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Rapid evolution in the tug-of-war between microbes and plants

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Meetings

Rapid evolution in the tug-of-war between microbes and plants

'Molecular mechanisms underlying the rapid evolution of plant–microbe interactions', New Phytologist/DFG SPP1819 Workshop, Vaals, the Netherlands, February 2018

Does the underlying co-evolutionary race between hosts and pathogens necessarily result in rapid evolution? Is the process of adaptation in these antagonistic interactions fundamentally different from other adaptive processes?

Members of the research priority programme SPP1819 (topic: 'Rapid evolutionary adaptation – potential and constraints') – funded by the German Science Foundation (DFG) – along with an international group of fellow scientists, met in February 2018 at the idyllic castle Bloemendal of Vaals in the Netherlands to discuss the latest advances on the emerging topic of evolutionary molecular plant–microbe interactions (EvoMPMI; for a recent review see Upson *et al.*, 2018). In the 20 talks delivered by both established and early career scientists in the field, the latest results covering a range of model systems were presented and discussed. While the limited space provided here does not allow for an extensive commentary on all of the talks, we present a few recurrent themes and highlights.

Can fungal pathogens shine light on the mechanisms of rapid evolution?

Much of the work presented at this workshop illustrated that plant-pathogenic fungi can be an invaluable tool for determining how pathogens adapt following the introduction of new host resistance specificities or during a shift to a new host. Their relatively small genomes (*c.* 20–200 Mb) can be easily (re-)sequenced, making them tractable for both comparative/population genomics and experimental evolution. A few laboratories have begun to incorporate genomic tracking with an experimental evolutionary approach involving serial passages of the pathogen through contrasting host species or genotypes, attempting to identify the mutations associated with host specialization. Since the price for short-read sequencing has decreased significantly in recent years, this genome 'monitoring' approach is also cost-efficient. In addition, advances in long-read sequencing can further aid in determining the contribution of structural changes such as chromosome length polymorphisms, large-scale deletions/duplications, and rearrangements in the process of adaptation. Considering the wide range of hosts, life-styles and propagation modes, fungi can deliver a cornucopia of insights for evolutionary biologists.

This notion was well reflected at the workshop. The laboratories of Antonio di Pietro (University of Córdoba, Spain), Jan Schirawski and Ralph Panstruga (both RWTH Aachen University, Germany) aim to understand the adaptive walk of three fungal pathogens (*Fusarium oxysporum*, *Sporisorium reilianum*, *Blumeria graminis*) to different host environments using experimental evolution. Using serial passaging of these pathogens through their respective hosts, they monitor the co-occurrence of genomic changes affecting virulence (Fig. 1). Preliminary results suggest that an increase in virulence on one host might come at a cost in other environments/hosts.

Utilizing a different approach, the laboratories of Bruce McDonald (ETH Zürich, Switzerland), Eva Stukenbrock (University of Kiel, Germany), Bart Thomma (Wageningen University & Research, the Netherlands) and Martijn Rep (University of Amsterdam, the Netherlands) are taking advantage of natural variation within and between species to home in on genetic factors that contribute qualitatively or quantitatively to the development of disease. The development of high-throughput imaging methods to collect data on the extent of infection including the number of pycnidia, the level of melanization or lesion area for the wheat pathogen, *Zymoseptoria tritici* (Karisto *et al.*, 2018) can provide major breakthroughs for the mapping of genetic factors associated with pathogenicity (Hartmann *et al.*, 2017). This approach has been extremely fruitful, providing not only insights on the

