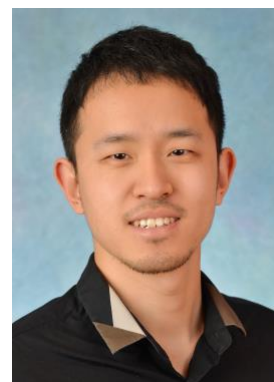


Yuchen Yang

BASIC INFORMATION

First name/Surname	Yuchen Yang
Position	Associate Professor
Affiliation	School of Ecology, Sun Yat-sen University
E-mail	yyuchen@email.unc.edu
Webpage	https://yuchenyanggroup.github.io
Google scholar	https://scholar.google.com/citations?user=0CK0320AAAAJ
Nationality	Chinese



RESEARCH INTERESTS

The focus of my recent research is in developing innovative approaches to investigate the mechanisms underlying plant metabolism and environmental adaptation. Our goal is to understand the molecular basis of plant's response to environmental stress (salt, heat, pollutants, etc.) and apply this knowledge to improve efficiency and ecological applicability of feature plants in ecosystem protection and environment repair. To achieve these goals, we utilize multi-omic technologies (RNA-seq, ATAC-seq, etc.) to discover the fundamental events and the basic mechanisms underlying the progression of various plant metabolisms and stress responses, such as plant hormone-mediated physiological and biochemical process, uptakes and efflux of heavy metal ions and so on. In addition, I also work on identifying and characterizing the genetic basis of plant's circadian events, such as light and tide oscillations.

RESEARCH EXPERIENCE

2021.09 - present	Associate Professor, School of Ecology, Sun Yat-sen University
2020.05 - 2021.08	Research Assistant Professor, Department of Pathology and Laboratory Medicine & McAllister Heart Institute, UNC at Chapel Hill
2016.09 - 2020.04	Postdoctoral Fellow, Department of Genetics, UNC at Chapel Hill Advisor: Dr. Yun Li

EDUCATION

2011.09 - 2016.06	Graduate/Ph.D. Student
Major	Biochemistry and Molecular Biology
Advisor	Dr. Suhua Shi
University	Sun Yat-sen University, Guangzhou, China
2007.09 - 2011.06	Undergraduate/B.S. Student
Major	Biotechnology
University	Sun Yat-sen University, Guangzhou, China

TECHNICAL SKILLS

Principal subjects	Having a good background in human genetics and computational biology, including single-cell RNA-seq analysis, chromatin interaction (Hi-C) data analysis, and comparative genomics.
Computational skills	Having a good expertise in transcriptome and genomic data analysis. Proficiency in Windows and Linux operating systems, C++ and Perl programming languages, and statistics programs R and Rcpp.
Experimental skills	Having a good training in field work and experimental skills for DNA & RNA extraction and PCR amplification.

FEATURE STUDIES

Project 1: **Molecular Dissection of Cadmium-responsive Transcriptome and Post-transcriptome Profile in a Low-cadmium-accumulating Cultivar of *Brassica parachinensis***

- ✦ Comparatively transcriptional analysis showed that, compared to high-Cd cultivar, many pathways involved in carbohydrate and amino acid metabolisms were exclusively up-regulated in roots of low-accumulating cultivar upon exposure to low Cd concentrations, which may produce more energy and metabolites for Cd detoxification.
- ✦ In shoots of low-accumulating cultivar, pathways of photosynthesis and cell growth were activated to mitigate Cd-induced damages.
- ✦ Cd transport genes, such as *MTP1*, *HMA3* and *CAX* family genes, were highly induced by Cd stress in low-Cd roots in accordance with the high Cd concentration in roots, while genes involved in root-to-shoot Cd translocation such as *FRD3* and *CESA3* were suppressed, which may contribute to the low Cd concentration in edible part of low-accumulating cultivar.
- ✦ Small RNA-seq showed that, in high-Cd cultivar, the overexpression of miR395 was engaged in Cd tolerance by regulating sulfur assimilation and associated with its high Cd accumulation, which in low-Cd cultivar, miRNA-mediated oxidative resistance was enhanced in response to Cd exposure.
- ✦ MiR397, miR393 and miR160 were involved in the Cd-induced growth improvement in both roots and shoots of the low-Cd-accumulating cultivar.

