YING CHANG

Yale-NUS College • 28 College Ave. West, Singapore 138533 • ying.chang@yale-nus.edu.sg

EDUCATION

Ph.D in Botany 09/2004-11/2011
Department of Botany, University of British Columbia

M.Sc in Biology 01/2001-01/2004
Department of Biological Sciences, National University of Singapore

B.Sc in Biochemistry 09/1996-07/2000
Department of Biochemistry, Nanjing University, China

RESEARCH EXPERIENCE

Assistant professor 10/2021 -
Division of Science, Yale-NUS college, Singapore

Visiting professor 07/2021 – 10/2021
Division of Science, Yale-NUS college, Singapore

Postdoctoral scholar 07/2015 – 07/2021
Department of Botany and Plant Pathology, Oregon State University

Postdoctoral fellow 01/2013-06/2015
University of British Columbia, Department of Botany

Research assistant 01/2004-07/2004
Department of Biological Sciences, National University of Singapore

TEACHING EXPERIENCE

Sessional instructor (part-time) 01/2013-04/2013

Department of Botany, University of British Columbia

Teaching assistant (part-time) 09/2004-04/2011

Department of Botany, University of British Columbia

Teaching assistant (part-time) 07/2001-11/2003

PUBLICATIONS AND CONFERENCE PRESENTATIONS

Publications in refereed journals

Chang, Y., S. Sekimoto, D. Rochon, Y. Wang., I. Grigoriev, J. E. Stajich, J. W. Spatafora. Phylogenomic analyses of *Olpidium* reveal hard polytomies of the backbone of Kingdom Fungi. 2021. *Scientific Reports* 11: 1-12.

Li Y., J. Steenwk, **Y. Chang**, Y. Wang, T. Y. James, J. E. Stajich, J. W. Spatafora, M. Groeneward, C. W. Dunn, C. T. Hittinger, X-X Shen, A. Rokas. A genome-scale phylogeny of Fungi: insights into early evolution, radiations, and the relationship between taxonomy and phylogeny. 2021. *Current Biology* 31: 1653-1665.

Tabima, J. F., I. Trautman, **Y. Chang**, Y. Wang, Y. Wang, S. Mondo, A. Kuo, A. Salamov, I. V. Grigoriev, J.E. Stajich, J.W. Spatafora. Phylogenomic analyses of non-Dikarya fungi support horizontal gene transfer driving diversification of secondary metabolism in the amphibian gastrointestinal symbiont, Basidiobolus. 2020. *G3: Genes, Genomes and Genetics* 120: 3417-3433.

Myers J. M., A. E. Bonds, R. A. Clemons, N. A. Thapa, D. R. Simmons, D. Carter-House, J. Ortanez, P. Liu, A. Miralles-Durán, A. Desirò, J. E. Longcore, G. Bonito, J. E. Stajich, J. W. Spatafora, **Y. Chang**, L. M. Corrochano, A. Gryganskyi, I. V. Grigoriev, T. Y. James. 2020. Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. *m*Bio 11: e02027-20.

Bell, D., W. K. Gerelle, Q. Lin, S. Joya, **Y. Chang**, Z. N. Taylor, C. J. Rothfels, A. Larsson, J. C. Villarreal, F-W Li, L. Pokorny, P. Szövényi, B. Crandall-Stotler, L. deGeronimo, D. Beerling, M. Deyholos, M. von Konrat, S. Ellis, T. Chen, D. Stevenson, J. D. Palmer and S. W. Graham. 2020. Organellomic datasets confirm a cryptic consensus on (unrooted) land-plant relationships, and provide new insights into bryophyte molecular evolution. 2020. *American Journal of Botany* 107: 91-115.

One Thousand Plant Transcriptomes (1KP) Initiative. One thousand plant transcriptomes and the phylogenomics of green plants. 2019. *Nature* 574: 679-685.

