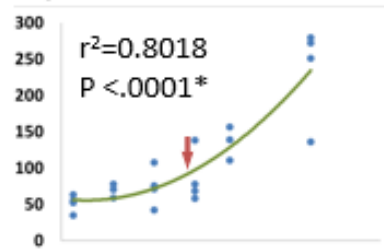
High

Rondo



Low

Sabine



Seasonal CH<sub>4</sub> emission [CH<sub>4</sub>-C g ha<sup>-1</sup>]

02-Oct12-Oct22-Oct01-Nov11-Nov21-Nov

1 5 9 13 17 21 25 29

1 5 9 13 17 21 25 29

1 2 3 4 5 6 7 8 9 10

Date

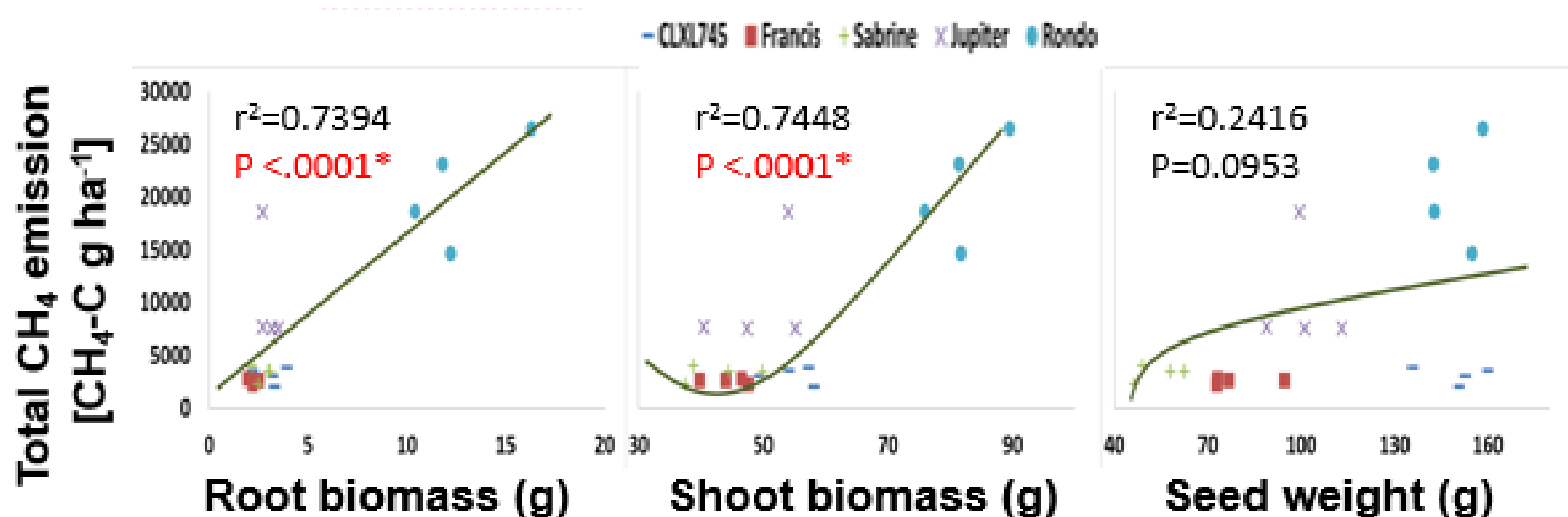
Tiller number

Panicle number

Reproductive stage (R)

