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### **A. Education**

Cornell University	Ithaca, NY	Plant Breeding and Molecular Genetics	Ph.D.	1991
University of the Philippines	Los Banos, Philippines	Plant Breeding and Genetics	M.S.	1986
Zhejiang University	Hangzhou, China	Agronomy ( <i>Summa Cum Laude</i> )	B.S.	1982

### **B. Appointments**

2000-present	Adjunct Professor (Assist 2000, Assoc 2003, and Full 2008)	Texas A&M University
1995-present	Research Geneticist (GS-15 since 2013)	USDA-ARS
1994-1995	Associate Research Scientist	Texas A&M University
1991-1994	Postdoctoral Research Associate	University of Florida
1986-1991	CNRRI/Rockefeller Research Fellow	Cornell University
1983-1985	Research Scholar	International Rice Research Institute
1982-1983	Research Assistant	China National Rice Research Institute

### **C. Publications** (10 selected from the most recent years)

1. Lu X, Fu X, Wang D, Wang J, Chen X, Hao M, Wang J, Gervers KA, Guo L, Wang S, Yin Z, Fan W, Shi C, Wang X, Peng J, Chen C, Cui R, Shu N, Zhang B, Han M, Zhao X, Mu M, Yu JZ, Ye W. 2018. Resequencing of cv CRI-12 family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. *Plant Biotechnology* <https://doi.org/10.1111/pbi.13030>
2. Reddy, U.K., P. Nimmakayala, V.L. Abburi, C.V.C.M. Reddy, T. Saminathan, R.G. Percy, J.Z. Yu, J. Frelichowski, J.A. Udall, J.T. Page, D. Zhang, T. Shehzad, and A.H. Paterson. 2017. Genome-wide divergence, haplotype distribution and population demographic histories for *Gossypium hirsutum* and *Gossypium barbadense* as revealed by genome-anchored SNPs. *Scientific Reports* 7:41285 doi:10.1038
3. Cox Jr, K., F. Meng, K. Wilkins, F. Li, P. Wang, N. Booher, S. Carpenter, L.-Q. Chen, H. Zheng, X. Gao, Y. Zheng, Z. Fei, J. Z. Yu, T. Isakeit, T. Wheeler, F.B. Wolf, P. He, A. Bogdanove, and L. Shan. 2017. TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. *Nature Communications* 8:15588 doi:10.1038
4. Abdurakhmonov, I.Y., M. Ayubov, K.A. Ubaydullaeva, B.T. Buriev, S.E. Shermatov, H. Ruziboev, U.M. Shapulatov, S. Saha, M. Ulloa, J.Z. Yu, R.G. Percy, E.J. Devor, S.C. Govind, V.R. Sripathi, S.P. Kumpatla, A. Van De Kroll, K.D. Hake, K. Khamidov, S.I. Salikhov, J.N. Jenkins, A. Abdurakarimov, and A.E. Pepper. 2016. RNA interference for functional genomics and improvement of cotton (*Gossypium* spp). *Frontiers in Plant Science* 7:202 doi:10.3389

