

AperTO - Archivio Istituzionale Open Access dell'Università di Torino

Traits affecting transmission rather than pathogenicity drive invasions by two fungal pathogens

This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1570484> since 2016-06-22T15:13:03Z

Publisher:

Ecological Science at the Frontier

Terms of use:

Open Access

Anyone can freely access the full text of works made available as "Open Access". Works made available under a Creative Commons license can be used according to the terms and conditions of said license. Use of all other works requires consent of the right holder (author or publisher) if not exempted from copyright protection by the applicable law.

(Article begins on next page)



UNIVERSITÀ DEGLI STUDI DI TORINO

This is an author version of the contribution:

Questa è la versione dell'autore dell'opera:

[Garbetotto M., Della Rocca G., Gonthier P., 2015. The 100th ESA (Ecological Science at the Frontier) Annual Meeting, Baltimore (MD), 9-14 August 2015. Paper 00S 23-7]

The definitive version is available at:

La versione definitiva è disponibile alla URL:

[<http://eco.confex.com/eco/2015/webprogram/Paper50829.html>]

OOS 23-7

Traits affecting transmission rather than pathogenicity drive invasions by two fungal pathogens

Tuesday, August 11, 2015: 10:10 AM

342, Baltimore Convention Center

Matteo Garbelotto, Espm, U.C. Berkeley Forest Pathology and Mycology Laboratory, Berkeley, CA, USA

Gianni Della Rocca, , CNR, Florence, Italy

Paolo Gonthier, , Universita Torino, Torino, Italy

Background/Question/Methods

In the past decades too much emphasis has been placed on the presumed high virulence of exotic pathogens on naive hosts to justify all invasions by plant pathogens. Here we present an analysis of several traits associated with invasiveness of two North American plant pathogens which have become invasive in the Mediterranean basin, namely the root rot agent *Heterobasidion irregulare* and *Seiridium cardinale*, the causal agent of cypress canker. In both cases, population genetic analyses have identified source populations and have reconstructed the history of both invasions allowing to perform comparative analyses between source, founder and invasive populations. We have previously shown through reciprocal inoculation trails that pathogenicity is not particularly elevated in the invasive populations of both pathogens. Here we present results from a series of studies evaluating traits of *Seiridium cardinale* such as spore size, spore production, spore viability temperature optima, and demographic phenotypic plasticity and results from comparative genomic analyses of *Heterobasidion irregulare* and of a close sister native taxon, *H. annosum*, which has been outcompeted by the invasive exotic species.

Results/Conclusions

We show that smaller spore size is strongly selected and adaptive both in the founder and invasive populations of *Seiridium cardinale*, in spite of a demonstrated trade off of reduced viability in smaller spores. We also show that intermediate virulence and an increase in sporulation are advantageous to the invasive populations. More strikingly we show that demographic plasticity increases for all traits in the founder compared to the source population, but such plasticity decreases sharply as the founder populations adapts to new environments and becomes invasive. In the case of *Heterobasidion irregulare*, results of the comparative genomic analysis shows the genomes of both the exotic and native species to be strikingly syntenic, despite 30-45 million years of isolation, and shows that while genes involved in pathogenicity are mostly unchanged, genes involved in saprobic growth, in fruiting, and gene regulation are mostly divergent between the native and the visibly more fit exotic species. We conclude that in both cases, traits affecting transmission and spread are key in explaining the invasive potential of two fungal pathogens. These traits do not involve high pathogenicity of exotic pathogens on naive hosts.