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EDUCATION

Ph. D. 2002 Department of Biology, University of Florida, Gainesville, FL.

Master of Science 2001 Computer Information Science and Engineering, Database Systems R&D Center, University of Florida, Gainesville, FL

Master of Science 1992 Kunming Institute of Zoology, the Chinese Academy of Sciences, Kunming, China

Bachelor of Science 1988 Northwest Normal University, Lanzhou, China.

WORKING EXPERIENCE

2021 - present Scientist ICBR, University of Florida, Gainesville, FL

2013 - 2020 Associate Scientist ICBR, University of Florida, Gainesville, FL

2009 - 2014 Interim scientific director of bioinformatics core, ICBR, University of Florida, Gainesville, FL

2004 - 2012 Assistant Scientist ICBR, University of Florida, Gainesville, FL

2002 - 2004 Postdoc Associate Department of Biochemistry and Molecular Biology, University of Florida, Gainesville, FL

1996 – 2002 Research and Teaching Assistant Department of Zoology and Department of Computer Information Science and Engineering, University of Florida, Gainesville, FL

1988 – 1996 Research Assistant Kunming Institute of Zoology, China.

TECHNICAL SKILLS

Familiar with most common bioinformatics and genomics databases and tools for data acquired from different sequencing platforms (Sanger, 454, SoLiD, Illumina, PacBio, NanoPore)

- **Molecular skills:** PCR, TA-Cloning, RFPL, Microsatellite, Microarray
- **Bioinformatics:** ChIP-seq (MACS, Cisgenome, PeakRanger), RNA-seq (Tophat, cufflinks, DESeq2, Star, Bowtie1/2, R-based stat packages), genome assembly & annotation (Spade, Trinity, Augustus, Soap, Abyss, Trinitotate), metagenomics (Canu, Flair, Rattle, metaFlye, metaQuast, MetaWrap, DADA2, QIIME2, checkM, etc)
- **Biostatistical analysis:** SAS, SPSS, R
- **Database:** GenBank, dbSNP, NCBI/JGI/Ensembl databases, Oracle, MS SQL server, MS excel
- **Operating Systems**: UNIX (SunOS & Solaris), Windows, DOS, Redhat Linux
- **Programming skills:** Java, Java Swing, Java Applets/Servlets, JSP (J2EE), JDBC, C/C++, SQL, Perl, XML, HTML, JavaScript

ACADEMIC MEMBERSHIP

American Society of Mammalogists

Sigma Xi, The Scientific Research Society

PUBLICATIONS

Here are the major publications associated with the bioinformatics work at ICBR. The whole list (90 publications) depends on request.

