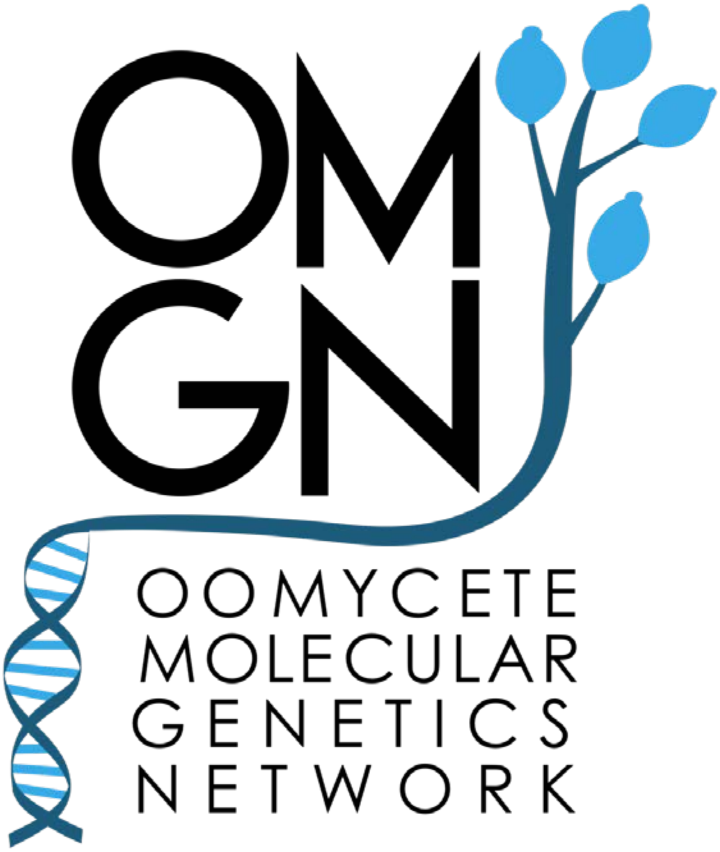
OMGN 2017

March 11 - 14, Asilomar Conference Grounds



Monday, March 13th		
3:50 - 5:10	**Oomycete biology, populations, and evolution I**	**Chair: Javier F. Tabima**
3:50 - 4:05	Phylogeography of the tropical oomycete *Phytophthora palmivora*	Erica M. Goss
4:10 - 4:25	Diversity of *Phytophthora* species from natural and semi-natural ecosystems in Portugal, Chile and Vietnam	Marília Horta Jung
4:30 - 4:45	Live cell imaging of the cytoskeleton in *Phytophthora* pathogens reveals unique actin and microtubule configurations	Kiki Kots
4:50 - 5:05	Morphological and molecular identification of *Phytophthora palmivora* Butler as causal agent of black pod rot of cocoa (*Theobroma cacao* L.) from coastal Ecuador	Miriam Escos

Phylogeography of the tropical oomycete *Phytophthora palmivora*

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The genetic structure and diversity of oomycetes are shaped by their evolutionary history, including coevolutionary interactions with hosts, geographic spread, and long-distance migration events, often mediated by humans. In turn, diversity and dispersal of present populations impact the risk of disease epidemics and strategies for controlling disease. *Phytophthora palmivora* is a globally distributed oomycete that infects a broad range of cash crops and fruit trees in the tropics and subtropics, including cocoa and palms. The center of diversity of *P. palmivora* is in Southeast Asia, but it is an important and widespread pathogen in South America. Our multilocus sequence analysis showed that the centers of origin of the pathogen are located in the Philippines and Indonesia. We then tested alternative models for the emergence of *P. palmivora*. We found genetic variation consistent with historical movement among Pacific Islands, likely associated with coconut. The population structure of *P. palmivora* is consistent with a bridgehead effect, such that the colonization of South America and host shift to cocoa led to further global dispersal, including gene flow back to Southeast Asia. We propose that the extensive genetic diversity in *P. palmivora* in Southeast Asia is the result of a complex history, including long-term co-evolution with native hosts, geographic isolation with migration, and re-introduction of genotypes from South America.

