**Dr. Vivian Irish**

[**vivian.irish@yale.edu**](mailto:vivian.irish@yale.edu)

Yale

She is exploring how floral pattern differences arise in a variety of species.  She works with *Arabidopsis* and other angiosperms to understand the underlying basis for the great variety in flowers.  Her work is focused on the evolution of the MADS domain containing transcription factors that regulate floral development.

Drea, S., Hileman, L.C., de Martino, G., and Irish, V.F. (2007). Functional analyses of genetic pathways controlling petal specification in poppy. Development 134: 4157-4166.

Chae, E., Tan, Q. K-G., Hill, T.A. and Irish, V.F. (2008). An Arabidopsis F-box protein acts as a transcriptional cofactor to regulate floral development. Development 135: 1235-1245.

**Dr. Leon Kochian**

[lvk1@cornell.edu](mailto:lvk1@cornell.edu)

Cornell University

He studies mineral nutrient uptake and abiotic stress tolerance in plants.  His main projects include: studying transport of nutritionally important minerals and toxic heavy metals, phytoremediation of heavy metal contaminated soils, and Aluminum tolerance, where he has been trying to identify Al tolerance genes in maize, sorghum and *Arabidopsis*.

Magalhaes JV, Liu J, Guimarães C, Lanal UGP, Alves VMC, Wang Y, Schaffert RE, Hoekenga OA, Piñeros MA, Shaff JE, Kochian LV. 2007. A gene in the multidrug and toxic compound extrusion (MATE) family confers aluminum tolerance in sorghum. Nature Genetics 39:1156-1161

**Dr. Wolf Frommer**

[wfrommer@carnegiescience.edu](mailto:wfrommer@carnegiescience.edu)

Carnegie Institution for Science

He studies how plants regulate nutrient uptake.  His major goals are to identify all components of this process such as exporters, transporters, and regulators, and to identify the signalling networks that underly homeostasis.

Sucrose Efflux Mediated by SWEET Proteins as a Key Step for Phloem Transport

Li-Qing Chen, Xiao-Qing Qu, Bi-Huei Hou, Davide Sosso, Sonia Osorio, Alisdair R. Fernie, and Wolf B. Frommer Science 13 January 2012: 207-211

Chen et al. 2010. Sugar transporters for intercellular exchange and nutrition of pathogens. Nature 468:527

**Dr. Anne Simon**

[simona@umd.edu](mailto:simona@umd.edu)

University of Maryland

She works on RNA secondary structure, RNA-RNA interactions, translational control (molecular and temporal aspects), and cap-independent translation. That probably sounds really boring to everyone except me, but I thought I would put in my nominee anyway! It's a nice mix between cell biology, structural biology, and plant pathology.

Papers attached to email (Guo 2011, 2012)

**Dr. Greg Gilbert**

[ggilbert@ucsc.edu](mailto:ggilbert@ucsc.edu)

University of California, Santa Cruz

Projects:

1. Fungal Dimensions: Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

2. Rare-species advantage: consequences of phylogenetic and numerical rarity of hosts for disease pressure and pathogen communities

3. Phyloepidemiology: Phylogenetic ecology of plant diseases

Papers attached to email (Gilbert papers)

**Dr. Niklaus Grunwald**

[grunwaln@science.oregonstate.edu](mailto:grunwaln@science.oregonstate.edu)

Oregon State University

We are primarily interested in the epidemiology, genetics and evolution of exotic and reemerging *Phytophthora* species with a current emphasis on the sudden oak death pathogen *P. ramorum*.

The genus *Phytophthora* contains some of the most destructive plant pathogens affecting agricultural and forest crops. Important examples include P. ramorum, a devastating exotic pathogen causing sudden oak death, and P. infestans, known as the cause of the Irish potato famine.

Much of our work is conducted with a focus on application towards improving disease management in horticultural and ornamental crops.

Fry, WE, McGrath, M. T, Seaman, A. , Zitter, T. A, McLeod, A. , Danies, G. , Small, I. M, et al. “The 2009 Late Blight Pandemic in the Eastern United States - Causes and Results”. Plant Disease 97 (2013): 296-306.

Cooke, David EL, Cano, Liliana M, Raffaele, Sylvain , Bain, Ruairidh A, Cooke, Louise R, Etherington, Graham J, Deahl, Kenneth L, et al. “Genome analyses of an aggressive and invasive lineage of the Irish potato famine pathogen.”. PLoS Pathog 8, no. 10 (2012): e1002940.

Grünwald, NJ, Garbelotto, M, Goss, EM, Heungens, K, and Prospero, S. “Emergence of the sudden oak death pathogen Phytophthora ramorum”. Trends in Microbiology 20 (2012): 131-138.

Grünwald, NJ, and Goss, EM. “Evolution and Population Genetics of Exotic and Re-Emerging Pathogens: Novel Tools and Approaches”. Annual Review of Phytopathology 49 (2011): 249-267.

**Dr. Joseph Spatafora**

[spatafoj@science.oregonstate.edu](mailto:spatafoj@science.oregonstate.edu)

Oregon State University

Research in our laboratory is focused on molecular systematics and population genetics of fungi. Particular emphases include the evolutionary biology of fungal symbioses as they relates to the evolution of host shifts, the phylogenetic integration of ecologically disparate groups of fungi, and population genetics of closely related organisms with different reproductive life histories.

Martin, F., Cullen, D., Hibbett, D., Pisabarro, A., Spatafora, J.W., Baker, S. E. and I.V. Grigoriev. 2011. Sequencing the Fungal Tree of Life. New Phytologist 190: 818-821.