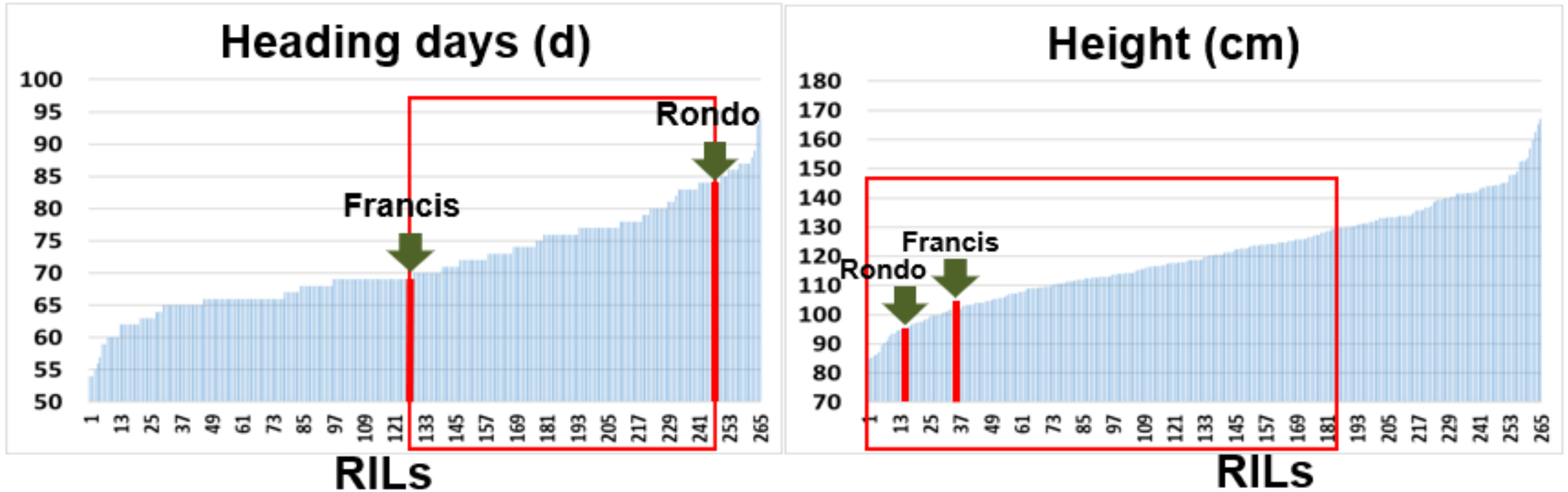


# CH<sub>4</sub> Emissions Were Highly Correlated with Root and Shoot Biomass at Maturity But Not Grain Yield



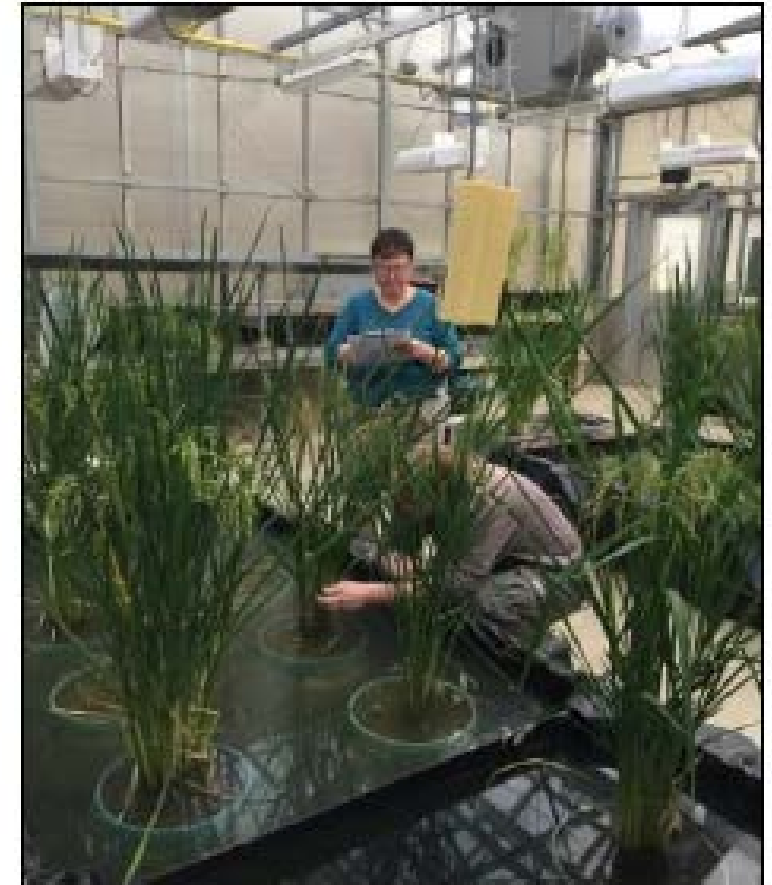
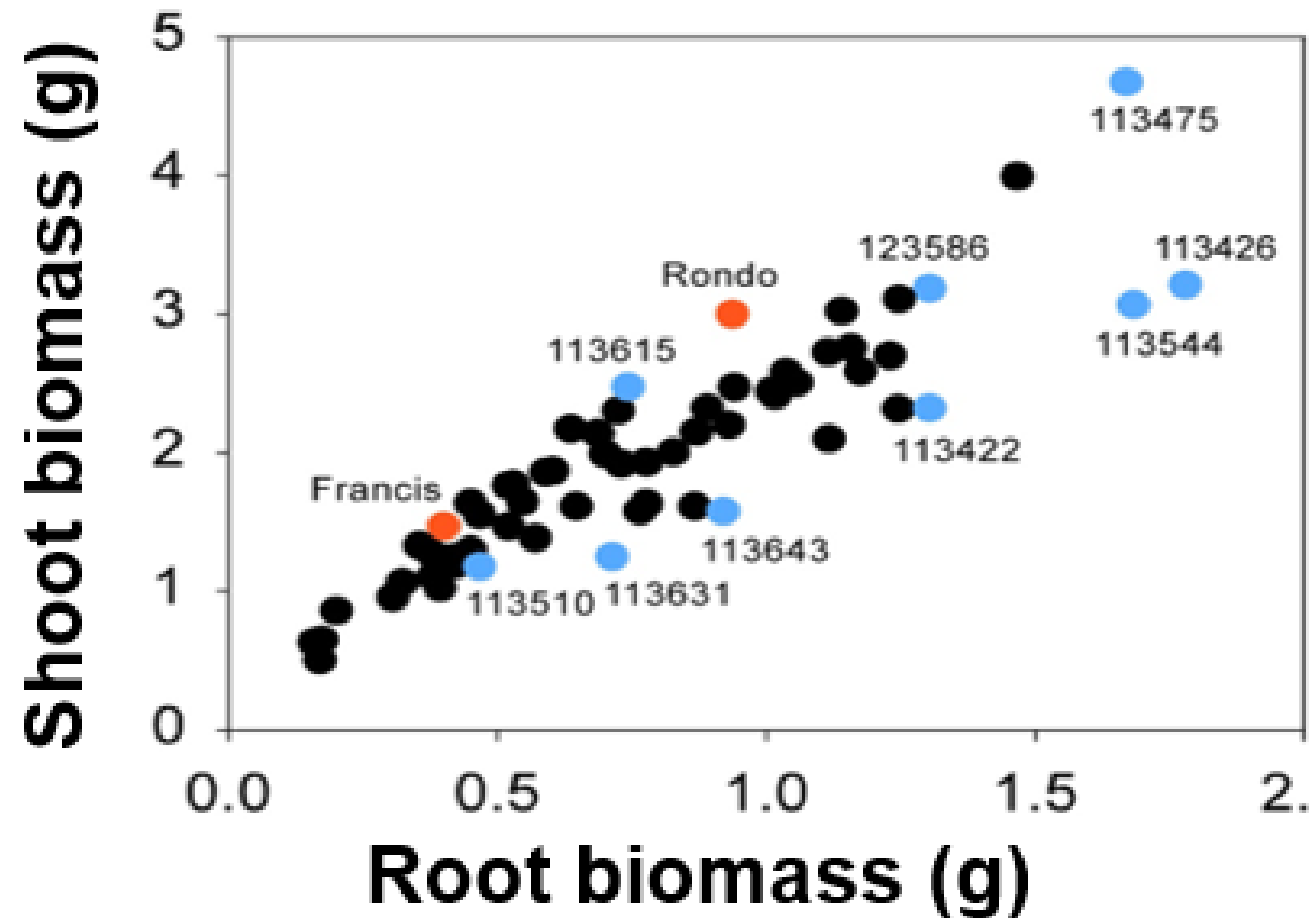
Francis (TRJ) and Rondo (Indica) Were Divergent for CH<sub>4</sub> Emissions and Root and Shoot Biomass