Diversity of *Phytophthora* species from natural and semi-natural ecosystems in Portugal, Chile and Vietnam

Thomas Jung[1,2,3], Bruno Scanu[4], József Bakonyi [5], Diána Seress [5], Alvaro Durán [6], Eugenio Sanfuentes von Stowasser [7], Leonardo Schena[8], Saveria Mosca [8], Pham Quang Thu[9], Chi Nguyen Minh[9], Sebastian Fajardo[7], Mariela González [7], Ana Pérez-Sierra [10], Helen Rees [10], Cristiana Maia[1], Beatriz Mora Sala[11], Giuseppe Carella[12], Salvatore Moricca[12], Alfredo Cravador[1], Marília Horta Jung[1,2]
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Surveys of *Phytophthora* diversity were performed using baiting assays and direct plating of necrotic plant tissues. Isolates were identified using both classical identification and sequence analysis of ITS and *cox1*. In Portugal, 68 forest stands, 12 forest nurseries, 38 river systems and 4 lagoon ecosystems were surveyed. The isolates obtained belonged to 29 known species, 3 informally designated taxa, and 1 previously unknown taxon of *Phytophthora*, nine new *Phytophthora* hybrid taxa from Clades 6 and 9, *Nothophytophthora homothallica* nom. prov., 1 known and 10 new *Halophytophthora* species, 7 known species and one new taxon of *Phytopythium*, and multiple *Pythium* species were isolated. In Chile, the survey was performed in 13 natural forest stands and 20 forest streams located in two protected areas near Valdivia and in a temperate mountain forest in the Concepción area, and in each one planted stand of the introduced tree species *Castanea sativa* and *Fagus sylvatica*. Eight described species (including *P. kernoviae*) and 2 previously unknown taxa of *Phytophthora* were isolated. In addition, a diverse array of Clade 6 hybrids, and *Nothophytophthora caduca* nom. prov., *Nothophytophthora chlamydospora* nom. prov. and *Nothophytophthora valdiviana* nom. prov., were obtained. In Vietnam the survey was performed in 23 natural forest stands and 10 forest streams and rivers in temperate montane and tropical lowland regions, and in 14 rubber plantations. Sixteen described species (including *P. ramorum*), 3 designated taxa and 23 previously unknown taxa of *Phytophthora*, amongst them 9 Clade 9 hybrid taxa, were isolated. In addition, *Nothophytophthora vietnamensis* nom. prov. and a diverse array of known and new taxa of *Phytopythium*, *Pythium* and *Elongisporangium* were recovered. The implications of these findings for plant biosecurity and the development of a deeper understanding of the evolution and adaptability of the genus *Phytophthora* will be discussed.

Live cell imaging of the cytoskeleton in *Phytophthora* pathogens reveals unique actin and microtubule configurations

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The cytoskeleton is a dynamic but well organized intracellular network that is essential for proper functioning of eukaryotic cells. We study the cytoskeleton in *Phytophthora* species, oomycete plant pathogens that cause devastating diseases worldwide. We use Lifeact-eGFP expressing *Phytophthora infestans* for live cell imaging of the actin cytoskeleton in various developmental stages. Previously we identified actin plaques as highly immobile, long-lived structures that are unique for oomycetes. Here we present two other unique actin configurations; one associated with plug deposition in germ tubes and the other with appressoria, infection structures formed prior to host cell penetration. Plugs are composed of cell wall material that is deposited in hyphae emerging from cysts to seal off the cytoplasm-depleted base after cytoplasm retraction towards the growing tip. Preceding plug formation a typical local actin accumulation was observed that remained associated with the leading edge during plug deposition. In appressoria we observed an aster-like actin configuration at the contact point with the underlying surface. These findings strongly suggest a role for the actin cytoskeleton in plug formation and plant cell penetration. For live cell imaging of the microtubule cytoskeleton we have generated a *Phytophthora palmivora* transformant expressing GFP-α-tubulin allowing us to visualize the dynamics of microtubules in oomycetes for the first time. The data presented here provide a better understanding of the structure and functioning of the *Phytophthora* cytoskeleton. The long term goal is to uncover oomycete or *Phytophthora* specific features in the cytoskeleton that might be instrumental for drug design.