

**Division-4-07**

**Development of Bioinformatics Capacity in Support of the KOICA-UPLB-IRRI Agricultural Genomics Research Center**

Ramil P. Mauleon<sup>1\*</sup>, Lord Hendrix Barboza<sup>1</sup>, Frances Nikki Borja<sup>1</sup>, Dmytro Chebotarov<sup>1</sup>, Jeffrey Detras<sup>1</sup>, Venice Juanillas<sup>1</sup>, Riza Pasco<sup>1</sup>, Kenneth L. McNally<sup>1</sup>

<sup>1</sup>Rice Breeding Innovation Platform, International Rice Research Institute, Los Baños, Laguna Philippines

**[Abstract]**

Capacity building for bioinformatics could be achieved with the systematic training of research staff and higher degree students in the current best practices for analysis of data from ‘omic-type experiments. It is anticipated that the KOICA-University of the Philippines Los Baños – International Rice Research Institute Agricultural Genomics Research Center activities will focus on the use of next generation sequencing technology for genome sequencing and annotation, genome variant discovery for use in GWAS and QTL mapping, and transcriptome analysis of organisms important to agriculture and food security. Such activities require that researchers have high levels of knowledge and skills in bioinformatics in order to gain insights from the results of the experiments performed. In this talk the bioinformatic tools/solutions and online training materials already available will be presented, as well the upcoming resources under development in support of the project.

**[Acknowledgement]**

The bioinformatics tools, portal development and support for training is supported through the KOICA project.

**[Short Biographical Sketch]**

Dr Ramil Mauleon is a Senior Scientist for bioinformatics at the International Rice Research Institute. He is a geneticist by training, with minors in Computer Science and Molecular Biology & Biotechnology from the University of the Philippines Los Baños (UPLB). His research interests include adoption, creation, and implementation of integrative analyses methods for genomics, transcriptomics, proteomics, metabolomics, and digital phenotyping in agricultural crops, leading to candidate gene discovery and marker development for breeding applications. On the biocomputing/IT side, he is involved in projects such as the development and adoption of re-usable analysis software workflows for large datasets with high computational resource demand, and exploration and implementation of FAIR (Findable, Accessible, interoperable, Reusable) -compliant technologies for biological databases and web applications (such as Rice SNP-Seek and Crop Galaxy). He is adjunct faculty at the UPLB and Southern Cross University in Australia.

\*Corresponding author: E-mail, r.mauleon@irri.org Tel. +63-580-5600