Annual TAA East Anglia Seminar

David Attenborough Building, Cambridge May 9th 2018

***Improving rural livelihoods by reducing crop losses**, with emphasis on Eastern Africa*

Presentation 1:
Plantwise: a programme to extend extension and improve plant health systems.
By Philip Taylor.

Philip Taylor went to Wye College to study plant sciences and then did a PhD on downy mildew of pea before embarking on a brief foray into molecular plant pathology in its early days. He became MD of a farm for 16 years growing both organic and GM crops along with more conventional crops. Then in 2010 he gave up farming and began working for CABI as the Plantwise training manager.

ABSTRACT
Plantwise is a donor-funded initiative aimed at improving extension services in developing countries. Simple training in field diagnostics is provided and the extension workers are encouraged to set up plant clinics in their local community, these are temporary events held once a week where farmers can bring samples of sick crops for diagnosis and advice. The details of the interaction is ultimately stored on a computer database which held securely by CABI on behalf of the country. In addition to the clinic data, Plantwise offers a knowledge bank, which is open access providing bespoke information for each country on the pests and diseases found there.

CABI is a not-for-profit intergovernmental organisation established in 1910 by a UN treaty; it provides scientific expertise and information about agriculture and the environment; it is owned by 48 member countries and has 500 dedicated staff worldwide in 21 locations.

The full paper will be published in Agriculture for Development, Issue 34, Summer 2018.

Presentation 2:
Maize Lethal Necrosis (MLN): using next-generation sequencing to characterise and develop genetic resistance to new disease outbreaks, such as MLN
By Luke Braidwood

Luke Braidwood is a Post Doctoral Research Associate in the Department of Plant Sciences, University of Cambridge.

ABSTRACT.
Crops suffer from a wide variety of pests and pathogens, which destroy around one third of global agricultural production annually (FAO). A growing global population, increasingly meat-hungry middle-class, and the expected

negative impacts of climate change mean that it will be vital to increase food production to attain global food security. Globalisation has brought with it the mass worldwide movement of crops, and with them new introductions of pests and pathogens. There are plant pathogen introductions every year, and rapidly responding to these new threats will mitigate potential crop losses. Many new technologies will be vital in this effort, and I will highlight the benefits of next-generation sequencing (NGS) for characterising new disease outbreaks when compared to older techniques such as PCR- or antibody-based methods, and explain how this has helped us respond to an emerging maize disease, maize lethal necrosis (MLN).

Maize is the most productive cereal crop in Sub-Saharan Africa (FAOSTAT). Maize production in the region is threatened by maize lethal necrosis (MLN), which has emerged due to a recently introduced virus: *maize chlorotic mottle virus* (MCMV). MCMV interacts synergistically with members of another viral family, the Potyviridae, to produce a more serious condition called maize lethal necrosis (MLND). MLND was first recorded in Africa in Kenya, 2011, but has since been reported in Tanzania (2012), Uganda (2013), Rwanda (2013), the Democratic Republic of the Congo (2013), and Ethiopia (2014). We began a research programme to generate MLN-resistant maize lines in 2014 and sampled maize in collaboration with the Kenya Agriculture and Livestock Research Organisation (KALRO).

NGS has two primary benefits compared to older techniques – less assumed knowledge, and data to both identify and characterise a pathogen. PCR- and antibody-based tests require selection of the primers or antibodies, and can detect a pathogen only if the correct primers (for PCR) or antibodies are present. In the case of MLN in East Africa, samples were tested with the correct antibodies, but the results were negative due to variation between strains of the viruses. NGS, by contrast, correctly identified that the viruses present were MCMV and *sugarcane mosaic virus* (SCMV), two viruses known to cause MLN. The NGS data showed that MCMV has very limited variation globally, while SCMV is highly variable. This informed our response to the MLN disease – we decided to target MCMV with artificial microRNAs (amiRNAs). amiRNAs direct part of the plant immune system called RNA silencing to destroy matching RNA molecules, such as viral genomes. Therefore, we designed amiRNAs to target the most conserved regions of the MCMV genome (identified using NGS data), and transformed these genes into Kenyan maize varieties in collaboration with Kenyatta University. We are now waiting for biosafety approval from the Kenyan Government to test the resistance in the maize lines.

Papers: Maize chlorotic mottle virus exhibits low divergence between differentiated regional sub-populations - https://www.nature.com/articles/s41598-018-19607-4

Extensive recombination challenges the utility of sugarcane mosaic virus phylogeny and strain typing (in preparation)