Project 2: **Transcriptome Analysis Unravelling the Molecular Mechanisms of Abscisic Acid-Mediated Drought-stress Alleviation in Pomegranate**

- ✦ Transcriptome data showed that exogenous ABA application substantially enhanced pomegranate drought resistance by strengthening some metabolic pathways, such as brassinosteroid synthesis, peroxisome biogenesis, photosynthesis and hemicelluloses synthesis.
- ✦ ABA degradation process was found to be triggered by over-dose ABA treatment, indicating there is a feedback loop in pomegranate to balance the ABA accumulation that exceeds the optimal ABA requirement, at the cost of suppressed growth process and stress resistance.

Project 3: **Identification and Characterization of Evolutionarily Conserved Alternative Splicing Events in Mangrove Genus *Sonneratia***

- ✦ Combining both transcriptome and genome sequences, I characterized conserved alternative splicing (AS) events in four *Sonneratia* species to investigate the post-transcriptional regulation in adaptation to intertidal environments.
- ✦ The conservation level of AS events was relevant to the genetic divergence in different species pairs. Compared with non-conserved events, conserved events are of shorter length and less possibility to introduce premature stop codons and frameshifts.
- ✦ For the genes containing conserved events, four of the 26 enriched GO terms are involved in proton transport, signal transduction and carbon metabolism, which may contribute to the evolutionarily adaptation of *Sonneratia* species to salt, dehydration and heat stresses.

PUBLICATIONS

† co-first author; * corresponding author

- Huang, L., Jiang, M., Li, G., Abnousi, A., Rosen, J., **Yang, Y.***, Hu, M.*, Li, Y.* (2021+) Leveraging deep learning methods developed for Hi-C data to enhance resolution of HiChIP/PLAC-seq data. *Briefings in Bioinformatics*. Preparing for submission.
- Xu, S., Guo, Z., Feng, X., Shao, S., **Yang, Y.**, Li, J., Zhong, C., He, Z., Shi, S. (2021+) Where whole-genome duplication is most beneficial – Mangroves invading the fluctuating environments between land and sea. *Molecular Ecology*. Major revision.
- Garbutt, T., Wang, Z., Ma, H., ..., **Yang, Y.***, Qian, L.*, Liu, J.* (2021+) Epigenetic regulation of cardiac maturation by arginine methyltransferase Carm1. *Circulation*. Major revision.
- Janghorban, M.†, **Yang, Y.†**, Zhao, N., Hamor, C., Nguyen, T., Zhang, X., Rosen, J. (2021+) Single Cell Analysis Unveils the Role of the Tumor Immune Microenvironment and Notch Signaling in Dormancy. *Cancer Research*. Major revision.
- Taylor, L., **Yang, Y.**, Harigaya, Y., Ulirsch, J., Sankaran, V., Hu, M., Reiner, A., Raffield, L., Wen, J., Li, Y. (2021+) Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. *PLOS Genetics*. Major revision. (bioRxiv, doi: <https://doi.org/10.1101/2021.03.15.435494>)
- Zhao, B., Li, T., Smith, S., ..., **Yang, Y.**, ..., Zhu, H. (2021+) Common variants contribute to intrinsic human brain functional networks. *Nature Genetics*. Major revision.
- Yang, Y.†, **Yang, Y.†**, Huang, L., Broome, J., Correa, A., Reiner, A., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Raffield, L., Li, Y. (2021+) eSCAN: Scan Regulatory Regions for Aggregate Association Testing using Whole Genome Sequencing Data. *Briefings in Bioinformatics*. Minor revision. (bioRxiv, doi: <https://doi.org/10.1101/2020.11.30.405266>)
- Giusti-Rodríguez, P.†, Lu, L.†, **Yang, Y.†**, Crowley, C., Liu, X., Juric, I., *et al.* (2021+) Using three-dimensional regulatory chromatin interactions from adult and fetal cortex to interpret genetic results for psychiatric disorders and cognitive traits. *Nature Neuroscience*. Major revision. (bioRxiv, doi: <https://doi.org/10.1101/406330>)
- 2022** Wang, H.†, **Yang Y.†**, Qian, Y., Liu, J., Qian, L. (2022) Delineating Chromatin Accessibility Re-patterning at Single Cell Level during Early Stage of Direct Cardiac Reprogramming. *Journal of Molecular and Cellular Cardiology*, 162: 62-71. PMID: 34509499.