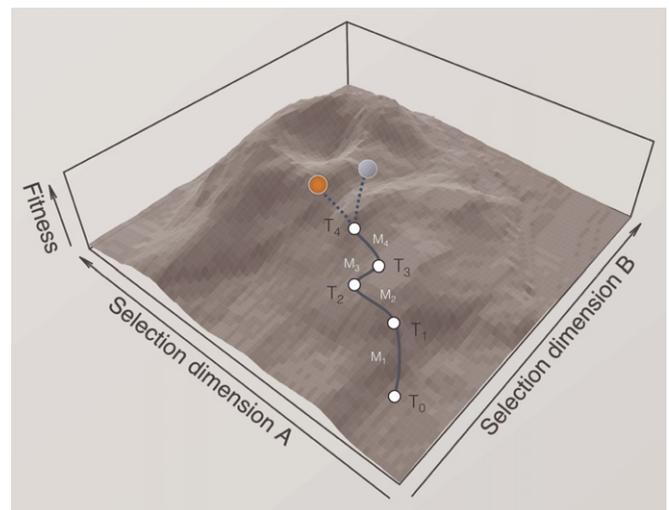


Fig. 1 Schematic representation of an adaptive walk a pathogen may take as it adapts to a new host species or to a new resistance specificity. Over time (T0–T4), adaptive mutations M1–M4 (e.g. gene duplications, deletions or nonsynonymous substitutions) will arise and be fixed in natural populations. The endpoint of an adaptive walk may be distinct fitness optima (represented here by red and blue dots) and these may correspond to different hosts or host genotypes.

quantitative effects of different pathogen effectors, but also offering a method to disentangle pathogen reproduction and virulence. Similar high-throughput experiments were presented by Dan Kliebenstein (University of California Davis, USA), in which *c.* 100 different *Botrytis cinerea* isolates were used to examine the polygenic basis of its virulence on tomato and other plant hosts (Soltis *et al.*, 2018). At the same time, comparative genomics between isolates of fungal species and their close relatives can reveal individual host-specific factors that are responsible for a large proportion of the colonization success and expose the role of lineage-specific, dispensable chromosomes or regions thereof in host shifts. This, for example, is nicely demonstrated by work on *Verticillium dahliae* and *F. oxysporum* (van Dam *et al.*, 2017; Shi-Kunne *et al.*, 2017).

Overall, it became evident that every research team is invigorated and blossoming in the new era of pathogenomics. Owing to the joint efforts of many laboratories around the world, resources have matured and now include multiple, curated and annotated datasets and nearly complete genomes, enabling the next generation of biologists to move forward and go beyond standard molecular genetics. Accumulating evidence, some of which was presented in this meeting, suggests that additional factors contribute to fungal virulence, and these might range from the life history of the isolates and their genetic backgrounds to the specific genome architecture (e.g. patterns of transposable element distribution, accessory chromosomes, etc.) and genome-wide epigenetic patterns (e.g. DNA methylation and histone marks).

The phyllosphere as a new frontier?

Embracing a taxonomically comprehensive approach, Eric Kemen (University of Tübingen, Germany) presented his work on the dynamics of the leaf microbe community. Following a series of combined experiments, the microbial community of the Arabidopsis phyllosphere could be reduced to a manageable number of culturable species to serve as synthetic microbial communities (SynComs). Alteration of the composition of these SynComs affected the infection success by the oomycete pathogen *Albugo laibachii*, suggesting that inter-microbe interactions may exert indirect effects on plant health. Joy Bergelson (University of Chicago, USA) pointed out that these plant microbial networks, despite being heritable across generations, are also vulnerable to disruptions originating from environmental change (Brachi *et al.*, 2017).

While binary host–pathogen interactions are still the standard model, the potential for a role of the associated microbial community to influence the outcome of host–pathogen interactions is widely acknowledged but rarely studied. Until now, the microbial community, as a third player in any host–pathogen interaction, has not been explicitly approached from the perspective of rapid evolution. However, it is likely that the process of adaptation of a pathogen to a new host also entails adapting to the associated indigenous microbial community. The associated microbial community may act in concert with the host immune system to negatively affect the pathogen or facilitate infection, depending on community structure. The experimental concepts that were presented in this workshop could be used to obtain a

deeper insight into how certain compositions of microbial communities can accelerate or hinder adaptation of phytopathogens to given plant species.

Rapid? Says who?

As new data accumulate, at what point can we generalize about specific scenarios conducive to rapid evolution? Is it as simple as characterizing the pathogen's own evolutionary potential (i.e. having a particular genome architecture, a given parasitic lifestyle, and a specific propagation mode; Dong *et al.*, 2015), or is it a sum of environmental factors (e.g. tighter co-association with certain other microbes)? Paraphrasing a quote from Oscar Wilde, factors associated with the rapid evolution of virulence and adaptation give an answer that at the moment is 'rarely pure and never simple'.