5. Kushanov, F.N., Pepper, A.E., Yu, J.Z., Buriev, Z.T., Shermatov, S.E., Saha, S., Ulloa, M., Jenkins, J.N., Abdurakimov, A., Abdurakhmonov, I.Y. 2016. Development, genetic mapping and QTL association of cotton PHYA, PHYB, and HY5-specific CAPS and dCAPS markers. *BioMed Central (BMC) Genetics* 17:141
6. Xu, Z., J. Yu, R.J. Kohel, R.G. Percy, W.D. Beavis, D. Main, and J.Z. Yu. 2015. Distribution and evolution of cotton fiber development genes in the fibreless *Gossypium raimondii* genome. *Genomics* 106: 61-69
7. Li, F., G. Fan, C. Lu, G. Xiao, C. Zou, R.J. Kohel, Z. Ma, H. Shang, X. Ma, J. Wu, X. Liang, G. Huang, R.G. Percy, K. Liu, W. Yang, W. Chen, X. Du, C. Shi, Y. Yuan, W. Ye, X. Liu, X. Zhang, W. Liu, H. Wei, S. Wei, G. Huang, X. Zhang, S. Zhu, H. Zhang, F. Sun, S. Wang, J. Liang, J. Wang, Q. He, L. Huang, J. Wang, J. Cui, G. Song, K. Wang, X. Xu, J.Z. Yu, Y. Zhu, and S. Yu. 2015. Genome sequence of cultivated Upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature Biotechnology* 33: 524-530
8. Yu, J.Z., M. Ulloa, S.M. Hoffman, R.J. Kohel, A.E. Pepper, D.D. Fang, R.G. Percy, and J.J. Burke. 2014. Mapping genomic loci for cotton plant architecture, yield components, and fiber properties in an interspecific (*Gossypium hirsutum* L. x *G. barbadense* L.) RIL population. *Molecular Genetics and Genomics* 289:1347-1367
9. Li, F., G. Fan, K. Wang, F. Sun, Y. Yuan, G. Song, Q. Li, Z. Ma, C. Lu, C. Zou, W. Chen, X. Liang, H. Shang, W. Liu, C. Shi, G. Xiao, C. Gou, W. Ye, X. Xu, X. Zhang, H. Wei, Z. Li, G. Zhang, J. Wang, K. Liu, R.J. Kohel, R.G. Percy, J.Z. Yu, Y.-X. Zhu, J. Wang, and S. Yu. 2014. Genome sequence of the cultivated cotton *G. arboreum*. *Nature Genetics* 46: 567-572
10. Yu, J.Z., R.J. Kohel, D.D. Fang, J. Cho, A. Van Deynze, M. Ulloa, S.M. Hoffman, A.E. Pepper, D.M. Stelly, J.N. Jenkins, S. Saha, S.P. Kumpatla, M.R. Shah, W.V. Hugie, and R.G. Percy. 2012. A high-density SSR and SNP genetic map of the tetraploid cotton genome. *G3: Genes, Genomes, Genetics* 2:43-58 doi:10.1534
11. Wang, K., Z. Wang, F. Li, W. Ye, J. Wang, G. Song, Z. Yue, L. Cong, H. Shang, S. Zhu, C. Zou, Q. Li, Y. Yuan, C. Lu, H. Wei, C. Gou, Z. Zheng, Y. Yin, X. Zhang, K. Liu, B. Wang, C. Song, N. Shi, R.J. Kohel, R.G. Percy, J.Z. Yu, Y.-X. Zhu, J. Wang, and S. Yu. 2012. The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics* 44:1098-1104

#### **D. Synergistic Activities** (5 selected from the most recent years)

- Conceived, designed and tested a strategy for molecular characterization of cotton germplasm accessions with DNA markers. The strategy has been used for characterizing U.S. and Uzbek Cotton Collections including genome-wide divergence and domestication process of *G. hirsutum* and *G. barbadense* cultivars and landrace accessions.
- Conceived, planned and led research that constructed TM-1 x 3-79 high-density genetic maps of SSR and SNP markers, which are recognized worldwide as portable references. Core DNA markers were developed from the maps for cotton germplasm characterization.
- Conceived, planned and led international efforts that generated, annotated and released the A (*G. arboreum*), D (*G. raimondii*), and AD (*G. hirsutum*) cotton genome sequences with 41,330, 40,976, and 76,943 genes identified in A, D, and AD genomes, respectively.
- Re-elected by his global peers to lead the International Cotton Genome Initiative (ICGI) as the Co-Chair (2015-2017) and as the Chair (2017-2019). Coordinated five ICGI workgroup initiatives to develop, integrate and disseminate cotton genomic resources and knowledge.
- Invited to serve as an expert member (and chair) of the USDA National Life Science Patent Committee (since 2014) in addition to numerous professional, editorial and scientific advisory roles including Nature Genetics, PNAS, Nucleic Acids Research, Scientific Reports, PLoS ONE, Molecular Genetics and Genomics, BMC Genomics, Breeding Science, etc. Trained numerous undergraduate, graduate and postdoctoral students and visiting scientists in plant genomics and molecular genetics.