# Francis x Rondo Mapping Population of 220 Recombinant Inbred Lines Were Used to Explore Traits Associated with CH<sub>4</sub> Emissions in A Common Genetic Background



Selection of ~70 RILs Within a Similar Heading and Height Range

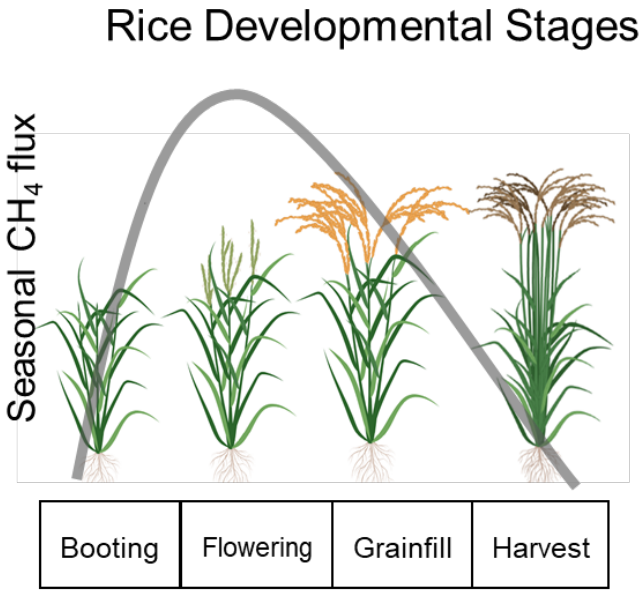
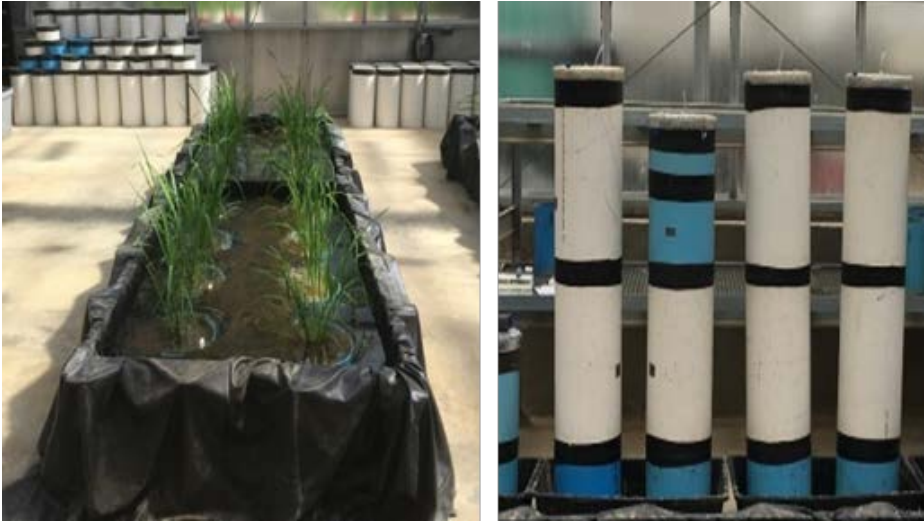
## RILs and Parents Were Evaluated for Shoot and Root Biomass at 6 wk stage and 9 RILs Were Selected for CH<sub>4</sub> Emission Evaluation



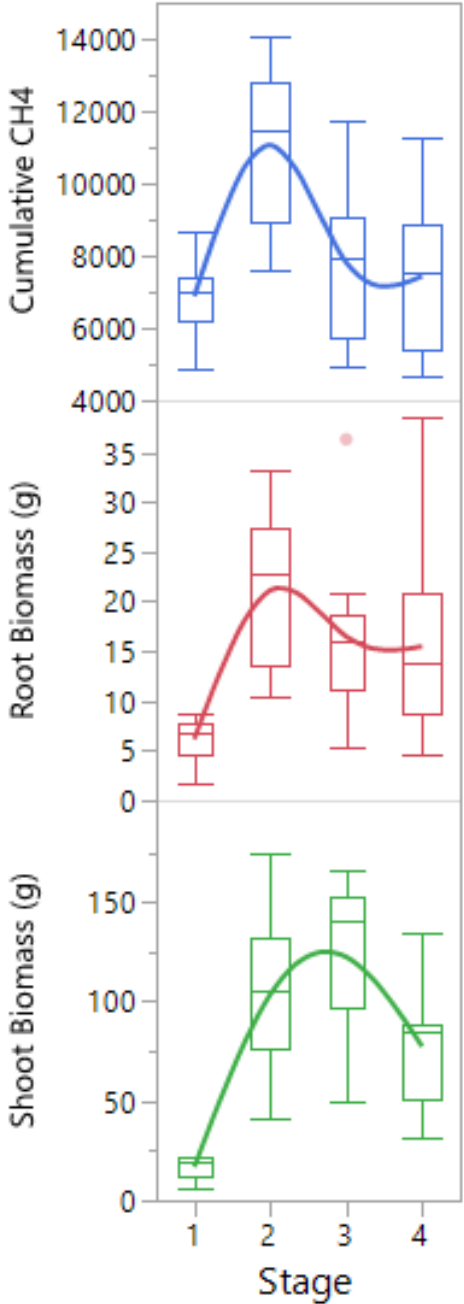
Barnaby, J.Y., Pinson, S.R., Chun, J. and Bui, L.T., 2019. Covariation among root biomass, shoot biomass, and tiller number in three rice populations. *Crop Science*, 59(4), pp.1516-1530.