1. Li Q., Zhou M.X., Chhajed S., **Yu F.H.**, Chen S.X., Zhang Y.P., Mou Z.L. 2023. N-hydroxypipecolic acid triggers systemic acquired resistance through extracellular NAD(P). Nature Communications, 14:6848.
2. Ghimire U., Pliakoni E., **Yu F.H.**, Brecht J.K., Liu T. 2023. Identifying genes regulated during natural, on-plant senescence in broccoli (*Brassica oleracea*) in contrast to postharvest senescence. Postharvest Biology and Technology, 206: 112535.
3. Maria M.D., Kroll K.J., **Yu F.H.**, Nouri M.Z., .. Denslow N.D. 2022. Endocrine, immune, and renal toxicity in male largemouth bass after chronic exposure to glyphosate and Rodeo. Aquatic Toxicology, 246: 1016142.
4. Sosa F., Carmickle A.T., Oliveira L.J., Sagheer M., Saleem M., **Yu F.H.**, et al. 2022, Effects of the bovine SLICK1 mutation in PRLR on sweat gland area, FOXA1 abundance, and global gene expression in skin. Journal of Dairy Science, 105:9206-9215.
5. Sidhu H., Bae H.S., Ogram A., O'Connor G., **Yu F.H**. 2021. Azithromycin and ciprofloxacin can promote antibiotic resistance in biosolids and biosolids-amended soils. Applied and Environmental Microbiology, 87:e00373-21. https://doi.org/10 .1128/AEM.00373-21.
6. Zhai Y.T., Lee S.Y., Teng L., Ma Z.X., **Yu F.H**., … Jeong K. 2021. Dissemination mechanisms of New Delhi metallo-B-lactamase genes in hospitalized patients. JAC-Antimicrobial Resistance, 3: dlab032 (https://doi.org/10.1093/jacamr/dlab032)
7. Santoro D., Fagan L., Zhang Y.P., **Yu F.H.** 2021. Clinical efficacy of spray-based heat-treated lactobacilli in canine atopic dermatitis: a preliminary, open-label, uncontrolled study. Veterinary Dermatology, 32: 114-e23. DOI: 10.1111/vde.12915.
8. Piersanti R., Block J., Ma Z.X., Leong K.C., Santos J., **Yu F.H.**, Sheldon I.M., Bromfield J. 2020. Uterine infusion of bacteria alters the transcriptome of bovine oocytes. FASEB BioAdvances, 2:506-520.
9. Laxensky R., Hunter M.E., Amador D.M., Al-Kehedery B., **Yu F.H.**, Walsh C., Matthew M., Gitzendanner M.A., Trip K., Walsh M., Denslow N.D. 2020. Investigating the gene transcription profiles of Florida manatees (*Trichechus manatus latirostris*) following a red tide exposure. PLoS One, 15: e0234150.
10. Horlock A.D., Piersanti R., **Yu F.H**., Block J., Santos J., Bromfield J., Sheldon I.M. 2020. Uterine infection alters bovine endometrium, oviduct, and granulosa transcriptome three months later. Reproduction, 160: 93-107.
11. Mesa, A.M., Mao, J.D., Nanjappa, K., Medrano, T.I., Tevosian, S., **Yu, F.H**., ... Cooke, P.S., 2020. Transcriptomic changes in mice lacking uterine enhancer of homolog 2 (EZH2) and association of transcript changes with unterine epithelial proliferation. Physiological Genomics, 52:81-95.
12. Brice, D.C., Figgins, E., **Yu, F.H.**, Diamond, G. 2019. Type I interferon and interferon-stimulated gene expression in oral epithelial cells. Molecular Oral Microbiology, 34:245-253.
13. Zhao, L.M., Alto, B.W., Shin, D.Y., **Yu, F.H**. 2018. The effect of permethrin resistance on Aedes aegypti transcriptome following ingestion of Zika virus infected blood. Viruses, 10: 470.
14. Lavelle, C., Smith, C., Bisesi Jr, J.H., **Yu, F.H**., Silva-Sanchez, C., Moraga-Amado, D., Buerger, A.N., Reyero, N.C., Sabo-Attwood, T., Denslow, N. 2018. Tissue-based mapping of the fathead minnow (*Pimephales promelas*) transcriptome and proteome. Frontiers in Endocrinology, 9: 1-18.
15. Shi, Q.C., Febres, V.J., Zhang, S.J., **Yu, F.H.**, McCollum, G., Hall, D.G., Moore, G.A., Stover E. 2018. Identification of gene candidates associated with Huanglongbing tolerance, using '*Candidatus* Liberacter *asiaticus*' Flagellin 22 as a proxy to challenge citrus. Molecular Plant-Microbe Interactions, 31:200-211.
16. Yu, Q.B., Chen, C.X., Du, D.L., Huang, M., Yao, J.Q., **Yu, F.H.**, Brlansky, R.H., Gmitter, F.G. 2017. Reprogramming of a defense signaling pathway in rough lemon and sweet orange is a critical element of the early response to '*Candidatus Liberibacter asiaticus*'. Horticulture Research, 4: 17063.
17. Kariithi, H.M., Yao, X., **Yu, F.H.**, Teal P.E., Verhoeven, C.P., Boucias, D.G. 2017. Impacts of the Hytrosavirus on the transcriptome of the housefly, *Musca domestica*. Frontiers in Microbiology, 8:1-23.
18. Bock, C.H., Chen, C.X., **Yu, F.H.**, Stevenson, K.L., Arias, R.S., Wood, B.W. 2016. Characterization of

microsatellites in *Fusicladium effusum*, cause of pecan scab. Forest Pathology, 46:600-609.

19. Yin, L., Yao, J., Chang, K.F., Gardner, B., **Yu, F.H.**, Giuliano, A., Goodenow, M. 2016. HPV population profiling in healthy men by next generation deep sequencing coupled with HPV-QUEST. Viruses, 8(2):28.