- 2021 Rosen, J., **Yang, Y.**, Abnoui, A., Chen, J., Song, M., Jones, I., Shen, Y., Hu, M., Li, Y. (2021) HPRep: Quantifying Reproducibility in HiChIP and PLAC-seq Datasets. *Current Issues in Molecular Biology*, 43: 1156-1170.
- Ma, H.[†], Liu, Z.[†], **Yang, Y.**[†], ..., Liu, J. (2021) Coordinated transcriptome and cell state dynamics of non-myocytes in heart regeneration. *EMBO reports*. e52901. PMID: 34523214.
- Li, G., Luan, C., Dong, Y., ..., Li, Y.* , **Yang, Y.*** (2021) ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-cardiomyocyte Cells. *International Journal of Molecular Sciences*, 22: 8943. PMID: 34445647.
- Yang, Y., Sun, H., Zhang, Y., ..., **Yang, Y.**, Wu, D., Yu, D. (2021) Dimensionality reduction by UMAP reinforces sample heterogeneity analysis in bulk transcriptomic data. *Cell Reports*, 36: 109442. PMID: 34320340.
- Yu, M., Abnoui, A., Zhang, Y., ..., **Yang, Y.**, ..., Ren, B., Hu, M. SnapHiC: a computational pipeline to identify chromatin loops from single cell Hi-C data. *Nature Methods*. <https://doi.org/10.1038/s41592-021-01231-2>. PMID: 34446921.
- Liu, W.[†], **Yang, Y.**[†], Abnoui, A., Zhang Q., Hu, M., Li, Y. (2021) MUNIn: A statistical framework for identifying long-range chromatin interactions from multiple samples. *Human Genetics and Genomics Advances*, 2: 100036. PMID: 34485947.
- Wang, L.[†], **Yang, Y.**[†], Ma, H., ..., Liu, J., Qian, L. (2021) Single cell dual-omics reveals the transcriptomic and epigenomic diversity of cardiac non-myocytes. *Cardiovascular Research*, cvab134. PMID: 33839759.
- Yang, Y.**, Li, G., Xie, Y., Wang, L., Lagler, T., Yang, Y., Liu, J., Qian, L., Li, Y. (2021) iSMNN: Batch Effect Correction for Single-cell RNA-seq data via Iterative Supervised Mutual Nearest Neighbor Refinement. *Briefings in Bioinformatics*, bbab122. PMID: 33839756.
- Yu, C., Littleton S., Giroux, N., ..., **Yang, Y.**, ..., Shen, X., Saban, D. (2021) Mucosal Associated Invariant T (MAIT) Cell Responses Differ by Sex in COVID-19. *Med*, 2: 755-772. PMID: 33870241.
- Jiang, Y., Li, W., Lindsey-Boltz, L., **Yang, Y.**, Li, Y., Sancar, A. (2021) Super-hotspots and -coldspots in the repair of UV-induced DNA damage in the human genome. *Journal of Biological Chemistry*. 296: 100581. PMID: 33771559.
- Jiang, W., **Yang, Y.**, Mercer-Smith, A., ..., Hingtgen S. (2021) Development of next-generation tumor-homing induced neural stem cells to enhance treatment of metastatic cancers. *Science Advances*, 7: eabf1526. PMID: 34108203.
- Wang, H., **Yang, Y.**, Liu, J., Qian, L. (2021) Direct cell reprogramming: approaches, mechanisms and progress. *Nature Reviews Molecular Cell Biology*, 22: 410–424. PMID: 33619373.
- Bruinsma, R., Fajgenbaum, K., **Yang, Y.**, del Mar Melendez-Gonzalez, M., Mohlke, K., Li, Y., Sayed, C. (2021) Assessment of Familial Risk in Patients with Hidradenitis Suppurativa. *British Journal of Dermatology*, 184: 753-754. PMID: 33152101.
- Lagler, T., Abnoui, A., Hu, M., **Yang, Y.***, Li, Y.* (2021) HiC-ACT: improved chromatin interactions from Hi-C data via aggregated Cauchy test. *American Journal of Human Genetics*, 108: 257-268. PMID: 33545029.
- Crowley, C., **Yang, Y.***, Qiu, Y., ..., Hu, M.* , Li, Y.* (2021) FIREcaller: Detecting Frequently Interacting Regions from Hi-C Data. *Computational and Structural Biotechnology Journal*, 19: 355-362. PMID: 33489005.
- Yang, Y.**[†], Li, G.[†], Qian, H., Wilhelmsen, K., Shen, Y., Li., Y. (2020) SMNN: Batch Effect Correction for Single-cell RNA-seq data via Supervised Mutual Nearest Neighbor Detection. *Briefings in Bioinformatics*, 22: bbaa097. PMID: 32591778.

