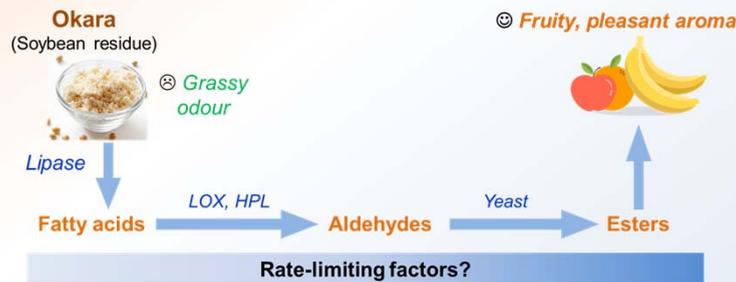


Bioconversion of Green volatiles in Okara (Soybean Residue) into Esters by Coupling Enzyme Catalysis and Yeast (*Lindnera saturnus*) Fermentation

By Ms. Vong Weng Chan

Abstract

Okara (soybean residue), a by-product from soymilk and tofu production, has a green, grassy off-odour as it contains a large amount of aldehydes. This work investigated the rate-limiting enzyme(s) in the formation of aldehydes in okara and the pathways leading to their bioconversion into fruity, pleasant-smelling esters by the yeast *Lindnera saturnus*. Lipase and hydroperoxide lyase were shown to be rate-limiting enzymes while endogenous soy lipoxygenase was also crucial for the production of aldehydes from okara. Subsequent fermentation of okara by *L. saturnus* increased the amount of esters by about 70 times to 165 – 277 µg/g dried okara. The generation of C7 esters followed our hypothesised pathway, while that for C6 esters was mainly affected by *L. saturnus*. This study presents a simple and inexpensive one-pot set-up for the natural bio-production of esters from okara.



About the Speaker



Miss Weng Chan VONG is a Ph.D. student in the Food Science and Technology programme at National University of Singapore, under the supervision of Assoc. Prof Shao-Quan LIU from the Flavour and Fermentation research group. Her work involves using microorganisms (yeasts, fungus, probiotics) and enzymes to convert okara into a more nutritious and tasty food product, such that the soy food by-product can find wider value-added applications.

ALL ARE WELCOME !

Role of Heteroresistance in Causing False Negatives When Predicting Antibiotic Resistance by Whole Genome Sequencing



By Mr. Zwe Ye htut

Abstract

As whole genome sequencing (WGS) becomes more affordable, it is increasingly being speculated as a potential replacement to the in vitro phenotypic testing for antibiotic resistance. Predicting resistance from a full complement of resistance determinants as determined from WGS data is rapid, inexpensive, and has the added advantages of discovering resistance to compounds not routinely tested and the ability to differentiate identical phenotypic resistance patterns caused by fundamentally different molecular mechanisms. However, its ability to accurately predict phenotype from genotype has yet to be unequivocally accepted. One major reason for this reservation is because in addition to the knowledge that a particular genetic feature may be correlated to a particular resistance, a firm grasp on the underlying reasons why disagreements between genotype and phenotype may occur, and how to reconcile or explain them, if possible, must also be well-defined.

In this study, the role of heteroresistance in causing false negative errors and the underlying reason as to why WGS is inherently limited in its ability to predict the resistance caused by this phenomenon will be discussed. The results from this study highlights but only one aspect that must be addressed before WGS can become the gold standard of antibiotic resistance prediction. .

About the Speaker



Mr Zwe Ye Htut (Ivan) obtained his Bachelor's Degree in Food Science & Technology from the Food Science & Technology (FST) Programme, NUS in 2015 before embarking on his Ph.D studies in the same programme. He is currently working on genomics and molecular aspects of antibiotic resistance in *Salmonella spp.*

Host: Dr. Liu Shao Quan **Date:** 17th Sep, 2018
Time: 12 to 1 pm **Venue:** Seminar Room S16-04-30