20. McFarland, K.N., Liu, J., Landrian, I., Godiska, R., Shanker, S., **Yu, F.H.**, Farmerie, W.G., Ashizawa, T. 2015. SMRT Sequencing of Long Tandem Nucleotide Repeats in SCA10 Reveals Unique Insight of Repeat Expansion Structure. PLoS One. 10(8): e0135906.

21. Lu, S., Zeumer, L., Sorensen, H., Yang, H., Ng, Y., **Yu, F.H.**, Riva, A., Croker, B., Wallet, S., Morel, L. 2015. The murine Pbx1-d lupus susceptibility allele accelerates mesenchymal stem cell differentiation and impairs their immunosuppressive function. Journal of Immunology, 194: 43-55.

22. Moroz, LL., Kocot, K.M., Citarella M.R., … **Yu, F.H.**, et al., 2014. The ctenophore genome and the evolutionary origins of neural systems. Nature, 510: 109-114.

23. Christiansen, H.E., Mehinto, A.C., **Yu, F.H.,** Perry, R.W., Denslow, N.D., Maule, A.G., Mesa, M.G. 2014. Correlation of gene expression and contaminant concentrations in wild largescale suckers: A field-based study. Science of The Total Environment. 484: 379-389.

24. Sefah, K., Yang, Z.Y., Bradley, K.M., Hoshika, S., Jiménez, E., Zhang, L.Q., Zhu, G.Z., Shanker, S., **Yu, F.H.**, Turek, D., Tan, W.H., Benner, S.A. 2014. In vitro selection with artificial expanded genetic information systems. PNAS, 111: 1449-1454.

25. Wang, Y., An, C., Zhang, X., Yao, J., Zhang, Y., Sun, Y., **Yu, F.H.**, Amador, D.M., Mou, Z. 2013. The Arabidopsis elongator complex subunit2 epigenetically regulates plant immune responses. Plant Cell, 25(2): 762-776.

26. Wang, Y., DeFraia, C.T., An,C., Zhang, X., Yao,J.Q., Zhang, Y.P., Sun, Y.J., **Yu, F.H.**, Amador, A.M., Mou, Z.L. 2013. Elongator Epigenetically Regulates Immune Responses in Arabidopsis thaliana. Plant Cell, 25(2): 762-76.

27. Puthanveettil, S.V., Antonov, I., Kalachikod, S., Rajasethupathy, P., Choi, Y.B., Kohn, A.B., Citarella, M., **Yu, F.H**., Karl, K.A., Kinet, M., Morozova, I., Russo J.J., Ju, J.Y., Moroz, L.L., Kandel E.R. 2013. A strategy to capture and characterize the synaptic transcriptome. PNAS, 110: 7464-7469.

28. Brockmeier, E.K., **Yu, F.H.**, Amador, D.M., Bargar, T.A., Denslow, N.D. 2013. Custom microarray construction and analysis for determining potential biomarkers of subchronic androgen exposure in the *Eastern Mosquitofish* (Gambusia holbrooki). BMC Genomics, 14: 660.

29. Jalan, N., Kumar, D., Andrade, M.O., **Yu, F.H**., Jones, J.B., Graham, J.H., White, F.F., Setubal, J.C., Wang, N. 2013. Comparative genomic and transcriptome analyses of pathotypes of *Xanthomonas citri* subsp citri provide insights into mechanisms of bacterial virulence and host range. BMC Genomics, 14: 551.

30. Nirmala, X., Schetelig, M.F., **Yu, F.H**., Handler, A.M. 2013. An EST database of the Caribbean fruit fly, *Anastrepha suspense* (Diptera: Tephritidae). Gene, 517:212-217.

31. Ozawa, M., Sakatani, M, Yao, J.Q., Shanker, S., **Yu, F.H.**, Yamashita, R., Wakabayashi, S., Nakai, K., Dobbs, K.B., Farmerie, W.G., Sudano, M.J., Hansen, P.J. 2012. Global gene expression of the inner cell mass and trophectoderm of the bovine blastocyst. BMC Developmental Biology, 12:33-46.

32. Koh, J., Chen, S.X., Zhu, N., **Yu, F.H.,** Soltis, P.S., Soltis, D.E. 2012. Comparative proteomics of the recently and recurrently formed natural allopolyploid Tragopogon mirus (Asteraceae) and its parents. New Phytologist, 196:292-305.

