

Workshop “pathogen-informed crop improvement”, April 8–10, 2015, Wageningen, The Netherlands

Cost Action Sustain (FA1208)

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Introduction

The workshop ‘Pathogen-Informed Crop Improvement’, held April 8–10, 2015, in Wageningen (The Netherlands), was organized by an international scientific committee lead by Aska Goverse from Wageningen University in the frame of the COST Action SUSTAIN (FA1208). This networking project supported since 2013 and for four years by the European Coordination in Science and Technology (COST) program aims at creating a European network of scientists and breeders for the accelerated transfer of knowledge on plant pathogen interactions into improved and innovative strategies for durable crop resistance. It unites more than 200 scientists from companies and public research and can, since COST Actions are open networking projects, still be joint by interested persons. For more details refer to <http://www.cost-sustain.org/>.

Sixty researchers with a large spectrum of different backgrounds from universities, academic institutes

and industry attended this two and a half-day workshop whose goals were

- to share latest knowledge regarding plant-pathogen interactions.
- to become aware of the desires and challenges in plant breeding companies.
- to discuss desires of the public/customers.
- to identify opportunities to leverage latest knowledge into applications for breeding companies, finally useful and accepted by the general public and with a broad and durable solution for future generations.

The workshop consisted of presentations and discussions based on propositions and statements submitted by the presenters and dealing essentially with three main topics

- Effector breeding.
- Effector diversity and host adaptation.
- Exploitation of novel resistance sources and strategies.

The program and abstract book can be downloaded at <http://www.cost-sustain.org/Media/Abstract-book-Wageningen>.

Effector breeding

In the workshop it became apparent that resistance breeding and research on plant-pathogen interactions

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is profoundly changing because genome sequencing and growing knowledge on pathogenicity is beginning to reveal the whole complement of virulence factors commonly called effectors in many phytopathogenic organisms (Dangl et al. 2013). This is directly instrumental for crop improvement because, frequently, crop resistance relies on the recognition of some of these effectors by the products of resistance genes. Innovative powerful screening procedures for resistance genes have been developed that exploit this knowledge. They rely on the infiltration of isolated effectors or their transient expression and promise to accelerate screening for new resistances in plant germplasm and to render introgression of the corresponding loci more straightforward. The feasibility of such simplified screening and effector breeding was demonstrated in pioneering work on major wheat and potato diseases presented during the workshop by R. Oliver Curtin University, Australia and V. Vleeshouwers, Wageningen University, NL (Vleeshouwers et al. 2008; Vleeshouwers and Oliver 2014). Discussion of the advantages and drawbacks of this approach highlighted that such simplified screening allows the analysis of large plant populations at extremely reduced costs since field or greenhouse infection assays can be replaced to a large extent (Lebrun 2015, INRA, France presentation at the workshop). However, these assays will not completely replace field trials and therefore proper trial sites (at proper locations with proper disease pressure to be able to select for the specific trait) and high throughput phenotyping remain important issues in this field.

Effector diversity and host adaptation

Monogenic resistance is threatened by resistance-breaking strains that lose or mutate the matching effector-coding avirulence (*Avr*) gene. However, such mutations are limited by the importance of the effector for pathogen virulence and the fitness cost their loss is associated with (Brown 2015a). Identifying central effectors that cannot easily be lost or modified by the pathogen and subsequently screen for corresponding resistances in germplasm collections is a promising strategy for durable resistance (Gawehns et al. 2013). Such strategies aiming at identifying central effectors are currently developed for many important crop pathogens (Gohari 2015, Wageningen University, The

Netherlands; Stukenbrock 2015, Christian-Albrecht University, Germany; Rep 2015, University of Amsterdam, The Netherlands; Schaffrath 2015, RWTH Aachen University, Germany, presentations at the workshop).

Knowledge on matching resistance (*R*) and avirulence (*Avr*) gene pairs allows to monitor the evolution of avirulence in pathogen populations at the molecular level and to understand the evolutionary mechanisms leading to resistance breakdown (Rouxel 2015, INRA, France, presentation at the workshop). Monitoring the presence and integrity of effector-coding *Avr*-genes in pathogen populations allows in addition, to protect *R* genes and to reduce pesticide treatments (Vleeshouwers et al. 2008).

