

***Root exudates impact plant performance
under abiotic stress and influence
bacterial communities***

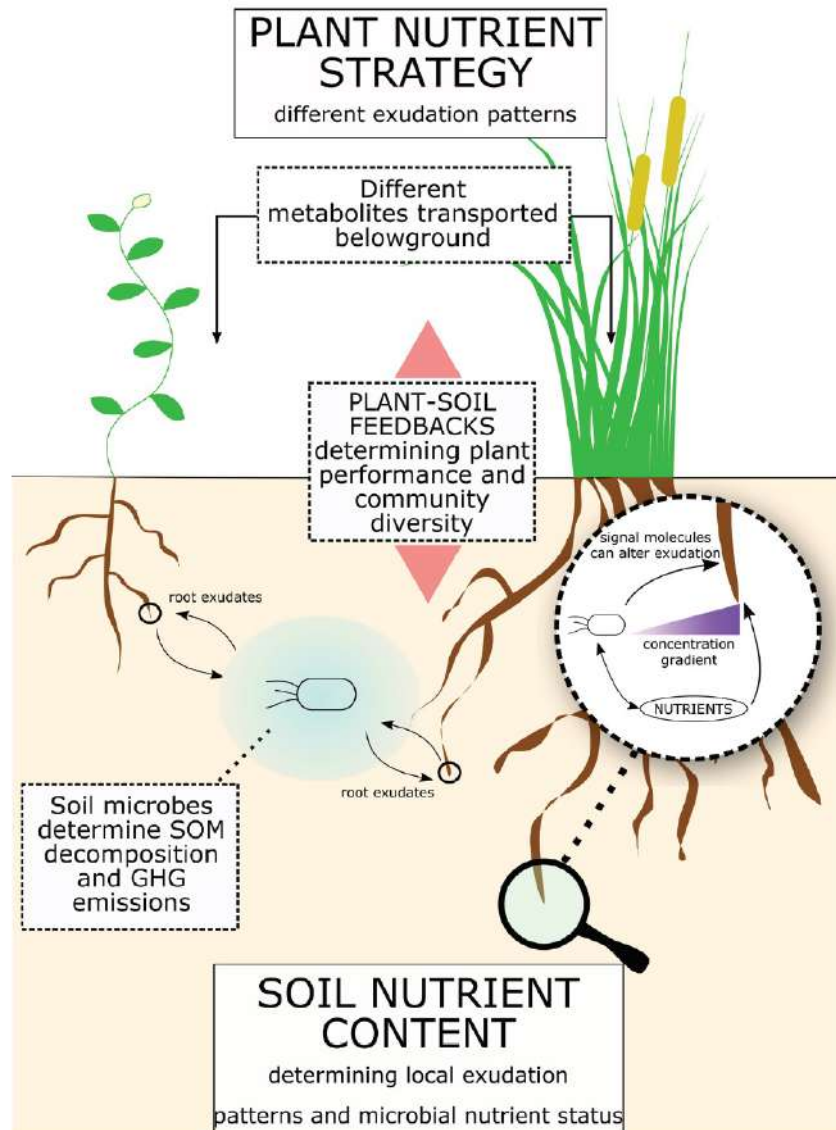
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Root exudates have multiple functional roles



