

•**Report Subgroup - Pathogen and host resistance:** (*Moderator: David Cooke, secretary: Geert Kessel*)

1. **Eric Magembe** – use of R-Gene resistance and monitoring population in Africa
 1. R was robust and the population stable EU2 – so far.
2. **Isaac Abuley** – Phenotypic traits of novel genotypes in Denmark
 1. Full back story on EU43 emergence and traits – emerged on ALL cvs and showed sensitivity to other a.i.s no obvious advantageous trait bar CAA R
3. **Jean Ristaino** - Predicting future P inf outbreaks: New tools to id new emerging lineages, virulence phenotypes and track spread
 1. Broad scope – tracking disease emergence via social media data mining, pensem of ancient lineages, status of USAblight and migrate to Plant Aid Database & in-field technologies
4. **Delphine Chauvin** – Rating potato varieties: 30 years of experiments to examine resistance and its variability
 1. >2500 data sets of cv response to infection – disease progress curves characterized to different categories strong to weak, late epidemics and resistance
5. **Amanpreet Kaur** - Use of PenSeq for studying P. infestans effectors
 1. Powerful tool for sequencing the key 0.2% of 240 MB genome – examples of virulence effector presence/absence and SNPs – method effective on FTA cards too. Expression levels with cDNA.
6. **Vikrant Singh** - Unveiling effectorome profiles of P. infestans during phases of infection
 1. Pros and cons of Pensem and Rensem emphasised

Explored details of pensem in detailed discussion.

Topic	Control strategies	Host-Pathogen	Alternaria
<p>What are the Key research questions in the subgroup</p>	<p>Write here</p>	<ul style="list-style-type: none"> • Unknown virulences - we are poor and characterising this at scale • What cv are grown where? Lack of knowledge on national/region scale • How can we pick up nascent clones earlier? Target 'Other' for key genes REAL-TIME REPORTING within season - • Proactive planning on other fungicide MOAs to keep them for longer • We need a more rapid and standardised system for phenotyping (e.g. fungicide and virulence) AND genotyping for fungicide R SNPs • A need to analyse the data we have in more detail • Maintain and improve connections with other networks 	<p>Write here</p>
<p>Suggest actions for improved Collaboration, shared facilities and outreach</p>	<p>Write here</p>	<ul style="list-style-type: none"> • Make list of what R genes are in which cvs to improve and share the differential series. Monitor and report virulence more widely • Open dialogue with those responsible for collection of cv area grown in EU countries. Suggestion – conact FAOSTAT. • Empasise in The Statement from EB to explain why above knowledge will benefit R gene stewardship • David and Jens to explore ways of reporting data early (as it is uploaded) • Design assays for rapid scoring of CAA and OSBPI SNPs – report early • Make list of labs & ways we can share and communicate information 	<p>Write here</p>