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Agronomic Practices Influence Soil Biodiversity with Strong Feedback to Plant growth

Yantai Gan, Chantal Hamel, Luke
Bainard, Zakir Hossain, Yining Niu

Canada

Diversified cropping systems

Benefits

- Reduce marketing risks
- Increase farming profits
- Decrease carbon footprints
- Optimize soil resources utilization
- Enhance environmental benefits

Questions

- How it influences soil health
- Long-term sustainability

Rotational benefits:

- ✓ Reduce production risks
- ✓ Break pathogen survival chain
- ✓ Offer more weed control options
- ✓ Use water in deeper soil layers
- ✓ Use soil residual nutrients
- ✓ Effect on soil health/quality
- ✓ Effect on soil microbiomes

Well documented

Well known

Well known

Well known

Many studies


Little is known

Black box





Recent Research at the Swift Current Research & Development Centre, AAFC

1. Determine the influences of agronomic practices on soil biology and soil health
 2. Evaluate the association of soil attributes and crop productivity at a system level
 3. Assess the probability of using soil beneficial microbiomes to suppress soil-borne pathogens
- 

Agronomic Practices and Soil Health

Main factors:

1. Fungicides use in pulse crops
2. Early-harvest pea vs late-harvest chickpea
3. Pulse-intensified rotations
4. Choice of crops and cultivars
5. Fertilizer N effect on microbiomes

Graduates and Post-Doc fellows



Ahmad Taheri



Sheng Min



Lobna Abdellatif



Adriana
Navarro-Borrell



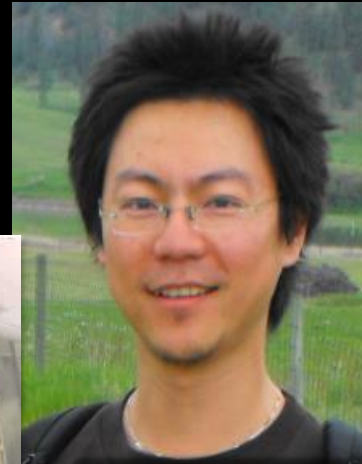
Walid Ellouze



Mulan Dai



Navid
Bazghaleh



Tony Yang



Yining Niu

Work Logistics



MAR-MAY

JUL

AUG

SEPT-OCT



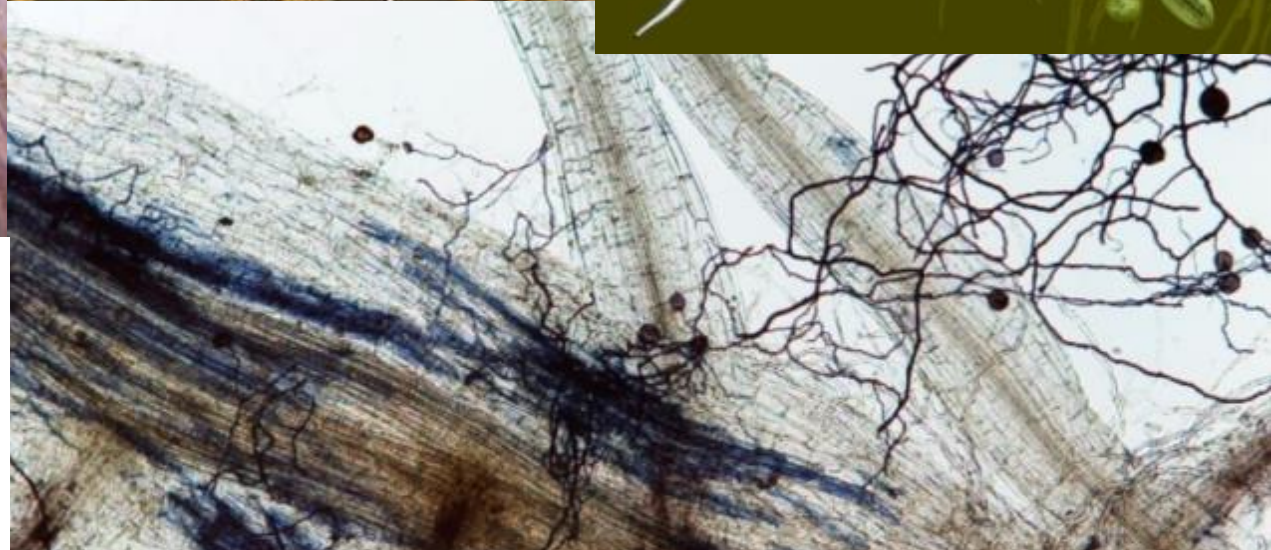
- ✓ Soil water, nutrient analyses
- ✓ Seeding
- ✓ Fertilizer & chemical application

- ✓ Rhizosphere soil and root sampling
- ✓ Root colonization
- ✓ Root DNA analysis
- ✓ Disease rating

- ✓ Soil sampling
- ✓ Soil DNA analysis
- ✓ Microbial activity



Agronomics - Microbial Community – Soil Health





Tag-encoded pyrosequencing analysis of the effects of fungicide application and plant genotype on rhizobacterial communities

Chao Yang^{a,b,c,*}, Chantal Hamel^{a,c}, Yantai Gan^{a,c}, Vladimir Vujanovic^{b,c}

^a Semiarid Prairie Agricultural Research Centre, AAFC, Swift Current, SK, Canada

^b Food & Bioproducts Sciences, University of Saskatchewan, Saskatoon, SK, Canada

^c Graduate School of Life and Environmental Sciences, Kyoto Prefectural University, 1-5 Shimogamohangi-cho, Sakyo-ku, Kyoto 606-8522, Japan

➤ **Fungicide use in pulse crops influenced the rhizobacterial community, and interacted with the choice of crop cultivars**

LI	0.43	1							
LII	0.38*	0.51	1						
LIII	0.34*	0.44	0.49	1					
VC	0.52	0.53	0.51	0.39*	1				
VI	0.49	0.57	0.55	0.37*	0.47	1			
VII	0.48	0.49	0.50	0.47	0.50	0.48	1		
VIII	0.40*	0.48	0.47	0.21*	0.48	0.47	0.45	1	

Note: Treatment codes as listed in Fig. 1.

* Significant difference according to Parsimony test at $P < 0.001$, $N = 64$.

