



14th International Conference on

Agriculture & Horticulture

August 15-16, 2019 | Rome, Italy

Keynote Forum Day 1

Agri 2019

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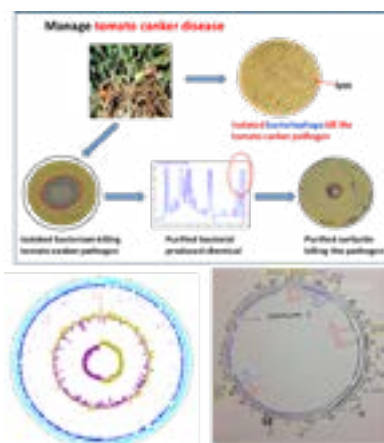
Ze-Chun Yuan

University of Western Ontario, Canada

Agriculture and Agri-Food Canada, Canada

Isolation, characterization and application of beneficial bacteria for sustainable agriculture and horticulture

Chemical fertilizers and pesticides have been heavily used in agriculture and horticulture food production, resulting in serious concerns including food safety and eco-system sustainability. Plant growth promoting bacteria are able to improve plant health and productivity and reduce pathogens and diseases, representing an ecologically-friendly alternative to chemical fertilizers and pesticides. We recently isolated various beneficial bacterial species including *Paenibacillus polymyxa* CR1 (*BMC Genomics* 2014; *Frontiers in Microbiology* 2015; *BMC Microbiology* 2016); *Bacillus velezensis* strain 9D-6 (*BMC Microbiology* 2019); *Bacillus velezensis* strain 1B-23 (*GenBank Accession*: NZ_CP033967.1) and *Burkholderia cenocepacia* CR318 (*Genome Announcements* 2017). These beneficial bacteria are capable of promoting crop health and inhibiting the growth of wide range of bacterial and fungal pathogens. In particular, *Bacillus velezensis* strain 9D-6 and 1B-23 produce surfactin, the most powerful biosurfactant. Surfactin aids in biocontrol through its antimicrobial action and through contribution to reducing biofilm formation. Our study further indicated that *Bacillus velezensis* strain 9D-6 and 1B-23 protect tomato plants from bacterial canker disease caused by *Clavibacter michiganensis* pv *michiganensis*. Interestingly, we found strain 1B-23 produces surfactin more efficiently at temperature between 16 to 20 °C. Our results suggest the potential of using beneficial bacteria to develop inoculants to protect agricultural important crops while reducing the use of chemical fertilizers and pesticides, towards more sustainable agriculture and horticulture.



Recent Publications

1. 2019. Elliot Grady; Jacqueline MacDonald; Margaret Ho; Brian Weselowski; Tim McDowell; Ori Solomon; Justin Renaud; Ze-Chun Yuan. Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium *Bacillus velezensis* 9D-6. BMC Microbiology. 2019. Jan 8;19(1):5. doi: 10.1186/s12866-018-1380-8.
2. 2019. Naeem Nathoo, Jacqueline MacDonald, Brian Weselowski and Ze-Chun Yuan. Comparative transcriptomic analysis reveals different responses of *Arabidopsis thaliana* roots and shoots to infection by *Agrobacterium tumefaciens* in a hydroponic co-cultivation system. 2019. Physiological and Molecular Plant Pathology. Volume 106, April 2019, Pages 109-119.
3. 2018. Munmun Nandi, Jacqueline MacDonald, Peng Liu, Brian Weselowski and Ze-Chun Yuan. *Clavibacter michiganensis* subsp. *michiganensis*: Bacterial Canker of Tomato, Molecular Interactions and Disease Management. Review. Molecular Plant Pathology. 2018 Mar 12. doi: 10.1111/mpp.12678.
4. 2017. Filip Zekic, Brian Weselowski, Ze-Chun Yuan. Complete Genome Sequence of *Burkholderia cenocepacia* CR318, a Phosphate-Solubilizing Bacterium Isolated from Corn Root. Genome Announcement. 2017. Jun 8;5(23). pii: e00490-17. doi: 10.1128/genomeA.00490-17.
5. 2017. Naeem Nathoo, Mark A. Bernards, Jacqueline MacDonald and Ze-Chun Yuan. A hydroponic co-cultivation system for simultaneous and systematic analysis of plant-microbe molecular interactions and signaling. 2017. Journal of Visualized Experiments. doi: 10.3791/55955. PMID: 28784965.
6. 2016. Elliot Nicholas Grady, Jacqueline MacDonald, Linda Liu, Alex Richman, Ze-Chun Yuan. Current Knowledge and Perspectives of *Paenibacillus*: A Review. BMC Microbial Cell Factories. 2016. 1;15(1):203.
7. 2016. Brian Weselowski, Naeem Amirali Nathoo, Alexander Eastman, Jacqueline MacDonald and Ze-Chun Yuan. Isolation, Identification and characterization of *Paenibacillus polymyxa* CR1 with potentials For biopesticide, biofertilization, biomass degradation and biofuel production. BMC Microbiology, 2016 Oct 18;16(1):244.

