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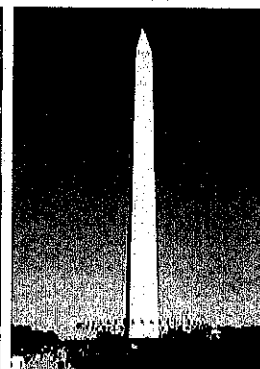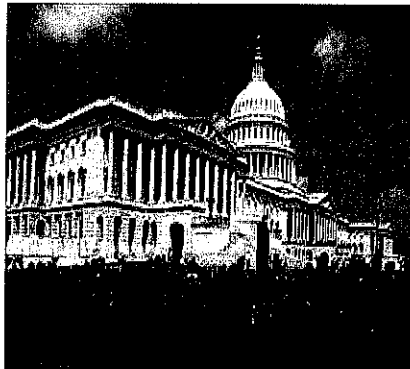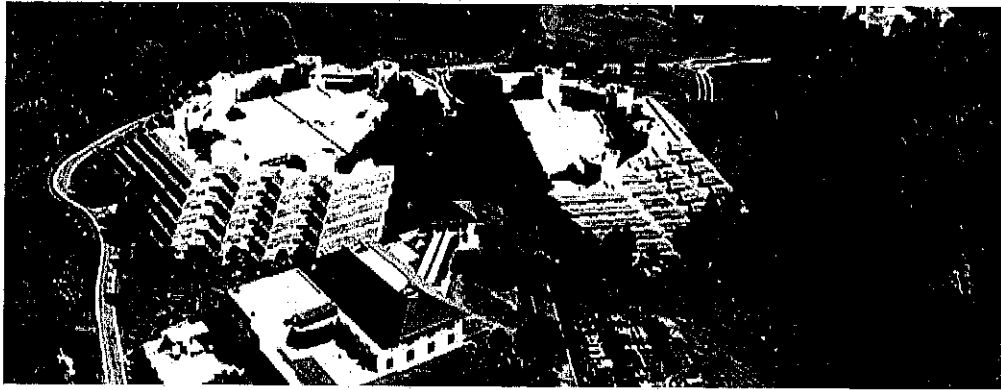# International Workshop
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Program and Book of Abstracts

Towards metagenomics-based diagnostics to detect and prevent plant pathogens

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Plant diseases are a major cause of food loss worldwide, contributing to losses in agricultural productivity ranging from 20% to 40%. These losses are either direct or indirect, resulting from a disruption of food quality and safety, and they have profound effects on food chains. In such a context, reliable diagnostic methods are needed to identify risks to plant health and promptly and efficiently administer plant protection products.

Current molecular diagnostic techniques, usually based on PCR, are very sensitive, specific and accurate. Some, especially those based on LAMP, are also very portable and allow for in the field molecular detection of plant pathogens, but they are always limited to detecting one or very few pathogens with each analysis. A completely non-targeted approach would provide an unbiased, holistic view of all the organisms (pathogenic or otherwise) in the sample of interest and would be of significant value in finding new and emerging pathogens, as well as for finding and identifying organisms that are unexpectedly present in a sample. A potential solution for surveillance in this type of material is a non-targeted approach based on High throughput Sequencing (HTS). Metabarcoding and shotgun metagenomics provide a useful tool for identifying at the same time a high number of possible pathogens in plants or seeds, but their application is still rare in the diagnostic field, except for shotgun metagenomics-based detection of viruses. Metabarcoding-based analyses are cheaper than shotgun metagenomics, they require less storage space, as well as less computational power, and they are easier to deal with from a bioinformatics point of view. However, the choice of the primers heavily influences the outcome, and for some genera, especially fungal ones, their resolution does not go beyond the genus-level. Shotgun metagenomics suffers no PCR-derived biases and allows for the analysis of the whole genome of pathogens, but it is expensive and can perform poorly when there is high biodiversity, many related strains are present and/or organism distribution is very uneven. The quality of databases is another central point to consider when applying any of these techniques for diagnostic purposes.

We consider the applicability of metagenomics in plant diseases diagnostics, discussing the limitations and applications of each technique. Problems that the scientific community needs to solve to enable the implementation of this tool are identified, and the interaction of metagenomics with other approaches, such as sampling of the airborne inoculum, is explored.