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NAME: Yu, John

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POSITION TITLE: Adjunct Professor of Plant Genetics (USDA Research Geneticist)

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Zhejiang University	BS	01/1982	Agronomy
University of the Philippines	MS	11/1985	Plant Breeding
Cornell University	PhD	05/1991	Plant Genetics
University of Florida	Postdoc	10/1994	Plant Molecular Genetics

**A. Personal Statement**

I am a research plant geneticist and an adjunct professor of plant genetics. I have about 40 years of research experience in plant breeding, genetics, and genomics at national and international institutions. I have published more than 100 peer-reviewed journal articles and other publications, which have 10,701 Google Scholar citations (3,985 since 2016). I have worked in the plant genetics area ranging from monocots to dicots and from diploids to polyploids. My recent 26 years with USDA-ARS at TAMU have been exclusively on cotton genomics including genome mapping and sequencing, characterization of gene pools, and identification of QTLs for molecular breeding. I have been playing a key role in international efforts of generating and releasing the genome sequences of core cotton species (*Gossypium arboreum*, *G. herbaceum*, *G. raimondii*, and *G. hirsutum*). These advances have brought about unprecedented revolution for genomics-assisted improvement of the cotton plants. I have trained more than 60 students and visiting scientists from the U.S. and abroad who came to work under my mentorship. My scientific leadership and research expertise have been demonstrated with my election in 2003 by my U.S. peers to lead the S-304 Multi-state Project; in this capacity I contributed to meeting project goals and to making successful efforts at project renewal to S-1036. Subsequently I was elected in 2005 and re-elected in 2015 by my global peers to lead the International Cotton Genome Initiative (ICGI), the first international organization to facilitate global collaborative research work on cotton genomics and genetics. My scientific leadership has significantly advanced the plant genetics research. Recently I have been serving in the USDA National Life Science Patent Committee (NLSPC). I am the recipient of the International Cotton Researcher of Year 2019 Award, selected by an independent panel of eminent experts around the world.

Citations:

1. **Yu, J.Z.**, Kohel, R.J., Fang, D.D., Cho, J., Van Deynze, A., Ulloa, M., Hoffman, S.M., Pepper, A.E., Stelly, D.M., Jenkins, J.N., Saha, S., Kumpatla, S.P., Shah, M.R., Hugie, W.V., and Percy, R.G.

- (2012). A high-density SSR and SNP genetic map of the tetraploid cotton genome. *G3: Genes, Genomes, Genetics* 2:43-58
2. Wang, K., Wang, Z., Li, F., Ye, W., Wang, J., Song, G., Yue, Z., Cong, L., Shang, H., Zhu, S., Zou, C., Li, Q., Yuan, Y., Lu, C., Wei, H., Gou, C., Zheng, Z., Yin, Y., Zhang, X., Liu, K., Wang, B., Song, C., Shi, N., Kohel, R.J., Percy, R.G., **Yu, J.Z.**, Zhu, Y.-X., Wang, J., and Yu, S. (2012). The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics* 44:1098-1104.
  3. Li, F., Fan, G., Wang, K., Sun, F., Yuan, Y., Song, G., Li, Q., Ma, Z., Lu, C., Zou, C., Chen, W., Liang, X., Shang, H., Liu, W., Shi, C., Xiao, G., Gou, C., Ye, W., Xu, X., Zhang, X., Wei, H., Li, Z., Zhang, G., Wang, J., Liu, K., Kohel, R.J., Percy, R.G., **Yu, J.Z.**, Zhu, Y.-X., Wang, J., and Yu, S. (2014). Genome sequence of the cultivated cotton *Gossypium arboreum*. *Nature Genetics* 46: 567-572
  4. **Yu, J.Z.**, Ulloa, M., Hoffman, S.M., Kohel, R.J., Pepper, A.E., Fang, D.D., Percy, R.G., and Burke, J.J. (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
  5. Li, F., Fan, G., Lu, C., Xiao, G., Zou, C., Kohel, R.J., Ma, Z., Shang, H., Ma, X., Wu, J., Liang, X., Huang, G., Percy, R.G., Liu, K., Yang, W., Chen, W., Du, X., Shi, C., Yuan, Y., Ye, W., Liu, X., Zhang, X., Liu, W., Wei, H., Wei, S., Huang, G., Zhang, X., Zhu, S., Zhang, H., Sun, F., Wang, X., Liang, J., Wang, J., He, Q., Huang, L., Wang, J., Cui, J., Song, G., Wang, K., Xu, X., **Yu, J.Z.**, Zhu, Y., and Yu, S. (2015). Genome sequence of cultivated Upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature Biotechnology* 33:524-530
  6. Huang, G., Wu, Z., Percy, R.G., Bai, M., Li, Y., Frelichowski, J.E., Hu, J., Wang, K., **Yu, J.Z.**, and Zhu, Y. (2020). Genome sequence of *Gossypium herbaceum* and genome updates of *Gossypium arboreum* and *Gossypium hirsutum* provide insights into cotton A-genome evolution. *Nature Genetics* 52:516–524