- 2020** Qian, J., Zhang, X., Yan, Y., Wang, N., Ge, W., Zhou, Q.* , **Yang, Y.*** (2020) Unravelling the molecular mechanisms of Abscisic acid-mediated drought-stress alleviation in pomegranate (*Punica granatum* L.). *Plant Physiology and Biochemistry*, 157: 211-218. PMID: 33120112.
- Wang, L., Ma, H., Huang, P., ..., **Yang, Y.**, ..., Qian, L. (2020) Down-regulation of Beclin1 promotes direct cardiac reprogramming. *Science Translational Medicine*, 12: eaay7856. PMID: 33087505.
- Yang, Y.**, Li, Y., Sancar, A., Oztas, O. (2020) The circadian clock shapes the Arabidopsis transcriptome through regulating alternative splicing and alternative polyadenylation. *Journal of Biological Chemistry*, 295: 7608-7619. PMID: 32303634.
- Feng, X., Xu, S., Li, J., **Yang, Y.**, Chen, Q., Lyu, H., Zhong, C., He, Z., Shi, S. (2020) Molecular adaptation to salinity fluctuation in tropical intertidal environments of a mangrove tree *Sonneratia alba*. *BMC Plant Biology*, 20: 178. PMID: 32321423.
- Johnson, N., Huang, L., Li, R., ..., **Yang, Y.**, ..., Conneely, K. (2020) Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. *Epigenetics*, 15: 294-306. PMID: 31506003.
- Huh, R.†, **Yang, Y.**†, Jiang, Y., Shen, Y., Li, Y. (2020) SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. *Nucleic Acids Research*, 48: 86-95. PMID: 31777938.
- 2019** Li, G., **Yang, Y.**, Van Buren, E., Li, Y. (2019) Dropout Imputation and Batch Effect Correction for Single-Cell RNA-seq Data. *Journal of Bio-X Research*, 2: 169-177.
- Giusti-Rodriguez, P., Lu, L., **Yang, Y.**, ..., Sullivan, P. (2019) SA72A HIGH-RESOLUTION MAP OF CHROMATIN INTERACTIONS IN ADULT AND FETAL CORTEX. *European Neuropsychopharmacology*, 29, S1227.
- Yang, Y.**, Huh, R., Culpepper, H., Lin, Y., Love, M., Li, Y. (2019) SAFE-clustering: Single-cell Aggregated (From Ensemble) Clustering for Single-cell RNA-seq Data. *Bioinformatics*, 35: 1269-1277. PMID: 30202935.
- Zhou Q.†, **Yang Y.**†, Yang Z. (2019) Molecular dissection of cadmium-responsive transcriptome profile in a low-cadmium-accumulating cultivar of *Brassica parachinensis*. *Ecotoxicology and Environmental Safety*, 176: 85-94. PMID: 30921700.
- Juric I., Yu M., Abnoui A., ..., **Yang Y.**, ..., Bing Ren B., Hu M. (2019) MAPS: model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. *PLOS Computational Biology*, 15: e1006982. PMID: 30986246.
- 2018** **Yang, Y.**, Guo, W., Shen, X., Li, J., Yang, S., Chen, S., He, Z., Zhou R., Shi, S. (2018) Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus *Sonneratia*. *Scientific Reports*, 8: 4425. PMID: 29535339.
- Guo, Z., Li, X., He, Z., **Yang, Y.**, Wang, W., Zhong, C., Greenberg, A.J., Wu, C-I, Duke N.C., Shi, S. (2018) Extremely low genetic diversity across mangrove taxa reflects past sea level changes and hints at poor future responses. *Global Change Biology*, 24: 1741–1748. PMID: 29087007.