# CH<sub>4</sub> Measurements At the Heading Stage (2) and During Late Grainfill (3) Captured the Peak Emissions

Pattern of Seasonal CH<sub>4</sub> Emissions

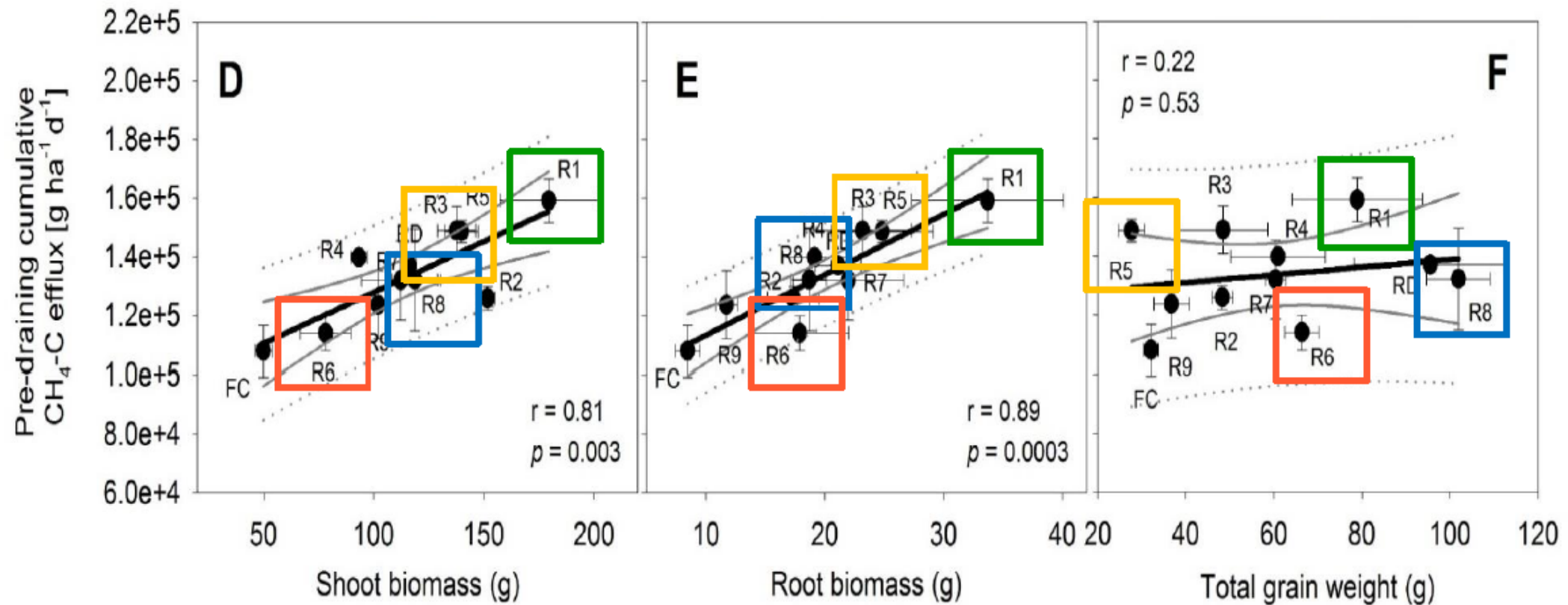


**Methane emissions peak  
at the flowering stage**