Modern, simplified agrosystems, characterized by monocultures with similar sets of *R* genes, push pathogens to fast evolution. In uniform environments, pathogen populations experience strong selection pressure and can adapt rapidly (Brown 2015b, John Innes Centre, UK; McDonald 2015, ETH Zurich, Switzerland, presentation at the workshop). Pathogens can only survive in monoculture agrosystems where *R* genes are present if mutations in *Avr* effector genes occur that prevent recognition. As a consequence, new resistances are frequently overcome in only a couple of years leading to the famous boom-and-bust cycles. On the contrary, more fragmented and diverse agrosystems slow down the evolution of pathogens and stabilize resistances. There was consensus that it is a great challenge to translate this fundamental knowledge on host-pathogen co-evolution into novel resistance employment and deployment strategies. Introduction of more diversity was considered as a key element and discussions turned a lot around the question whether this has to occur at the plant, the field or the agrosystem level:

- Combining different types of resistances (quantitative and qualitative) and pyramiding *R* genes or *R* genes and susceptibility (*S*) genes to create highly resistant varieties. This solution is technically still challenging but should lead to varieties with higher and more durable resistance. However, due to the strong selection pressure in monocultures, it can be expected that also this resistance will erode or break down after a certain period. In addition, emergence or re-emergence of pathogens may cause new problems and antagonistic effects

may render varieties that are highly resistant to one disease highly susceptible to others.

- Cultivar mixtures combining different cultivars with different resistances in one single field are known to slow down epidemics even if defeated resistances are used. Although widely recognized as a powerful, durable and environment friendly solution for disease resistance, variety mixtures raise technical problems. The non-homogenous fields and yields comprise specific management requirements. Different harvest times require for example additional logistics and specific harvest machines which prevent damage of neighbouring (not yet harvestable) plants. Moreover, variety mixes are prohibited by European regulation (the DUS principle of “Distinguishable, “Uniform” and “Stable”). Similar, promising solutions are either: (I) intercropping that strongly reduces disease development by introducing diversity at the field level. (II) Creating a landscape that is non-homogenous for pathogens and diverse at the local level by planting many different varieties with different resistance spectra at a local level and on smaller fields. (III) Employ crop rotation to reduce disease pressure and diversify the Agro-system.

Discovery and exploitation of *R* and *S* genes

Advanced marker and sequencing technologies allow the accelerated discovery of *R* genes even in complex genomes such as wheat and potato, and to better mine crop genome diversity. This was exemplified in the workshop by the cloning of the first wheat *R* gene against Septoria net blotch disease (Saintenac 2015, INRA, France, presentation at the workshop) and improved mining of the potato genome for *R* gene analogs by Renseq (Jupé et al. 2013; Hein 2015, James Hutton Institute, UK, presentation at the workshop). Future developments in these techniques promise to further revolutionize gene cloning and resistance breeding. In addition to classical NB-LRR proteins, membrane immune receptors of the class of receptor-like proteins and receptor kinases are also increasingly recognized as important *R* protein classes that can have generally large spectra and show sometimes broad phylogenetic distribution (Liebrand et al. 2013).

An alternative to *R* genes are *S* genes. *S* genes are required for susceptibility; their loss leads to loss of disease and therefore protects crops. *S* gene-mediated resistance is believed to be often more durable than resistance conferred by *R* genes (Pavan et al. 2010). Identification of *S* genes can profit from studies in model species as shown for the *DRM6* that provides, when inactivated, resistance to biotrophic pathogens in the model plant *Arabidopsis* but also in crops such as lettuce and spinach (van Damme et al. 2008; Van den Ackerveken 2015, Utrecht University, The Netherlands, presentation at the workshop). Novel non-GMO gene knockout technologies such as TILLING and CRISPR-based genome engineering render this approach highly attractive and complement the search for susceptibility loci in germplasm populations (Ahman 2015, Swedish University of Agricultural Sciences, Sweden; Bai 2015, Wageningen University, The Netherlands; Smant 2015, Wageningen University, The Netherlands, presentations at the workshop).

Conclusions

In conclusion, the workshop highlighted that there is a strong need for innovative approaches and new solutions to achieve durable disease resistance in crops. Breeding more durably resistant varieties and introducing more diversity at all levels, from the plant to the agrosystem, are required. The huge progress in the understanding of plant pathogen interactions opens many exciting new ways to achieve this goal that is crucial for a sustainable high yielding and environment friendly agriculture. Intensifying exchange between academic research and companies appears as a prime solution to accelerate the implementation of innovative knowledge-based strategies in this important field.

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