**Dr. Vivian Irish**

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

Yale

She is understanding how floral pattern differences arise in a variety of species.  She has work on 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. Sheng Yang He**

[hes@msu.edu](mailto:hes@msu.edu)

Michigan State University

He studies how microbial pathogens cause disease and what cellular mechanisms underlie pathogenesis by using the models Arabidopsis and *P syringae*.  His goal is to understand how the effector proteins secreted from *P* *syringae* manipulates innate immunity, vesicle trafficking, JA signaling, and stomata functions.

Yang DL, Yao J, Mei CS, Tong XH, Zeng LJ, Li Q, Xiao LT, Sun TP, Li J, Deng XW, Lee CM, Thomashow MF, Yang Y, He Z, He SY (2012) Plant hormone jasmonate prioritizes defense over growth by interfering with gibberellin signaling cascade. Proc Nat Acad Sci USA 109(19):E1192-200.

Withers J, Yao J, Mecey C, Howe GA, Melotto M, He SY (2012) Transcription factor-dependent nuclear localization of a transcriptional repressor in jasmonate hormone signaling. Proc Natl Acad Sci USA 109: 20148-20153.

**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

**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

**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.