## B. Positions, Scientific Appointments, and Honors

### Positions and Scientific Appointments

2015 – 2019	Co-chair (2015-2017) and Chair (2017-2019), the International Cotton Genome Initiative (ICGI)
2013 – Present	Member, USDA National Life Science Patent Committee (NLSPC)
2005 – 2009	Co-chair (2005-2007) and Chair (2007-2009), the International Cotton Genome Initiative (ICGI)
2003 – 2006	Vice Chair (2003-2004) and Chair (2005-2006), the S-304 Committee of the U.S. Beltwide Multi-state Cotton Research Project
2000 – Present	Adjunct Professor, Texas A&M Univ., College Station, TX
1995 – Present	Research Geneticist, USDA, ARS, College Station, TX
1994 – 1995	Associate Research Scientist, Texas A&M Univ., College Station, TX
1991 – 1994	Postdoctoral Research Associate, Univ. Florida, Gainesville, FL
1986 – 1991	Research Fellow, World Bank/Rockefeller Foundation, Cornell Univ., Ithaca, NY
1983 – 1985	Research Scholar, International Rice Research Institute, Los Banos, Philippines
1982 – 1983	Research Assistant, China National Rice Research Institute, Hangzhou, China

### Honors

1991	Bradfield Award in Plant Genome Research, Cornell Univ., NY
2017	Excellent Scholar Award, XIX International Botanical Congress
2019	ICAC International Cotton Researcher of the Year Award, The International Cotton Advisory Committee (ICAC), Washington, DC

## C. Contributions to Science

1. **Genome sequencing of allotetraploid cotton and its diploid progenitors.** My recent contributions to science were the conception, development, and release of reference genome sequences for Upland tetraploid cotton (*Gossypium hirsutum*) and its probable diploid progenitors (*G. arboreum*, *G. herbaceum*, and *G. raimondii*). The genome of *G. hirsutum* was particularly difficult to assemble owing

to its allotetraploid genome and there was no literature existed on the cotton genome of any allotetraploid cotton species. Successful deciphering of Upland cotton genome represented an important benchmark for many polyploid plants. The breakthrough from such international collaborative research opened a new paradigm in cotton genomics that revolutionizes genetic improvement of cotton plants through better exploitation of genetic variation otherwise buried in *Gossypium* germplasm. The ground-breaking work has moved cotton into post-genome era, where molecular genetic advances will refocus on cotton functional traits.