33. Hoy, M.A., **Yu, F.H**, Meye,r J.M., Tarazona, O.A., Jeyaprakash, A., Wu, K. 2012. Transcriptome sequencing and annotation of the predatory mite *Metaseiulus occidentalis* (Acari: Phytoseiidae): a cautionary tale about possible contamination by prey sequences. Experimental and Applied Acarology, (DOI) 10.1007/s10493-012-9603-4.

34. **Yu, F.H**., Li, S.P., Kilpatrick, C.W., McGuire, P.M., He, K., Wei, W.H. 2012. Biogeographical study of plateau pika *Ochotona curzoniae* (Lagomorpha, *Ochotona*). Zoological Sciences, 29:518-526.

35. Valles, S.M., Oi, D.H., **Yu, F.H.,** Tan, X.X., Buss, E.A. 2012. Application of metagenomics and pyrosequencing to facilitate discovery of potential viral natural enemies of the invasive Caribbean crazy ant, *Nylanderia pubens* (Forel). Plos One, 7: e31828.

36. Jalan, N., Aritua V., Kumar D., **Yu, F.H.,** Jones J.B., Graham J.H., Setubal, J.C., Wang, N. 2011. Comparative genomic analysis of *Xanthomonas axonopodis pv. Citrumelo* F1 causing citrus bacterial spot and related strains provides insights into virulence and host-specificity. Journal of Bacteriology, 193: 6342-6357.

37. Yao, J.Q., **Yu, F.H**. 2011. DEB: A web interface for RNA-seq digital gene expression analysis. Bioinformation Volume 7 (Open access: *www.bioinformation.net*).

38. Sun, Y., Cai, Y., Mai, V., Farmerie, V., **Yu, F.H.,** Li, J., Goodison, S. 2010. Advanced computational algorithms for microbial community analysis using mass 16S rRNA sequence data. Nucleic Acid Research, 38: e205.

39. Wellehan, J.F.X., **Yu. F.H.,** Venn-Watson, S. K., Jensen, E. D., Smith, C. R., Farmerie, W. G., Nollens, H. N. 2010. Characterization of San Migue sea lion virus populations using pyrosequencing based methods. Infection, Genetics and Evolution, 10:254-260.

40. **Yu, F.H**., Sun, Y.J., Liu, L., Farmerie. W. 2009. GSTaxClassfier3: a genomic signature based taxonomic classifier for metagenomic data analysis. *Bioinformation* (Open access: *www.bioinformation.net*).

41. Sun, Y., Cai, Y., Liu, L., **Yu, F.,** Farrell, M. L., McKendree, W., Farmerie, W. 2009. ESPRIT: estimating species richness using large collections of 16S rRNA pyrosequences**.** Nucleic Acids Research, 37: e76.

42. Ding X.D., Richter T., Chen M., Fujii H., Xie M.T., Zheng X.W., Kanrar S., Stevenson B., Dardick C., Li Y., Jiang H., Zhang Y., **Yu F.H.**, Zhu L.H., Farmerie W.G., Gribskov M., Zh J.K., Fromm M.E., Ronald P.C., Song W.Y, 2009. A rice kinase-protein interaction map. Plant Physiology, 149(3):1478-1492.

43. Yu F.R., Lu S.Q., **Yu F.H.**, Shi J.N., McGuire P.M., Wang R. 2008. Cytotoxic activity of unsaturated fatty acids from *Euphorbia kansui* on human tumor cell strains. Journal of Pharmacy and Pharmacology, 60:253-259.

44. Moroz, L. L., Edwards, J.R., Puthanveettil S.V., Kohn A., Ha T., Heyland A., Knudsen B., Sahni A.**, Yu F.H.**, Liu L., et al. 2006. The neuronal transcriptome of *Aplysia californica*: neuronal compartments and neuronal circuitry. Cell, 127: 1453-1467**.**

45. Xu C.J., Xu L.Z., **Yu F.H.**, Tan W.H., Moroz L.L., Li J. 2006. Nonparametric estimation of the number of unique mRNA transcripts expressed in a biological tissue. IEEE Transactions on Signal Processing, 54 (10), 3759-3767.