ROD A. WING

Professor, University of Arizona

Thank you. This is my first time attending a policy congress. I am a scientist who has a large lab in Arizona and I will talk to you today about some of the work that we have been doing on rice. The title of my talk is the International Oryza Map Alignment Project, the development of a genus wide comparative genomics platform to help solve the 9 billion people question – and it could also be the 10 billion people question. I am a professor at the University of Arizona and I also have a position at the International Rice Research Institute in Los Banos, the Philippines.

One of the big questions that our community is interested in is what we call the 9 billion people question, which has now gone up to the 9 10 billion people question, and rice will play an important role in helping us solve this problem. Rice feeds half the world and it is estimated that the rice dependant population will double by about 2050. Our goal is to develop new varieties of rice that are higher yielding and more nutritious but require less of an environmental footprint – i.e. rice that requires less water, fertiliser and pesticides and can grow on marginal lands. In India, this is called designer rice, while in China it is called Green Super Rice, and we call the general concept the nextgen super crops.

A big part of developing these new types of crops is the concept of capturing the natural variation that exists in the landraces, accessions and wild relatives. Essentially, you can find diversity in almost any trait and I have a number of examples here of seed colour, size, yield, drought tolerance and so on. A tremendous amount of natural variation therefore already exists in the plant community and this has still to be tapped into because of what is called 'the domestication bottleneck'. A few plants were domesticated and during the domestic process a lot of wild traits were shed. However, many of these wild traits can be used, if they are captured properly, to improve crops, including rice.

In terms of the amount of variation that exists for rice, the International Rice Research Institute (IRRI) has a gene bank with more than 125,000 accessions which are waiting to be characterised. In fact, we are using less than 5% of this material for modern varieties that we are working with. One gene that was identified recently and has now been introgressed into mega varieties around the world is the submergence 1 (Sub1) gene. Sub1 allows a plant to resist flooding, where plants can be under water for up to two weeks and still survive. Many rice plants have never had this gene. It was identified in a wild species of rice and then crossed into cultivated species using standard genetic crossing methods. Today, the majority of rice varieties that we eat have this Sub1 gene, and this is not considered a "genetically modified organism" (GMO) that everyone is afraid of but is actually created by traditional crossing.

In our lab at Arizona and in a number of other groups, we are interested in the wild relatives of rice where we try to extract traits from these accessions and cross them into cultivated species. The two cultivated species are Oryza sativa – Asian rice – and Oryza glaberrima – African rice. O. rufipogon is the progenitor of Asian rice and there are then a number of other species, such as O. punctata, all the way through to O. coarctata. What we say is that these species are agronomically inferior but they contain a virtually untapped reservoir of genes that can be used for crop improvement. One dramatic example is O. coarctata, which can actually grow in salt water to the level of ocean water. If we were able to transfer the salt loving genes of O. coarctata into Asian rice, we would be able to grow rice in more extreme environments.

It turns out that Africa has the highest diversity of Oryza genomes in the world, with six different species of rice. O. barthii is the progenitor of O. glaberrima and O. longistaminata is the first species where a disease resistant gene was isolated from. The Africa Rice Centre was first located in the Ivory Coast and then moved to Benin, and Africa holds the future for the world's rice farming because the continent has great untapped potential, which is benchmarked by its large land distribution and barely used water resources.

The International Oryza Map Alignment Project has been involved in generating reference genome sequences for all of the wild relatives of rice and African rice. These species contain a treasure trove traits related to abiotic and biotic stress, drought tolerance, mineral content in the soil, as well bacterial, viral and mosquito resistances. These have all been identified in these species and are currently being crossed to transfer these traits into Asian and African rice. Our lab was involved in sequencing the Asian rice genome about 10 years ago and we just celebrated that anniversary two weeks ago. We have also recently published the genome of African rice in Nature Genetics.

Asian rice was domesticated about 10,000 years ago in China from Oryza rufipogon and Oryza nivara. 7,000 years later, African rice was domesticated from Oryza barthii in West Africa, along the Niger River. This was a completely independent domestication event, which is an amazing thing in and of itself. Our lab has also sequenced the Oryza glaberrima, the African rice parent for the NERICA lines that we heard about earlier today, and amongst the things that we discovered was that African rice was domesticated in a single domestication centre. In fact, there are two theories about this: either Africe rice was domesticated throughout the continent or it was just in a small area. It turns out that our data supports the hypothesis that African rice was domesticated in a single cente of domestication and moved into to two secondary centres in West Africa.

