



THE CHINESE UNIVERSITY OF HONG KONG  
SCHOOL OF LIFE SCIENCES

# LIFE SCIENCES SEMINAR SERIES

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*Life Sciences Seminar is a seminar series aiming to provide up-to-date research ideas and experimental approaches to graduate students in the School*

Will the Pacific oysters invade and attack  
Hong Kong by 2100?

*by*

Dr. Vengatesen Thiyagarajan  
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*on*

9 January 2014  
(Thursday)

*at*

12:30 – 1:15 pm

*at*

LT2, Mong Man Wai Building  
The Chinese University of Hong Kong

*ALL ARE WELCOME*

## Will the Pacific oysters invade and attack Hong Kong by 2100?

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Oyster consumption is expected to rise with the increasing human population. However, increasing anthropogenic CO<sub>2</sub> taken up by the ocean is causing ocean acidification (OA) and threatening oyster survival. The impacts of OA on oysters are already clear, e.g., the collapse of oyster production in the United States, and OA is at a tipping point for many oyster culturing regions in Europe and Asia. This is a serious warning to China, which produces >80% of the world's oysters. Certainly, OA and other stressors will produce winners and losers among the three commercially cultivated oysters, the Hong Kong, the Pacific and the Portuguese oysters. The invasive oysters (Pacific and Portuguese) appear to be winners and they may have the capacity to invade and replace the native Hong Kong oyster. A mechanistic understanding of the effect of OA is therefore a pressing issue for Hong Kong scientists, oyster farmers in South China and policy makers of Asia. OA is expected to alter oyster physiology to cope with new challenges through adjusting protein expression pattern at proteome level. Such proteome wide stress related alterations can provide early life stages of these three oysters necessary physiological or cellular or phenotypic plasticity to deal with stressors. Recently, in collaboration with proteomics experts, we have begun to understand oyster larval proteome plasticity to multiple climate change stressors. We have successfully used the high-resolution shotgun proteomics technology (iTRAQ-coupled 2D nano LC-MS/MS) to understand how the Pacific oyster larval proteome was altered to cope with multiple stressors including elevated CO<sub>2</sub> and temperature. As the complete genome of this oyster species is available, we have identified thousands of oyster larval proteins with high confidence and also quantitatively mapped molecular pathways used by them to tackle climate stressors. In this presentation, I will show these results and discuss their implications. In the end, I will show that some of the challenging climate change and larval biology questions could be answered if we integrate the rapidly advancing proteomics with larval biology in this era of multidisciplinary collaboration.