Davis, W. J., K. R. Amses, G. L. Benny, D. Carter-House, **Y. Chang**, I. Grigoriev, M. E. Smith, J. W. Spatafora, J. E. Stajich, T. Y. James. Genome-scale phylogenetic analyses reveal a monophyletic Zoopagales (Zoopagomycota, Fungi) with predacious taxa evolving from mycoparasite ancestors. 2019. *Molecular Phylogenetics and Evolution* 133: 152-163.

Chang, Y., A. Desirò, H. Na, L. Sandor, A. Lipzen, A. Clum, K. Barry, I. Grigoriev, F. Martin, J. Stajich, M. Smith, G. Bonito, Spatafora, J.W. Phylogenomics of Endogonaceae and evolution of mycorrhizae within Mucoromycota. 2019. *New Phytologist* 222: 511-525.

Spatafora, J. W., **Y. Chang,** G. L. Benny, K. Lazarus, M. E. Smith, M. L. Berbee, G. Bonito, N. Corradi, I. Grigoriev, A. Gryganskyi, T. Y. James, K. O'donnell, R. W. Roberson, T. N. Taylor, J. Uehling, R. Vilgalys, M. M. White, And J. E. Stajch. 2016. Zygomycete Genealogy Of Life (Zygolife): a phylum-level phylogenetic classfication of zygomycete fungi based on genome-scale data. *Mycologia* 108: 1028-1046.

Chang, Y., S. Wang, S. Sekimoto, A. Aerts, C. Choi, A. Clum, K. LaButti, E. Lindquist, C.Y. Nagn, R. A. Ohm, A. Salamov, I. V. Grigoriev, J. W. Spatafora and M. L. Berbee. 2015. Phylogenomic analyses indicate that early fungi evolved digesting cell walls of algal ancestors of land plants. *Genome Evolution and Biology* 7: 1590-1601

Chang, Y., and S. W. Graham. 2014. Patterns of clade support along the backbone of moss phylogeny. *Cladistics* 30: 590-606.

Chang, Y., and S. W. Graham. 2011. Inferring the higher-order phylogeny of mosses (Bryophyta) and relatives using a large, multigene plastid data set. *American Journal of Botany* 98: 839-849.

Chang, Y., and S. W. Graham. 2011. Bryophyte-specific primers for retrieving plastid genes suitable for phylogenetic inference. *American Journal of Botany* 98: e109-e113.

Akiyama, H., **Y. Chang**, T. Yamaguchi, and B. C. Tan. 2011. *Yakushimabryum longissimum* (Pylaisiadelphaceae) gen. & sp. nov., from the Yakushima Island, Japan. *Journal of Bryology* 33: 42-49.

Akiyama, H., **Y. Chang**, and B. C. Tan. 2010. *Clastobryopsis imbricata* (Pylaisiadelphaceae) sp. nov. from Doi Inthanon, northern Thailand. *The Bryologist* 113: 752-759.

Chang, Y., C.-W. Khiong, S. W. Graham and B. C. Tan. 2006. Molecular evidence for the systematic positions of two enigmatic mosses: *Pterogonidium pulchellum* (Sematophyllaceae, Musci) and *Piloecium pseudorufescens* (Myuriaceae, Musci). *Canadian Journal of Botany* 84: 501–507.

Tan, B. C. and **Y. Chang**. 2004. Molecular contribution to the systematic position of *Mastopoma scabrifolium* (Broth. *in* Moell.) B. C. Tan & Tran Ninh (Sematophyllaceae, Bryopsida). *Cryptogamie, Bryologie* 25: 301-308.

Conference proceeding

Hedenas, L., B. C. Tan and **Y. Chang**. 2008. Morphological and molecular data suggest different evolutionary relationships among species of *Acroporium* and closely related genera (Sematophyllaceae). In: *Mohamed H., Baki B. B., Nasrulhaq-Boyce A. and L. P. K. Yuen.* (eds). Bryology in the new millenmium. Kuala Lumpur: University of Malaya, pp. 259-276.

