Scientific Review and Planning Workshop

"Management of critical pests and diseases of RTBs through enhanced risk assessment and surveillance (CRP-RTB)"

"Modeling climate impacts on pests and diseases"

Program

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Book of Abstracts

10-14 December 2012

Lima, Peru

Foreword

Within the new structure of the Consultative Group on International Agricultural Research (CGIAR), new defined Research Programs (CRPs) should bring together the research synergies, strengths, and resources from multiple centers to increase efficiencies and enhance impacts in achieving global development goals. The **Roots, Tubers, and Bananas Research Program** (RTB Research Program) is one of these initiatives; it is led by the International Potato Center (CIP) together with its sister centers Bioversity International, International Center for Tropical Agriculture (CIAT), and the International Institute for Tropical Agriculture (IITA). The Research Program on **Climate Change, Agriculture and Food Security** (CCAFS) is led by CIAT. It seeks to overcome the threats to agriculture and food security in a changing climate, exploring new ways of helping vulnerable rural communities adjust to global changes in climate. The approach of CCAFS is to bring together the world's best researchers in agricultural science, climate science, environmental and social sciences to identify and address the most important interactions, synergies and trade-offs between climate change and agriculture.

Endemic and non-endemic pests and plant pathogens are a major threat to the productivity of Roots, Tubers and Bananas (RTB) and all other mandate crops of the CGIAR as systems adapt to changing global needs. These threats persistently challenge food security, income generation and trade with cropping intensification, increased human mobility and climate change challenging our ability to manage plant health. Assessment and forecasting of future shifts in the distribution and impact of plant pests and pathogens combined with early and accurate diagnoses and surveillance at local, regional, and global scales are necessary to deploy pre-emptive mitigation strategies.

The objective of the scientific review and planning workshop is to contribute to:

- Link experts in pest and pathogen ecology, epidemiology, risk analysis, modeling and mapping, detection and surveillance, trade regulations etc. across the globe to identify scientific challenges, to review available resources and set priorities, and to create synergies between CG centers and other stakeholders to efficiently address the challenges of pest risks assessments and surveillance under a changing climate.

- Establish a priority list of pests and pathogens through evaluation of their risk to food security and income generation.

- Develop new modeling tools addressing the effects of climate change on agricultural pests and diseases, and especially assemble and evaluate a general platform for pest and disease risk assessments under climate change.

- Identify and recommend appropriate methods for diagnostics, risk assessments and surveillance.

- Develop a harmonized and shared science based framework and planning document (MTP) for pests and disease risk assessment and modeling and surveillance research that identifies major research products, milestones, and outcomes, target regions, countries and key research teams for future collaborative research and capacity building initiatives.

Fen Beed

IITA, Nigeria

Karen Garrett

Kansas State University

Jürgen Kroschel

CIP, Lima

Program

Monday, December 10	
08:00 - 08:30	Registration
08:30 - 08:45	Welcome note by P. Donini (DDG-Research)
08:45 - 09:15	Introduction into workshop objectives and program (J. Kroschel, F. Beed)
09:15 - 09:30	Self introduction of participants
Theme 1:	**Target pests and diseases: justification and distribution (Chair: J. Smith)**
09:30 - 10:00	Banana and plantain: target pests and diseases (P. Lepoint)
10:00 - 10:30	Cassava: target pests and diseases (B. Herrera)
10:30 - 11:00	*Coffee break*
11:00 - 11:30	Potato and sweetpotato: target pests and diseases (J. Kroschel, J. Kreuze)
11:30 - 12:00	Banana, cassava and yam: target pests and diseases (F. Beed)
Theme 2:	**Pest, disease and weed risk assessment and modeling under current and future climates (Chairs: J. Kroschel & K. Garrett)**
12:00 – 12:30	Predicting crop risks under climate change: progress and opportunities (A. Challinor, via skype)
12:30 – 13:30	*Lunch*
13:30 – 13:45	Platform for pest and disease risk assessments under climate change (K. Garrett)
13:45 – 14:00	Climate change adaption in disease management: a framework for evaluating the likely utility of decision support systems and index insurance (K. Garrett)
14:00 – 14:15	Disease risk assessments and modeling at IRRI (A. Sparks)
14:15 – 14:30	Disease risk assessments and modeling at CIP (G. Forbes)
14:30 – 14:45	Insect pest risk assessments using phenology modeling (J. Kroschel)
14:45 – 15:00	Insect Life Cycle Modeling (ILCYM) software for phenology models development and life table parameters estimation (H. Tonnang)
15:00 – 15:15	*Coffee break*
15:15 – 15:30	Spatial analysis tools in ILCYM software for risk assessment (H. Juarez)
15:30 – 15:45	Weed and pest risk assessments with Maxent (R. Simon)
15:45 – 16:00	Linking crop and pest models for assessing risks on crop losses using intelligent systems (H. Tonnang)
16:00 – 16:15	Management of critical banana pests and diseases through

	enhanced risk assessment and modeling (E. Karamura)
16:15 – 16:30	Risk assessments and modeling at CIAT (S. Parsa)
16:30 – 16:45	Risk assessments and modeling at CIMMYT (P. Likhayo)
16:45 – 17:00	Risk assessments and modeling of biotic stresses in ICRISAT mandate crops (H. Sharma)
17:00 – 17:15	Pest Risk assessments and activities in modeling impacts of climate change on pest dynamics at *icipe* (S. Subramanian)
17:15 – 17:30	Risk assessments and modeling: IITA (M. Tamu)
17:30 – 18:00	*Open discussion*
18:00	*Cocktail in CIP's garden*
Tuesday, December 11	
Theme 3:	**Risk based surveillance (Skype presentation plus q & a) (Chair: F. Beed)**
08:00 – 08:45	Regulation of pest to protect trade and plant health (FAO-IPPC-O. Sosa)
08:45 – 09:15	Targeted surveillance to promote food security (FAO-AGP-M. Robson)
09:15 – 09:30	Sampling strategies for trade shipments (J. Smith)
09:30 – 10:00	*Open discussion*
10:00 – 10:30	*Coffee break*
Theme 4:	**Current surveillance strategies (Chair: J. Kroschel)**
10:30 – 10:45	Current surveillance strategies for banana pests and diseases (M. Dita)
10:45 – 11:00	Current surveillance strategies for potato and sweet potato pests and diseases (G. Forbes)
11:00 – 11:15	Current surveillance strategies for banana, cassava and yam pests and diseases (F. Beed)
11:15 – 12:00	*Open discussion*
12:00 – 13:00	*Lunch*
Theme 5:	**Detection and diagnostics (Chair: M. Tamo)**
13:00 –13:15	Symptom recognition mediated by mobile plant clinics (T. Holmes)
13:15 –13:30	Classical disease and pest diagnostic methods (S. Miller)
13:30 –13:45	Barcoding for pathogens and insect pests (J. Kreuze)
13:45 –14:00	Virus disease detection methods (J. Kreuze)
14:00 –14:15	LAMP and next generation sequencing (J. Smith)
14:15 – 15:00	A new low-cost diagnostic tool for detecting regulated (quarantine) cassava and banana diseases (E. Alvarez)
15:00 –15:15	*Open discussion*
15:15 – 15:45	*Coffee break*

Theme 6:	Data management and reporting (Chair: S. Parsa)
15:45 – 16:00	Plantwise knowledge bank (T. Holmes)
16:00 – 16:15	Valuing pest risk analysis in pest outbreak prevention (J. Smith)
16:15 – 16:30	Networks for diagnostics and capacity building (S. Miller)
16:00 – 16:45	Climate data management for species distribution models (H. Juarez)
16:45 – 17:00	Innovations to increase efficiency of data management (R. Simon)
17:00 – 17:30	*Open discussion*
Wednesday, December 12	
08:00 – 08:30	Orientation to group work and outputs (J. Kroschel, F. Beed)
08:30 – 10:00	Working group A:**Targeting**
Group A1:	Targeting priority pests for RTB & CCAFS
Group A2:	Targeting priority pests for RTB & CCAFS
Group A3:	Targeting priority diseases for RTB & CCAFS
Group A4:	Targeting priority diseases for RTB & CCAFS
10:00 – 10:30	*Coffee break*
10:00 – 10:20	Reporting to plenary: group A1 & A2
10:20 – 10:40	Reporting to plenary: group A3 & A4
10:40 – 12:10	Working group B:**Capacity and needs for modeling**
Group B1:	Modeling of pests
Group B2:	Modeling of pests
Group B3:	Modeling of diseases
Group B4:	Modeling of diseases
12:10 – 12:30	Reporting to plenary: group B1 & B2
12:30 – 12:50	Reporting to plenary: group B3 & B4
12:50 – 14:00	*Lunch*
14:00 – 15:30	Working group C:**Capacity and needs for risk assessment under current and future climates**
Group C1:	Risk assessments for pests
Group C2:	Risk assessments for pests
Group C3:	Risk assessments for diseases
Group C4:	Risk assessments for diseases
15:30 – 16:00	*Coffee break*
16:00 – 16:20	Reporting to plenary: group C1 & C2
16:20 – 16:40	Reporting to plenary: group C3 & C4
16:20 – 17:00	Open discussion (J. Kroschel, F. Beed)
Thursday, December 13	
08:00 – 08:30	Orientation to group work and outputs (J. Kroschel, F. Beed)
08:30 – 10:00	Working group D:**Risk based surveillance strategies**
Group D1:	Risk based surveillance for pests