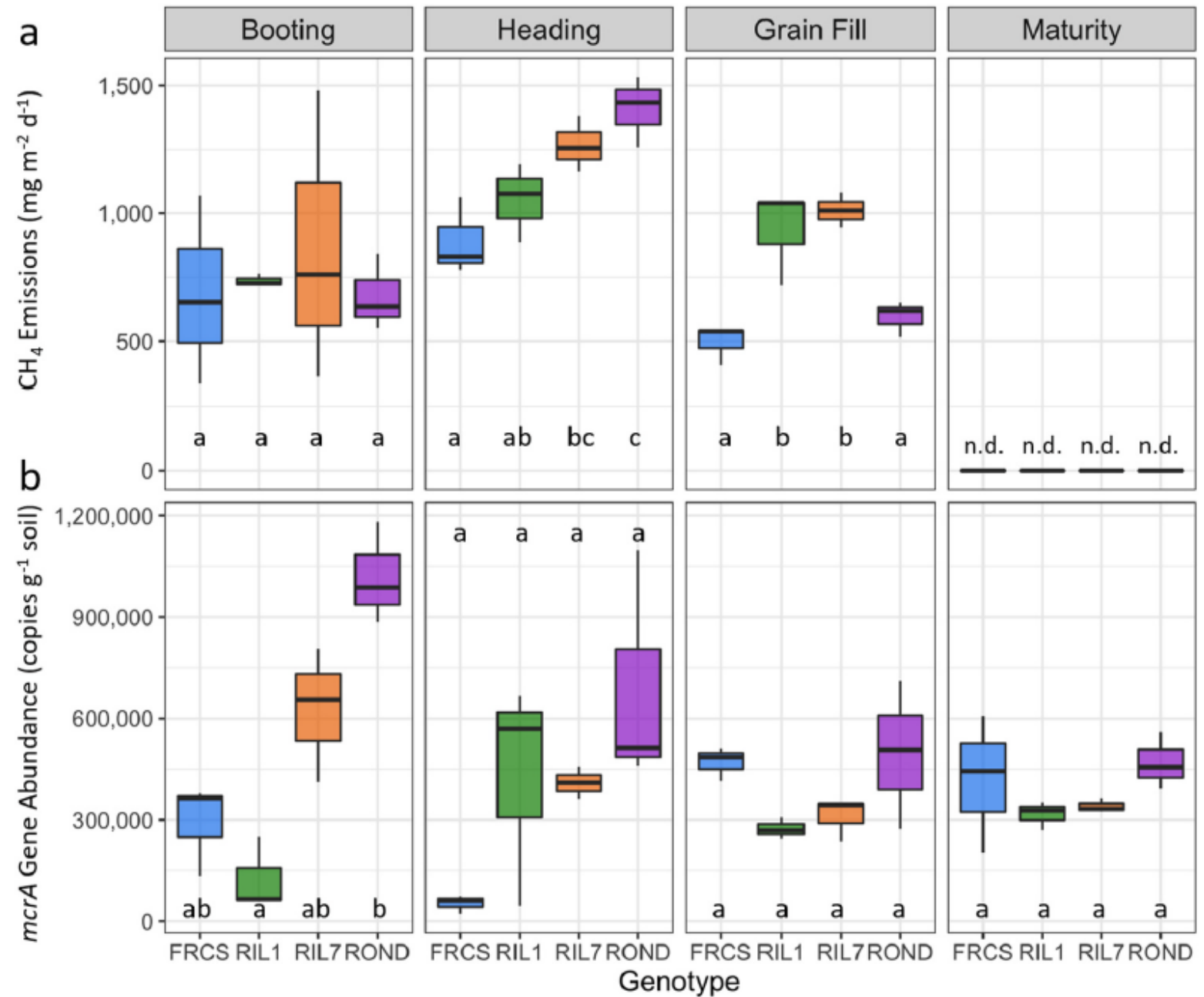




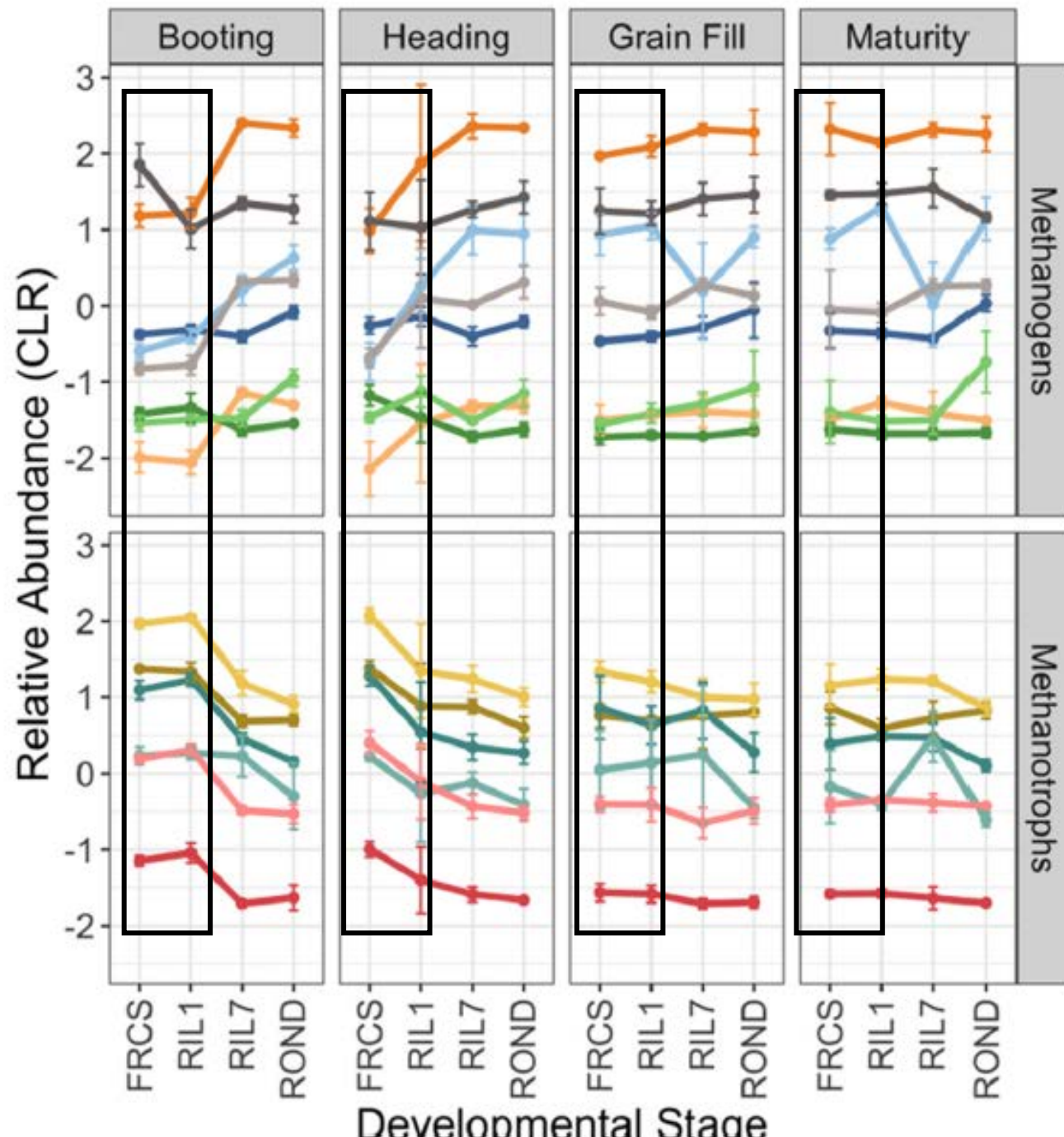
# As Among the Different Cultivars, CH<sub>4</sub> Emissions Were Correlated with Root and Shoot Biomass but Not Yield.