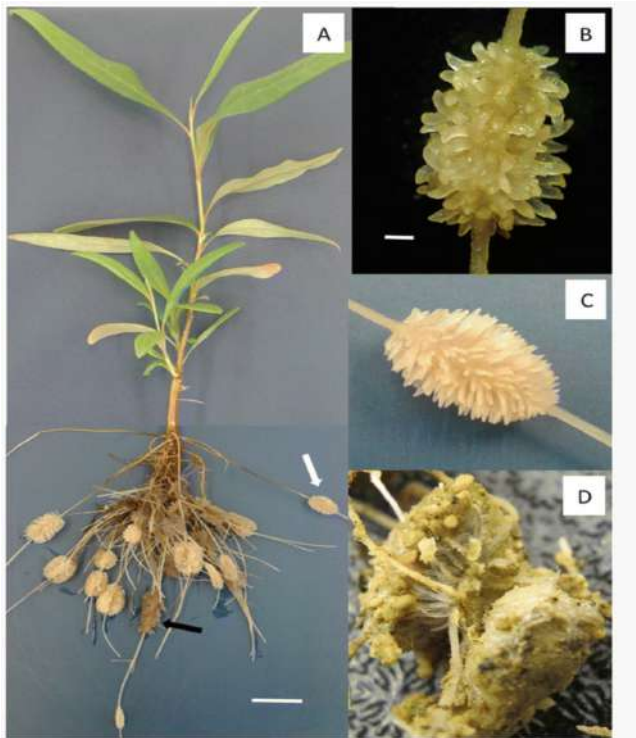
- Account for up to 21% of plant net photosynthates
- Primary metabolites – essential for cell growth and functioning
 - Organic acids
 - Amino acids
 - Sugars
- Secondary metabolites – not directly involved in cell growth and maintenance
 - Phenolics
 - Hormones

(Canarini et. al., 2019)

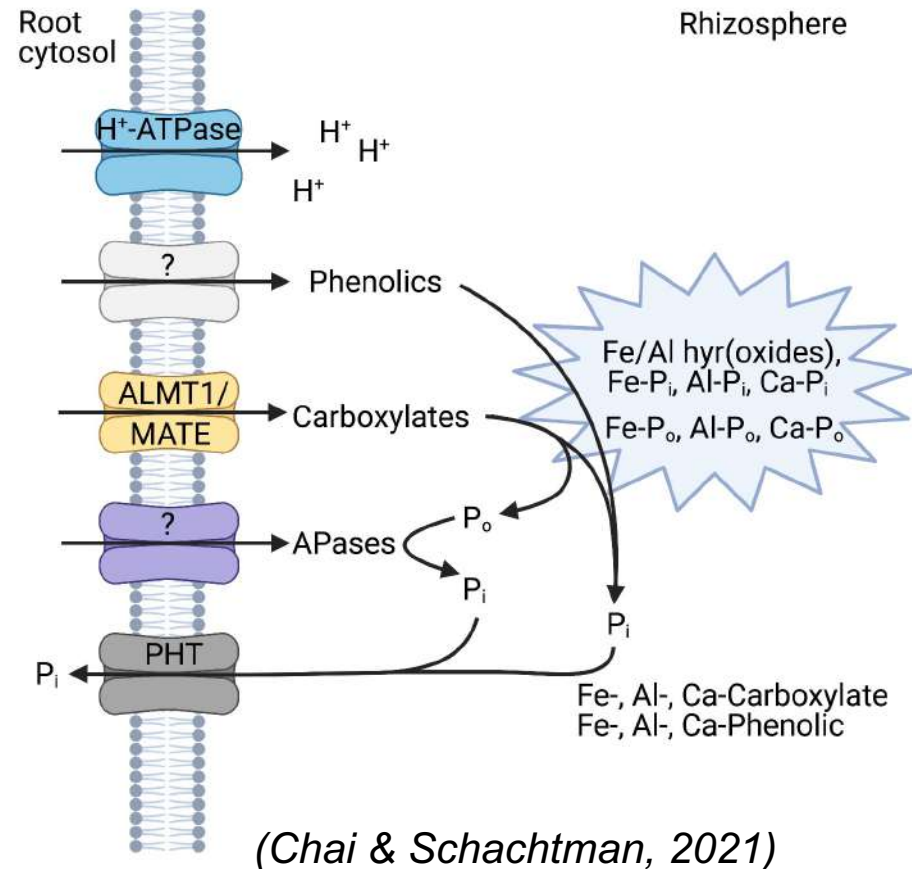


Exudates enhance plant P acquisition

- Up to 80% of soil phosphorus is not available for plant uptake
- Plant mechanisms in coping with P stress
 - Phenolics and carboxylates
 - Acid phosphatases (APases)