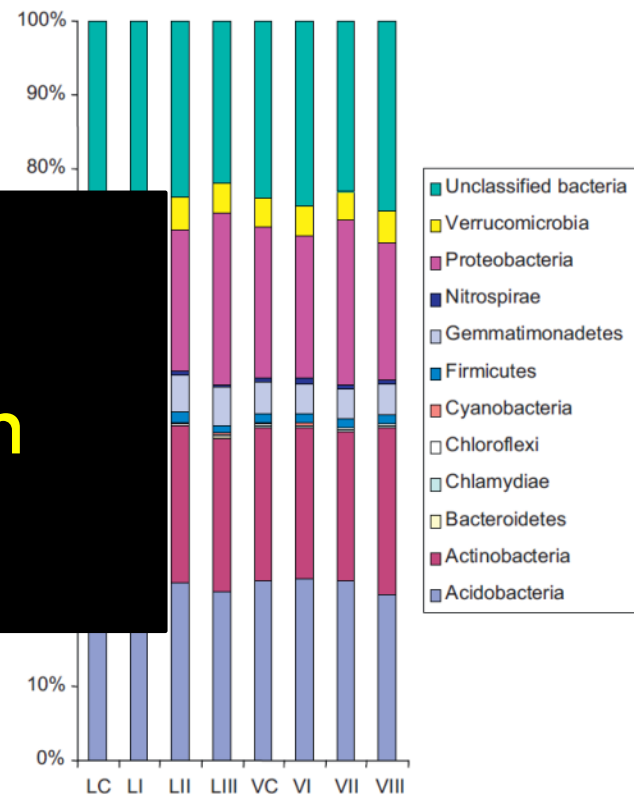


Fig. 1. Relative abundances of phylogenetic groups in rhizosphere soils derived from the different fungicide treatments and chickpea genotypes classified at the phylum level. VC: CDC Vanguard Control; VI: CDC Vanguard treatment I; VII: CDC Vanguard treatment II; VIII: CDC Vanguard treatment III; LC: CDC Luna Control; LI: CDC Luna treatment I; LII: CDC Luna treatment II; LIII: CDC Luna treatment III.

ORIGINAL ARTICLE

Nontarget effects of foliar fungicide application on the rhizosphere: diversity of *nifH* gene and nodulation in chickpea field

C. Yang^{1,2}, C. Hamel¹, V. Vujanovic² and Y. Gan¹

¹ Semiarid Prairie Agricultural Research Centre, AAFC, Swift Current, SK, Canada

² Food and Bioproducts Sciences, University of Saskatchewan, Saskatoon, SK, Canada

- Fungicide use in pulses influenced the community of *nifH* N-fixing gene and the carriers;
- Fungicide use in pulses affected phytochemicals on the roots, thus, causing a shift of N-fixing Rhizobacterial community

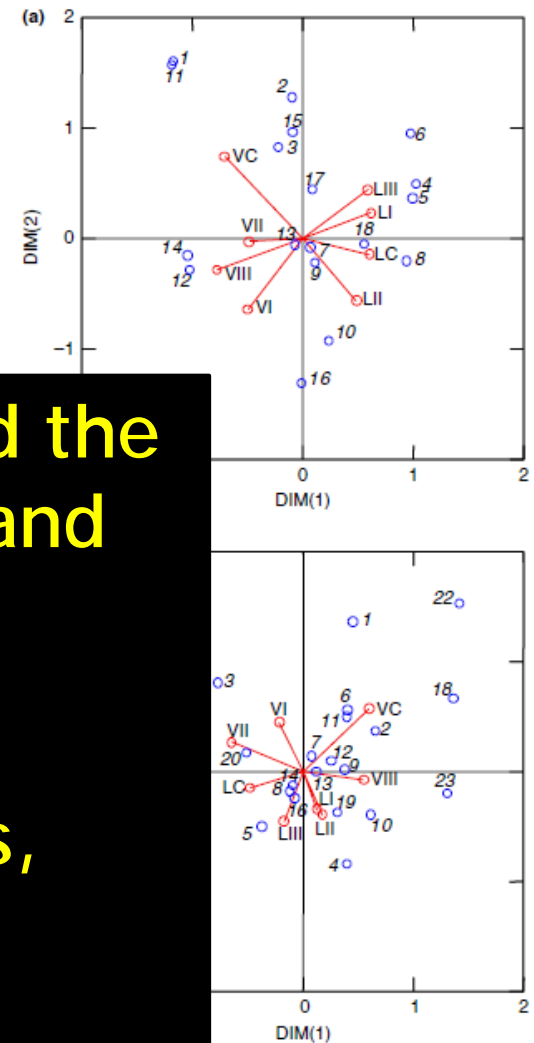
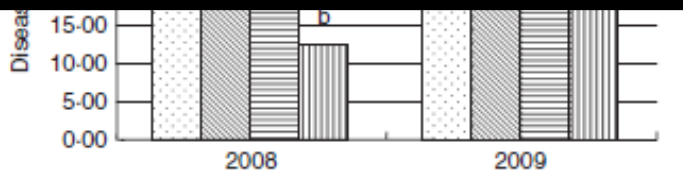


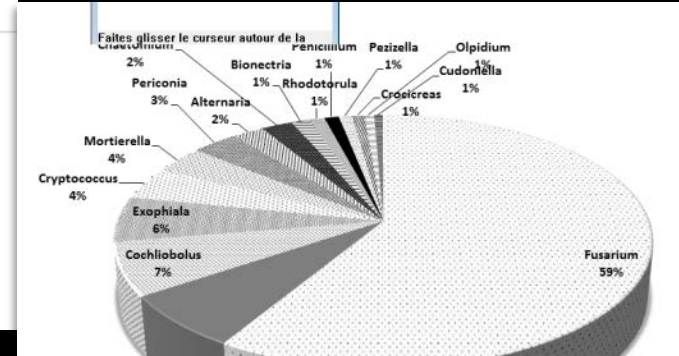
Figure 1 Correspondence analysis (CA) of relationships between disease control treatments and identified dominant N₂-fixing bacteria in the rhizosphere of both chickpea cultivars in 2008 (a) and 2009 (b), as revealed by *nifH* gene. C: control; I, II and III: increasing intensity of fungicide application; V: CDC Vanguard; L: CDC Luna; Numbers correspond to the identified N₂-fixing bacteria shown in Table 2. $P = 0.014$ in 2008, $P > 0.05$ in 2009, $N = 32$.





Pyrosequencing reveals the impact of foliar fungicide application to chickpea on root fungal communities of durum wheat in subsequent year

Ahmad Esmaili Taheri^{a, b, c}, Chantal Hamel^c, Yantai Gan^c



- *Fusarium* made up 59% and 23% of all fungal reads in the roots of durum wheat in 2009 and 2010, respectively;
- Fungicide use in chickpea increased *Fusarium* in the seminal roots of the subsequent durum wheat, but inconsistent

