Summary of Workshop Deliberations on Improving Plant Health

Area	Needs/Gaps	Opportunities	Approaches[1]	Immediate priorities & short term deliverables	Long-term Deliverables	Opportunities for Collaboration: Between US & UK	Opportunities for Collaboration: With Developing Countries	Opportunities for Collaboration: Other International
Foundational Research Needs, Opportunities, and Challenges								
Improving genetic resistance:								
Increasing the durability of resistance to pathogens and pests	Identification of resistance (R) genes that are likely to be durable. Improvement of genome editing technologies to enable pyramiding.	Development of strategies that maximize hurdles to pathogen virulence.	Pyramiding of resistance genes, preferrably with multiple modes of action.	Development protocols for testing durability under experimental conditions of accelerated pathogen evolution. Identification of R genes that detect conserved effectors. Techniques for rapidly stacking genes at single chromosomal sites.	Pyramids of resistance genes in adapted germplasm of crop species.	Studies in model pathosystems defining pathogen components recognized by R genes. Comparative functional genomics to identigy commonalities or novelties with non-model interactions.	Field studies characterizing pathogen evasion of R genes. Characterization of pathogen diversity and evolutionary potential.	Expansion of types of pathosystems studied. Widespread translational trials to evaluate durability of R gene resistance in diverse locations.
Identifying and engineering pathogen-recognition receptors	Identification of large numbers of R genes, including cell surface and apoplastic receptors. Detailed understanding of R gene function.	Characterization of R gene repertoires in crop species and function of multiple types of R genes.	Mining of wild species for canonical R genes. Structure-function studies of natural and designed R proteins, including use of synthetic biology, cryo-EM, and high resolution cell biology.	High-throughput screens for novel recognition abilities of R proteins. Expression systems to produce R proteins for structural studies. Structures of R proteins and complexes.	R gene catalogs from wild relatives of crop plants. R genes available for pyramiding. Engineered R genes with novel specificities.	Synthetic and structural biology approaches to understand structure-function relations of NLR proteins.	Screens of biodiverse plants and crop wild relatives for novel recognition capabilities.	Prospecting wild plant species for novel resistance functions. Development and deployment of field-scale, high throughput phenotyping platforms for gene discovery. Coordination with international genome projects.
Identifying and deploying diverse R genes	Detailed understanding of quantitative disease resistance and infection processes to identify opportunities for interventions.	Molecular characterization of polygenic resistance, responsiveness of defense response pathways, susceptibility genes, and effector targets in major and minor crop species.	Genome mining, expression analyses, high resolution cell biology, genome editing.	Evaluation of genetic materials at locations where variation can be assessed. Development of resistant cultivars with pyramids of R genes through marker-assisted breeding. Manipulation of S and defense response (DR) genes in crops using genome editing technologies.	New targets for interventions. Genes with different modes of action for incorporation into gene pyramids. Dissection and exploitation of large effect QTLs in major and minor crops for marker-assisted and genomic-informed breeding.	Experiments to transfer known resistance mechanisms to new crop species. Increased interaction with programs such as Rosbreed II for durable disease resistance in speciality fruit crops.	Develop (improved) transformation protocols for locally important crops. Testing of variability in efficacy of QDR in target crops at multiple locations.	Widespread translational trials to evaluate efficacy and durability of QDR under diverse conditions. Engagement with EU FP7 and H-2020 programs. Excellent opportunities exist for collaboration with Australia, New Zealand, Canada and Brazil.
Modulating plant-microbe interactions:								
Manipulating small RNAs to alter plant-pathogen interactions	Better understanding of the roles of small RNAs in regulating plant disease resistance and pathogen virulence and how they move between plant and pathogen.	Manipulation of regulatory pathways to enhance resistance. Identification of points of pathogen vulnerability .	High resolution detection of small RNAs. Characterization of small RNA dynamics by sequencing. Host-induced gene silencing (HIGS) of pathogens.	Identification of host-pathogen small RNA transfer mechanisms. Identification of targets for HIGS. Assessment of HIGS efficacy against different classess of pathogens; field tests with crop plants.	Novel intervention strategies. Crops with HIGS-mediated resistance. Assessment of durability of HIGS.	Evaluation of HIGS and RNA interference for efficacy against hard-to-control pathogens.	Deployment of crops with HIGS.	