We were also able to identify 73 regions across the genome that are under selection, which means that many regions of the genome have been identified which could be important for the adaption of African rice to the African continent and utilised to understand their function and improve rice. We were also able to show that many of the genes that were selected for domestication in Asian rice were also selected in African rice. It is therefore a fascinating story. The work in the future will be to try to identify traits in genes that are adapted to the African environment that can be used for crop improvement.

There is a wonderful book by Judith Carney called Black Rice about the historical significance of African rice in America. At one point in the 1700s, South Carolina was one of the largest exporters of rice in the world and the story was that the slave owners taught the slaves how to grow rice. This is completely false; it was actually the slaves who knew everything about rice production. They knew how to cultivate, irrigate, harvest and cook rice. The book is a fascinating story setting out that slavery was not just about muscle but also a transfer of knowledge from one culture to another. The book is definitely worth reading.

I have talked about the wild relatives of rice and I would now like to talk a little about genomics. We will soon have the genomes of all the wild relatives of rice and we can use this information to pinpoint agriculturally important genes that can be used to improve crops. The cost of sequencing has gone down and because of this the number of plant genomes has increased significantly. There are therefore lots and lots of genomes but what we do not have is an efficient mechanism for understanding the biology of these plants. This is what we call the genome bottleneck and one of the greatest challenges that we face in plant breeding is to be able to link genome sequences to functional traits that could be used to create superior and sustainable varieties, which is what we call genotype to phenotype. The phenotype is what the plant is expressing – its number of seeds and resistance to disease and drought, for example.

There are regions around the world that are developing state of the art phenotyping centres that can phenotype thousands and thousands of plants at a time. We collaborate with Qifa Zhang at Huazhong Agricultural University in Wuhan in China, where they have developed a phenotyping greenhouse that can assay 4,000 plants a day. This information is used to understand and capture natural variation and associate it with specific loctions on the genome. Once you have that information you can use it to learn and incorporate new variation into breeding programs.

HZAU has built a state of the art greenhouse phenotyping center, while IRRI has some wonderful high throughput phenotyping field scanners, which are tractors with booms and lots of sensors. The tractors go through a field where there are plots of 25 plants with the same genetic makeup and they can cover 3,000 25 plant plots per hour, using just one or two people. IRRI has recently released the sequences of 3,000 of these 125,000 accessions and is interested in trying to plant all of them out in the field and then phenotyping them in various locations to associate genotype with phenotype.

A couple of weeks ago, we held the International Symposium on Rice Functional Genomics in Tucson, Arizona to celebrate the 10th anniversary of the completion of the rice genome. At the meeting we held two think tank sessions where we discussed a concept that Qifa Zhang and I have been working on for the past two years, which we call ‘9 billion to help solve the 9 billion people question’. In terms of functional genomics, the challenges here are stress biology, evolutionary biology, natural variation and ecosystems genomics, which is not only looking at the genetics of the plant but also the environment, the microbiome in the soil and and above ground and its relationship with climate change. We are working on some White Papers to try to raise money for developing a coordinated activity to do phenotyping worldwide.

Part of this coordination is the concept of generating five or six nextgen super crops science and technology centres and we have put forward the proposal to build centres in Africa, China and possibly India, Europe, South America and the United States. The idea is to take the 120,000 rice accessions and plant them in various locations around the world, phenotype them and capture the natural variation so that we can create the nextgen super crops that will allow us to keep up with the world’s population.

Qifa Zhang and I were in Wudangshan, a main centre for Taoism – Taoism refers to the path – and we believe that we have developed a path to helping solve this problem.

Jean-Yves Carfantan, Senior Consultant, AgroBrasConsult

Thank you. It is fascinating because you have shown that Africa is part of the solution. If it is studied well, Africa has resources that can be a huge contribution to the solution.

Rod A. Wing, Professor, University of Arizona

This is a huge solution, not only for Africa but for the whole world.