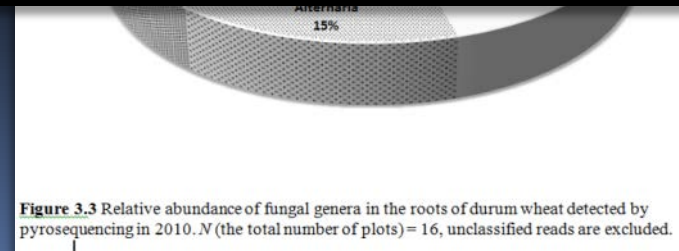
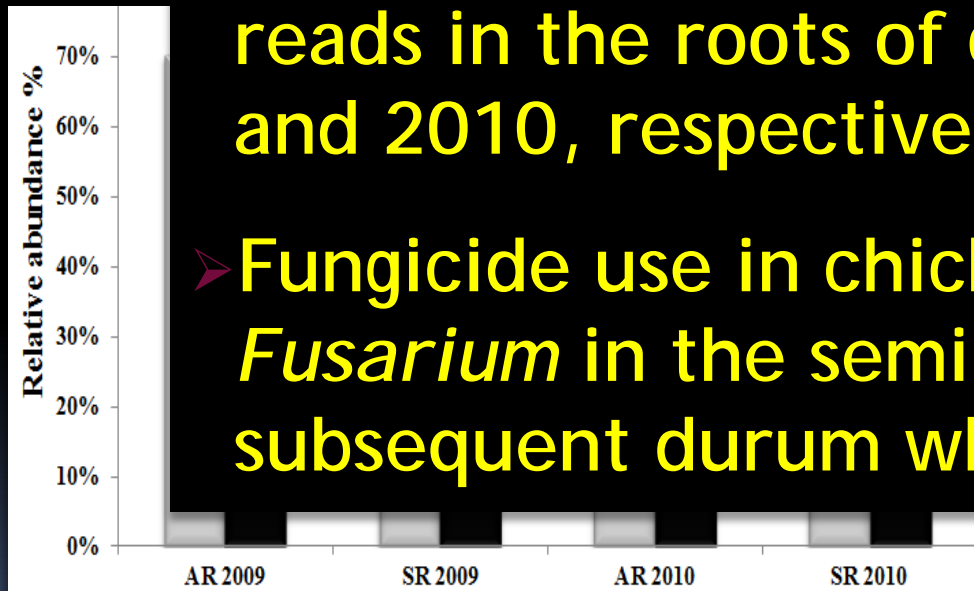
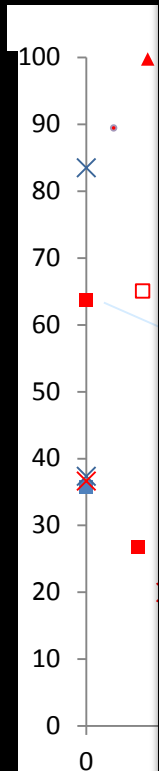


Figure 3.6 The effect of fungicide treatments on chickpea on the relative abundance of the genus *Fusarium* in seminal roots (SR) and adventitious roots (AR) of subsequent durum wheat at early seedling as determined by pyrosequencing. $P = 0.012$, $n = 4$.

Figure 3.3 Relative abundance of fungal genera in the roots of durum wheat detected by pyrosequencing in 2010. N (the total number of plots) = 16, unclassified reads are excluded.

Changes in the Fungal Functional Diversity of Durum Wheat Roots in Relation to Previous Year Farming Practices

Ahmad Esmacili Taheri^{1,2*}, Chantal Hamel², and Yantai Gan²



- Previous pulses influenced the abundance of antagonist and pathogenic fungal species in the subsequent durum wheat.
- Previous chickpea increased virulent fungal pathogens in the subsequent durum wheat more than previous pea
- Durum wheat grown after pea had greater fungal antagonists than durum wheat grown after chickpea

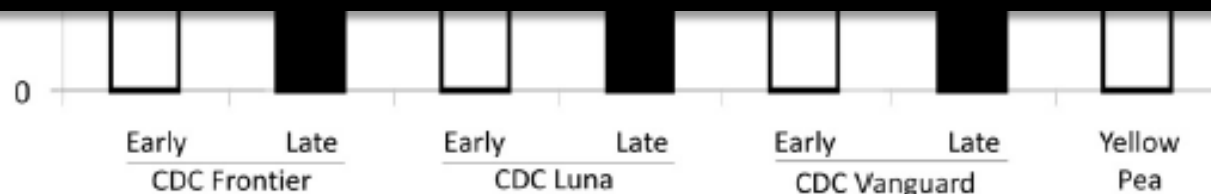
Vanguard

Luna

Pea

Bacterial endophytes mediate positive feedback effects of early legume termination times on the yield of subsequent durum wheat crops

- Early pulse termination promoted beneficial bacterial community in durum plant roots the following year
- Dry weather during pulse crop growth prevented this legacy from occurring
- The drought-resistant *Firmicutes* dominated after late pulse termination, and *Actinobacteria* dominated after early pulse termination.



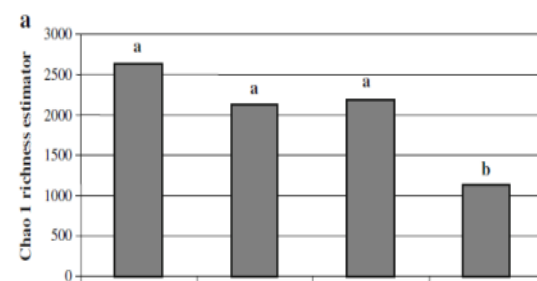
Pyrosequencing reveals how pulses influence rhizobacterial communities with feedback on wheat growth in the semiarid Prairie

Chao Yang · Chantal Hamel · Yantai Gan · Vladimir Vujanovic

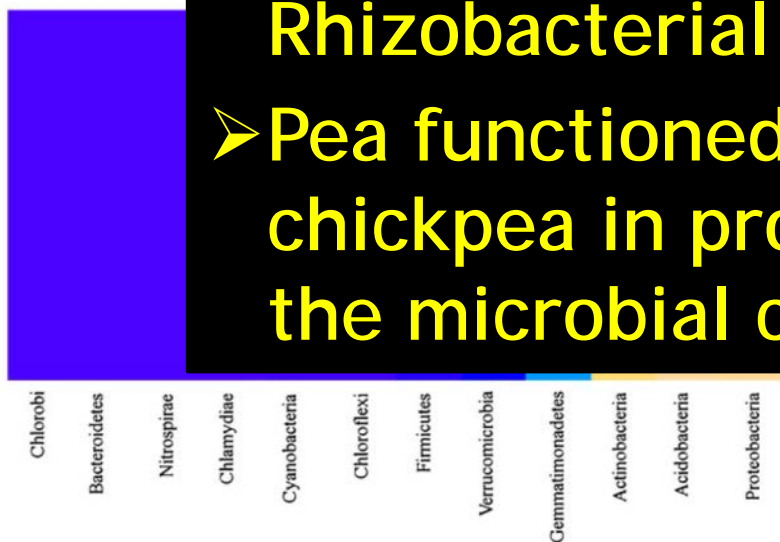
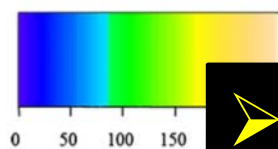
500

Plant Soil (2013) 367:493–505

Fig. 4 Influence of pulse crops on the diversity of their rhizobacterial community in September of 2008. a Chao 1 richness estimating index; b ACE richness estimating index; c Shannon (H') diversity index. Different small letters indicate significant differences based on protected Fisher-LSD test at $P < 0.05$ ($N = 16$)



Plant Soil (2013) 367:493–505



- Different crops selected different Rhizobacterial communities in the soil;
- Pea functioned differently from chickpea in promoting biodiversity of the microbial community.