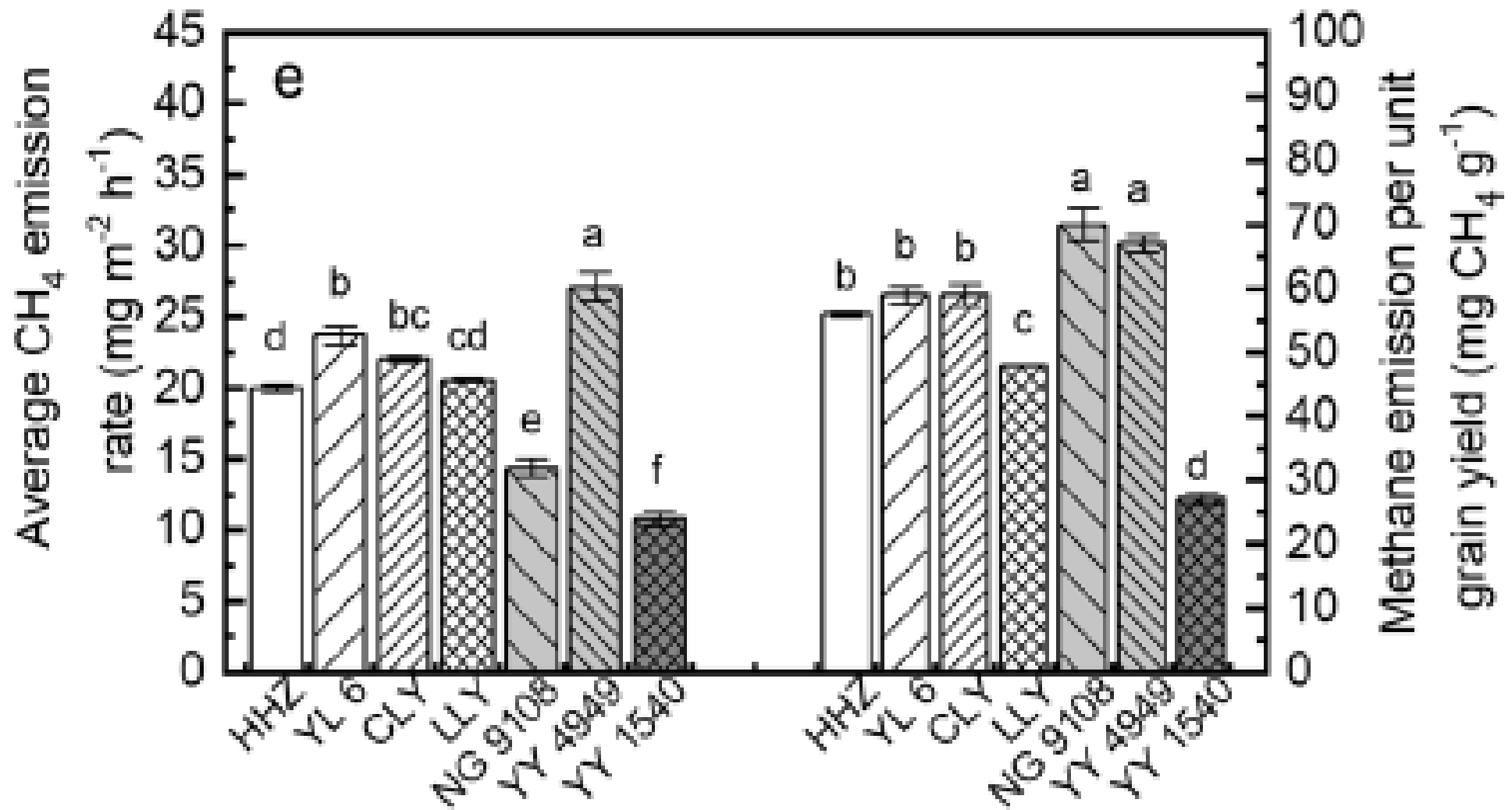
RILS Differing in CH<sub>4</sub> Emissions Were Selected for Soil Microbiome Studies



Fernández-Baca, C.P., Rivers, A.R., Kim, W., Iwata, R., McClung, A.M., Roberts, D.P., Reddy, V.R. and Barnaby, J.Y., 2021. Changes in rhizosphere soil microbial communities across plant developmental stages of high and low methane emitting rice genotypes. *Soil Biology and Biochemistry*, 156, p.108233.