Group D2:	Risk based surveillance for pests
Group D3:	Risk based surveillance for diseases
Group D4:	Risk based surveillance for diseases
10:00 – 10:30	*Coffee break*
10:00 – 10:20	Reporting to plenary: group D1 & D2
10:20 – 10:40	Reporting to plenary: group D3 & D4
10:40 – 11:40	Working group E:**Detection and diagnostics**
Group E1:	Detection and diagnostics of pests
Group E2:	Detection and diagnostics of pests
Group E3:	Detection and diagnostics of diseases
Group E4:	Detection and diagnostics of diseases
11:40 – 12:00	Reporting to plenary: group E1 & E2
12:00 – 12:20	Reporting to plenary: group E3 & E4
12:20 – 13:30	*Lunch*
13:30 – 14:30	Working group F: **Data management and reporting**
Group F1:	Data management and reporting
Group F2:	Data management and reporting
Group F3:	Data management and reporting
Group F4:	Data management and reporting
14:30 – 14:50	Reporting to plenary: group F1 & F2
14:50 – 15:10	Reporting to plenary: group F3 & F4
15:10 – 15:40	*Coffee break*
15:40 – 17:00	Working group G:**Planning of products, milestones, outcomes, and responsibilities**
Group G1:	CRP-RTB Theme 3
Group G2:	CRP-RTB Theme 3
Group G3:	CCAFS
Group G4:	CCAFS
Friday, December 14	
08:30 – 09:00	Orientation to group work and outputs (J. Kroschel, F. Beed)
09:00 – 10:30	Working group G (cont.): **Planning of products, milestones, outcomes, and responsibilities**
Group G1:	CRP-RTB Theme 3
Group G2:	CRP-RTB Theme 3
Group G3:	CCAFS
Group G4:	CCAFS
10:30 – 11:00	*Coffee break*
11:00 – 11:20	Reporting to plenary: group G1 & G2
11:20 – 11:40	Reporting to plenary: group G3 & G4
11:40 – 12:30	Final discussion; assignment of responsibilities; plan to

	disseminate for refinement and development of proposals
12:30 – 14:00	*Lunch & Faire well cocktail*
	DEPARTURE

THEME 1

TARGET PESTS AND DISEASES:

JUSTIFICATION AND DISTRIBUTION

Banana and plantain: target pests and diseases

P. Lepoint[1], M. Dita[2], A. Molina[4], C. Staver[3], G. Blomme[1], E. Karamura[1]

[1]Bioversity International Africa, [2]South America, [3]Montpellier, [4]Asia

A wide range of pests and diseases including fungal, viral and bacterial diseases, and nematodes and weevils affect banana and plantain (*Musa* spp.) production worldwide. In Asia, the primary center of origin of *Musa* spp., the major fungal diseases affecting bananas consist of Fusarium wilt (*Fusarium oxysporum* f.sp. *cubense*, *Foc*) including its most virulent strain the Tropical Race 4 (TR4) and black sigatoka (*Mycosphaerella fijienis*). *Mycosphaerella eumusa* causing banana leaf spot in India and Sri Lanka and Freckle disease caused by *Guignardia musae* are two emerging fungal diseases of importance in the region. Key virus diseases in Asia include Banana bunchy top disease (BBTD) and banana bract mosaic. Moko and Bugtok caused by (*Ralstonia solanacearum*) are serious banana bacterial diseases but so far limited to the Philippines, while Blood Disease caused by *Pseudomonas celebensis* (taxonomic identity is being established) are causing epidemics in Indonesia and Malaysia. Latin America and the Caribbean (LAC), although neither the center of origin of bananas nor a center of domestication or secondary diversity, grow 28% of the global *Musa* production and seven countries of the region are in the top 10 banana exporting nations. In spite of considerable technical change in recent decades, bananas in LAC continue to face important challenges for sustainable pest and disease management of *Foc*, banana rust thrips (*Chaetanaphothrips signipennis*), Erwinia soft rot (*Dickeya* spp.) and Moko (*Ralstonia solanacearum*). While the latter are specific to certain production systems, *M. fijienis* is still the major phytosanitary challenge for banana production in LAC and Foc TR4 and BBTD are listed as quarantine diseases. In Africa, center of secondary diversification for the East African Highland bananas (EAHB) and plantain, key pests and diseases include BBTD, banana Xanthomonas wilt (XW), black sigatoka, weevils and nematodes, of which some singly or in various combinations cause major damage in Cavendish, EAHB and plantain systems significantly reducing yield. The continent is dominated by smallholder systems, often perennial and subtended by informal seed systems with minimum attention to seed quality. Foc TR4 is equally listed as a quarantine disease in Africa whereas XW is endemic to the African continent and was first described on *Musa* in 1974. A systematic prioritization of banana pests and diseases is currently under way to guide research investment. Steps include mapping of cultivar group/production system, estimation of yield impacts of pests and diseases, review of current production practices, technology under use and costs of production.

Cassava: target pests and diseases

B.V. Herrera Campo, J.M. Pardo

Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia

Cassava production worldwide is significantly affected by pests and diseases. Although the cassava pest complex is large, the most limiting pests are mites, mealybugs and whiteflies. Several caused by viruses, fungi, bacteria, phytoplasma are also of significant concern. CIAT's phytosanitary research has focused on a few species, prioritized on their economic impact and their potential risk of introduction into important production centers, where they are absent. Recent efforts have been made in order to know the current and the potential distribution of cassava green mite, cassava mealybug and the whitefly, regarding pests, and Cassava Mosaic disease, Cassava Brown Streak disease and Cassava frog skin disease, concerning to diseases. Cassava mealybugs and mites are present in South America, their origin center, and Africa, where they caused considerable losses after being introduced in 1970´s. They were successfully controlled in late 1980´s. Regardless the large absent of these pest in Southeast Asia, cassava production areas become threatened in the last years, due to recent introduction of the cassava mealybug and a cassava mite in this area. Results from species distribution models carried out at CIAT show that environmental conditions ensure the potential establishment of these pests. Whiteflies are widely spread pests, directly affecting cassava. Their importance varies between different regions and continents. However, their major risk refers to their capacity to transmit several cassava-related viruses. Most important diseases affecting cassava in Africa are Cassava Mosaic disease and Cassava Brown Streak disease. The former´s distribution embraces the entire cassava belt in Africa and the western coast of India where cassava is cultivated. The latter was largely confined to the Eastern coast of the continent but recently has moved to other central places in the continent. Cassava Frog Skin disease is an important constraint to cassava production in some areas of Latin America and cassava bacterial blight is the major issue in Asia.

Potato and sweetpotato: target pests

J. Kroschel

International Potato Center (CIP), Lima, Peru

Potato producing farmers in developing countries worldwide have to contend with about 20 insect pests. The potato tuber moth, *Phthorimaea operculella*, and the Andean potato tuber moth, *Symmetrischema tangolias,* have evolved in the center of potato origin. *P. operculella* has become very invasive and is reported from more than 90 countries worldwide. It is considered the most damaging potato pest in the developing world. The Andean potato tuber moth is widely distributed in the Andean region; it is less invasive but has been also reported outside its range of origin; e.g., Australia. The Guatemalan potato tuber moth, *Tecia solanivora,* started invading South America in 1983 and reached Ecuador in 1996. In 2000, it reached the Canary Islands (Tenerife) and is considered major threat to potato production of southern Europe. The leaf miner fly *Liriomyza huidobrenis*, also of neotropical origin, is reported today from 66 countries; recently we could report its occurrence in Nepal. The bud midge, *Prodiplosis longifilia,* can be very damaging and is likely to become more invasive under climate change. The green peach aphid (*Myzus persicae*), the potato aphid (*Macrosiphum euporbiae*) and cutworms (*Agrotis* spp.) are found worldwide. Aphids are mainly a risk for virus infection and seed degeneration. Cutworms are extremely polyphagous and damaging in the Hindu Kush-Himalaya. The Colorado potato beetle, *Leptinotarsa decemlineata*, which originated in central Mexico, has become the main threat to potato production in developing countries of Central Asia, the Caucasus, and has also been reported from western China.

Sweetpotato weevils (*Cylas* sp.) are the most serious insect pests of sweetpotato in Central America, Africa and Asia; *C. formicarius* is found globally, whereas *C. puncticollis* and *C. brunneus* are reported only from Africa. These are considered as the main target pests although a large complex of pests may occur regionally, e.g. in East Africa consisting of: (i) stem and root feeders, (ii) defoliators, and (iii) virus transmitters.