Exploiting immunomodulatory chemicals	Identification and detailed knowledge of immunomodulatory repertoires from both plants and pathogens. Development of a chemical registry of metabolites.	Leveraging state of the art analytical instrumentation. Integration of metabolomic profiling with genomic and genetic resources.	Bioassays, genetic and chemical analyses to resolve activities and compound identities at biologically relevant levels. Spatial imaging of chemicals.	Profiling of plant and microbe immunomodulatory metabolites coupled with assays for bioactivity. Elucidated regulatory and biosynthetic mechanisms for metabolite production.	Deployment of molecules modulating resistance. Engineered biochemical defence pathways. New bioactive chemicals. Metabolite biosensors.	Integration of high-quality metabolite databases. Identification of mechanisms underlying metabolite-mediated resistance. Technology transfer to multiple cropping systems.	Bioassay-based screens for identification of candidate immunomodulatory metabolites. Deployment of crops with optimized biochemically-based immunity.	Collect diverse samples for profiling metabolites, bioactivity and underlying genetic control. Assess durability of resistance mechanisms in diverse environments.
Exploiting organismal interactions with plants:								
Characterizing pathogen effectors	Comprehensive characterization of effector repertoires from multiple pathogens and their modes of action. Knowledge of effector function outside of defense suppression.	Availability of genome sequences and high-throughput sequencing technologies to characterize effector repertoires. High resolution imaging to identify common subcellular targets exploited by effectors.	Large scale genome sequencing and mining. Determination of effector expression patterns. Genetic and biochemical functional screens and analyses.	Improved transformation technologies to support rapid functional analyses in pathogens/pests and vectors. Identification of conserved effectors and shared effector targets.	Expedited discovery, functional analyses, and stacking of R genes. Understanding of plant resistance and pathogen virulence. Tools for manipulating plant processes.	Reporter-based phenomics screens for biological pathways targeted by effectors. Development of novel functional assays. Organize collaborations based on pathways targeted rather than by pathogen.	Screens of non-host plant species for detecting effectors to identify novel resistance genes. Rapid genome/transcriptome sequencing of emerging pathogen lineages to identify effector repertoires and inform R-gene deployment.	Screens of diverse pathosystems to expand the repertoirs of effectors from disparate types of pathogen. Coordinate systematic genome sequencing of emerging pathogens.
Exploiting phytobiomes to enhance plant health	Characterization of the composition, evolution, and function of phytobiomes, and approaches to modulate the phytobiome for plant benefit.	Sequencing and analytical technologies to identify components of complex microbial communities, signaling cues, and interactions that influence plant health.	Metagenomic analyses of microbial communities above and below ground in heathy and diseased states using reductionist and natural settings. Co-analysis of genotype performance and phytobiome composition/ function.	Identification of major drivers of plant microbiome structure and function. Identification of management practices that favor beneficial phytobiomes. Deciphering of cross-kingdom signaling within the phytobiome.	Agricultural biologicals, including microbial inoculants and bio-based chemicals as novel biostimulants and biopesticides. Plant genotypes that enhance beneficial associations.	Co-screens of genotype performance and beneficial phytobiome recruitment potential under low input conditions.	Screens of microbes, microbial mixtures and bio-based chemicals for biocontrol, biopesticides and biostimulation.	Commercialization of agricultural biologicals, including microbes and small molecules for exogenous applications.

Modifying virus-plant interactions	More complete knowledge of mechanisms underlying viral evolution, replication, movement, and virulence.	New high resolution techniques such as single-cell genomics, high resolution imaging, and RNA sequencing for analysis of viral activities in plants and vectors.	High resolution cell biology. Cryo-EM. Single cell RNA and DNA sequencing. Genome editing of genes critical for viral infection.	Elaboration of the molecular signatures of vector and plant responses to infection. Single cell approaches to identify common sRNA/microRNAs that influence pathogenesis of multiple viruses. Optimization of approaches for engineering resistance to DNA viruses.	Identification of new opportunities for intervention and engineering resistance to both RNA and DNA viruses. Genome editing to alter S genes to effect viral but not plant processes.	Identification and manipulation of vector, host, and phytobiome factors that limit viral repication and vector dissemination.	Development and deployment of viral and vector control strategies.	International collaborations to obtain genome sequences of important vector species such as plasmodiophorids.
Minimizing and monitoring weed, pathogen and pest challenges:								
Controlling weeds	Genomic information on major weeds. Understanding of beneficial and deleterious plant-plant interactions.	Minimizing herbicide resistance through a better understanding of its genomic basis in weeds. Development of precision agriculture and integrated management practices.	Functional genomic studies of weeds. Research into cultural practices. Crop phenotyping for weed control traits.	Genome sequencing of major agronomic weeds including resistant biotypes. Screening plant germplasm for weed suppression and microbes and microbial products for weed control.	Understanding of the evolution and basis of herbicide resistance. Better diagnostic and predictive tools for durable herbicide use. New strategies for controlling weeds and parasitic plants. Reduced reliance on herbicides.	Identification of mechanisms of herbicide resistance.	Development of cultural practices that maximize weed control and herbicide durability.	Expansion of traning programs focused on optimized cultural practices for weed control and durable herbicide use.