Biography

Ze-Chun Yuan is a research scientist and principal investigator at Agriculture and Agri-Food Canada. He is also a research professor and graduate student supervisor at the Department of Microbiology and Immunology, University of Western Ontario, Canada. He has expertise in soil microbiology, bacterial genetics and genomics with great passion in improving crop health and productivity through alternative strategies. He has been isolating and characterizing beneficial microorganisms to manage crop disease or improve crop health and productivity, in particular, developing biofertilizers and biopesticides to reduce the use of classical chemical fertilizers and pesticides in agriculture and horticulture. Ze-Chun Yuan is also interested in developing renewable bioproducts from biomass, in particular, crop residues. His research also involves synthetic biology and microbial engineering aiming at rewiring microbial metabolic pathways towards higher productivity of bio-based products and biochemicals. Ze-Chun Yuan looks for opportunities for collaborative research and training of highly qualified personnel including graduate students and postdoctoral fellows.

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An application on rice of reasonably using canopy temperature to improve the precision of water stress monitoring

Crop water stress index (CWSI) has been recognized as a water stress indicator and as a potential tool for irrigation scheduling. In present study, CWSI calculated based minimizing the low temperature impact was suitable to improve the precision of water stress monitoring. Thermal images were taken with FLIR thermal infrared imager at 14:00. Upper, sunlit and non-covered temperatures derived from canopy images, and canopy temperature cumulative frequency curves were discovered as discrete distribution under different degrees of water stress. CWSI used canopy temperature as the main driver for evaluation, and was calculated based on average temperature over a certain quantile. Regression equation between different CWSI and photosynthetic activity were built to find which one is the most sensitive index. Statistical analysis revealed that higher correlation coefficients were found after minimizing the low temperature. Further, the most sensitive CWSI also showed better relation to root soil moisture. CWSI thresholds were redefined. Optimal diagnose of the water stress was based on reasonably using canopy temperature. The results of this study were promising in precise irrigation scheduling.

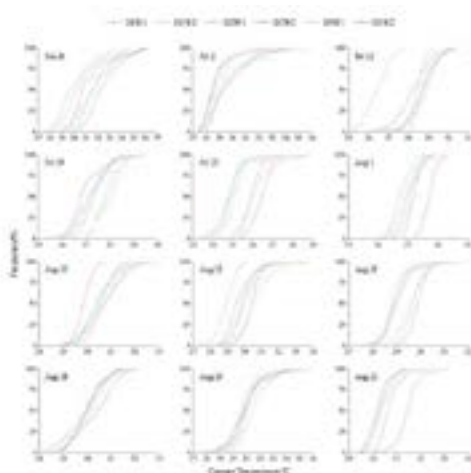


Fig.2 The cumulative frequency curve of canopy temperature on different dates.