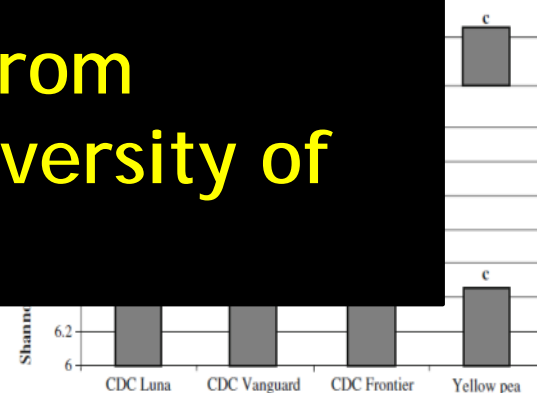


Fig. 3 Abundance of the OTUs belonging to the identified rhizobacterial phyla found in the rhizosphere of field-grown pulses July and late September, in 2008 (Number shown on the scale represent the number of OTUs)

Chickpea genotypes shape the soil microbiome and affect the establishment of the subsequent durum wheat crop in the semiarid North American Great Plains

Walid Ellouze^{a,b,c,*}, Chantal Hamel^b, Vladimir Vujanovic^d, Yantai Gan^b, Sadok Bouzid^c, Marc St-Arnaud^a

^a Institut de recherche en biologie végétale, Université de Montréal and Jardin botanique de Montréal, 4101 rue Sherbrooke est, Montréal, Québec, Canada H1X 2B2

^b Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Airport Road, Swift Current, SK, Canada S9H 3X2

^c Département de Sciences Biologiques, Faculté des Sciences de Tunis, Université Tunis El Manar, Campus Universitaire, Tunis 1060, Tunisia

^d Department of Applied Microbiology and Food Science, University of Saskatchewan, Agricultural Bldg., 51 Campus Dr., Saskatoon, SK, Canada S7N 5A8



- Cultivars differed in the ability of interacting with soil microbiomes;
- CDC Anna hosted the highest level of soil fungal diversity; Amit selected for antagonist species, hosted the lowest diversity.

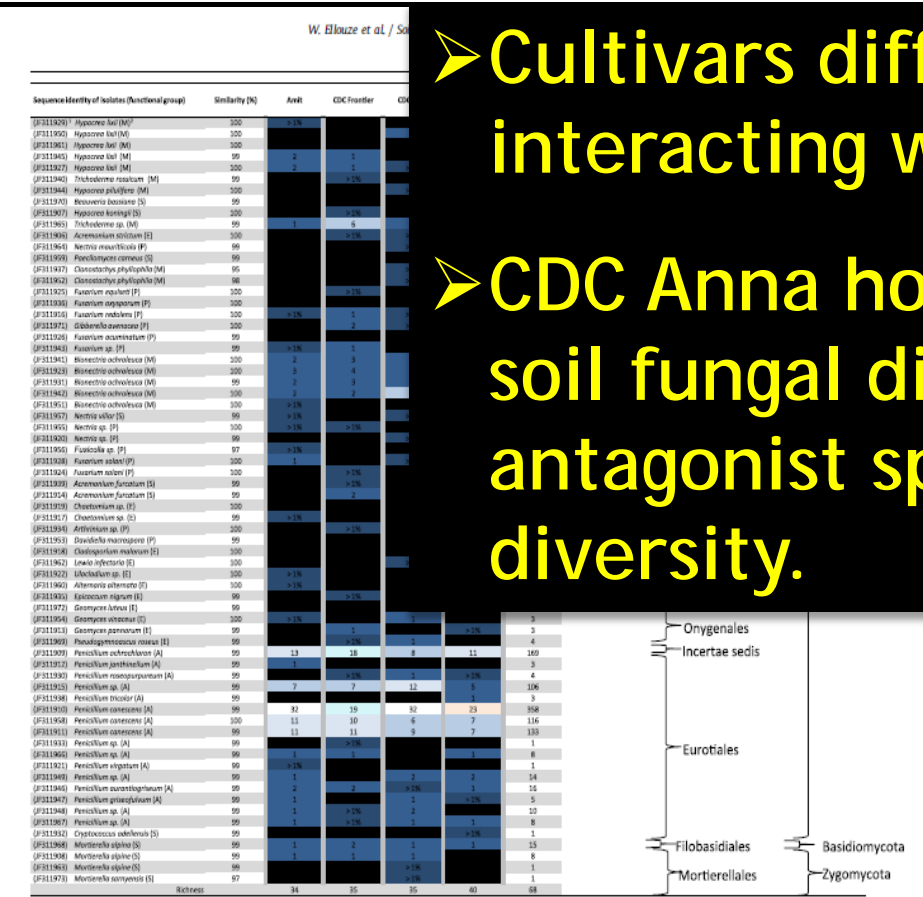


Table 2
Indices of diversity of the culturable fungal communities living in the top 0–7.5 cm of soil planted with different chickpea genotypes in 2005.

Diversity index	Chickpea genotypes			
	Amit ^a	CDC Frontier	CDC Xena	CDC Anna
Simpson's index of diversity (1 - D)	0.828 b	0.881 ab	0.869 ab	0.003 a
Shannon's diversity Index (H')	1.998 b	2.223 ab	2.192 ab	2.284 a

^a Least square means are not significantly different according to ANOVA-protected LSMeans Student's *t* tests when followed by the same letter on the same row ($\alpha = 0.05$; $n = 8$).

Fig. 2. Profiles of the community of culturable fungi in the top 0–7.5 cm soil layer planted with the different chickpea genotypes in 2005. High frequencies of recovery from the chickpea root zone due to soil dilution and plating are shown by lighter shades, whereas darker shades show low frequencies and black rectangles indicate undetected taxa. Sequence identities, determined by comparison with known sequences, are followed by the percentages of similarity with the closest match in GenBank and preceded by their accession number in GenBank. The functional group to which they belong is indicated in parentheses.