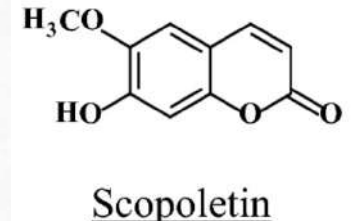
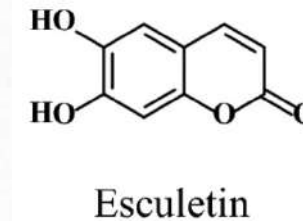
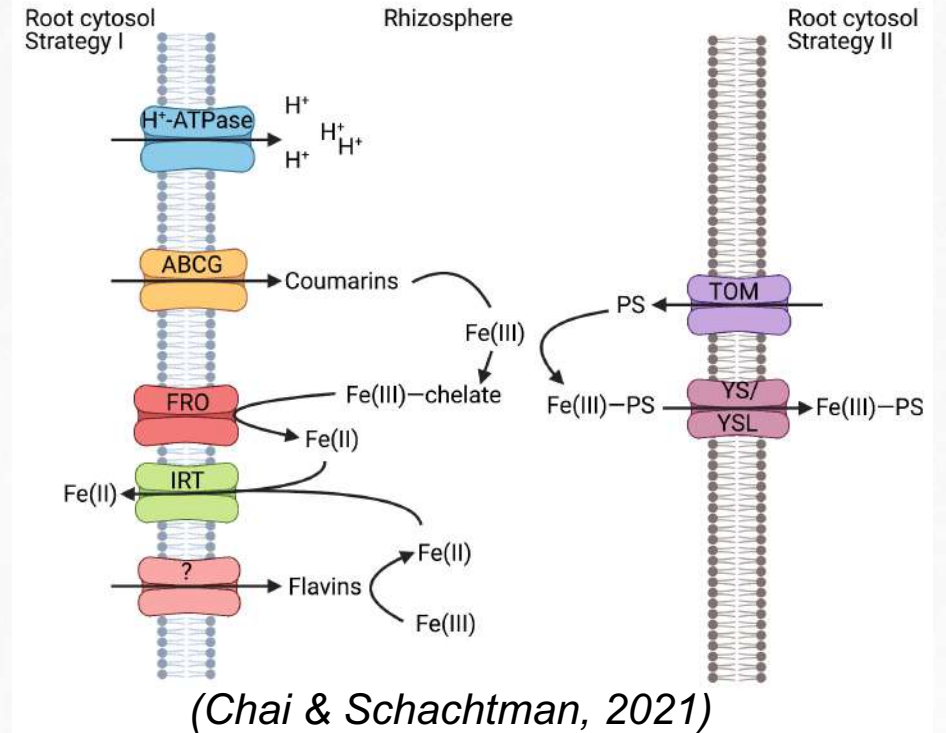


Cluster roots of *Embothrium coccineum* seedling (Kleinert et al., 2018)



Exudates enhance plant Fe acquisition

- Fe largely exists in the ferric form (Fe^{3+}), but only ferrous form (Fe^{2+}) can be used by plants
- Coumarins, flavins, and phytosiderophores chelate with Fe
- Coumarins also affect root-associated microbiome
 - Scopoletin
 - Selective antimicrobial activity against fungal pathogens
 - Harmless to beneficial rhizobacteria (*Stringlis et. al., 2018*)



(An, Choi, & Ahn, 2020)