Potato and sweetpotato: target diseases

J. Kreuze, G. Forbes, L. Gutarra

International Potato Center (CIP), Lima, Peru

A very large number of pathogens have been reported in association with potato production, but a smaller number of them are generally considered to the primary agents of disease worldwide. One of the primary potato diseases is late blight caused by the oomycete pathogen *Phytophthora infestans.* Late blight is a global problem and its significance in terms of both yield loss and fungicide usages has been estimated to be over 10 billion USD annually. Bacterial wilt, caused by *Ralstonia solanacearum* is a major disease in many parts of the developing world, particularly in warm, humid areas. *R. solanacearum* is a soilborne pathogen mainly transmitted through tuber seed leading to a condition often referred to as seed degeneration. Similarly, a number of viruses also accumulate through generations and participate in seed degeneration; the most important seed degeneration viruses are PVY and PLRV, and to a lesser extent PVX. Other mild viruses such as PVS, PVM, PVA, PVV are also widespread and may contribute to degeneration of potatoes, but their presence in developing countries has not been systematically surveyed in many places and the effect on yields poorly quantified. Surveys on native potatoes in Peru and Ecuador determined the high incidence of PVX and PVS viruses however their infection not always were related to decreased performance on some native varieties. Several other viruses such as APMV, PYVV, APLV, PYV, PVT, AMV, PAMV, and PBRSV are only important in Latin America whereas Potato spindle tuber viroid and phytoplasma diseases may be of importance locally in some regions. As with bacterial wilt, several pathogens may be seed- and soilborne pathogens (e.g. *Rhizoctonia solani, Streptomyces* spp. and *Clavibacter michiganensis* subsp. *sepedonicus*) and may participate in seed degeneration, which overall is probably the main biotic constraint to potato productivity in developing countries. There are several diseases which have local importance, and may also be considered quarantine problems. Powdery scab, caused by *Spongospora subterranea* and potato wart, caused by *Synchtrium endobioticum,* are diseases caused by pathogens with a great survival capacity reason by wich they are very difficult to manage. The bacterial complex of black leg and soft rot caused by *Pectobacterium* spp. and *Dickeya* spp. can be extremely severe under the conducive environmental conditions, although we are unaware that *Dickeya* spp. have been reported in developing countries. Nematodes of the species *Globodera* spp. in temperate regions and highlands and *Melodoigyne* spp. in warm areas are widespread and can cause significant damage also by increasing the incidence of other bacterial and fungal diseases on roots.

The major disease problem of sweetpotato on a worldwide scale is caused by viruses which often occur in a complex reducing yield considerably. Of the about 30 known sweetpotato infecting viruses the most widespread are Sweet potato feathery mottle virus and Sweet potato virus C, and Sweet potato chlorotic stunt virus (SPCSV). Recently it

has been realized that sweetpotato begomoviruses or 'sweepoviruses' are also very common worldwide, although their impact is not clear yet as they have been relatively little studied. Whereas most sweetpotato infecting viruses (with the exception of SPCSV) often cause no, or only mild symptoms in most sweetpotato cultivars, mixed infection with SPCSV causes increased titers with all currently investigated viruses and severe disease complexes with many of them. Therefore SPCSV is probably the single most serious disease problem for sweetpotato worldwide. Nematodes (particularly *Meloidogyne* spp.) are also a significant problem in many sweetpotato producing areas. Numerous bacteria and fungi, including *Ceratocystis fimbriata, Altenaria bataticola, Elsinoe batatas, Fusarium solani, F. oxysporum, R. solanacearum, Rhizopus stolonifer, Diplodia* gossypina, *Macrophomina phaseolina, Streptomyces ipomoeae, Dickeya sp.(E. chrysanthemi)* have also been reported to cause various types of root or stem rot diseases or foliar blemishes, although they are much less important on a global scale and/or only important locally.

Banana, cassava and yam: target pests and diseases

F. Beed

International Institute for Tropical Agriculture (IITA), Dar es Salaam, Tanzania

Cassava is a staple food across Africa, banana across the great lakes region and yam is a favored food in West Africa. All three crops are of critical importance to food security and income generation to Africa. While cassava and banana have been introduced to Africa from Latin America and Asia, respectively, yam is indigenous. The productivity of all three crops is threatened by current and emerging pests and diseases that are indigenous to Africa, and further, due to the potential introduction of other pests and diseases from elsewhere in the world. Taking cassava as an example; indigenous pathogens and pests include African cassava mosaic virus, East African cassava mosaic virus complex, South African cassava mosaic virus, whiteflies, fungal diseases and root scales. However, some of the most devastating viruses have restricted distribution such as brown streak, Ugandan brown streak virus and East African mosaic virus – Uganda (EACMV-UG). Exotic pests that are now established on cassava in Africa include Green spider mite (*Mononychellus tanajoa*), Cassava mealy bug, (*Phenacoccus manihoti*), Cassava Bacterial Blight (*Xanthomonas axonopodis*) and Indian cassava mosaic virus. While important pests and pathogens not present in Africa but present in South America include; common mosaic virus, green mosaic virus, vein virus, X virus, Frog Skin Disease, antholysis, Super Elongation (*Sphaceloma manihoticola*) and from southeast Asia; witches broom (Phytoplasma) and from South Asia; Sri Lankan mosaic virus.

For banana an indigenous bacterium that is spreading across the great lakes region and devastating production is Xanthomonas Wilt (*Xanthomonas campestris* pv. *musacearum*) while another bacterium, *Ralstonia solanacearum* Race 2, that causes Moko disease, is currently restricted to Australia, South Pacific and Latin America. A fungal disease caused by *Fusarium oxysporum* f.sp *cubense* is divided into different races based on which clones are attacked. Races 1 and 2 are already established in Africa; race 1 attacks clones of AAA, AAB, ABB and AAAA while race 2 attacks ABB and AAAA clones. Perhaps the greatest threat to banana production in Africa, and potentially the world, is Tropical race 4 (TR4) of this fungus. This is because it kills all clones susceptible to race 1 and 2 plus cultivars in the Cavendish clones (AAA) which were specifically bred for resistance to race 1. Currently TR4 is spreading from Southeast Asia and Australia to China and beyond. Another disease, caused by a virus, that is increasingly devastating all clones of banana in Africa, is a variant of Banana Bunchy Top Disease that is more virulent than other forms elsewhere in the world.

A risk assessment will be provided, based on distribution and impact of pests and diseases of cassava, banana and yam, to prioritize those that justify management interventions such as targeted surveillance, to prevent their introduction, establishment and spread.

