

Chapter 13

A Web Portal for Rice Crop Improvements

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ABSTRACT

High quality models of factors influencing rice crop yield are needed in countries where rice is a staple food. These models can help select optimal rice varieties for expected field conditions. Development of a system to help scientist track and make decisions using this data is challenging. It involves incorporation of complex data structures - genomic, phenotypic, and remote sensing - with computationally intensive statistical modeling. In this article, the authors present a web portal designed to help researchers to manage and analyze their datasets, apply machine learning to detect how factors taken together influence crop production, and summarize the results to help scientists make decisions based on the learned models. The authors developed the system to be easily accessed by the entire team including rice scientist, genetics, and farmers. As such, they developed a system on a server architecture comprised of a SQLite database, a web interface developed in Python, the Celery job scheduler, and statistical computing in R.

1. INTRODUCTION

Rice is a staple food throughout the world. Production of foods like rice must increase to meet global demands. There is a gap between production of rice and expected rice consumption. Shrinking rice field area, water scarcity, climate change, and disease creates challenges in ensuring and increasing rice production. Climate change is negatively impacting rice plants through its effect on environmental factors that influence crop yield (Challinor et al., 2014). A threat to rice crops translates into food insecurity

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due to its widespread consumption throughout the world. Therefore, there is a need to revolutionize the way existing rice plant varieties are improved and new varieties are developed and introduced. Robust rice varieties are needed to handle prolonged droughts, extreme wet conditions, and water source depletion (Toha, 2011).

Potential land for agriculture in Indonesia is approximately 96 million hectares, comprising 71 million hectares of dry land, 5 million hectares of wet land, and 20 million hectares of marsh land (Kementan, 2015). From the total area, only about 1.2 million hectares of dry land is being used for the production of rice and low productivity is a problem. The average yield is about 3.3 tons/ha, contributing to about 5% of national rice production (Kementan, 2014). In an effort to improve production, rice scientists in Indonesia are keeping track of genomic and field factors and production outcomes. The objective is to use these data to help improve crops through selection of optimal seeds for expected field conditions and using genetic markers to inform plant breeding. The goal of the latter is to produce rice varieties with good production qualities, such as resistance to disease.

Increasing production is a challenging task. Rice farmers can provide agricultural researchers with valuable information on the current conditions of rice farming. Conversely, researchers are the main providers of information to farmers on new or improved rice varieties. Information must be passed in both directions to make informed decisions on how to improve rice production. Additionally, plant characteristics as well as environmental factors influence production traits. A deep understanding of these factors are needed to optimize production. A genomic approach can be useful in identifying the molecular features that predicts resistant to environmental conditions such as drought and salt tolerance (Papageorgiou, 2017).

1.1. Rice Genetics

The rice genome is relatively small (430 megabase-pairs) and well mapped (Sasaki et al., 2002). The rice genome was one of the first genome sequencing projects. It is the smallest genome among cereals (Eckardt, 2000). Because of these characteristics, rice is considered to be a model plant and research into the rice genome has been ongoing over the last decades. The rice genome consists of 12 chromosome pairs. Along these chromosomes, there are points where the nucleotides vary from plant to plant. The most common type of genetic variation found at these sites are single-nucleotide polymorphisms (SNPs). The nucleotides at these points of variation are called alleles, and since the chromosomes are paired, two alleles make up a genotype. Genotypes for variants in nearby proximity are often correlated because they are more likely to be copied together. Genotypes are captured with DNA genotyping or sequencing technologies.

Research programs analyze the rice genome in order to understand genomic diversity and support development of new varieties. These programs began in the 1990s in Japan (Sasaki, 2003) focusing on two rice subspecies: *Indica* and *Japonica*. This provided the groundwork for scientist to improve the quality of rice, and also the quality of cereals in general. Today, given its importance for food security, rice genomics is one of the top research areas in life sciences, after human and mouse (Wang, Xia, Li, Hou, & Yu, 2013). Much work is focused on marker-assisted selection (MAS). This approach uses genetic markers to screen plants for breeding. This process is used to create new varieties of plants with desirable traits, such as yield improvement, drought and disease resistance (He et al., 2014). These technologies allows scientists to create new plant varieties more efficiently by genetically predicting the phenotype rather than observing it after the plant has grown.

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