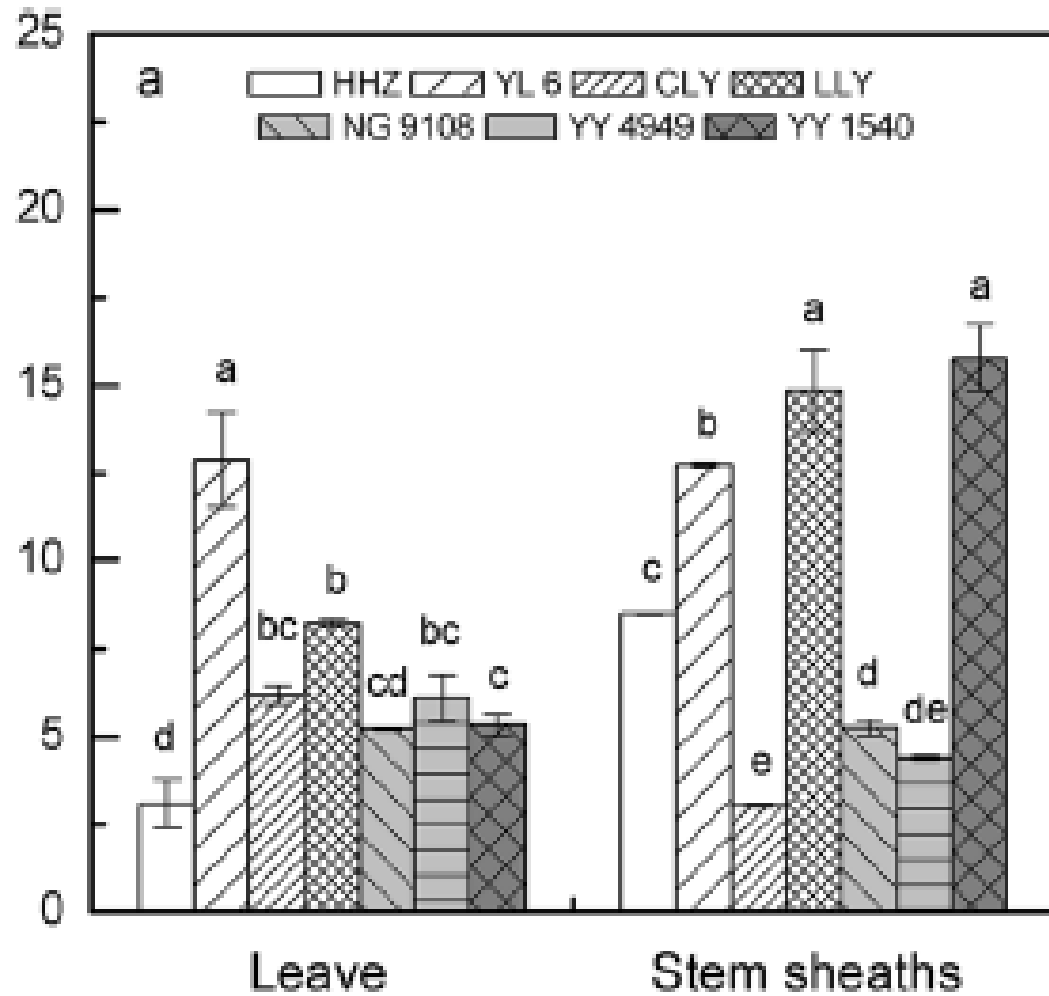


Low Emitters- lower methogens and greater methanotrophs during booting and heading