THEME 2

PEST, DISEASE AND WEEK RISK ASSESSMENT

AND MODELING UNDER CURRENT

AND FUTURE CLIMATES

Predicting crops risks under climate change: progress and opportunities

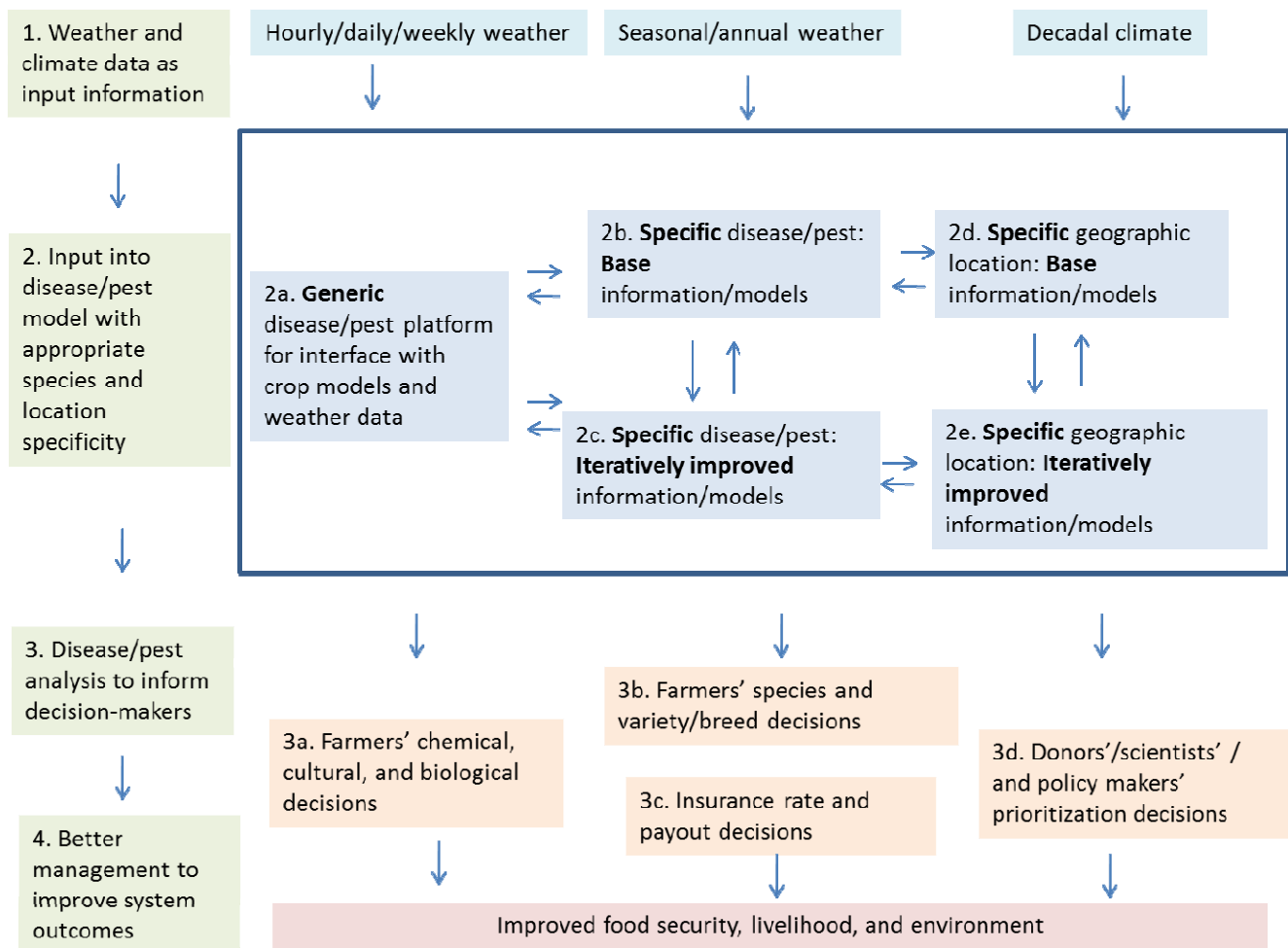### A. Challinor

University of Leeds, UK

Over the last decade, there have been significant advances in the combined simulation of climate and crop yield. Ensemble techniques to quantify uncertainty are now routinely used, and crop model inter-comparisons' are starting to occur. After a review of these techniques, two areas for future development are suggested: i. greater integration of crop models with models of pests and diseases; ii. greater awareness of the uncertainties inherent in downscaling and climate model bias correction; and ii. re-framing the way in which uncertainty is presented in order to obtain robust information on when changes are expected to occur.

Platform for pest and disease risk assessments under climate change

K. Garrett and CCAFS scoping study team

Kansas State University

Based on the scoping study, we recommend that CCAFS participants work together to assemble and evaluate a general platform for pest and disease models, to the extent useful. Points for synergy would include: 1. Use of shared global and regional weather and climate databases as input; 2. Use of shared programs for predicting losses to pests and disease, where the core models will differ from one pest/disease to another, but the general programming structure for estimating risk and yield losses can be similar; 3. Use of shared conceptual frameworks for how the core pest/disease models can be used in within-season forecasting, seasonal forecasting, scenario analysis and prioritization, and potential index insurance programs; 4. Use of shared platforms for communicating results to stakeholders; 5. Use of shared methodologies for evaluating the impact of CCAFS activities and forming strategies to increase impact.

Climate change adaptation in disease management: a framework for evaluating the likely utility of decision support systems and index insurance

K. Garrett, G.M. Ramirez, B. Natarajan

Kansas State University

The same core models of the relationship between weather and loss to viruses are needed for climate change scenario analysis, decision support systems (DSS), and other potential applications such as index insurance. We have developed a framework for evaluating the likely effectiveness of DSS and index insurance for pests and diseases, as a function of a number of key factors. First, we consider the time series of weather conditions, in terms of baseline temporal autocorrelation and the type of non-stationarity imposed by climate change, and how these patterns make DSS and index insurance more and less feasible. Second, the framework within which the DSS is constructed is considered, in terms of the number of years of data available and how good initial parameter estimates are. We use these system traits to identify parameter combinations or scenarios where DSS and index insurance are likely to be effective or not. We are beginning the work of placing particular diseases and geographic locations in the theoretical parameter space. Ultimately we plan to use this framework to identify pathosystems and locations that are particularly good targets for implementing tools such as DSS and index insurance. We also are addressing the general question of when DSS developed in baseline climate scenarios can still work well in new climate scenarios, versus when DSS must be modified to maintain utility.

Disease risk assessments and modeling at IRRI

A. Sparks

International Rice Research Institute (IRRI), Los Banos, The Philippines

IRRI is actively working to better understand and mitigate uncertainty in rice yields due to short and long-term changes in weather patterns and concurrent shifts in pest and disease severity and distribution. This work focuses both on in-field research and modeling efforts. In-field research is being undertaken to characterize change in diseases due to the transformation of production situations and provide data for modeling efforts. Currently two models are being developed and used by IRRI. EPIRICE predicts the severity of unmanaged epidemics for five rice diseases using weather data. RICEPEST is a mechanistic model capable of simulating yield losses due to six diseases, three insect injuries and a range of weeds using weather and field observation data. Using these models it is possible to estimate relative risks and yield losses under current and future climate conditions for select pests and diseases.

Disease risk assessments and modeling at CIP

G. Forbes, J. Kreuze

International Potato Center (CIP), Lima, Peru

In CIP, plant disease risk modeling and assessment has been primarily limited to potato late blight with some recent activities on potato and sweet potato viruses. Late blight has been modeled at the plot level for research purposes using a process based simulation model. Late blight risk is also estimated at the plot level using simple decision support systems adapted low input farmers. At a larger scale, a disease forecasting model was incorporated into a geographical information system (GIS); this gave the potential for estimating potential disease intensity at various spatial scales. This technology has since been modified to use geo-referenced weather data of much lower temporal resolution, and has been used to estimate effects of climate change. Pathogen evolution for pathogenicity has been of major concern at CIP and efforts to estimate risk are currently underway. Risk of late blight pathogen evolution for fungicide insensitivity has been monitored, which can also provide some degree of predictability because of the clonal nature of the pathogen. Overall risk to farmer health and environment has been estimated using the environmental impact quotient. Recently siRNA technology is being used to monitor viruses in sweet potato and to a lesser degree potato, which can provide insight into the risk of emerging diseases. This technology is discussed more in the session on monitoring.

Insect pest risk assessments using phenology modeling

J. Kroschel, H. Tonanng, H. Juarez

International Potato Center (CIP), Lima, Peru

Temperature has a strong and direct influence on insect development, reproduction and survival and is considered under climate change the dominant abiotic factor directly affecting herbivorous insects (pests). It is also expected that climate change may dissociate predator-prey relationships, because of a higher sensitivity of higher trophic levels to climatic variability or of different temperature optima compared with pests. Two modeling approaches are used to understand and predict effects of increasing temperature on insects: the inductive modeling approach uses the combination of occurrence records and environmental variables and through the application of climate match functions it estimates the establishment potential of a species to new areas. Limitations are that it does not consider detailed biological characteristics of the insect in the modeling framework. It uses degree day models which describe the linear development of insects using the accumulation of temperature above the min. temperature threshold. However, due to the non-linearity of the development curve degree-day models are poor predictors of insect development. Advantages are that it can use minimal data sets and simple functions to describe the species' response to temperature and other climatic factors, which allow quite quick assessments. Software programs which support such kind of modeling are CLIMEX, BIOCLIM and others. The deductive modeling approach uses a process-based climatic response model (i.e., phenology model) for a particular insect species of interest. The temperature dependency of insects is applied in a process-oriented framework; forecasting the potential distribution of insect species is completely independent of observed occurrences. The Insect Life Cycle Modeling (ILCYM) software, developed by CIP, supports the development of process-based temperature-driven and age-stage structured insect phenology models and applies these models in a GIS environment for insect species distribution and risk mapping. For studying the effects of climate change on insects the software provides downscaled future climate scenarios from different projections (e.g., SRES-A1B of the year 2050). The potato tuber moth will be used as an example to demonstrate modelling outputs and global and regional risk maps.

Insect Life Cycle Modeling (ILCYM) software for phenology models development and life table parameters estimation

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The relationship between aspects of insects' life-history (development, survival, reproduction, etc.) and environmental variables (temperature) can be well described by process-based phenology models. The present paper describes the model builder of the Insect Life Cycle Modelling (ILCYM) software as a tool to support the development of process-based temperature-driven and age-stage structured insect phenology models. ILCYM's model builder contains a library of several empirical linear and nonlinear models, including the derivations of the biophysical models which have been proposed to define critical temperatures of insects' development. Several statistical measures are provided for the estimation of parameters and the comparison models. Additionally, phenology models can be applied for estimating insect population increase and abundance using deterministic and stochastic simulations under constant and fluctuating temperatures. Outputs of the simulations are life table parameters that include net reproduction rate, mean generation time, intrinsic rate of increase, finite rate of increase and the doubling time. Through these analyses, the biology and temperature requirements of insects can be defined, as well as the effects of different diets or host plants on insects' life table parameters. ILCYM also supports investigation between natural enemies (e.g., parasitoids) interactions and its target pests as well as the natural enemy potential control efficiency in integrated pest management system. Further, possible outbreaks of pest populations in relation to changes in temperature can be simulated.

Spatial analysis tools in ILCYM software for risk assessments

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ILCYM is an open-source computer-aided tool built on R and Java codes and linked to uDig platform, which is a basic geographic information system (GIS). The software package consists of three modules the "*model builder*", the "*validation and simulation*", and the "*potential population distribution and risk mapping*". This paper only focuses on the GIS component of ILCYM. Under this later module, insect phenology models are simulated in a defined area according to grid-specific daily/monthly temperatures obtained from available databases. Outputs of the simulations are used for calculating life table parameters that include: the net reproduction rate, mean generation time, intrinsic rate of increase, finite rate of increase and the doubling time. From life table parameters, three indices are estimated (the establishment risk index (*EI*), the generation index (*GI*) and the activity index (*AI*)) and mapped for assessing the potential population distribution and abundance of a particular species. Several functionalities for vector (dbf to shape, raster to points, raster to polygons, extract by points, etc.) and raster analysis (merge, cut, mask, aggregate/disaggregate, re-class, describe, raster calculator, etc.) are part of the ILCYM-GIS component. Such tools improve the manipulation of large datasets and help ILCYM's users in analyzing and visualizing the risk assessment maps. Additionally, a sub-module (*index interpolator*) for analysing the index at higher spatial (pixel size of 90m) and temporal resolution (daily data) for capturing small-scale of insect population distribution and abundance is also presented.