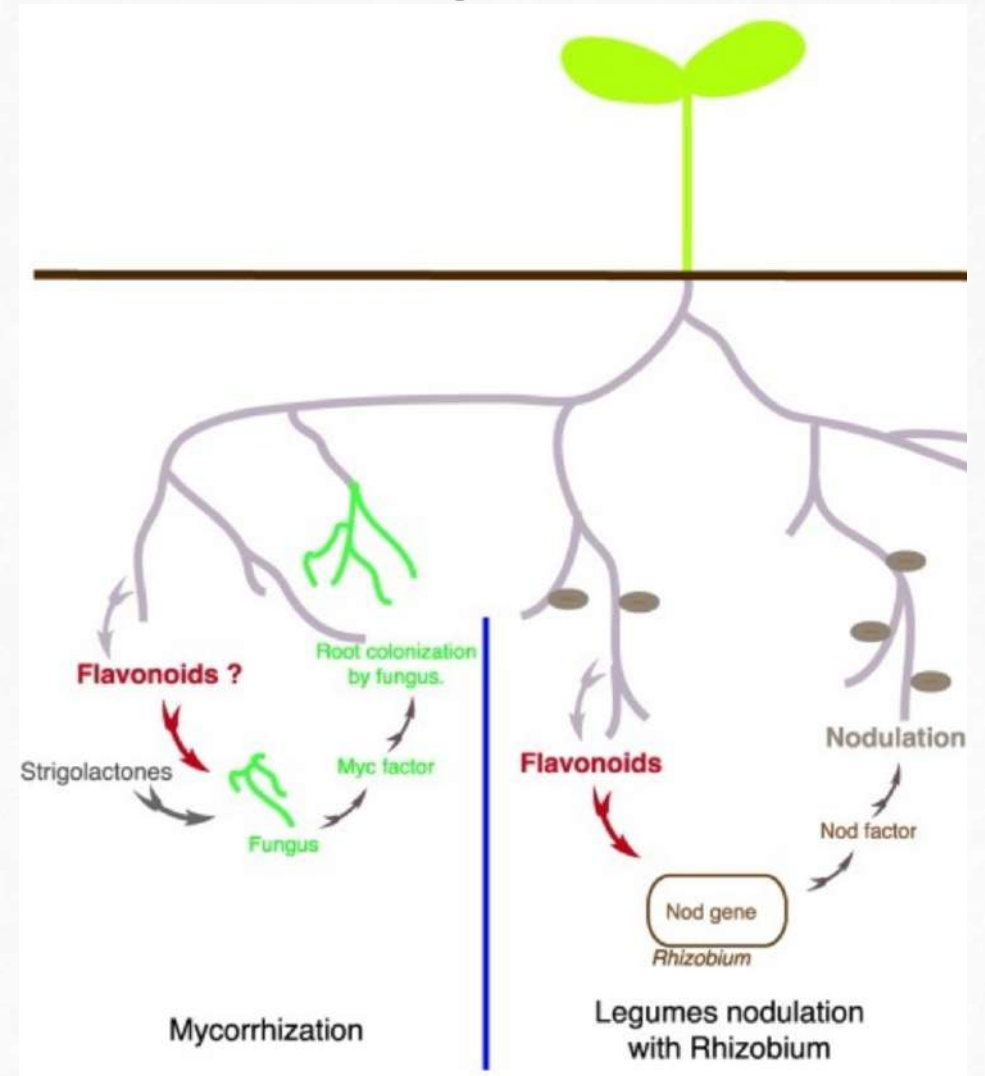
Root exudates play a key role in signaling beneficial bacteria and fungi

Arbuscular mycorrhizal fungi

- Strigolactones
- Flavonoids

Rhizobia

- Flavonoids



(Abdel-Lateif, Bogusz & Hocher, 2012)



Maize root exudates and their role in shaping root-associated microbial communities

Two major questions:

- Is there natural variation in exudates of maize?
- Can the natural variation in exudate concentration be used to study their impact on the root-associated microbiome?