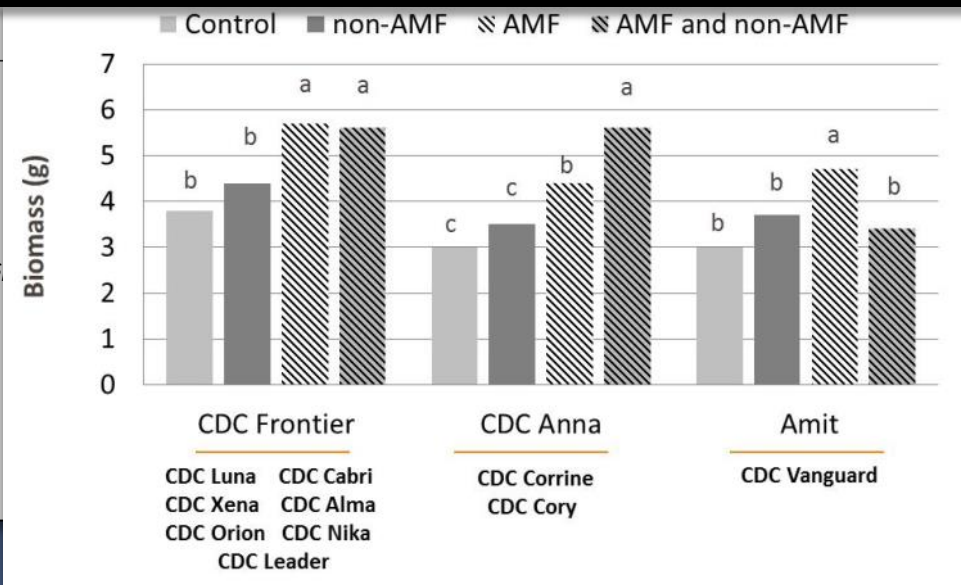
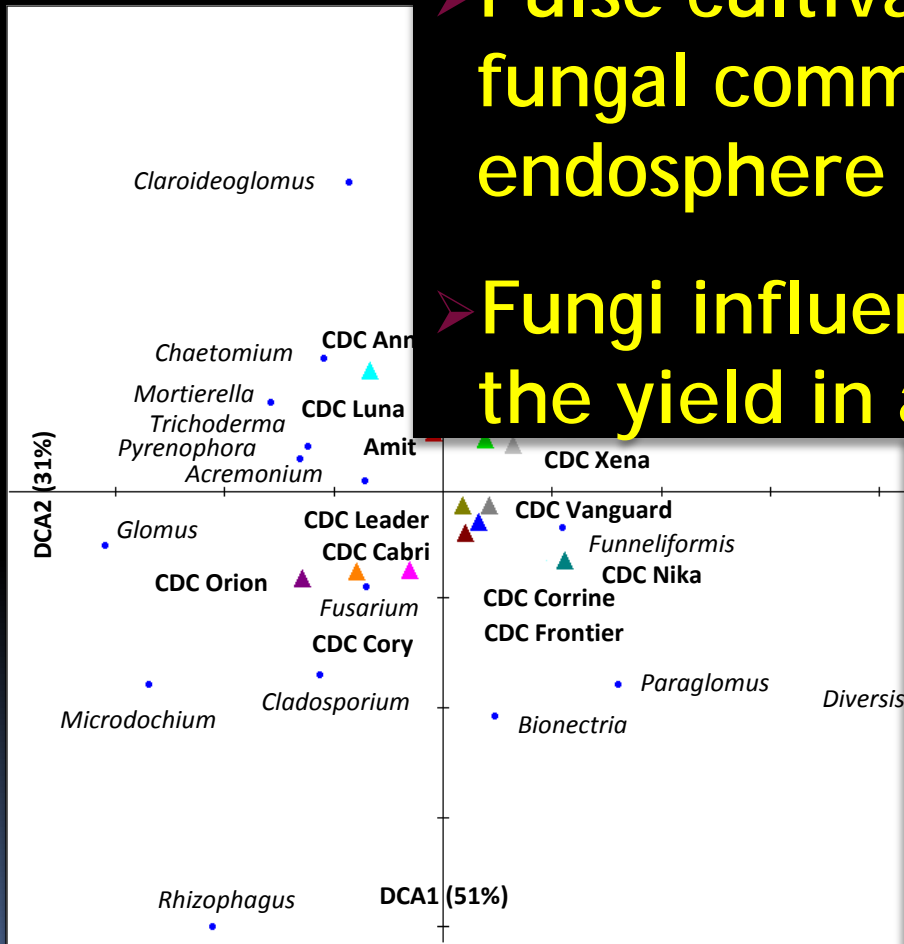
Genotype-Specific Variation in the Structure of Root Fungal Communities Is Related to Chickpea Plant Productivity

Navid Bazghaleh,^{a,b} Chantal Hamel,^{a,b} Yantal Gan,^{a,c} Bunyamin Tar'an,^c Joan Diane Knight^b

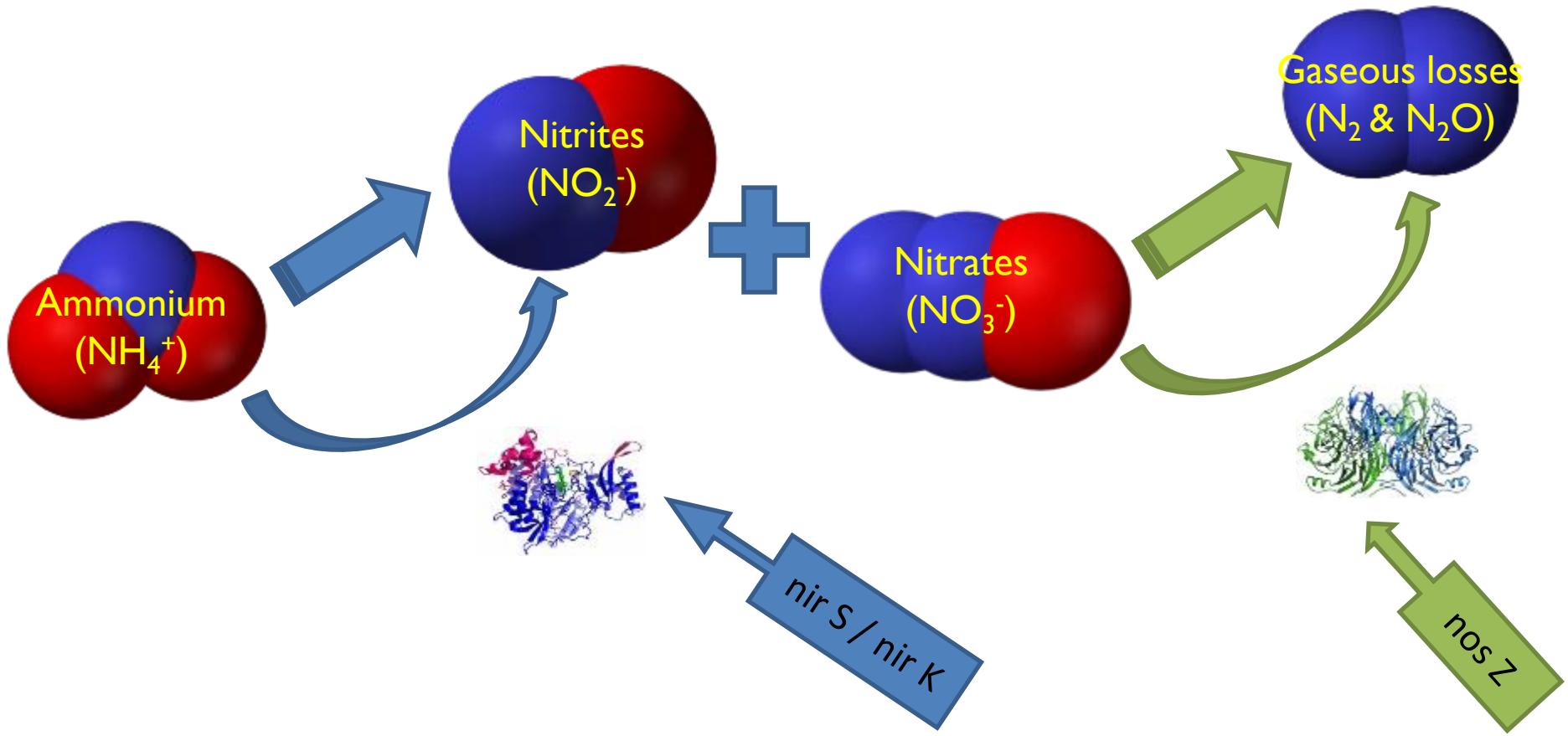
Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada^a; Department of Soil Science, University of Saskatchewan, Saskatoon, SK, Canada^b; Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada^c