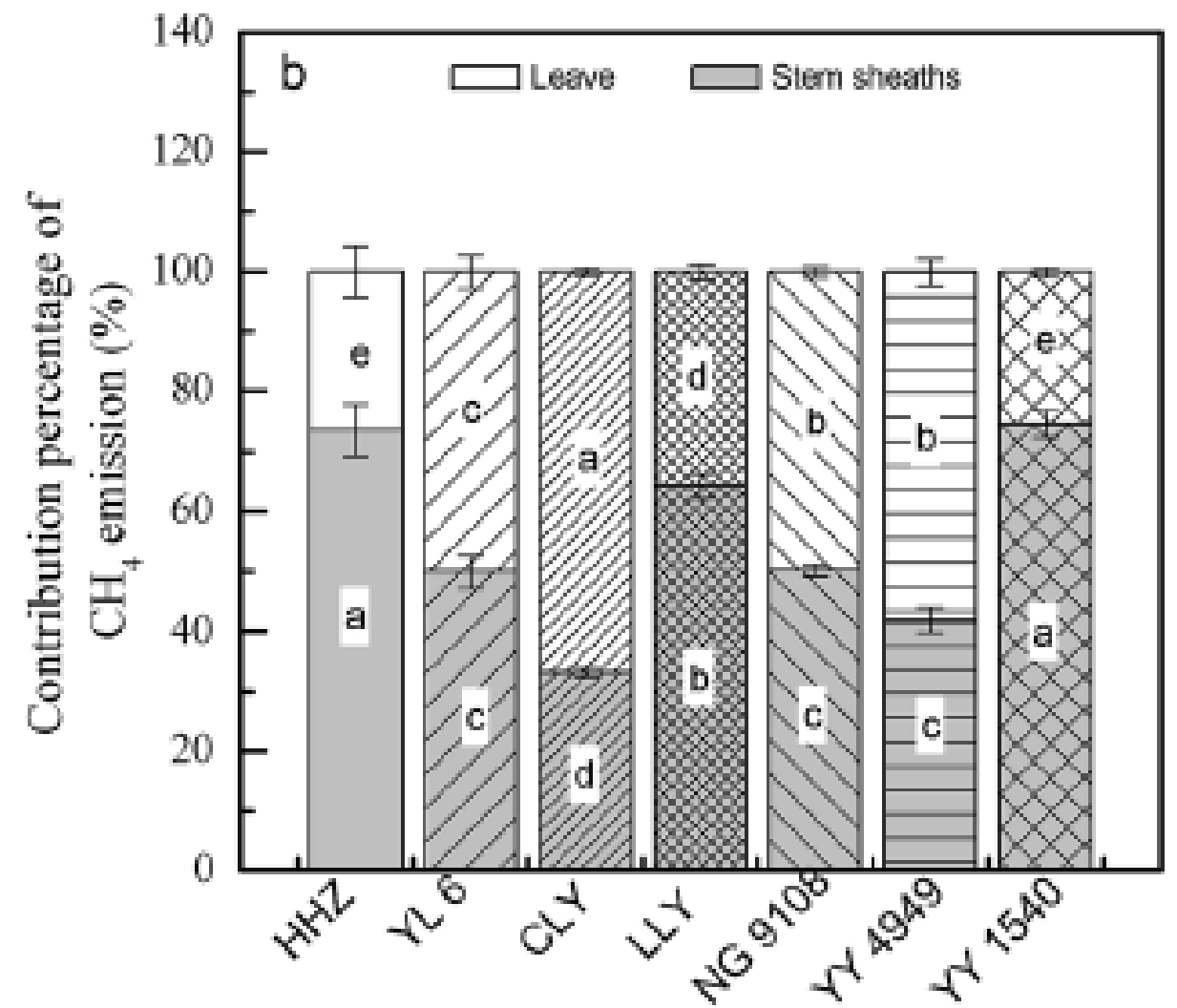




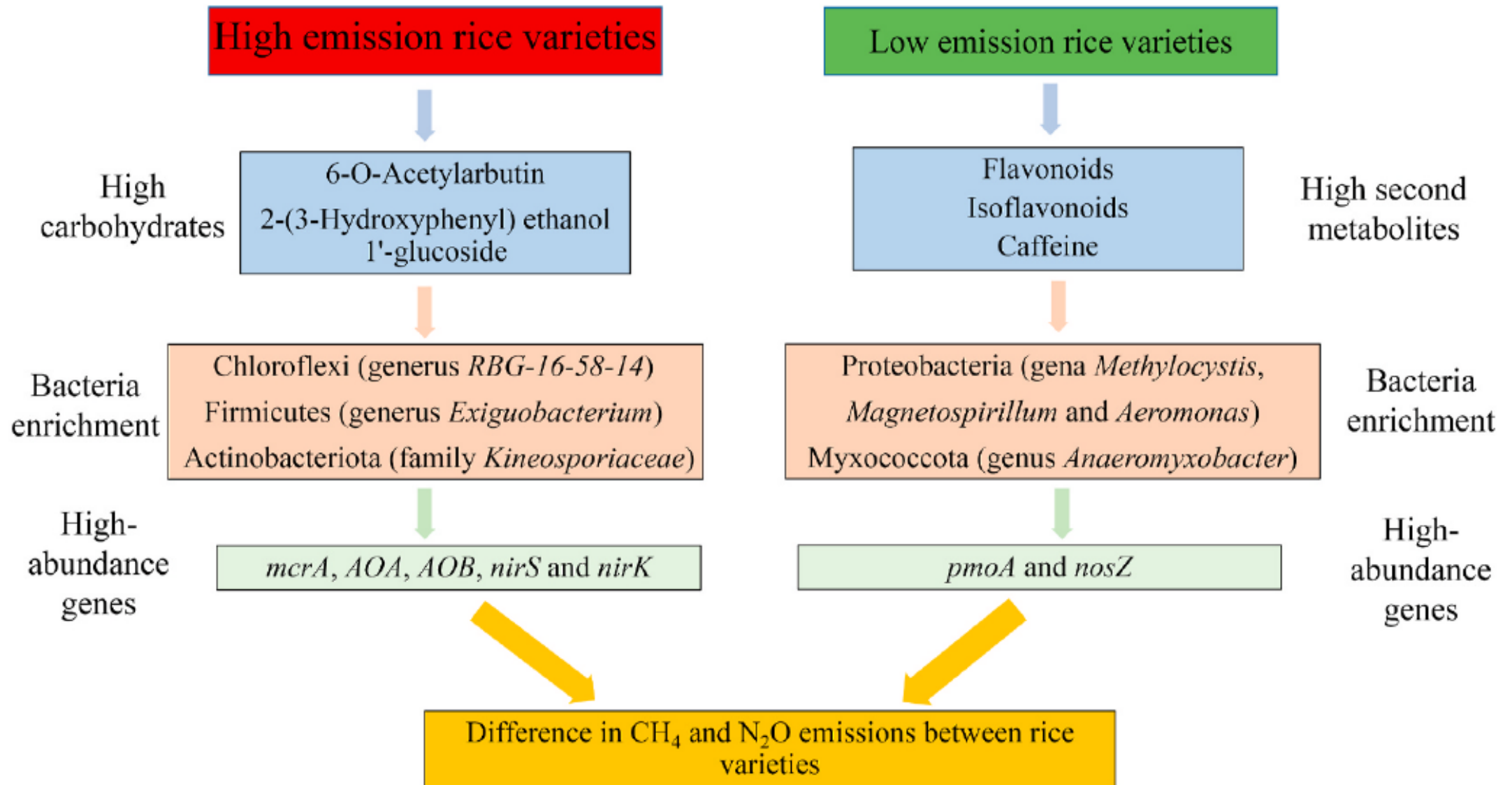
## Other Plant Parts Need to Be Studied for Their Role in GHGE



Different parts of rice plant



Different rice varieties



Ding 2022. Effect of microbial community structures and metabolite profile on greenhouse gas emissions in rice varieties. Env. Poll. 356

# Summary

- Rice cultivars differ in methane emissions and can be part of the mitigation process
- Mapping populations serve as a means of identifying traits and QTL that are related to GHGE that may help in developing new low emitting varieties
- Results demonstrate that different genotypes can influence the soil microbiome that impact GHGE
- Considering the complex G x E X M interactions affecting GHGE, screening for varieties that support lower methanogen and higher methanotroph abundances, may be a means of a high throughput selection method valuable for breeding low GHGE rice