Hibbett, D.S. Binder, M., Bischoff, J.F., Blackwell, M., Cannon, P.F., Eriksson, O.E., Huhndorf, S., James, T.Y., Kirk, P.M., Lucking, R., Lumbsch, H.T., Lutzoni, F.L., Matheny, P.B., McLaughlin, D.J., Powell, M.J., Redhead, S., Schoch, C.L., Spatafora, J.W., Stalpers, J.A., Vilgalys, R., Aime, M.C., Aptroot, A., Bauer, R., Begerow, D., Benny, G.L., Castlebury, L.A., Crous, P.W., Dai, Y.-C., Gams, W., Geiser, D.M., Griffith, G.W., Gueidan, C., Hawksworth, D.L., Hestmark, G., Hosaka, K., Humber, R.A., Hyde, K.D., Ironside, J.E., Koljag, U., Kurtzman, C.P., Larsson, K.-H., Lichtwardt, R., Longcore, J., Miadlikowska, J., Miller, A., Moncalvo, J.-M., Mozley-Standridge, S., Oberwinkler, F., Parmasto, E., Reeb, V., Rogers, J.D., Roux, C., Ryvarden, L., Sampaio, J.P., Schußler, A., Sugiyama, J., Thorn, R.G., Tibell, L., Untereiner, W.A., Walker, C., Wang, Z., Weir, A., Weiss, M., White, M.M., Winka, K., Yao, Y.-J., and Zhang, N. 2007. A higher-level phylogenetic classification of the Fungi. Mycological Research 111: 509-547

Spatafora, J.W., G.-H. Sung, N.L. Hywel-Jones, J.-M. Sung and J.F. White. 2007. Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. Molecular Ecology 16: 1701-1711.

**Matteo Garbelotto**

UC Berkeley

[matteog@berkeley.edu](mailto:matteog@berkeley.edu)

His work centers broadly on forest pathology and mycology but his lab works on a variety of projects including: understanding the mechanisms behind invasions by exotic forest pathogens including Sudden Oak death and Cypress canker, understanding community structure and island biogeography using beneficial and pathogenic fungi as model systems, highlighting how genetic diversity is structured intraspecifically using population genetics and phylogeography, studying the efficacy and longevity of direct chemical controls on forest diseases and understanding the role of insects as vectors of vascular diseases and otherwise spreading native forest pathogens.

Garbelotto M., Guglielmo, F., Mascheretti, S., Croucher, P., Gonthier, P. 2013. Population genetic analyses provide insights on the introduction pathway and spread patterns of the North American forest pathogen *Heterobasidion irregulare* in Italy. Molecular Ecology, 22: 4855-4869.

Garbelotto, M., Gonthier, P. 2013. Biology, Epidemiology and Control of *Heterobasidion* Species Worldwide. Annu. Rev. Phytopathol. 51:39-59.

**Ignacio Chapela**

UC Berkeley

[chapela@berkeley.edu](mailto:ichapela@berkeley.edu)

A microbial ecologist whose current emphasis is the Ecoscope, a project developed in collaboration with GenØk, the National Center for Biosafety in Norway, and constructed with the goal of producing the instrumentation and methods necessary for the first ever mapping capability for microbial life. The idea of this project is to develop an understanding of the patterns of abundance and distribution to enable mapping of microbial organisms at geographical scales, with DNA-sequence specificity.

Chapela, IH and Garbelotto, M. 2004. Phylogeography and evolution in matsutake and close allies inferred by analyses of ITS sequences and AFLPs. Mycologia, 96(4), 2004, pp. 730-741.

Henn, MH & Chapela, IH. 2004. Isotopic Fractionation during Ammonium Assimilation by Basidiomycete Fungi and Its Implications for Natural Nitrogen Isotope Patterns. New Phytologist 162:771-781

**Dr. Colleen McMahan**

Research Chemist

USDA-ARS - Albany, CA

[colleen.mcmahan@ars.usda.gov](mailto:colleen.mcmahan@ars.usda.gov" \t "_blank)

Current Projects:

- Improvement and Utilization of Natural Rubber- and Castor Oil-producing Industrial Crops

- Genetic and Biochemical Regulation of Rubber Biosynthesis

- Guayule Rubber Crystallization Studies

- POLYMER-PROTEIN INTERACTIONS IN NATURAL RUBBER LATEX

Examples of publications can be found here:

<http://www.ars.usda.gov/pandp/people/people.htm?personid=45781>

**Dr. Christine Queitsch**

University of Washinton

[queitsch@uw.edu](mailto:queitsch@uw.edu)

http://queitschlab.gs.washington.edu/research.shtml

She studies the molecular underpinnings of "evolvability" in *Arabidopsis*.

Wild-type phenotypes are remarkably robust to environmental and genetic variation, yet evolutionary novelty continues to arise. What are the molecular underpinnings of phenotypic robustness? How do novel shapes and functions evolve from a robust wild-type phenotype? Natural selection draws upon phenotypic variation among individuals. Although selection can only fix traits with an underlying genetic basis, phenotypic variance results from a complex interplay of genetic, epigenetic, and environmental factors. We seek to identify and understand molecular mechanisms that have the potential to rapidly generate selectable phenotypic variation. Our current projects focus on Hsp90- and Pol V-mediated evolutionary capacitance, the interactions of microRNA-mediated regulation with HSP90, the phenotypic consequences of length variability polymorphisms in microsatellites, and the dynamics of the plant chromatin landscape across development and different environments.

Phenotypic capacitance

Microsatellites in local adaptation and population genetics

The Plant Chromatin landscape

Phenotypic Robustness and the Missing Heritability of Disease

pubs here: http://queitschlab.gs.washington.edu/publications.shtml