Weed and pest risk assessments with Maxent

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Distribution modeling of biological species is an important tool for biologists to understand and predict past, current or future presence based on typically few observations on the ground. Applications include species under threats like climate change or predictions of epidemic outbreaks of organisms damaging to health or food production. Three main classes of modeling tools are available: a) mechanistic models like the EcoCrop approach; b) process oriented models like ILCYM or c) probabilistic or machine learning tools like MaxEnt. There is currently no consensus on a best modeling tool or approach across biological taxa for different reasons. These include for regression approaches the problem of presence only data - that is, the need for absence data. However, assumption or imputation of absence data is unreliable. Similarly, data obtained under laboratory conditions may not be of value for extrapolation under in-situ conditions since many organisms act like integrative sensors. Therefore, the predictive value of independent variables like temperature may be changed. However, recently the maximum entropy approach as implemented in MaxEnt has shown success across a wide taxonomic range. We therefore review the basic algorithm of Maxent and compare it to the other two approaches. We use it for three applications: a) predicting the distribution of a wild potato species with a well defined habitat; b) a weedy potato species and c) for predicting one insect species (*Phthorimea operculella*).

Linking crop and pest models for assessing risks on crop losses using intelligent systems

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Proper estimation of actual crop yield with the help of computer assisted simulation models requires detailed quantitative knowledge of the interactions between the crop and its pests. Because of the complexity of such systems, most crop growth models do not include routines for the simulation of damage caused by pests. In this paper, novel ways for linking pest and crop models via intelligent systems are presented. A detailed example of linking the Insect Life Cycle Modeling (ILCYM) software to a potato crop model using fuzzy logic system is given. The framework is based on coupling pest damage of various types into the crop model. Coupling points are identified in the model for simulating damage to leaves, stems, roots, seeds, whole plants, and to the supply of assimilate. This intelligent model coupling is being developed and will be tested by simulating potato yield with measured pest damage levels due to *Liriomyza huidobrensis* (foliar feeding insect) and *Phthorimaea operculella* (foliar and tuber insect) and comparing observed and simulated crop growth and yield results. Such approach for coupling pests with crop models has potential for extending the practical applications of crop models to a broad range of problems.

Management of critical banana pests and diseases through enhanced risk assessment and modeling

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The success of banana pests and diseases across the globe is linked to their modes of spread. Some diseases are transmitted via vectors over short and long distances accidentally and/or intentionally (XW, BBTV, BSV, etc.) others via air (BLS, Cladosporium) and yet others through host planting material/soil (BBTV, BSV, BBrMV, CMV, BMMV, weevils, nematodes, *Foc*, BXW*)* as well as a combination of the three. These multiple modes of spread, when combined with informal seed systems, provide reservoirs of pests/diseases making it difficult to achieve control. The situation is made worse by weak and/or non-existent quarantine services linked to the lack of surveillance and limited information exchange within and between countries and regions. Moreover for most pests and diseases there is limited capacity for efficient/effective pest and disease detection in support of quarantine. Although yield is a product of complex interactions between genotype, soil fertility, and pests and diseases nevertheless, pests and diseases probably contribute a significant proportion of the yield gap. Studies on level of yield reduction which is attributed to pests and diseases are nevertheless very limited for banana pests. Methods remain variable, making comparisons difficult. The use of chemical control is still limited in smallholder systems but may increase with changing farming objectives; wide spread adoption of resistant varieties may lead to monoculture and reduction of diversity, while and extensive rouging to reduce inoculum may lead to loss of associated biodiversity. For both BXW and *Foc* TR4, probably the most important diseases, a number of diagnostic tools have been developed to facilitate disease surveillance and strengthen quarantine efforts to control the spread. The 2009 PRA for Xanthomonas wilt of bananas is currently undergoing revision as part of 2012 RTB deliverables. In general, however other risk factors such as climate change and its effects on environment and yield; institutional frameworks and associated resource availability and the largely informal seed systems all combine to hamper the management of risks associated with banana pests and diseases. In assessing the risks associated with banana pests and diseases, a holistic perspective needs to be taken into account, including associated biotic, abiotic and socioeconomic factors in the quest to develop effective models for the management of the pests and diseases.

Risk Assessment and Modeling: CIAT

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Under the pest risk analysis paradigm, risk assessment is the obligate prerequisite for risk management. The process for risk assessment is often divided into three steps: (1) pest categorization, (2) assessment of the probability of introduction and spread, and (3) assessment of the potential economic consequences. Risk assessment work at CIAT has focused on the second of these steps; more specifically, on environmental suitability assessments via species distribution modeling. Both statistical and mechanistic models have been used to assess global environmental suitability for critical cassava pests and diseases. Our approach has been integrative; taking advantage of ensemble modeling techniques and joint inductive-deductive approaches to derive the "best" risk maps given available data. Ongoing efforts seek to refine modeling expertise; but more importantly, to broaden capacities for pest risk assessment and analysis.

Risk Assessment and Modeling: CIMMYT

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Climate change will contribute to increased prevalence of insect pests in many agro – ecosystems. The spotted stem borer (Crambidae: Lepidotera), maize weevil and the larger grain borer (Bostrichidae: Coleoptera), are key economically important pests of maize that impacts on millions of African's livelihoods. The former infests cereal crops in the field while the latter two attacks cereal grain in storage. Larger grain borer is an invasive exotic pest that has shown resistance to commonly used insecticide and its expansion to new area could threaten the grain industry and contribution of agriculture to the GDP due to its feeding activities in converting grains into flour. Further, the new range of expansions could present economic impacts through increased seed and insecticide costs and food security. The focus will be directed towards generating missing gaps in life tables' data, based on literature review, to estimate the pest threshold requirements for development time, fecundity and longevity using Insect Life Cycle Modeling (ILCYM) software to project potential future ranges under changing climate. The data will be generated under temperature conditions of $10 – 35^{o}C$ in steps of $5^{o}C$ and humidity of 40 -75 % in steps of 5% in the laboratory.

Risk Assessment and Modeling of Biotic Stresses in ICRISAT Mandate Crops

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Climate change is likely to make rainfed agriculture even more risk prone in the semi-arid tropics (SAT), and the crop and pest management systems need to adapt to these changes at a faster pace in the near future. However, the exact nature of these changes is quite uncertain. The major areas of our research effort on insect pests is focused on and predicting potential risks, changes in geographical distribution, and modeling population dynamics of legume pod borers, *Helicoverpa armigera*, *Maruca vitrata*, defoliators, *Spodoptera litura* and *S. exigua*, spotted stem borer, *Chilo partellus*, and sorghum head bugs, *Calocoris angstatus* and *Eurystylus oldi*. We are also studying the effects of climate change on pest incidence and population dynamics of the target pests and their natural enemies. In grain legumes, the historical information on wilt and dry root rot in chickpea; and wilt, sterility mosaic, and *Phytophthora* blight in pigeonpea as impacted by climate change is being analysed to predict the likely effects of climate change on disease severity in these crops. Investigations are also in progress on the effect of epidemiological parameters on *Phytophthora* blight disease development in pigeonpea under greenhouse conditions. In dryland cereals, blast disease caused by *Magnaporthe grisea* has emerged as a new threat to pearl millet production in India. We are studying the effect of weather variables on blast development in pearl millet. In groundnut, we will validate a model for the severity of late leaf spot. The studies on climate effects on biotic stresses are aimed at gaining a better understanding of the effect of climate variability and global warming on pest – host – environment interactions to develop strategies for mitigating the effects of climate change on crop production in the SAT Asia and Africa.