Recent Publications

1. Xu JZ, Bai WH, Li YW, Wang HY, Yang SH*, Zhang JG. 2019. Calibration and validation of AquaCrop in simulating rice growth, yield and field water balance under drying-wetting cycle condition in eastern China. *Agricultural Water Management*, 213: 289-297
2. Xu JZ*, Liu BY, Wang HY, Liu WH, Li YW, Dai YB, Lu T. 2019. Ammonia volatilization and nitrogen leaching following top dressing of urea from water saving irrigated rice field: impact of two-split surge irrigation. *Paddy and Water Environment*, 17: 46-51
3. Lv YP, Wei Q, Luan YJ, Xu JZ*, Fazli Hameed, Twecan Dalson, Wei Z. 2019. Coupling Effect of Soil Water Deficit and Air Aridity on Crop Water Stress of Pepper. *International Journal of Agriculture and Biology*, 21 (3): 506-512
4. Xu JZ, Wei Q*, Yang SH, Liao LX, Qi ZM, Wang WG. Soil degassing during watering: an overlooked soil N₂O emission process. *Environmental Pollution*, 242(A): 257-263.
5. Xu Junzeng, Xiaoyin Liu, Shihong Yang*, Zhiming Qi, Yijiang Wang. 2017. Modeling rice evapotranspiration under water-saving irrigation by calibrating canopy resistance model parameters in the Penman-Monteith equation. *Agricultural Water Management*, 182:55-66.

Biography

Junzeng Xu, Male, Professor of Hohai University. Research interests were: Efficient irrigation and drainage management, Eco-environmental aspects of efficient irrigation and drainage management in rice paddy and so on, and more than 50 papers have been published during the last 5 years.

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Notes:



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Jianlong Xu

Chinese Academy of Agricultural Sciences, China

Selective introgression lines-based QTL mapping and QTL-designed breeding in rice

Advances in re-sequencing and fast phenotyping technologies greatly facilitate gene mapping and favorable allele mining of important agronomic traits from germplasms and mapping populations in crops. However, separation of QTL mapping studies from breeding practice results in difficult use of most mapping results in breeding program due to sensitivity of QTL to genetic background and environment. Here, we proposed a selective introgression line strategy to tightly connect QTL mapping and QTL-designed breeding together. Using three sets of trait-specific introgression lines (ILs) in a *Xian (indica)* variety Huanghuazhan (HHZ) background, we identified nine drought tolerance QTL (DT-QTL) and seven low nitrogen tolerance QTL (LNT-QTL) by a segregation distortion approach and a genome-wide association study, respectively. Based on performances of DT and LNT and genotypes at the detected QTL, two ILs M79 and M387 with DT and LNT were selected for cross-making to validate the identified QTL and to develop DT and LNT rice lines by pyramiding two DT-QTL (*qDT3.9* and *qDT6.3*) and two LNT-QTL (*qGY1* and *qSF8*). Using four pairs of kompetitive allele specific PCR (KASP) SNP markers, we selected 66 F₂ individuals with different combinations of the target DT- and LNT-QTL favorable alleles and they showed expected improvement in DT and/or LNT, which were further validated by the significant improvement in DT and/or LNT of their F₃ progeny testing. Based on evaluation of pyramiding lines in F₃ lines under drought, low nitrogen (LN) and normal conditions, four promising pyramiding lines having different QTL favorable alleles were selected, which showed significantly improved tolerances to drought and/or LN than HHZ and their IL parents. Our results demonstrated that trait-specific ILs could effectively connect QTL mapping and QTL pyramiding breeding, and designed QTL pyramiding (DQP) using ILs could be more effective in molecular rice breeding for complex quantitative traits.

Recent publication:

1. Ali J, Xu JL, Gao YM, et al (2017) Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerance in rice (*Oryza sativa* L.). PLoS One 12: e0172515.
2. Cui Y, Zhang F, Xu J, et al (2015) Mapping quantitative trait loci in selected breeding populations: a segregation distortion approach. Heredity 115, 538–546.
3. Li ZK, Fu BY, Gao YM, X, et al (2005) Genome- wide introgression lines and their use in genetic and molecular dissection of complex phenotypes in rice (*Oryza sativa* L.). Plant Mol Biol 59, 33–52.

Biography

Jianlong Xu got PhD degree on Crop Genetics & Breeding in 2001 in Zhejiang University, China. After finishing postdoctoral career of molecular rice breeding for two years at IRRI, he joined the Institute of Crop Sciences, Chinese Academy Agricultural Sciences, focusing on gene mapping and favorable allele mining for molecular rice breeding in high yield, high grain quality, abiotic and biotic stress tolerance. So far, he has published 70 papers in international journals, obtained four provincial awards and 13 patents.

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