➤ Pulse cultivars developed different fungal communities in the root endosphere

➤ Fungi influenced pulse plant roots and the yield in an interactive manner

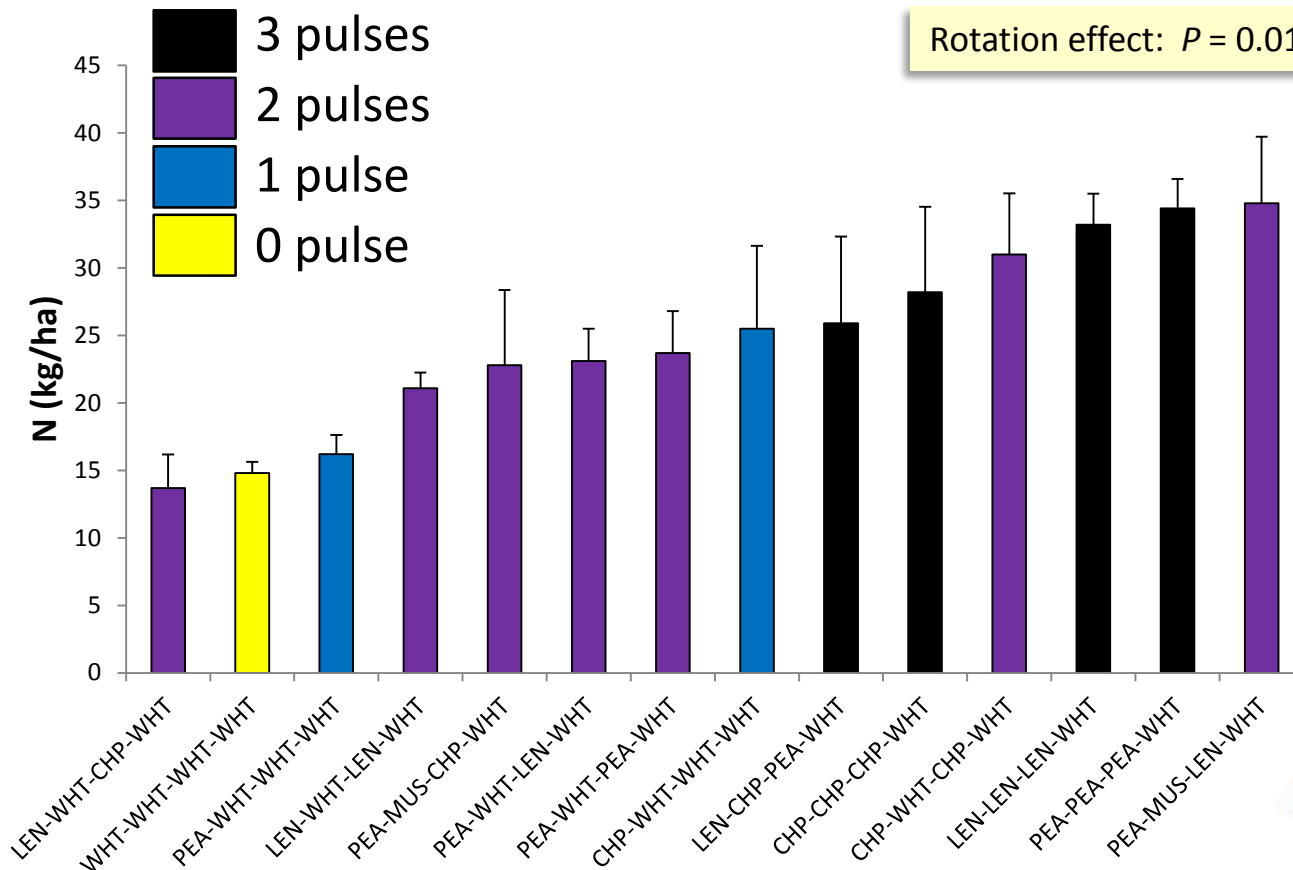


Enzymes and gene-groups involved in denitrification in soil



Soil residual N after 4-years of rotations (in the 0-120 cm depth)