~240 lines of maize for studying natural variation in exudates

"Buckler Goodman Association Panel" (*Flint-Garcia et al., 2005*)

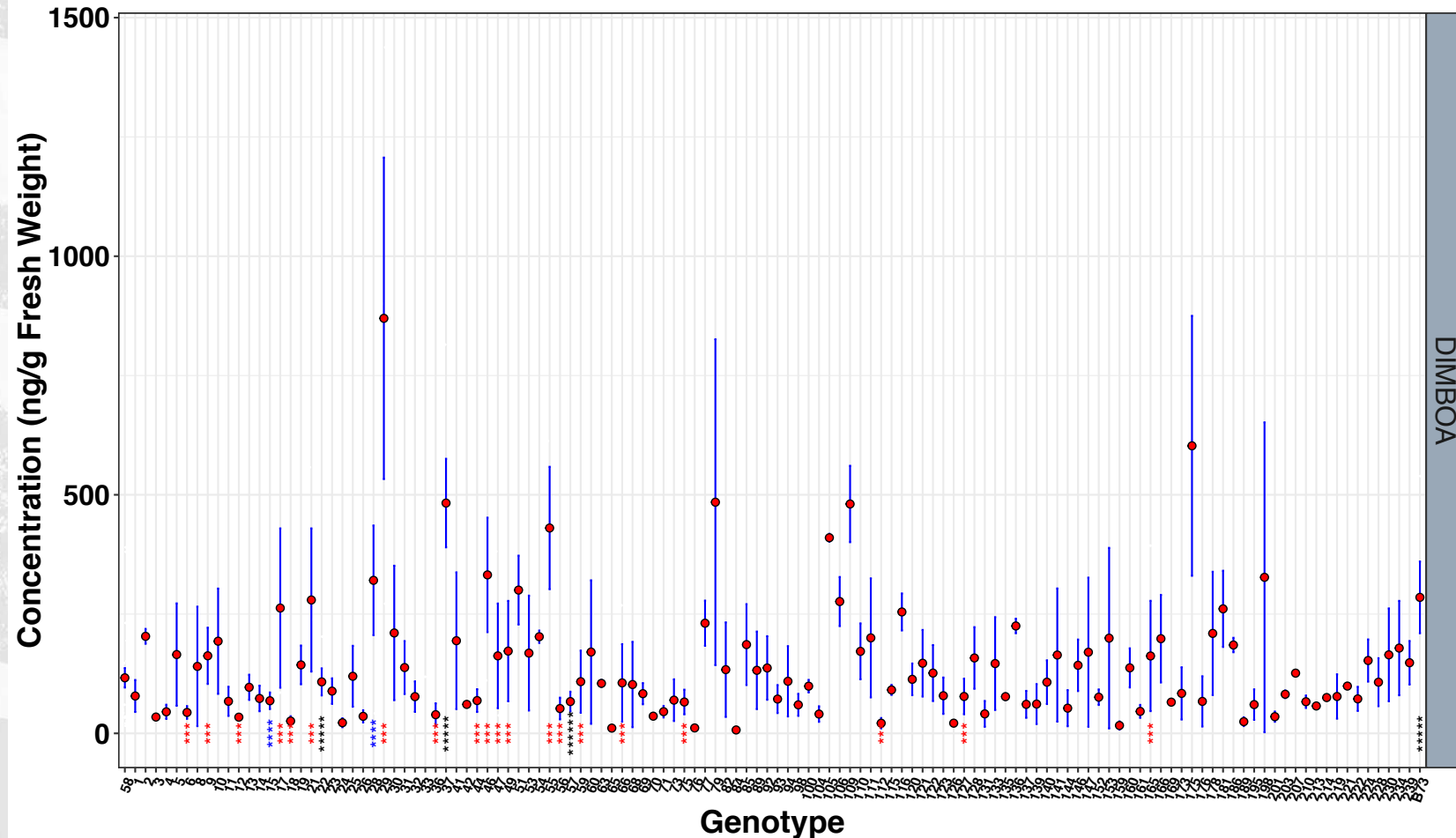
Targeted metabolite analysis



OA or sugar	Detected	AA	Detected	AA	Detected	Hormone	Detected
Succinic acid (SUC)	x	Ala	x	Pro	x	Indole-3-acetic acid (IAA1)	x
Citric acid (CIT)		Arg	x	Ser	x	IAA-Asp1	x
Fumaric acid (FUM)	x	Asn	x	Thr	x	trans-zeatin (tZ1)	
Lactic acid (LAC)	x	Asp	x	Trp	x	cis-zeatin (cZ1)	x
Malic acid (MAL)	x	Gln	x	Tyr	x	trans-zeatin riboside (ZR1)	x