- 2017** Yang, Y., Li, J., Yang, S., Li, X., Fang, L., Zhong, C., Duke, N., Zhou, R., Shi, S. (2017) Effects of Pleistocene sea-level fluctuations on mangrove population dynamics: A lesson from *Sonneratia alba*. *BMC Evolutionary Biology*, 17: 22. PMID: 28100168.
- Li, J., Yang, Y., Yang, S., Zhang, Z., Chen, S., Zhong, C., Zhou, R., Shi, S. (2017) Comparative transcriptome analyses of a mangrove tree *Sonneratia caseolaris* and its non-mangrove relatives, *Trapa bispinosa* and *Duabanga grandiflora*. *Marine Genomics*, 31: 13-15. PMID: 27810366.
- Zhou, Q., Yang, Y., Shen, C., He, C., Yuan, J., Yang, Z. (2017) Comparative analysis between low- and high-cadmium-accumulating cultivars of *Brassica parachinensis* to identify difference of cadmium-induced microRNA and their targets. *Plant and Soil*, 420: 223-237.
- Du, Y., Martin, J., McGee, J., Yang, Y., Liu, E., Sun, Y., Geihs, M., Kong, X., Zhou, E., Li, Y., Huang, J. (2017) A SNP panel and online tool for checking genotype concordance through comparing QR codes. *PLoS ONE*, 12(9): e0182438. PMID: 28926565.
- 2016** Yang, Y., Duke, N.C., Peng, F., Li, J., Yang, S., Zhong, C., Zhou, R., Shi, S. (2016) Ancient geographical barriers drive differentiation among *Sonneratia caseolaris* populations and recent divergence from *S. lanceolata*. *Frontiers in Plant Science*, 7: 1618. PMID: 27833634.
- Li, J., Yang, Y., Chen, Q., ..., Zhou R., Shi. S. (2016) Pronounced genetic differentiation and recent secondary contact in the mangrove tree *Lumnitzera racemosa* revealed by population genomic analyses. *Scientific Reports*, 6: 29486. PMID: 27380895.
- Fang, L., Yang, Y., Guo, W., Li, J., Zhong, C., Huang, Y., Zhou, R., Shi, S. (2016) *De novo* assembly of the transcriptome of *Aegiceras corniculatum*, a mangrove species in the Indo-West Pacific region. *Marine Genomics*, 28: 49–52. PMID: 27296448.
- Li, X., Duke, N., Yang, Y., Huang, L., Zhu, Y., Zhang, Z., Zhou, R., Zhong, C., Huang, Y., Shi, S. (2016) Re-Evaluation of Phylogenetic Relationships among Species of the Mangrove Genus *Avicennia* from Indo-West Pacific Based on Multilocus Analyses. *PLoS ONE*, 11(10): e0164453. PMID: 27716800.
- Wang, S., Chen, Y., Yang, Y., Wu, W., Liu, Y., Fan, Q., Zhou, R. (2016) Phylogenetic relationships and natural hybridization in *Triadica* inferred from nuclear and chloroplast DNA analyses. *Biochemical Systematics and Ecology*, 64: 142-148.
- Zhang, Z., He, Z., Xu, S., Li, X., Guo, W., Yang, Y., Zhong, C., Zhou, R., Shi, S. (2016) Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus *Acrostichum*. *Scientific Reports*, 6: 35634. PMID: 27782130.
- Shi, L., Li, N., Wang, S., Zhou, Y., Huang, W., Yang, Y., Ma, Y., Zhou, R. (2016) Molecular Evidence for the Hybrid Origin of *Ilex dabieshanensis* (Aquifoliaceae). *PLoS ONE*, 11(1): e0147825. PMID: 26808531.
- 2015** Yang Y., Yang, S., Li, J., Deng, Y., Zhang, Z., Xu, S., Guo, W., Zhong, C., Zhou, R., Shi, S. (2015) Transcriptome analysis of the Holly mangrove *Acanthus ilicifolius* and its terrestrial relative, *Acanthus leucostachyus*, provides insights into adaptation to intertidal zones. *BMC Genomics*, 16: 605. PMID: 26272068.
- Yang, Y., Yang, S., Li, J., Li, X., Zhong, C., Huang, Y., Zhou, R., Shi, S. (2015) *De novo* assembly of the transcriptomes of two yellow mangroves, *Ceriops tagal* and *C. zippeliana*, and one of their terrestrial relatives, *Pellacalyx yunnanensis*. *Marine Genomics*, 23: 33-36. PMID: 25899405.
- Yang, Y., Yang, S., Fang, L., Li, J., Zhong, C., Zhou, R., Shi, S. (2015) Phylogenetic position of *Sonneratia griffithii* based on sequences of the nuclear ribosomal internal transcribed spacer and 13 nuclear genes. *Journal of Systematics and Evolution*, 53(1): 47-52.