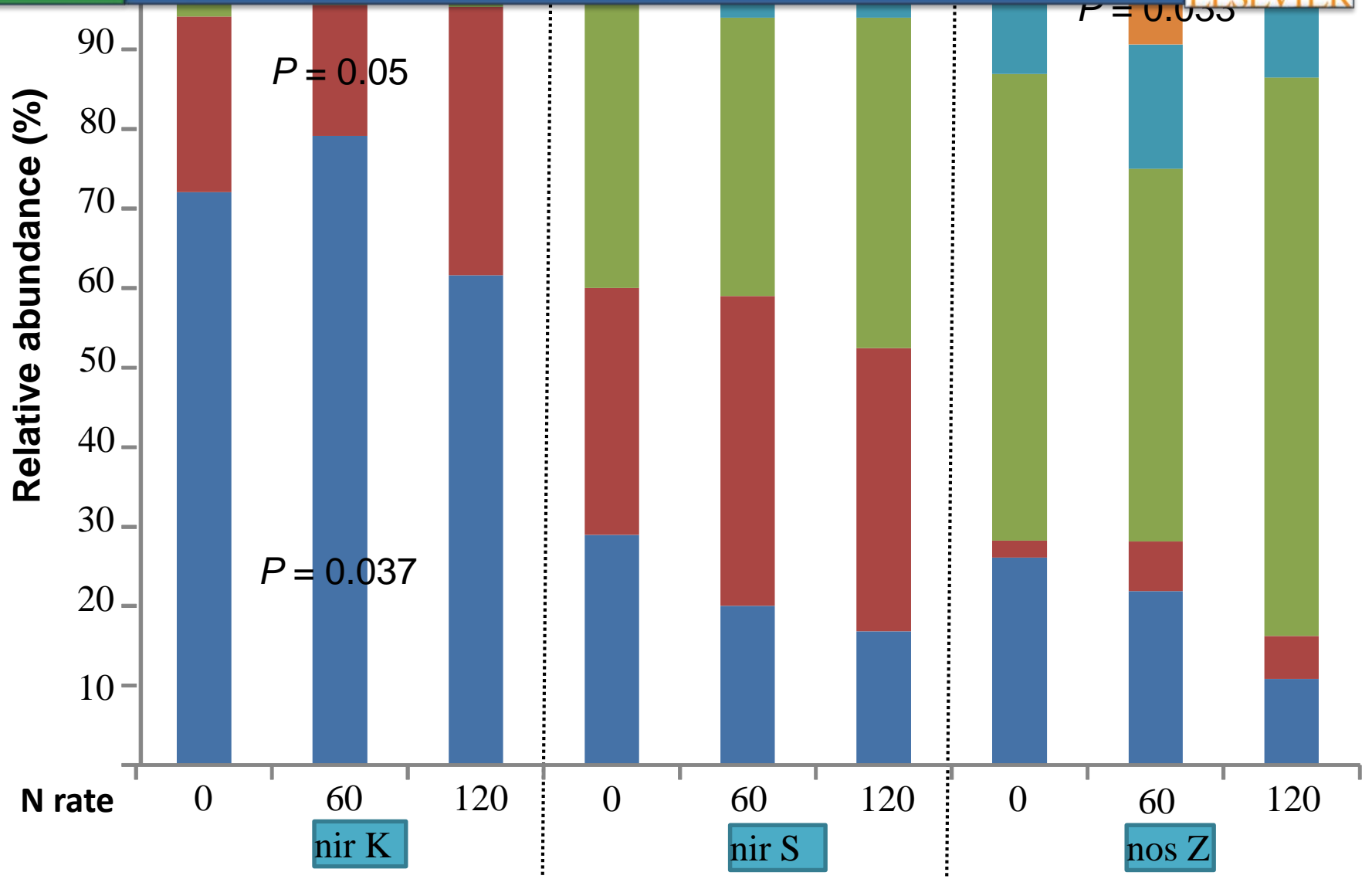
Pulse frequency



Incongruous variation of denitrifying bacterial communities as soil N level rises in Canadian canola fields

Chao Yang, Chantal Hamel, Yantai Gan *

Agriculture and Agri-Food Canada, Swift Current, Saskatchewan, Canada





Studies on “soil N chemistry” show:

- 1. N chemistry in the soil is regulated by several gene groups (with different codes)**
- 2. A higher frequency of pulses in a rotation leads to more N available in the soil**
- 3. Some of the pulse fixed-N is wasted, most likely through pulse-stubble decomposition**
- 4. Good choices of varieties and rotations may help optimize the use of soil N**

RESEARCH ARTICLE

Spatial and temporal structuring of arbuscular mycorrhizal communities is differentially influenced by abiotic factors and host crop in a semi-arid prairie agroecosystem

Luke D. Bainard, Jillian D. Bainard, Chantal Hamel & Yantai Gan

Semi-arid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada

Table 3. PERMANOVA results for AMF fungal community composition in root and soil samples

	Root AMF community			Soil AMF community		
	d.f.	F	P	d.f.	F	P
Crop	2	2.890	0.0558	2	1.155	0.3732
Sampling period	3	5.081	0.0001	3	2.636	0.0010
Crop*Sampling period	6	1.655	0.0488	6	0.905	0.6269

Bold values are significant at $P \leq 0.05$.



Fig. 3. Nonmetric multidimensional scaling (NMS) ordination of AM fungal communities detected in the soil associated with the different crops and across sampling periods. Symbols are the mean (\pm standard error) ordination coordinates of samples at each of the sampling periods for each crop. Numbers inside the symbols indicate the sampling period (1 = June 14, 2 = July 5, 3 = July 26, and 4 = August 16). Environmental variables that were significantly correlated with the AMF community composition in the NMS analysis were included in the biplot. Stress of the final NMS solution was 0.087.

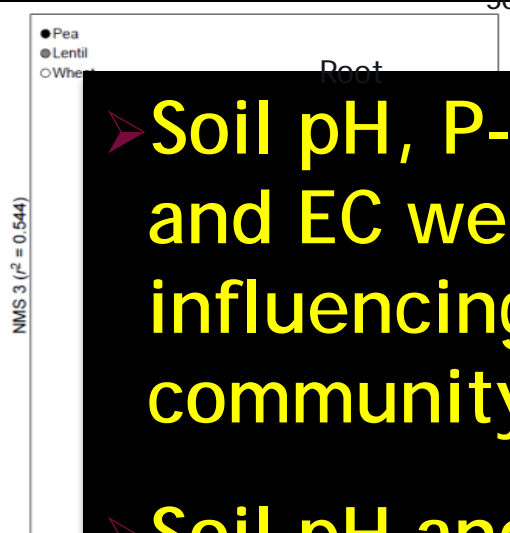


Fig. 1. Nonmetric multidimensional scaling (NMS) ordination of AM fungal communities detected in the root associated with the different crops and across sampling periods. Symbols are the mean (\pm standard error) ordination coordinates of samples at each of the sampling periods for each crop. Numbers inside the symbols indicate the sampling period (1 = June 14, 2 = July 5, 3 = July 26, and 4 = August 16). Environmental variables that were significantly correlated with the AMF community composition in the NMS analysis were included in the biplot. Stress of the final NMS solution was 0.087.

- Soil pH, P-availability, moisture, temperature, and EC were found to be key factors influencing the composition of the AM fungal community in crop roots.
- Soil pH and EC influenced the composition of the AM fungal community in the soil.