- a. Wang, K., Wang, Z., Li, F., Ye, W., Wang, J., Song, G., Yue, Z., Cong, L., Shang, H., Zhu, S., Zou, C., Li, Q., Yuan, Y., Lu, C., Wei, H., Gou, C., Zheng, Z., Yin, Y., Zhang, X., Liu, K., Wang, B., Song, C., Shi, N., Kohel, R.J., Percy, R.G., **Yu, J.Z.**, Zhu, Y.-X., Wang, J. & Yu, S. (2012). The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics* 44:1098-1104.
- b. Li, F., Fan, G., Wang, K., Sun, F., Yuan, Y., Song, G., Li, Q., Ma, Z., Lu, C., Zou, C., Chen, W., Liang, X., Shang, H., Liu, W., Shi, C., Xiao, G., Gou, C., Ye, W., Xu, X., Zhang, X., Wei, H., Li, Z., Zhang, G., Wang, J., Liu, K., Kohel, R.J., Percy, R.G., **Yu, J.Z.**, Zhu, Y.-X., Wang, J. & Yu, S. (2014). Genome sequence of the cultivated cotton *Gossypium arboreum*. *Nature Genetics* 46: 567-572
- c. Li, F., Fan, G., Lu, C., Xiao, G., Zou, C., Kohel, R.J., Ma, Z., Shang, H., Ma, X., Wu, J., Liang, X., Huang, G., Percy, R.G., Liu, K., Yang, W., Chen, W., Du, X., Shi, C., Yuan, Y., Ye, W., Liu, X., Zhang, X., Liu, W., Wei, H., Wei, S., Huang, G., Zhang, X., Zhu, S., Zhang, H., Sun, F., Wang, X., Liang, J., Wang, J., He, Q., Huang, L., Wang, J., Cui, J., Song, G., Wang, K., Xu, X., **Yu, J.Z.**, Zhu, Y. & Yu, S. (2015). Genome sequence of cultivated Upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature Biotechnology* 33:524-530
- d. Lu, X., Fu, X., Wang, D., Wang, J., Chen, X., Hao, M., Wang, J. Gervers, K.A., 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, J.Z.** & Ye, W. (2018). Resequencing of cv CRI-12 family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. *Plant Biotechnology* 17:945-955.
- e. Huang, G., Wu, Z., Percy, R.G., Bai, M., Li, Y., Frelichowski, J.E., Hu, J., Wang, K., **Yu, J.Z.** & Zhu, Y. (2020). Genome sequence of *Gossypium herbaceum* and genome updates of *Gossypium arboreum* and *Gossypium hirsutum* provide insights into cotton A-genome evolution. *Nature Genetics* 52:516–524

**2. Integrated genetic, physical and transcript mapping of tetraploid cotton genomes.** Upland cotton, the world's leading fiber crop, has a complex allotetraploid genome that hinders advances in genomics research for much needed genetic improvement. Prior to the genome sequencing efforts stated above, I conceived and led collaborative research to develop the first integrated genetic, physical, and transcript maps of partially homologous tetraploid cotton chromosomes with large insert DNA clones, molecular markers, and EST genes. High-density genetic maps of tetraploid cotton and core DNA markers were developed, which are highly recognized and widely used by the global cotton research community as a reference genome map and standard marker set for cotton germplasm characterization and many other genetic applications. The concepts and methodologies with core sets of portable DNA markers make it possible for cotton researchers worldwide to collaborate, relate, and utilize genetic diversity data systematically among respective cotton germplasm collections.

- a. Xu, Z., Kohel, R.J., Song, G., Cho, J., Yu, J., Yu, S., Tomkins, J. & **Yu, J. Z.** (2008). An integrated genetic and physical map of homoeologous chromosomes 12 and 26 in Upland cotton (*G. hirsutum* L.). *BMC Genomics* 9:108
- b. **Yu, J.Z.**, Kohel, R.J., Fang, D.D., Cho, J., Van Deynze, A., Ulloa, M., Hoffman, S.M., Pepper, A.E., Stelly, D.M., Jenkins, J.N., Saha, S., Kumpatla, S.P., Shah, M.R., Hugie, W.V. & Percy, R.G. (2012). A high-density SSR and SNP genetic map of the tetraploid cotton genome. *G3: Genes, Genomes, Genetics* 2:43-58
- c. **Yu, J.Z.**, Fang, D.D., Kohel, R.J., Ulloa, M., Hinze, L.L., Percy, R.G., Zhang, J., Chee, P., Scheffler, B.E. & Jones, D.C. (2012). Development of a core set of SSR markers for the characterization of *Gossypium* germplasm. *Euphytica* 187:203–213