Invited conference presentations (*presenter)

J. W. Spatafora*, **Y. Chang,** Y. Wang, J. Ortanez, D. Carter-House, G. Benny, M. E. Smith, N. Reynolds, T. Y. James, W. Davis, K. Ames, I. Grigoriev, J. E. Stajich. Phylo-secretomics of zygomycete fungi: “Fungi are what they secrete”. 2019. MSA 2019 (Annual meeting of the Mycologial Society of America). Minneapolis, MN.

Chang, Y.*, A. Desirò, G. Bonito, I. Grigoriev, A. Clum, A. Lipzen, J. W. Spatafora. 2018. Endogonales (Mucoromycotina) genomes reveal imprints of ectomycorrhizal lifestyle. International Mycological Conference. San Juan, PR.

Chang, Y.*, A. Desirò, G. Bonito, I. Grigoriev, A. Clum, A. Lipzen, J. W. Spatafora. 2017. The Metagenomes of *Endogone* (Mucoromycota) sporocarps. Joint Genome Institute User Meeting. Walnut Creek, CA.

Chang, Y., S. Sekimoto, S. Wang, J. W. Spatafora, M. L. Berbee* and the AFTOL2 group. 2014. Pectinases link early fungal evolution to the land plant lineage. New Phytologist Workshop, London, UK.

Chang, Y. and S. W. Graham*. 2011. Progress in inferring the deep phylogenetic relationships of mosses using plastid data. International Botanical Congress. Melbourne, Australia.

Regular conference presentations (*presenter)

Chang, Y.*, S. Sekimoto, Y. Wang, D'Ann Rochon, Igor Grigoriev, Mary Berbee, Jason E. Stajich, Joseph W. Spatafora. Phylogenomic analyses of *Olpidium* reveal hard polytomies of the backbone of Kingdom Fungi. MSA 2019 (Annual meeting of the Mycological Society of America). Minneapolis, MN.

Chang, Y.*, J. E. Stajich, F. Martin, M. Hainaut, M. Marcet-Houben, T. Gabaldón, B. Henrissat, J. W. Spatafora. 2016. Phylogenomic analyses suggest early origins of major fungal clades and independent diversifications to break down cellulose-rich cell walls. MSA 2016 (Annual meeting of the Mycologial Society of America). Berkeley, CA.

Chang, Y.*, S. Sekimoto, S. Wang, J. W. Spatafora, M. L. Berbee and the AFTOL2 group. 2014. Early diverging fungi and evolutionary origins of enzymes for Breakdown of the pectins in plant cell walls. MSA 2014 (Annual meeting of the Mycologial Society of America). East Lansing, MI.

Lam, V.*, E. Biffin, H. Rai, **Y. Chang**, and S. W. Graham. 2011. Phylogenetics of mycoheterotrophic monocots and gymnosperms using plastid loci. International Botanical Congress. Melbourne, Australia.

Chang, Y.*, B. M. Murray, and S. W. Graham. 2010. Molecular phylogenetics of costate Andreaeaceae. Botany 2010 (Joint annual meeting of the Botanical Society of America and other societies). Providence, RI.

Chang, Y.* and S. W. Graham. 2009. The deep phylogeny of mosses in the context of land-plant evolution. Botany and Mycology 2009 (Joint annual meeting of the Botanical Society of America, Mycological Society of America and other societies). Snowbird, Utah.

Chang, Y.* and S. W. Graham. 2008. The placement of Andreaeaceae in moss phylogeny and phylogenetic relationships in the family. Botany 2008 (Joint annual meeting of the Botanical Society of America and other societies). Vancouver, BC.

Chang, Y.* and S. W. Graham. 2007. Inference of higher-order relationships in Bryophyta using multiple plastid genes. World Conference of Bryology (Biennial congress of the International Association of Bryologists). Kuala Lumpur, Malaysia.

Chang, Y.*, W.-K. Chan, and B. C. Tan. 2002. The systematics of Sematophyllaceae (Musci) in Peninsular Malaysia and adjacent regions based on *rbc*L gene sequences. 7th Biological Science Graduate Congress (National University of Singapore and Chulalunkong University, Thailand). Bangkok, Thailand.