Fructose	x	Glu	x	Val	x	Strigolactone (Orobanchol)	x
Glucose	x	His	x	Cys		Jasmonyl-isoleucine (JA-ILE1)	x
Sucrose	x	Ile	x	Gly		12-oxo-phytodienoic acid (OPDA1)	x
Galactose	x	Leu	x	Sec		Jasmonic acid (JA1)	x
Ribose		Lys	x	GABA	x	Abscisic acid (ABA1)	x
Raffinose		Met	x			Salicylic acid (SA1)	x
Arabinose	x	Phe	x			Gibberellins	x
Xylose	x					DIMBOA	x
Pinitol-soybean							
Mannose	x						
Threhalose	x						



Natural variation in DIMBOA concentration of the root exudates in 126 lines

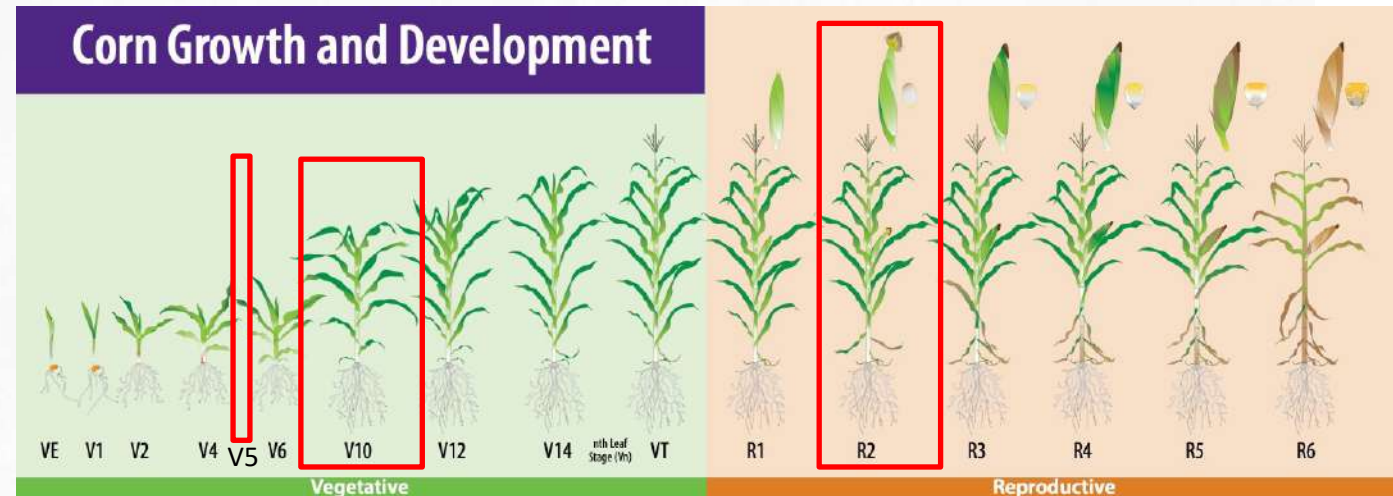
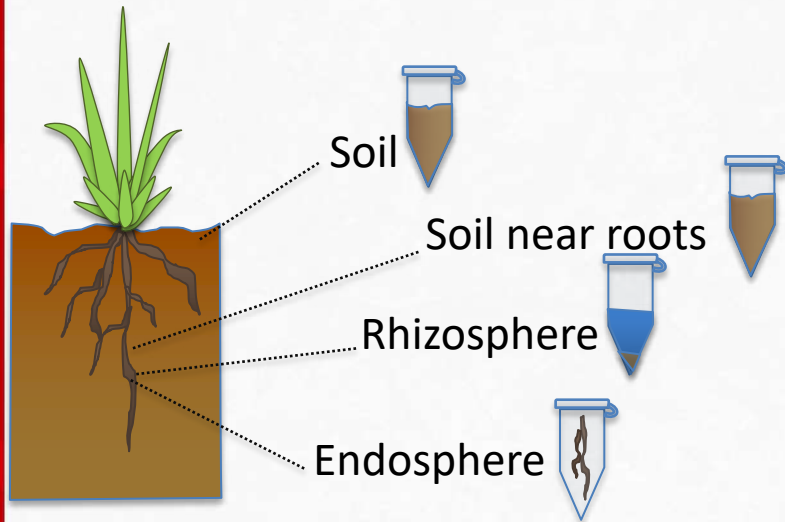


