



4-2019

# Unwelcomed stowaways and their role in thousand cankers disease spread

Aaron Onufrak  
*University of Tennessee, Knoxville*

Emel Oren  
*University of Tennessee, Knoxville*

Romina Gazis  
*University of Florida*

William Klingeman  
*University of Tennessee, Knoxville*

Massimo Faccoli  
*University of Padua, Italy*

*See next page for additional authors*

Follow this and additional works at: <https://trace.tennessee.edu/masmc>

## Recommended Citation

Onufrak, Aaron; Oren, Emel; Gazis, Romina; Klingeman, William; Faccoli, Massimo; Chalal, Karandeep; Windham, Mark; Ginzel, Matthew; and Hadziabdic, Denita, "Unwelcomed stowaways and their role in thousand cankers disease spread" (2019). *Middle Atlantic States Mycological Conference 2019*.  
<https://trace.tennessee.edu/masmc/7>

This Poster is brought to you for free and open access by the Conferences at UT at Trace: Tennessee Research and Creative Exchange. It has been accepted for inclusion in Middle Atlantic States Mycological Conference 2019 by an authorized administrator of Trace: Tennessee Research and Creative Exchange. For more information, please contact [trace@utk.edu](mailto:trace@utk.edu).

---

**Authors**

Aaron Onufrak, Emel Oren, Romina Gazis, William Klingeman, Massimo Faccoli, Karandeep Chalal, Mark Windham, Matthew Ginzel, and Denita Hadziabdic

Mid-Atlantic States Mycological Conference (MASMC)  
University of Tennessee – Knoxville  
12-14 April 2019

ABSTRACTS – Posters

**Unwelcomed stowaways and their role in thousand cankers disease spread**

Aaron Onufrak<sup>1</sup>, Emel Oren<sup>1,2</sup>, Romina Gazis<sup>3</sup>, William Klingeman<sup>4</sup>, Massimo Faccoli<sup>5</sup>, Karandeep Chahal<sup>1,6</sup>, Mark Windham<sup>1</sup>, Matthew Ginzel<sup>7</sup>, Denita Hadziabdic<sup>1</sup>

<sup>1</sup>Department of Entomology and Plant Pathology, University of Tennessee, <sup>2</sup>University of Tennessee, Department of Entomology and Plant Pathology, Current address: Diyarbakir Plant Protection Research Institute, Diyarbakir, Turkey, <sup>3</sup>University of Florida, Department of Plant Pathology/Tropical Research and Education Center, <sup>4</sup>Department of Plant Sciences, University of Tennessee, <sup>5</sup>Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padua, Italy, <sup>6</sup>Department of Entomology and Plant Pathology, University of Tennessee, Current address: Department of Plant, Soil and Microbial Sciences, Michigan State University, <sup>7</sup>Departments of Entomology and Forestry & Natural Resources, Purdue University

*Geosmithia morbida* is a plant pathogenic fungus primarily vectored by the walnut twig beetle, *Pityophthorus juglandis* (WTB). Together, these species cause thousand cankers disease (TCD) in walnut (*Juglans* spp.) and wingnut (*Pterocarya* spp.) trees. TCD was originally described in the western United States and later detected in 2010 in the eastern U.S. within the native distribution of black walnut (*J. nigra*). In 2013, TCD was discovered in Italy on both black and English walnut (*J. regia*). Due to regional and global movement of TCD, there is a critical need to understand the basic biology and genetics of both the pathogen and vector(s) of TCD, including genetic diversity and population structure of disease complex members. Using traditional and molecular tools, our group has provided an insight into biology, life cycle, and population genetics of TCD members. Current research supports two overlapping WTB generations per season in the U.S. and Italy and potential alternative disease vectors, which could help sustain localized disease presence once the pathogen is introduced. We have also detected high genetic diversity among *G. morbida* subpopulations in the U.S. with spatial clustering and evidence of gene flow providing support for multiple anthropogenic introductions of *G. morbida* from multiple sources. Additionally, we have developed rapid molecular detection methods for both *G. morbida* and *P. juglandis*, significantly reducing disease confirmation time. Future TCD research plans are focused on identifying pathogenicity genes, as well as developing a potential biocontrol for TCD, and understanding how these potential biocontrol methods impact the host microbiome.