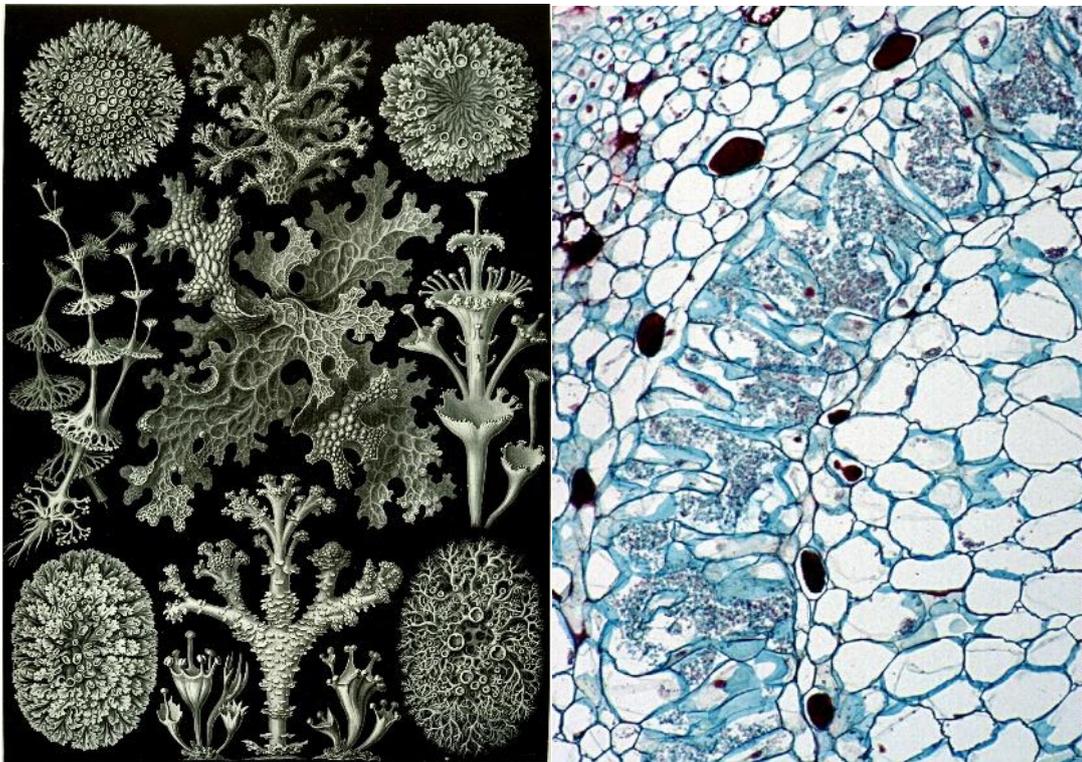




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Conference Abstracts



Spatial metagenomics illuminate the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale

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Our knowledge about plant virus diversity in nature is still limited. Indeed, studies of plant-virus interactions have primarily focused on cultivated areas. This lack of knowledge about patterns of virus diversity and distribution in nature is hampering our understanding of plant virus ecology and evolution in the long term. In addition, this scarcity of knowledge does not allow to fully understand, model and predict the micro- and/or macro-evolutionary processes that are taking place across the agro-ecosystem. Consequently, it is still difficult to quantify the impact of human activities (agricultural intensification, plants transport, climate change, etc.) on host-pathogen interactions. We developed a new metagenomics approach, the so-called geo-metagenomics approach, in order to provide information about the virus biodiversity, the prevalence of unknown and asymptomatic viruses and the spatial distributions of those plant viruses in two pilot ecosystems: the Western Cape Region of South Africa and the Camargue region in France. This approach provides geographically tagged cDNA from known and unknown viruses, and further allows linking viral sequences obtained by the metagenomics approach to a specific host, and hence to geographic coordinates. The objectives of this study were to assess (i) if wild areas can be considered as reservoir of plant virus biodiversity (ii) if there exists patterns of spatio-temporal distribution of plant viruses at the agro-ecosystem scale and (ii) if ecological parameters can account for these distributions. This new approach allowed us to estimate plant virus diversity associated with both pilot agro-ecosystems. This study led to the discovery of 94 potential new plant viral species and highlighted patterns of spatial distribution of plant viral families. Plant virus prevalence associated with cultivated areas was found to be significantly greater than those associated with non-cultivated areas. Furthermore, exotic plants from South African fynbos showed significantly higher prevalence than native plants. These results emphasize the direct or indirect impact of human activity on plant virus dynamics at the agro-ecosystem scale.

Keywords

Metagenomics, agro-ecosystem, plant viruses, diversity