Monitoring pathogens, pests, and weeds.	Real-time monitoring of pathogens. New detection technologies to diagnose and quantify diseases. Gobal collections of pathogen isolates/ecotypes/biotypes.	Advances in remote sensing, sequencing technologies, and computational power. Opportunities to test germplasm using relevant pathogen isolates.	Development of global networks for monitoring key pathogens of major crops. High throughput sequencing of field samples of pathogens and crops. Integration with remote sensor data. Establishment of global pathogen collections.	Linking remote sensing data with ground-truthing data on disease and pathogen presence. Identification of pathosystems requiring investment in monitoring.	Deployment of control measures driven by knowledge of pathogen variation. Germplasm with widespread efficacy.	Development of cost-effective, high-resolution diagnostic methods for field pathogenomics for surveilling major crop pathogens.	Development of partnerships to integrate data from farmer observations with remote sensing data. Development of disease assessments appropriate for each area.	Implementation of (volatile) detection methods for detecting pathogens during global trade. Exchange of data for development of science-based regulations for pathogen detection/validation and quarantine restrictions.
Assessing the impacts of climate change on pathosystems.	Understanding the impacts of climate change. Data to inform the pathogen layer of climate models.	Advances in tools for organism level measurements. Increasing sophistication of climate models.	Detailed phenomic and molecular analyses under controlled perturbations and field experiments.	Characterizing the impact of environmental conditions on pathogen epidemiology and on resistance in major crops.	More accurate predictive models. Global approaches to disease management. Modified R genes with efficacy under future climatic conditions. Attenuated increases in mycotoxin contamination of food.	Generation of data for climate change models using high-throughput characterization of environmental impacts on biotic stresses. Analysis and prediction of pathogen and vector responses to climatic change.	Generation of data for climate change models using field-based characterization of environmental impacts on biotic stresses.	Global integration of disease data to better predict and respond to existing and emerging pathogen threats.
Translational opportunities, needs and challenges:								
Translational activities.	Two way knowledge exchanges. Tools for handling unprecedented amounts of data. Development of decision trees. Coordinated efforts of multiple entities.	Tools for handling big datasets from electronic social media.	Recruitment of bioinformaticans and computer scientists to the plant health area.	Meta-analysis of plant, pathogen, and phytobiome compnents influencing crop productivity.	More effective translation.	Development of disease resistant potato, wheat, barley, and sugar beet varieties. Development of HIGS systems that target rust fungi and nematodes.	Translation to perennial crop systems (e.g. banana). Translation to minor (orphan) crops of local importance for food security.	Development of disease resistant wheat, corn, and soybean cultivars.
Building capacity in developing countries.	Increased capacity building. Models for successful partnerships in knowledge transfer.	Social media capabilities. On-going activities of professional societies, foundations, research universities, and government agencies.	Establishment of bidirectional partnerships. Two-way exchanges of information between partners. Engagement of extension and farmer networks.	Training of graduate students from developing coutries. Short-term training of research scientists from developing countries in collaboration with CGIAR.	Targeting relevant interventions to hotpsots.		Identify needs in priority crops. Collaborations facilitated by e.g. multiple national BBSRC, DFID, NSF, USDA, USAID and BMGF programs.	
GMO deployment.	Increased discourse to promote GMO acceptance. Rational, evidence-based decisions. Public appreciation and enthusiasm for improved crops.	Traits that appeal to consumers. Genome editing as a non-GM technology.	Improved communication with decision makers and general public.	Assistance for publicly-funded projects and those aimed at minor crops to comply with regulatory hurdles.	More efficient path to deployment of GM and edited crops. Increased consumer trust. Reduced environmental impact of agriculture.	Collaborate to develop science-based regulatory framework for GMOs. Share experiences and informational materials.	Involve existing and nascent regulatory agencies in GMO framework discussions.	
Genome editing.	Efficient methods for allele replacement and knock-ins. Technologies for reagent delivery that do not involve tissue culture.	Generation of stacks of R, DR, and/or S genes.	Technology development through multi-institutional collaborations with private sector and exchange of information and protocols.	Technologies for non-DNA-mediated genome editing of crops. Non-tissue culture based protocols.	Genome-edited, non-transgenic crops with enhanced disease resistance.	Exchange of methods and protocols. Collaborations with the private sector.	Targeting crops and cultivars relevant to developing countries.	

[1] Approaches: These are some of the most salient that could be applied and are not comprehensive. There are also overlaps and redundancies between areas that are not repeated.

Due to space constraints, the term "pathogen" in this table is inclusive of all types of biotic interactors including viral, bacterial, fungal and oomycete pathogens, insect pests, nematodes, parasitic plants, and where appropriate beneficial symbionts and weeds.