Phytochemicals to suppress Fusarium head blight in wheat–chickpea rotation

Andre F. Cruz^b, Chantal Hamel^{a,*}, Chao Yang^a, Tomoko Matsubara^b, Yantai Gan^a, Asheesh K. Singh^a, Kousaku Kuwada^c, Takaaki Ishii^b

^aSemiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Box 1030, 1 Airport Rd., Swift Current, SK, Canada S9H 3X2

^bGraduate School of Life and Environmental Sciences, Kyoto Prefectural University, 1-5 Shimogamohangi-cho, Sakyo-ku, Kyoto 606-8522, Japan

^cResearch Laboratory, Yamaki Co. Ltd., 1698-6 Kominato, Iyo, Ehime 799-3194, Japan

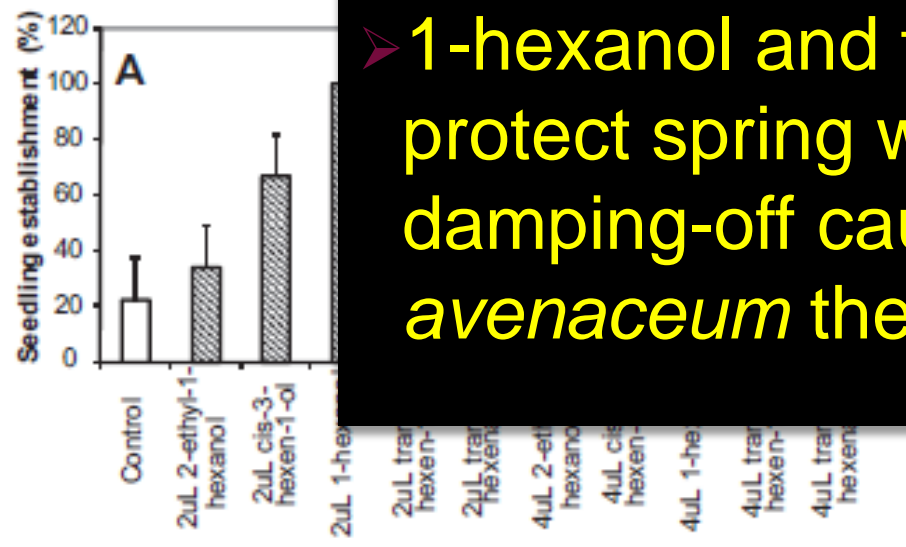
Table 1

Concentrations (nL g⁻¹ fresh weight) of volatile organic compounds in the leaves and roots of chickpea tissues as influenced by genotype and fungicide application.

Chickpea variety	Leaf			Root	Nodule
	1-Penten-3-ol	Cis-3-hexen-1-ol	Trans-2-hexen-1-ol	1-Penten-3-ol	1-Penten-3-ol
CDC Frontier	155 b*	93 b	87.2 a	53 c	nd
CDC Luna					
CDC Vanguard					
CDC Luna + fungicide					
CDC Vanguard + fungicide					
LSD					
ANOVA					

* Means (n = 3) followed by different letters are significantly different (p < 0.05), nd, not detected, n/a; detection limit

- Infection by *Ascochyta rabiae* in chickpea triggered the production of phytochemicals in shoots and roots;
- 1-hexanol and trans-2-hexen-1-ol could protect spring wheat seedlings against damping-off caused by *Fusarium avenaceum* the following year



Soil health management

Pesticides
Soil N, P

Soil

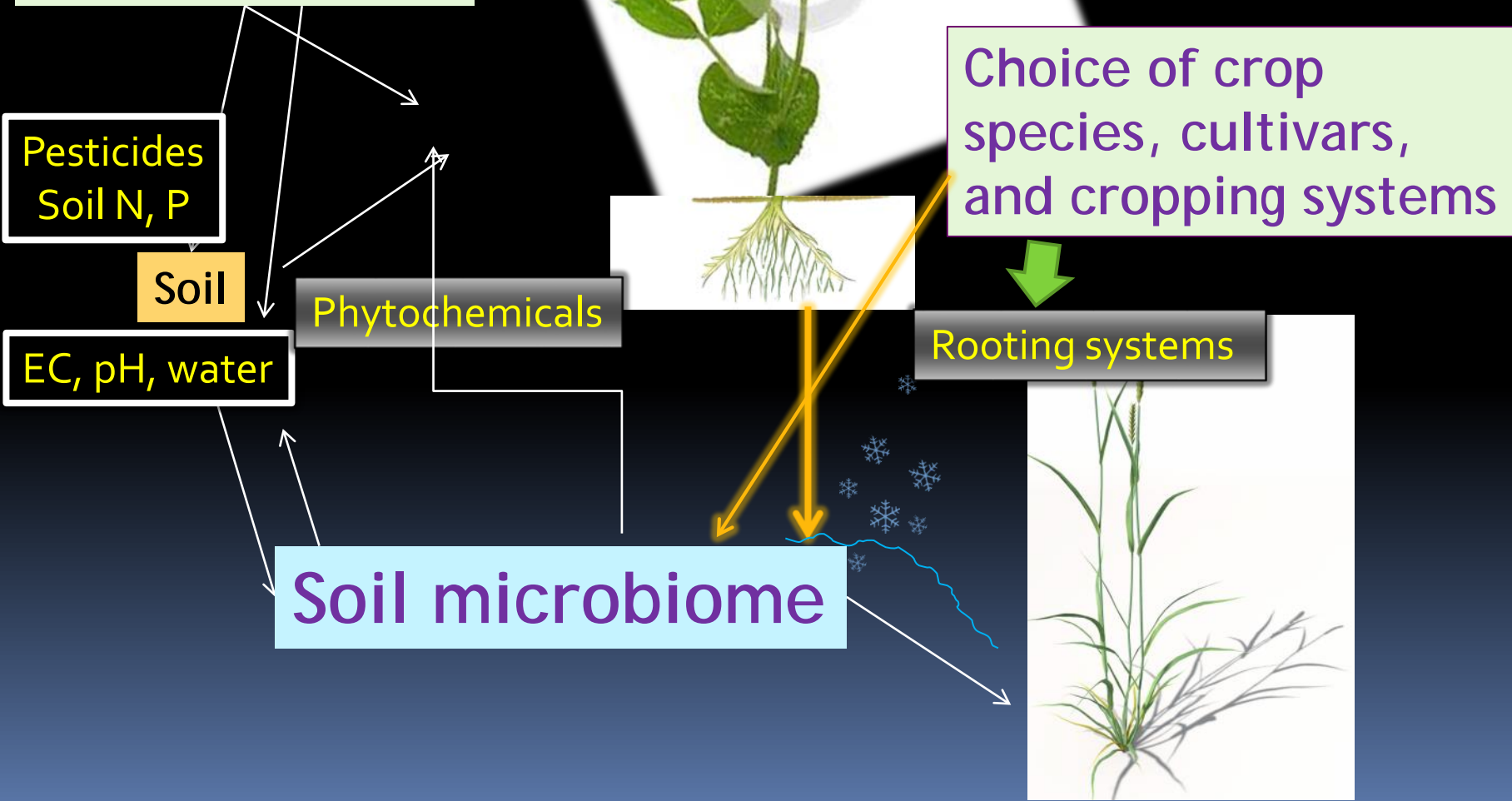
EC, pH, water

Phytochemicals

Soil microbiome

Choice of crop species, cultivars, and cropping systems

Rooting systems



KEY POINTS

- There are beneficial and pathogenic microbes in the prairie soil
- Beneficial microbes often appear in healthy plant roots; the magnitude of the effect varies with crop species and cultivars
- Higher microbial diversity = healthy soil
- **Avenues to Utilize Soil Microbiomes:**
 - To improve agronomic strategies and practices with system approaches
 - Use pesticides in an efficient way
 - Genetic improvement through breeding to enhance phytochemical profile (future goal)



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