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BOOK OF ABSTRACTS

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POPULATION HISTORY AND PATHWAYS OF SPREAD OF THE PLANT PATHOGEN PHYTOPHTHORA PLURIVORA**CORINE SCHOEBEL⁽¹⁾, JANE STEWART⁽²⁾, NIKLAUS GRUENWALD⁽³⁾, DANIEL RIGLING⁽¹⁾, SIMONE PROSPERO⁽¹⁾**⁽¹⁾ SWISS FED RES INSTITUTE WSL, SWITZERLAND, ⁽²⁾ UNIVERSITY OF GEORGIA, USA, ⁽³⁾ USDA-ARS-HORTICULTURAL CROPS, USA

Human activity has been shown to considerably affect the spread of dangerous pests and pathogens worldwide. Therefore, strict regulations of international trade exist for particularly harmful pathogenic organisms. Our study organism, *Phytophthora plurivora*, which is not subject to regulations, is a plant pathogen frequently found on a broad range of host species, both in natural and artificial environments. It is supposed to be native to Europe while resident populations are also present in the US. We characterized a hierarchical sample of isolates from Europe and the US and conducted coalescent-, migration, and population genetic analysis of sequence and microsatellite data, to determine the pathways of spread and the demographic history of this pathogen. We found *P. plurivora* populations to be moderately diverse but not geographically structured. High levels of gene flow were observed within Europe and unidirectional from Europe to the US. Coalescent analyses revealed a signal of a recent expansion of the global *P. plurivora* population. Our study shows that *P. plurivora* has most likely been spread around the world by nursery trade of diseased plant material. In particular, *P. plurivora* was introduced into the US from Europe. International trade has allowed the pathogen to colonize new environments and/or hosts, resulting in population growth.

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RESURRECTION OF ANCESTRAL OXIDOREDUCTASES: AN IN SILICO APPROACH**IVAN AYUSO, JAVIER RUIZ-DUEÑAS, ANGEL T. MARTÍNEZ**

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The evolution of gene function is a central issue in molecular evolution and ancestral sequence reconstruction is a powerful tool in these studies. It has the advantage of inferring ancient gene sequences that act as hypothesis that can be tested in laboratory by resurrection of those sequences. During the past years the resurrection of genes had help to prove several hypothesis about how was life on Earth, and how some enzymes had evolved and obtained the functions they have today. The basis of this technique is the use of extant proteins to infer the ancestral sequences of interest, which will be expressed and characterized in vitro. Resurrected proteins are of interest not only because the basic information about evolution that they give us, but also because these proteins have great biotechnological potential: the resurrected proteins catalyzed reactions in a planet where the conditions were very different from actual Earth, with different temperature, pH, oxidation conditions, etc. Recently, it has been published the Paleozoic origin of lignin degradation using 31 genomes, where 6 genomes of Polyporales were used, reconstructing the ancestral state of discrete characters in ligninolytic and generic peroxidases, such as the appearance or disappearance of the oxidizing sites that defines the catalytic activities of these peroxidases. This study has been amplified and concreted using 10 genomes of Polyporales. In this way, we propose the reconstruction not only of those discrete characters, but the whole protein by inferring the ancestral sequences using the information of extant basidiomycete peroxidases. Thereby, by resurrection and characterization of those sequences in the laboratory we will be able to determine the mechanisms that lead the ancient proteins to the functions and properties they have today including the ability to degrade the recalcitrant lignin polymer, a key issue for development of land ecosystems. Here we present the preliminary results based on in silico resurrection and modeling of the ancestral PODs, with special interest in the oxidizing sites and their modification through the evolution.



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