What is your idea?

An informed-Decision platform to reduce the risk of RIce Diseases (DRuIDs)

Reducing disease epidemics is only possible if we understand the interaction among host, pathogen, and environment. In this project, we plan to integrate these three key elements into a decision tool that allows local agriculture agencies to reduce the chance of future epidemics by deciding which variety will be promoted next season. The tool will also drive future breeding priorities with an emphasis on developing the right variety for specific regions and protect long-term investments in the rice sector by making disease resistance more durable. We are not proposing to create a traditional disease alert tool, but rather a real-time integrated system for decision-making. The platform will link the resistance spectrum of local rice varieties with high throughput field information to generate the most convenient strategy for deployment or breeding intervention. This platform will be used by government officials, research scientists and extension specialists who will be able to receive up-to-date information when they need it most.

We will use bacterial blight (BB) (causal agent *Xanthomonas oryzea* pv. *oryzae*; (*Xoo*)) of rice as a pilot problem because the disease is widely distributed across rice-growing regions worldwide and based on work by IRRI and AfricaRice it is predicted to become more severe with climate change. As with other important diseases of rice, BB resistance has a strong race-specific component, making host plant resistance the most effective way to manage the disease. The fact that we can control disease outbreaks by deploying resistance genes offers a unique opportunity to scale up the platform to most of the important rice diseases in the future. The pilot will be tested in the Philippines with the help of scientists at the International Rice Research Institute (IRRI) and University of Southern Queensland (USQ). We expect to integrate early-season field information to recommend a set of varieties that will carry resistance to the disease in the next season and reduce the risk for rice farmers. In addition, breeders can monitor the platform to design breeding priorities in real-time.

How will you pilot it?

The platform represents a real-time interface between seasonal field information (host, pathogen, and weather components) and the decision makers (extension agencies, breeders, and other officials). IRRI has already developed a web-based platform, the Philippine Rice Information System (PRiSM), http://riceinfo.ph, which has demonstrated the usefulness of web and cloud-based technologies for agriculture in developing countries. Following this path, users will be log in to a web platform and receive up-to-date information regarding the geographic locations of the pathogen races and occurrence of the disease.

In this scenario, IRRI and USQ scientists have developed new technologies to help mapping and monitoring the components that contribute to disease epidemics: i) IRRI have validated a panel of SNP markers that can identify pathogen races directly from an infected leaf sample. This innovation was developed with a service provider, allowing high throughput genotyping and genetic mapping of virulent factors in few days, providing critical information for resistance gene deployment; ii) IRRI is also developing a catalog of released rice varieties in regards to the resistance spectrum and presence of resistance genes for *Xoo*. This is an ongoing work and is supported by molecular markers and greenhouse pathotyping; iii) USQ is currently working to characterize agricultural environments and develop disease models that can be used to represent the rice landscape. Additional data than can be included in this platform that can provide useful information for researchers and extension specialists include farmers' agronomic practices, farmers' market preferences, grain quality, and other biotic or abiotic stresses in the area; iv) having been involved in the development of PRiSM, USQ scientists have experience in the integration of data for decision making and development of decision tools in a web-based platform. In line with the Inspire Challenge guidelines, open source tools will be used to develop this platform, v) USQ scientists have experience developing packages for R to extend its functionality and have participated in both reviewing code for R packages and having R packages peer reviewed. These experiences will provide expertise necessary to complete this project.

While the research budget will be distributed equally between both institutions, IRRI will assume the administrative effort. USQ will build the platform interface and operational components of the pilot platform. Meanwhile, IRRI will lead the seasonal groundtruthing and cataloging of resistance genes in a database. Data collected will include local weather patterns, pathogen and rice geo-references, pathogen genotypes, race determinations of leaf samples, resistance spectrum and agronomic components of rice varieties. Output information will include maps of the distribution of *Xoo* races, a list of candidate varieties based on local agronomic preferences, deployment strategies suggested for the region, a list of donors with useful resistance genes for breeding.

Leveraging the power of open source tools provided by the R software and the R shiny package, http://shiny.rstudio.com; information will be presented in an easy-to-use dashboard. Users will be able to view maps of distribution of rice varieties, *Xoo* races and create combination maps where resistance genes in rice varieties planted and *Xoo* races occur. Breeders will be able to generate downloadable lists of candidate donors by selecting their desired criteria from maps and other data in the database. The proof-of-concept dashboard will be hosted with https://www.shinyapps.io.

Source-code for the dashboard will be readily available via GitHub as an installable R package for interested parties released under the MIT license.

If the pilot is technically successful, future plans include: i) expansion of the tools to other countries in Southeast Asia (SEA), South Asia (SA) and northern Australia. For instance, SNP markers appear to be effective in Indonesia, Taiwan, Cambodia, India and Thailand populations as well; ii) expansion of the operational platform to other diseases such as blast, Rice Yellow Mottle Virus (RYMV), and others; iii) engage with national rice programs from SEA and SA regions and the rice industry in Australia to customize the platform for their particular needs. And iv) move the platform to Amazon Web Services to provide hosting infrastructure and backup capacity in a fashion similar to that of PRiSM with relational databases and full redundancy with Amazon data archiving services.