- d. Fang, D.D. & Yu, J.Z. (2012). Addition of four-hundred fifty-five microsatellite marker loci to the high-density *Gossypium hirsutum* TM-1 x *G. barbadense* 3-79 genetic map. *J. Cotton Sci.* 16:229–248
- e. Buyyarapu, R., Kantety, R.V., Yu, J.Z., Xu, Z., Kohel, R.J., Percy, R.G., Macmil, S., Wiley, G.B., Roe, B.A. & Sharma, G.C. (2013). BAC-pool sequencing and analysis of large segments of A12 and D12 homoeologous chromosomes in Upland cotton. *PLoS ONE* 8(10): e76757
- f. Reddy, U.K., Nimmakayala, P., Abburi, V.L., Reddy, C.V.C.M., Saminathan, T., Percy, R.G., Yu, J.Z., Frelichowski, J., Udall, J.A., Page, J.T., Zhang, D., Shehzad, T. & Paterson, A.H. (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

**3. Identification of cotton genes and QTLs.** Molecular breeding technologies empower cotton producers with an efficient means of improving fiber yield and quality, but only if accurate marker-trait association is developed. I planned and led the research to identify cotton genes and QTLs that confer fiber yield and quality among other traits. Gene-rich islands and sub-genomic roles were discovered in Upland cotton, providing critical information for genetic applications. The trait-linked DNA markers identified in the cotton genome facilitate understanding and dissection of genetic factors, underlying these important traits and marker-assisted selection in cotton.

- a. Xu, Z., Kohel, R.J., Song, G., Cho, J., Alabady, M., Yu, J., Koo, P., Chu, J., Yu, S., Wilkins, T.A., Zhu, Y. & Yu, J.Z. (2008). Gene-rich islands for fiber development in the cotton genome. *Genomics* 92:173-183
- b. Yu, J.Z., Ulloa, M., Hoffman, S.M., Kohel, R.J., Pepper, A.E., Fang, D.D., Percy, R.G. & Burke, J.J. (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
- c. Xu, Z., Yu, J., Kohel, R.J., Percy, R.G., Beavis, W.D., Main, D. & Yu, J.Z. (2015). Distribution and evolution of cotton fiber development genes in the fibreless *Gossypium raimondii* genome. *Genomics* 106: 61-69
- d. Abdurakhmonov, I.Y., Ayubov, M., Ubaydullaeva, K.A., Buriev, B.T., Shermatov, S.E., Ruziboev, H., Shapulatov, U.M., Saha, S., Ulloa, M., Yu, J.Z., Percy, R.G., Devor, E.J., Govind, S.C., Sripathi, V.R., Kumpatla, S.P., Van De Kroll, A., Hake, K.D., Khamidov, K., Salikhov, S.I., Jenkins, J.N., Abdugarimov, A. & Pepper, A.E. (2016). RNA interference for functional genomics and improvement of cotton (*Gossypium* spp.). *Front. Plant Sci.* 7:202
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- i. Yu, J.Z. & Gervers, K.A. (2019). Genomic analysis of marker-associated fiber development genes in Upland cotton (*Gossypium hirsutum* L). *Euphytica* 215(4) pp.74
- j. Fan, Y., Lu, X., Chen, X., Wang, J., Wang, D., Wang, S., Guo, L., Rui, C., Zhang, Y., Cui, R., Wang, Q., Yu, J.Z. & Ye, W. (2021). Cotton transcriptome analysis reveals novel biological pathways that eliminate reactive oxygen species (ROS) under sodium bicarbonate (*NaHCO<sub>3</sub>*) alkaline stress. *Genomics* 113(3):1157-1169