PROFESSIONAL ACTIVITIES

Manuscript reviews for Nucleic Acids Research; Briefings in Bioinformatics; Science of the Total Environment; Guided Open Access; Bioinformatics; Genes; Evolutionary Applications; Human Genomics; PLOS Computational Biology; International Journal of Molecular Sciences; Molecular Genetics and Genomics; Computational Biology and Chemistry; Frontiers in Genetics; Frontiers in Plant Science; All Life; Scientific Reports; PLoS ONE.

TEACHING EXPERIENCE

Every semester **Brief introduction to R** at Basic Bioinformatics Tools (BBT) Workshops of UNC-CH
2018.02 Teaching R software and single-cell RNA clustering at NGS Workshop of UNC-CH

SELECTED CONFERENCE PRESENTATIONS

IVB/MHI cardiovascular research symposium 2020, UNC Coordinated transcriptome and cell state dynamics of non-myocytes in heart regeneration (**oral presentation**)
American Society of Human Genetics 2019 SMNN: Batch Effect Correction for Single-cell RNA-seq data via Supervised Mutual Nearest Neighbor Detection (**platform (oral) presentation**)
American Society of Human Genetics 2018 MUNIn (Multiple tissue UNifying long-range chromatin Interaction detector): a statistical framework for identifying long-range chromatin interactions from multiple tissues (**Reviewers' Choice Abstracts**)

HONORS & AWARDS

2015 - 2017 Academic Scholarship Award of Chang Hungta Science Foundation, Sun Yat-sen University
2015 National Scholarship Award for Graduate Students, China
2015 Wang Bosun Ecology Scholarship Award, Sun Yat-sen University
2015 Second Prize for Outstanding Graduate Award, State Key Laboratory of Biocontrol, Sun Yat-sen University
2008 - 2010 First Prize Scholarship Award for Undergraduate Students, Sun Yat-Sen University