Pest Risk Assessments and activities on modeling impacts of climate change on pest dynamics at icipe

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Indigenous and invasive insect pests and diseases are key constraints to crop productivity and better livelihoods in Africa. Dynamics of these pests, diseases and their natural enemies are influenced by several biotic and abiotic factors. Climate change affects these biotic and abiotic factors and thereby disturbs their entire dynamics. Globalization and movement of commodities and communities across borders has increased the risk of accidental introductions of Alien Invasive Species (AIS) that negatively impact on agriculture. This is exacerbated by ineffective natural regulatory factors. Surveillance and pest risk assessments for development of develop timely management strategies were undertaken at *icipe* for indigenous and invasive species such as cereal stem borers including *Chilo partellus* and *Busseola fusca*; fruit flies including *Bactrocera invadens*; the tomato red spider mite, *Tetranychus evansi*; red palm weevil, *Rhynchophorus ferrugineus*; the coffee berry borer *Hypothenemus hampei* and *Iris yellow spot virus*. Ecological Niche Modeling like Maximum Entropy (MAXENT), Genetic Algorithm for Rule Set Production (GARP) and Climate and population modeling software (CLIMEX) were used for predicting pest distributions and risk assessments. The modeling approach also guides exploration for potential natural enemies for introduction into Africa for biological control of the target pests. *icipe* in collaboration with International Potato Center (CIP) is elucidating the impact of climate change on pest and disease dynamics through pest risk mapping with temperature dependent life table-data based insect phenology models using Insect Life Cycle Modeling software (ILCYM) for cereal stem borers and their parasitoids, western flower thrips and *Liriomyza* leafminers. Similar activities are also planned with the diamondback moth and their parasitoids, bean flower thrips, natural enemies of the coffee berry borer, avocado thrips and fruit borers. Montane ecosystems are characterized by graded changes in regional climate and associated agro-ecologies across altitudes and can act as surrogates for future climate change scenarios. *icipe* is evaluating the dynamics of key pests of maize, coffee, crucifers and avocado across altitudes in three montane ecosystems of East Africa. Such dynamics will be modeled with downscaled weather data sets derived from a network of existing and newly installed automatic weather stations and data loggers across altitudes to predict impacts of climate change. Predictions using ecological niche- and phenology modeling will be compared and refined with other geospatial data layers such as plant and soil characteristics, hydrology, crop seasonality, land cover and land use-changes.

Theme 2: Pest, disease and weed risk assessment and modeling under current and future climates

The uncertainties of various climate change models will be assessed with a Multi-model Ensemble using the CORDEX–Africa program. The optimal models will be used to predict target species distribution in present, past and future climate change scenarios.

Risk Assessment and Modeling: IITA

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Recent and current efforts at IITA to assess risks due to the various biotic stresses, arthropod pests and diseases, are presented for different cropping systems. In the case of cassava arthropod pests, the focus is on temperature-mediated interactions between the pest and its natural enemy which has been introduced to keep the former under control. Modeling approaches are currently on-going for the cassava mealybug *Phenacoccus manihoti* and its hymenopteran parasitoid *Anagyrus lopezi*, the green mite *Mononychellus tanajoae* and its phytoseiid predator *Thyphlodromalus aripo*, the fruit fly *Bactrocera invadens* and its parasitoid *Fopius arisanus*, and the banana aphid *Pentalonia nigronervosa* as a single species model. Preliminary results from these studies indicate a higher risk for natural enemies to be affected by increasing temperatures due to their generally smaller size than the pest. Also, possible asynchronization of the pest-natural enemy is being investigated. In cowpea, experiments have just begun to assess the complex interactions between different drought regimes, beneficial microorganisms such as the endophytic entomopathogenic fungus *Beauveria bassiana* and mycorrhiza, the cowpea plant and one of its key pests, the legume pod borer *Maruca vitrata*. The first sowing date in the rain-out shelter has been harvested, and the data show a negative correlation between the intensity of drought stress and infestation by the pod borer. Cowpea plant co-inoculated with both the endophyte and mycorrhiza were less affected by the drought, and had also less damage by the pod borer. Detection of the endophyte in various plant tissues (roots, leaves, flowers and pods) will be carried out by PCR using *B. bassiana* specific SCAR markers. The experiment is planned to continue until March 2013, and is currently replicated under field conditions. For banana weevils *Cosmopolites sordidus*, our data suggest a positive correlation between temperature and yield loss attributable to increased infestation levels by the weevil. Also, the range of expansion of the weevil in higher altitudes needs to be investigated in more details. This is also the case for white flies attacking cassava and transmitting the devastating CMV and CBSV. With a change in climate and ambient temperature, so likely will the distribution of nematode pests. The three major groups of nematode pests, cyst, root knot and lesion nematodes, have already been predicted to expand in their geographical range according to World Bank studies. However, a major impact of climate change will be through more irregular or reduced availability of water. Under lower water availability nematode damage to roots will further limit water access by plants, in effect exacerbating the effects of climate change. Thus, while there is general consensus for a greater need of drought resistant crops and varieties, a similar, or greater need for root pest and disease resistance is also needed, but often overlooked. A further impact of climate change will be through expanded ranges of nematodes due to changes in temperature. The potential

impact of *Radopholus similis* on bananas in the East African Central Highlands illustrates this well. Currently, the nematode occurs only up to approximately 1400 m asl, due to temperature limits. A rise in temperature would result in a corresponding rise in *R. similis* damage at higher altitudes. For plant viruses, the main thrust of our efforts is concentrating on diagnosis for disease surveillance and early warning, and developing mitigating the climate change effects on disease emergence and outbreaks.

THEME 3

RISK BASED SURVEILLANCE

Regulation of pest to protect trade and plant health

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The International Plant Protection Convention is an international agreement on plant health with 177 current signatories. It aims to protect cultivated and wild plants by preventing the introduction and spread of pests. The Secretariat of the IPPC is provided by the Food and Agriculture Organization of the United Nations. The IPPC provides an international framework for plant protection that includes developing International Standards for Phytosanitary Measures (ISPMs) for safeguarding plant resources. The IPPC is recognized by the WTO-SPS agreement as the standard setting organization for global plant health. The presentation will highlight key definitions used in the convention with relevant to pest regulation and introduces the IPPC framework for pest regulation. It will underscore the key activity of Pest Risk Analysis as the basis countries by which countries prepare the requirements to trade commodities and protect plant resources in their territories. The principal steps involved in the PRA will be briefly reviewed. It underscores the importance of pest surveillance and pest diagnostics as key to support the conduct of PRA and the preparation of regulated pest lists and by extension key enabling activities for countries to regulate pests.

Targeted surveillance to promote food security

Mike Robson

FAO-AGP, Rome, Italy

Sampling strategies for trade shipments

J. Smith

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Plant pathologists often give undue emphasis to the efficacy of the diagnostics and insufficient attention to how the diagnostics can be applied. Yet the challenges associated with sampling and the positioning of the diagnostic in time and space are considerable and fundamental to realising the value of a diagnostic test. In this context a critical initial question relates to what is it I need to be able to say; what is the policy position I need to support. And there are many questions that will require distinct sampling and testing approaches. By example of a few: Freeness from a pest in seed, or for a level of tolerance, as with seed certification schemes; in a pest survey to establish prevalence of a common pest, or to ascertain if a pest is absent or of limited distribution; to assess for GM or aflatoxin contamination in grain shipments; inspection regimes at portside for purposes on regulation and monitoring of trade. Layered on these questions is consideration of the target. How easy is it to diagnose? Is it likely to be uniformly distributed or clumped? The lack of homogeneity of aflatoxin in grain provides for particular challenge in sampling. Then there is the layer of resources, both human and infrastructure, and what is practicable and affordable, relating to issues of a governments willingness to accept the costs of testing, or if the costs can be borne by, or shared with, the private sector. These factors all boil down to a position of what is it I need to be able to prove and what uncertainty can I support in my answer i.e. do I have to be with 95% confidence in detecting a zero, 1 or 5% level of pest prevalence in grain or in seed, or in stating an area is free of a named pest. Brief review of some of these aspects will be given.

THEME 4

CURRENT SURVEILLANCE STRATEGIES

Current surveillance strategies for banana pests and diseases

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Early diagnostic of plant diseases is a critical step for preventing pathogen dissemination, precluding incursions into areas where the disease has not been observed and reducing the inoculum pressure. This is especially true for tropical race 4 (TR4) of *Fusarium oxysporum* f.sp. *cubense* (*Foc*), the causal agent of Fusarium wilt of bananas. *Foc* TR4 is a quarantine pathogen in many *Musa* spp. producing regions of the world and considered a major threat to the banana industry. Trading of symptomless, but infected banana planting material, movement of machinery with adhering infested soil and contaminated irrigation water facilitate the spread of *Foc*. A PCR-based detection tool for TR4 has been developed and subsequently improved (nested and qPRCs) enabling detection at different levels, including symptomatic and symptomless banana tissues, soil and water. In parallel, the use of Vegetative Compatibility Group (VCG) pairing with international VCG-tester sets has enabled the identification of nine VCGs (1213/16, 0120/15, 0121, 0123, 0124/5, 0126, 0128, 01218, 01220) in Asia. VCG1213/16, the group that comprises *Foc* TR4, was the dominant VCG from samples collected in China, Indonesia, Malaysia, Philippines, and Taiwan but not found in samples from the other countries. VCG 0124/5, a VCG associated to *Foc* Race 1, was the dominant VCG in samples from India, Bangladesh, Cambodia, Sri Lanka, Vietnam, and Thailand. No *Foc* infection of banana was found in Papua New Guinea. Awareness campaigns coupled with training courses on diagnostic, surveillance and management of TR4 have been carried out by Bioversity International and National Plant Health organizations in Latin America and several countries (Mexico, Nicaragua, Costa Rica, Cuba, Colombia, Ecuador) have been already capacitated. These results are a key step towards designing policies and measures to prevent further spread of TR4 through effective quarantine measures.

