

FITOPATOLOGÍA

Publicación oficial de la Sociedad Española de Fitopatología



Año 2018

Número 2



Miguel Cambra, SEF fotografía 2016

Libro de Resúmenes



XIX CONGRESO

DE LA SOCIEDAD

ESPAÑOLA DE FITOPATOLOGÍA

TOLEDO 2018

8 al 10 de octubre

An update on the genetic population structure of the invasive ash dieback pathogen *Hymenoscyphus fraxineus*

Ana Pérez-Sierra¹, Vahideh Rafiei², Concepción Olivares³, Helen Rees¹, Sietse Van Der Linde¹, Nenad Keča⁴, Katharina Schwanda⁵, Venche Talgø⁶, Blanca B. Landa^{3*}

¹Forest Research, Alice Holt Lodge, Farnham, Surrey GU10 4LH, UK. ²Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran. ³Instituto de Agricultura Sostenible, CSIC, Avda. Menéndez Pidal s/n. 14004 Córdoba. ⁴Faculty of Forestry, University of Belgrade, Kneza Višeslava 1, 11030 Belgrade, Serbia. ⁵Federal Research and Training Centre for Forests, Natural Hazards and Landscape, Seckendorff-Gudent-Weg 8, Vienna 1131, Austria. ⁶Norwegian Institute of Bioeconomy Research, NIBIO, Pb 115, NO-1431 Ås, Norway.

Understanding the genetic diversity and structure of invasive pathogens in their source of origin or in areas where they have been recently introduced is crucial to reconstruct the course of invasions and to establish effective control measures. *Hymenoscyphus fraxineus* (*Hf*) jumped from Asian ash species (*Fraxinus* spp.) where it is a leaf pathogen with little impact to European ash (*F. excelsior*) and narrow-leafed ash (*F. angustifolia*) in Europe on which is causing severe disease symptoms and often mortality. Previous studies showed that the European *Hf* population was originated by two divergent haploid individuals. Subsequent introductions from this source would greatly increase the adaptive potential of this pathogen and represents a potential threat to European ash. Therefore, a need to analyse the *Hf* genetic population structure in new areas was identified as the main objective of this study.

In this study 11 microsatellite markers (MM) were used to characterize the genetic structure and diversity of 111 new isolates obtained from nine locations (five of them with no previous MM information in Serbia and the UK) and compare them with a published dataset of 1377 isolates from a total of 11 European countries, Russia and Japan. After combining the two data sets, 270 alleles were observed from 1488 isolates resulting in 778 Multilocus genotypes (MLGs) which were collapsed, based on Bruvo's genetic distance matrix, into 591 contracted MLGs that were used to draw minimum spanning networks (MSN). MSN, STRUCTURE and PCA analyses validated previous findings that indicated that European and Japanese populations are partially intermingling although consistently associated to separate clusters. Results did not reveal any evident population structure of European strains, including the *Hf* isolates sampled from new locations, pointing to a single introduction in Europe by few individuals and a recent genetic bottleneck.

Funded by the EU's Horizon 2020 Project No 635646 POnTE.