Variation in exudate concentrations also found in:

- GABA
- Total sugars
- JA
- IAA
- ABA

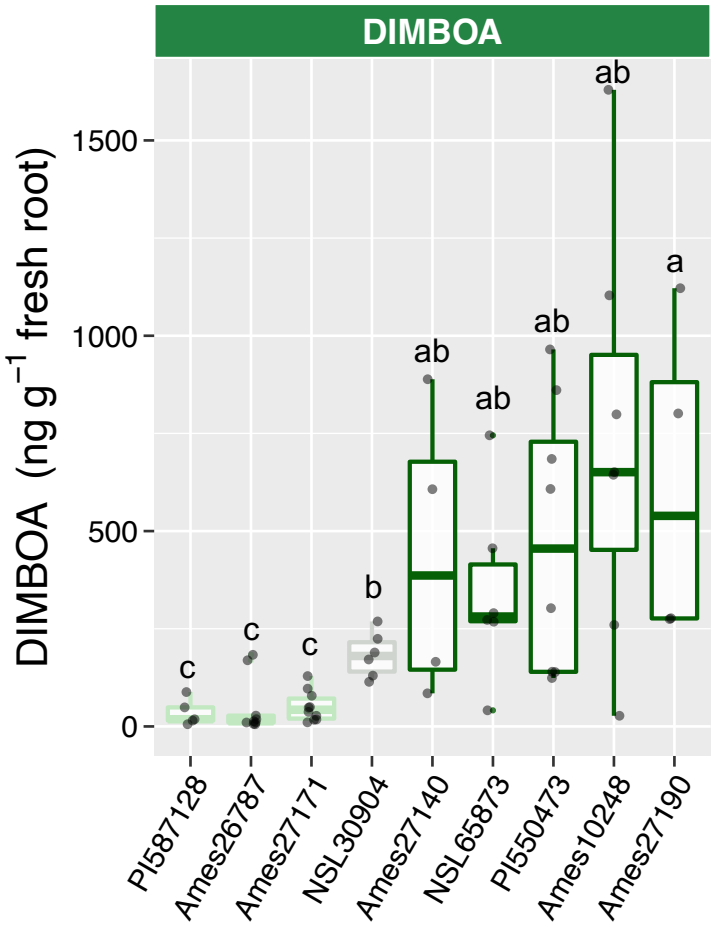
Note: "***": genotype having three replicates; "****": genotype having four replicates; "*****": genotype having five replicates. Others: two replicates; 58: 29 replicates

Field experiments to test the relationship between exudates and root associated microbiome composition