Depending on the pathogen species, different types of genetic variants were found to be associated with host specialization and adaptation (e.g. accessory chromosomes, copy number variation, the presence of active transposable elements, structural rearrangements and/or nucleotide polymorphisms). However, despite attempts to place these examples in a common framework, each pathogen still appears to represent a unique evolutionary trajectory and no single type of genetic variation serves as a predictor for a high rate of adaptive evolution.

Many factors, both intrinsic (such as genome flexibility, mating system, pathogen life style and/or mode of dispersal), and extrinsic (such as climatic variability, the structure of the host-associated microbial community and the spatial distribution/landscape coverage of the host relative to the mode of pathogen dispersal), influence the potential rate of adaptation. A new framework to study the presence of rapid evolution in plant–pathogen systems should not only address the all-important underlying genomic changes that lead to differences in host specificity or susceptibility, but also consider how these other factors have shaped the evolutionary trajectories.

Finally, an important first step to better understand the process of rapid adaptation is to characterize the underlying genetic changes associated with specialization and pathogenicity. Studying pathogens from many kingdoms, including bacteria, viruses, fungi and oomycetes, our field is making rapid progress to decipher these genetic changes associated with rapid evolution and can even deliver some new case studies (Inoue *et al.*, 2017). Looking into the future, our next challenge is to determine if there are any common, underlying patterns. Finding the answer to this question will likely require integration of many different research fields, including epidemiology, ecology, molecular biology, population genomics and computer science, to work on the common theme of rapid evolution.

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References

- Brachi B, Filaault D, Darne P, Mentec M Le, Kerdaffrec E, Rabanal F, Anastasio A, Box M, Duncan S, Morton T *et al.* 2017. Plant genes influence microbial hubs that shape beneficial leaf communities. *bioRxiv*. doi: 10.1101/181198
- van Dam P, Fokkens L, Ayukawa Y, van der Gragt M, ter Horst A, Brankovics B, Houterman PM, Arie T, Rep M. 2017. A mobile pathogenicity chromosome in *Fusarium oxysporum* for infection of multiple cucurbit species. *Scientific Reports* 7: 9042.
- Dong S, Raffaele S, Kamoun S. 2015. The two-speed genomes of filamentous pathogens: waltz with plants. *Current Opinion in Genetics & Development* 35: 57–65.
- Hartmann FE, Sánchez-vallet A, McDonald BA, Croll D. 2017. A fungal wheat pathogen evolved host specialization by extensive chromosomal rearrangements. *The ISME Journal* 11: 1189–1204.
- Inoue Y, Vy TTP, Yoshida K, Asano H, Mitsuoka C, Asuke S, Anh VL, Cumagun CJR, Chuma I, Terauchi R *et al.* 2017. Evolution of the wheat blast fungus through functional losses in a host specificity determinant. *Science* 357: 80–83.
- Karisto P, Hund A, Yu K, Anderegg J, Walter A, Mascher F, McDonald BA, Mikaberidze A. 2018. Ranking quantitative resistance to *Septoria tritici* blotch in elite wheat cultivars using automated image analysis. *Phytopathology* 108: 568–581.
- Shi-Kunne X, Faino L, van den Berg GCM, Thomma BPHJ, Seidl MF. 2017. Evolution within the fungal genus *Verticillium* is characterized by chromosomal rearrangement and gene loss. *Environmental Microbiology* 20: 1362–1373.
- Soltis NE, Atwell S, Shi G, Fordyce R, Gwinner R, Gao D, Shafi A, Kliebenstein DJ. 2018. Crop domestication and pathogen virulence: interactions of tomato and *Botrytis* genetic diversity. *bioRxiv*. doi: 10.1101/255992
- Upson JL, Zess EK, Białas A, Wu C, Kamoun S. 2018. The coming of age of EvoMPMI: evolutionary molecular plant–microbe interactions across multiple timescales. *Current Opinion in Plant Biology* 44: 108–116.

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