Current surveillance strategies for potato and sweet potato pests and diseases

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Several diseases and insect pests of potato and sweet potato have been monitored throughout the history of CIP. After its inception, CIP commissioned a number of country wide disease surveys by expert consultants. These remain today the only geographic record of a number of diseases. One of the most concerted efforts to monitor a pathogen in CIP has been that of *Phytophthora infestans*, the causal agent of late blight. Within the context of the global initiative on late blight, CIP and partners mapped major pathogen strains, sometimes by direct evaluation, but also by reviewing published pathogen population studies. More recently there has been an effort to link this pathogen monitoring with the Euroblight initiative. For viruses, CIP is currently applying a technology based on siRNA sequencing and assembly to determine the 'virome' of sweetpotato throughout Africa. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. The same technique has been used at a smaller scale to identify potato and yam bean viruses in Peru. Incidence and damage of insect pests of potato have been surveyed recently in Ecuador, Peru, Nepal and Kenya along with collections and identifications of natural enemies; likewise for sweetpotato in Africa in Kenya, Rwanda and Uganda. Major results of the surveys are the presence of serious secondary pests in the Andean region, which had been overlooked previously; the confirmation of the introduction of the invasive leafminer fly, *Liriomyza huidobrensis*, in Nepal; the confirmation of establishment and wider distribution of *Copidosoma koehleri,* parasitoid of the potato tuber moth, *Phthorimaea operculella*, which was introduced to Kenya in the 1970s. Further surveys are planned for different potato systems in Africa.

Current surveillance strategies for banana, cassava and yam pests and diseases

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In an optimal world, the distribution, spread and impact of pests and diseases would be nationally documented and updated using results from routine surveillance to facilitate regional pre-emptive management interventions. Alas, this is not the reality and particularly not for African countries where resources and diagnostic capacities are limited. Therefore, cost effective and practical surveillance mechanisms are needed. Further, mechanisms are needed to disseminate results from surveillance exercises as widely and efficiently as possible. Different methods that have been tested will be reviewed, including design and implementation of spatial surveys to represent landscapes and production of easy to interpret GIS maps, going public exercises, media based awareness campaigns, community based actions, use of SMS alerts and java based surveys for mobile phones, farmer field schools and how these can be feasibly and sustainably supported by appropriate (rapid, precise and practical) diagnostic capacities.

Many surveillance schemes have been instigated by discrete projects but often these are only active as long as there is funding. The future aim for surveillance strategies for critically important diseases of cassava, banana and yam is to target locations and mechanisms for surveillance and to link these to protocols that become refined as experiences are accrued. Such practices can be housed in open access working documents such as Pest Risk Analyses (PRA) to increase information sharing between countries, ing the same threats. Sustainability of such lic and private sector recognized their benefit to efore contributed funds.

Nematode pests are a good example of where surveillance mechanisms need to become more robust as they often go unmonitored and yet they cause devastating diseases in their own right and also exacerbate the impact of other biotic and abiotic stresses. Some species have been highlighted for monitoring for quarantine purposes due to their status as serious pests on key crops, such as *Meloidogyne chitwooodi*. However, the status of many nematode pests in many areas is poorly understood. Species such as *Meloidogyne enterolobii* appears to be an aggressive pest of numerous crops, but due to difficulties with its identification, and a limited nematology capacity across the world, knowledge of distribution and impact is limited. While the critically important nematodes for cassava, banana and yam have been prioritized during session 1, emerging nematode species also need to be considered and offer the potential to discuss novel surveillance methods such as barcoding soil biota? For example, the yam nematode, *Scutellonema bradys*, has recently been recovered from potato in West Africa, and shown to cause severe damage to production and quality. However, its distribution on potato, varietal susceptibility, and its environmental plasticity is virtually unknown.

THEME 5

DETECTION AND DIAGNOSTICS

Symptom recognition mediated by mobile plant clinics

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Plantwise helps developing countries to establish an integrated plant health system. This system links the farmer – via a plant clinic - with an integrated support network, consisting of input suppliers (e.g. pesticide manufacturers), diagnostic laboratories, researchers, national plant protection organizations (NPPOs) and policy makers. Plantwise clinics are made accessible to farmers by holding them on a regular basis in a prominent local meeting place, such as a market. When the farmer has a problem with a crop, he/she can bring a sample along to the plant clinic. At the clinic a trained 'plant doctor' listens to the farmer, examines the sample, diagnoses the problem and offers a suggested treatment. Treatment suggestions are made with five key things in mind. Is the treatment: effective?; practical?; locally available and farmer-friendly?; economic?; and safe?. IPM practices are often the approaches that fulfil these criteria most successfully. The correct chemicals are recommended only when necessary; brand-names are avoided. With access to these services farmers can tackle pests and diseases and produce healthy crops and productive yields. With successful harvests farmers can feed and support their families. Diagnosis is not always straightforward. Sometimes plant doctors need to send samples to a laboratory (in exactly the same way that a family doctor sends samples to a hospital laboratory). Plantwise helps link clinics with diagnostic laboratories and other resources they need. We offer comprehensive support in disease identification and management. We work with all crops in all countries, particularly tropical crops, and offer expert identification services for fungi, bacteria, nematodes, viruses and phytoplasmas.A free service is available for eligible clients in developing countries. The service, based at CABI in the UK, receives more than 500 samples each year from more than 80 countries. Plantwise (formerly Global Plant Clinic (GPC)) is closely involved in surveillance and identification of new diseases and has published 31 new disease records with its global partners since 2001, 11 from Africa alone.

Classical Disease and Pest Diagnostic Methods

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On a practical level the majority of plant disease and pest diagnoses are based on classical diagnostic methods. Field diagnoses rely on evaluation of symptoms and signs, usually aided by no more than experience, a good hand lens and reference materials. In the laboratory, classical techniques range from the use of microscopy to culturing and pathogenicity tests. Most classical laboratory methods require a great deal of experience on the part of the practitioner, and may be very time- and space- consuming. For insect pests and nematodes, classical identification is largely based on observation of specific physical characteristics. For plant diseases, a suite of structured tests, many based on light microscopy, differentiate potential causal agents into basic pathogen groups, in a process generally referred to as triage. For example, a simple bacterial streaming test differentiates bacterial pathogens from other groups of pathogens and abiotic disorders. A specific series of tests is then carried out depending on the results of the streaming test and the host plant. After a positive streaming test, culturing on general and selective media, sub-culturing, simple determinative biochemical tests, and a hypersensitive reaction (HR) test in tobacco are often sufficient to identify bacterial pathogens to the genus level. Production of key structures in and on plant tissues often allow for identification of fungal and oomycete pathogens to the genus level, but follow-up with culturing and further tests may be necessary. Serological assays have been used for diagnosis of diseases caused by viruses for so long that they may be considered "classical", and are important tools in the field and laboratory. Improved selective media, diagnostic reference materials such as on-line image libraries and Lucid keys, and laptop- and smartphone-based microscopes are among the innovations in classical methods that continue to improve the speed and quality of plant pathogen diagnostics.

Barcoding for pathogens and insect pests

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DNA barcoding is a taxonomic method that uses a short genetic marker in an organism's DNA to identify it as belonging to a particular species. Although the DNA sequences of related species are generally very similar, there are differences to be found. The part of the DNA sequence that is different is specific to that particular organism and forms a unique and specific molecular DNA barcode. DNA barcoding has arisen as a robust and standardized approach to species identification. Through the project QBOL, DNA barcoding has been developed for plant health diagnostics generating DNA barcodes and an associated database of key disease and pest species.

Virus disease detection methods

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For many years now CIP has produces a set of kits based on ELISA for the detection of key potato and sweetpotato viruses and bacterial wilt. These kits have the benefit of being easy to use, require minimum equipment and are easy to interpret. However the downside is that they are limited in their sensitivity and only detect a subset of all known viruses of these crops.

The power of modern high throughput DNA sequencers is enabling a new generation of virological studies in which metagenomes of ecosystems can be determined to understand evolution and variability of viruses. We are currently applying a technology based on siRNA sequencing and assembly to determine the 'virome' of sweetpotato throughout Africa. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. Such technologies however are still too expensive and knowledge intensive to be applied by most national diagnostic laboratories (NDL) which still mostly rely on ELISA and sometimes PCR methods for testing single viruses at a time. Platforms for the sensitive detection of multiple viruses at the same time such as microarrays may be practical and efficient solutions for NDLs with the need to test many plants against many viruses with sufficient sensitivity. Results from validation experiments of ClonDiag tube arrays for potato and sweetpotato will be presented. On the other hand, for diagnostics at the field level, simple and straight forward methods are needed that are robust, require minimum equipment but still are sensitive and easy to interpret. Loop-mediated isothermal Amplification (LAMP) is a highly sensitive and specific nucleic acid amplification method that does not to require complex thermal cycling equipment. Reagents can be lyophilized and reactions performed with low cost re-usable heat-packs, whereas color changes or lateral flow devices may be used to identify positive reactions. The challenges to bring the technology to field use rely on optimizing the way of detecting positive reactions and developing of simple enough nucleic acid extractions that can be used under field conditions.