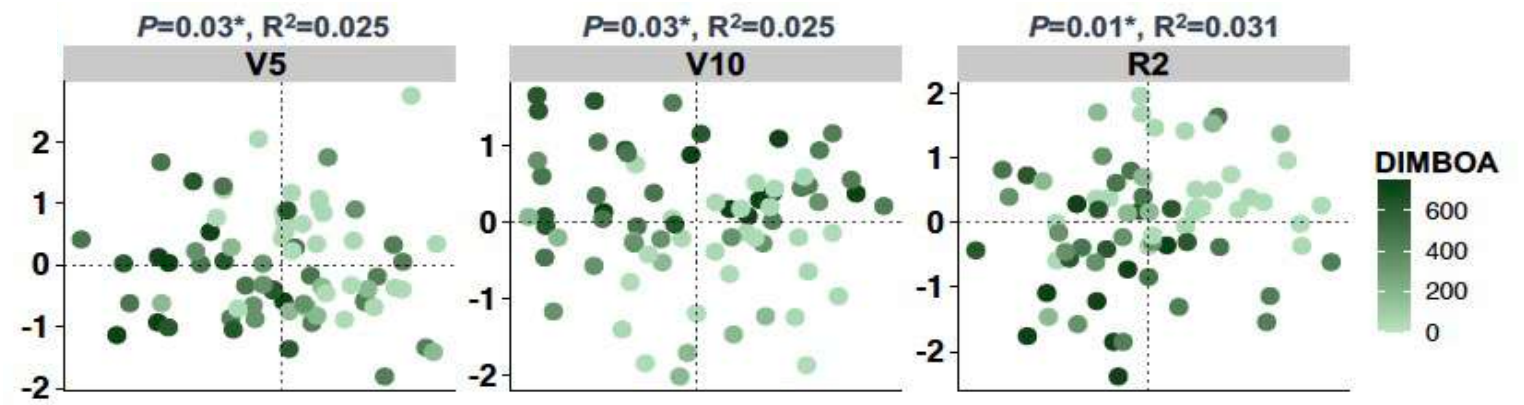


Root associated microbiome is temporally dynamic so sampling done at three time points – V5, V10, R2

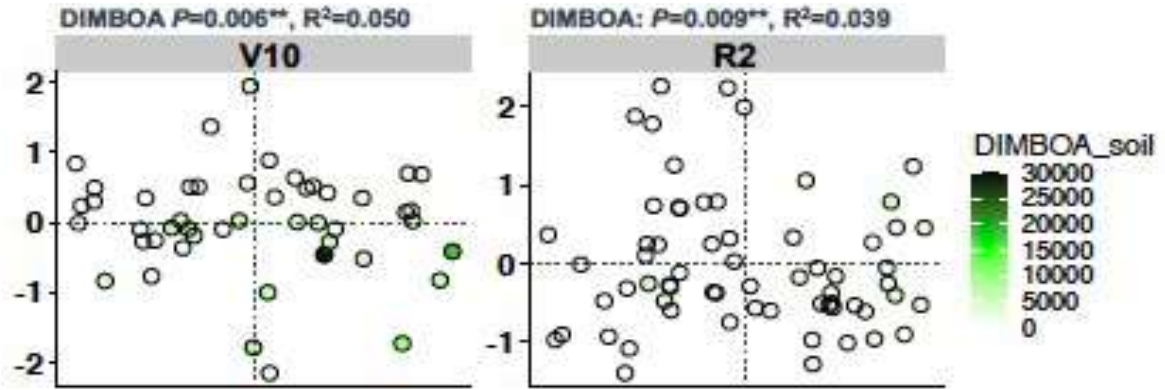
Natural variation in maize inbred lines can be used to study changes in community composition - validated using DIMBOA



Growth chamber DIMBOA exudate concentrations



DIMBOA measured in the field



Wang et. al., 2021, Natural variation in root exudation of GABA and DIMBOA impacts the maize root endosphere and rhizosphere microbiomes, bioRxiv
 doi: <https://doi.org/10.1101/2021.11.05.467511>

Significant changes in bacterial community composition due to DIMBOA

Root exudates are critical for plant interactions with environment

- Root exudates play important roles in plant tolerance to abiotic stress and influence microbiome structure and activity
- Large variation found in the concentration of many root exudates in maize
- First evidence that plant hormone jasmonic acid is exudated from maize roots and impacts bacterial community composition and activity

Future – to modify/breed for root exudates to enhance microbiome beneficial functions and to improve abiotic stress tolerance more work will need to be done on which exudates influence key changes and which genes contribute to variation exudate concentrations.

