SEMINAR

ALL ARE WELCOME

TEMASEK LIFESCIENCES LABORATORY

21 September 2015 (Monday), 11am
Seminar Rm 05-41 (Level 5)

Hosted by: Dr Laszlo Orban

Genomics, Diversity and Evolution

Professor Christopher M. Austin
Monash University, Malaysia



Prior to his current appointment at Monash University in 2011 Professor Austin was at Charles Darwin University, Australia, for 6 years where he was Head of School and responsible for building research capacity and the Higher Degree by Research student program for the School of Environmental and Life Science. Professor Austin has now established vibrant and productive molecular genetic and genomic research laboratories at three Australia Universities over the last 10 years and developed and supported courses, workshops and training programs in molecular genetics, genomics, scientific writing, research methods and biostatistics in Australia, Malaysia, Vietnam and Indonesia. Professor Austin has recently embraced next-gen DNA sequencing having set up a new genomics laboratory and research platform at Monash University Malaysia with 2 of the latest bench-top sequencers. His research interests and expertise are in animal biodiversity and evolution with a major emphasis on genomics, molecular genetics and conservation of aquatic organisms and commercial fish and shellfish species. Prof Austin has formed many productive collaborations with Australian and international scientists. Over the last 20 years Professor Austin has authored over 130 publications and reports, the majority of which are articles in refereed international journals and he regularly acts as an expert reviewer for leading journals in the biological sciences.

The recent development of next-generation sequencing technologies provides opportunities to characterize the genomic composition of individuals, populations and species in unprecedented detail. It is now possible to obtain genetic information from throughout the genome and to address a variety of questions relating to evolutionary and comparative genomic research that can contribute to may disciplines of the biological and health sciences. Nevertheless there are many fields of study that are only slowly taking advantage of this sequencing revolution and there are many animal groups for which there is only limited genomic information. In this presentation I am going to describe some recent genomic studies on fish, mollusks and crustaceans conducted at Monash University Malaysia that attempt to fill important knowledge gaps and contribute to our understanding of the evolution and diversity of these groups. These case studies include (1) genome sequencing projects for the Malaysian arowana or dragon fish, the Australian Murray cod and the red claw crayfish, (2) mitogenome evolution in decapod crustaceans and (3) new approaches to genotyping molecular markers for conservation studies and fisheries management.

Recent Publications:

1. Tan, Mun Hua; Gan, Han Ming; Schultz, Mark; **Austin, Christopher**. (2015). MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes. Molecular Phylogenetics and Evolution 85:180-188
2. Tan, Mun Hua; Gan, Han Ming; Schultz, Mark; Miller, Adam, Croft, Larry, **Austin, Christopher** (2015). First comprehensive multi-tissue transcriptome of Cherax quadricarinatus (Decapoda: Parastacidae) reveals unexpected diversity of endogenous cellulase. Accepted Organism Diversity and Evolution.
3. **Austin CM,** MH Tan, YP Lee, LJ Croft, HM Gan (2014). The complete mitogenome of the Murray Cod, Maccullochella peelii (Mitchell, 1838)(Teleostei: Percichthyidae). Mitochondrial DNA, 1-2 DOI: 10.3109/19401736.2014.880897.Gan HM, Schultz, MB