LAMP and next generation sequencing

J. Smith

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As a general direction of travel, crop pest diagnostics have seen a move from antibody based diagnostics (eg ELISA) to nucleic acid based PCR and real-time PCR, with stepwise progression realised in sensitivity, specificity, robustness and facility for design and redesign. However, whilst we have become increasingly competent at laboratory diagnostics for known pathogens, we have struggled to achieve the same levels of specificity and sensitivity with field diagnostics, where ELISA-based technologies have been foremost retained, and we remain at a loss of how to identify or provide surveillance against unknown pathogens. Recent advances in sequencing and amplification chemistries have however, provided a step change in these two areas. Loop Mediated Isothermal Amplification (LAMP) is essentially the same as PCR in that it relies on primers designed to target and amplify nucleic acid sequence, but differs in one major area in that the amplification reaction proceeds at a steady temperature (~60°C); as opposed to PCR cycling. As an outcome of this difference the infrastructure needed to support LAMP is much less, limited to a hot block. The products of LAMP can be viewed on a gel, or on a dip-stick styled Lateral Flow Device, and thus the diagnostics can be performed in a lab of basic infrastructure or in a field. The power of nucleic sequencing has transformed over the past 5 years. What used to take weeks, months or years is now achievable in hours and days. Commonly referred to as a next generation sequencing (NGS), one application is the unbiased amplification of nucleic acid sequence that is present in a sample that can then be interrogated for 'signature sequences' of interest. This approach may be used to identify the signatures of unknown pests without recourse for a priori knowledge. By brief example of Cassava Brown Streak Disease and Maize Lethal Necrosis Disease example will be provided on LAMP and NGS, for the development of a diagnostic suited for basic lab or field and in discovery of an unknown pathogen, respectively.

A new low-cost diagnostic tool for detecting regulated (quarantine) cassava and banana diseases

E. Alvarez

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Cassava and banana are important staple food for millions of people worldwide. In South Asia and LAC, sustainable cassava and banana production, respectively, is currently threatened by the proliferation of emerging diseases. Unchecked, they threaten the livelihoods of small farmers for whom cassava and banana may be their only means of generating income. Climate change aggravates the problem, influencing disease distribution and incidence. Sustainability needs to be fostered for this and future generations through effective, innovative, and improved technologies. Traditional processes for identifying plant pathogens can take days, even weeks, preventing timely decision-making while allowing problems to advance. We therefore propose develop and implement an innovative diagnostic technology for cassava and banana protection: a small low-cost device called Gene-Z, which is a new, simple, low-cost, hand-held platform for diagnosing emerging infectious diseases caused by plant pathogens, such as fungi, bacteria and virus. This portable isothermal platform is operated by an iPod Touch or Google Android tablet. It performs genetic analyses on microRNAs and other genetic markers. It is fast (10 to 30 min), highly specific, insensitive to PCR inhibitors, does not require complicated DNA extraction protocols, and can be used in the field. The Gen Z technology will contribute towards strategies that respond to challenges of food security and climate change.

THEME 6

DATA MANAGEMENT AND REPORTING

Plantwise knowledge bank

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Plant doctors, extension workers and researchers all need access to the latest information in order to be able to best assist the farmer. Plantwise offers online diagnosis and treatment support information as well as practical on the ground training for potential plant doctors. As a result of helping farmers Plantwise collects valuable data about plant pest and disease distribution that is shared with the participating countries. Working with the relevant NPPO (National Plant Protection Organization) Plantwise will publish validated pest and disease distribution data. This information, harnessed effectively, can form this basis of an early warning system alerting the plant health community to a change in distribution of existing pests/diseases or the threat of a disease in a new region. Data gathering from plant clinics is currently the focus of two pilot approaches: a paper form-based system with translation to a digital format away from the clinic; and a mobile tablet/smartphone/pc system with direct data entry at the clinic. Both approaches have challenges in: provision of equipment, ease of use and scalability. It may emerge that multiple approaches are useful; a toolkit from which the most appropriate system for a country or region can be chosen. In fact it is likely that a one-size-fits-all solution is not achievable. The Plantwise Knowledge Bank will help with the local, national and regional fight against pests and diseases. In addition to local distribution data captured at the clinics Plantwise will capture data about new pests and diseases from scientists, published sources and official bodies, and map this information in greater detail than ever before. Working with partners this data will be combined with the best information in the field to provide a comprehensive knowledge bank on crops, pests, diseases and weeds.

Valuing Pest Risk Analysis in pest outbreak prevention

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A signature of a successful and resilient cropping system is one which invests in pest outbreak prevention more than cure, where actions are taken that prevent an outbreak or mitigate an outbreak as to make its impact insignificant. It is thus a major objective of governments to anticipate future pest threats (either new, emerging, or evolved) and to mitigate accordingly. Unfortunately, for Africa, and many developing countries, the track-record for pest outbreak prevention provides for example of having achieved too-little too late. Yet with an increase in trade, trade-routes and the influence of climate change the likelihood of future new events is high. The challenge for all countries is to promote free-trade and mitigate pest risks and, where pest risks are seen, to implement measures that are not disproportionate and based on the good evidence as would otherwise contravene WTO guidance. To facilitate in these processes of attributing pest risk to trade, and in providing the evidence required for policy development of phytosanitary measures, the practice of Pest Risk Analysis (PRA) is advocated by the International Plant Protection Convention (IPPC) as set out under its various International Standards for Phytosanitary Measures (ISPMs). In review of PRA literature many schemes are evident as preferred by countries and regions. These variously attempt to bring in risk assessment and risk management and qualitative *versus* quantitative judgements, but also share features about risk related to entry, establishment, spread and consequences. Each also strives to bring together a state-of-knowledge through a desk review of literature on what is known and not known and to attribute risk and uncertainty to these knowledge sets. Further a good PRA may aim to set-out a research agenda and provide for a communication of findings in formats that are both technical and non-technical, for targeted audiences. In this talk example will be made of two PRAs that have been led on by Fera in recent years progressing states-of knowledge for the causal agents of Cassava Brown Streak Disease of cassava and Banana Xanthomonas Wilt of banana.

Networks for diagnostics and capacity building

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Early and accurate diagnoses and effective pathogen surveillance are necessary on local, regional and global scales to identify invasive species, predict disease outbreaks and allow timely deployment of appropriate mitigation strategies. The quality of plant disease diagnoses and ultimately their usefulness in both plant safeguarding and disease management decision-making is a function of 1) human resources, 2) technology and 3) infrastructure. For all but the most simple and obvious diagnostic problems, well-trained individuals, readily available technology and/or adequate infrastructure for conducting diagnostic tests and protocols are required. However, significant gaps in capacity to diagnose plant diseases exist in both the developing and developed world. The lack of human capital will not be remedied in the near future by a large influx of well-trained diagnosticians. Therefore, sharing of expertise across borders through well-supported networks can compensate for the lack of human capacity in a given country. For example, the International Plant Diagnostic Network (IPDN), established in 2004, assists local diagnosticians through training, diagnostic technology research and development, preparation and sourcing of reference materials and sharing of diagnostic expertise in 12 countries. The expertise of individuals within networks is a rich source of knowledge for development of diagnostic protocols appropriate to various levels of physical and human capacity. Such standardized operating procedures provide guidance on diagnostics for important pests and diseases and engender confidence in the outcomes of the diagnostic processes.   Focused regional workshops introduce classical and modern diagnostic methods at a reasonable cost, and provide much needed networking opportunities. Short-term intensive training results in greater knowledge acquisition through repeated practice and exposure to a wide array of plant problems.   Both types of training also improve capacity to identify invasive species and therefore mobilize prevention and/or management efforts.

Climate data management for species distribution models

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Climate has long been considered as the primary factor constraining potential distribution of many organisms. Proper climate data storage, manipulation and dissemination are therefore the backbones for species distribution models. However, available data bases are characterized by missing values, and other factors leading to numerous data anomalies. Serious care is therefore required during their inclusion into models. Most available tools use 'climate surfaces' for different scenarios. Climate surfaces at very high resolution are essential for studies in mountain environments and areas with great change in gradients. Available data bases contain information for several scenarios at different spatial resolutions starting from 10 arc-minute (18 km) to 30 arc-second (0.9 km). The aim here is to explain how modeling tools manage these datasets using Insect Life Cycle Modeling (ILCYM) software, Maximum entropy (MaxEnt) and CLIMEX for illustrations.

Innovations to increase efficiency of data management

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Amongst the principal challenges for data management and reporting in the context of pest and disease monitoring will be the ability to handle highly distributed data since a classical global monitoring schema would typically rely on a large number of local human observers (like crowd-sourcing) or also on smart specialized sensors. Alternatively or complementary remote sensing data could be used for pest and disease monitoring. This leads us to the second challenge of high volume data in the form of images or fine-grained time series data from sensors in weather stations. As indicated, the data may come from a variety of data collecting devices (like laptops, smartphones, mobile sensors, micro-drones, satellites) hence the need for unified communication and data format protocols. The last challenge is to make these data available for browsing, analysis and decision-making in a highly responsive and in a near real-time manner. In this paper we will review informatics tools for these purposes. These include: a) physical infrastructure with high accessibility and availability; b) efficient data structures for near real-time data discovery, integration, analysis and high availability; c) efficient statistical algorithms and platforms that can handle large datasets; d) data standards that facilitate the analysis; and e) highly automatable statistical reporting tools. Finally, an example scenario briefly shows the integration of these components to address the above listed challenges in data management.

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