

2023

1. **Antifungal mechanism of volatile compounds emitted by Actinomycetota *Paenarthrobacter ureafaciens* from a disease-suppressive soil on *Saccharomyces cerevisiae***

Nguyen, T. P., Meng, D. R., Chang, C. H., Su, P. Y., Ou, C. A., Hou, P. F., Sung, H. M., Chou, C. H., Ohme-Takagi, M. & Huang, H. J. (2023). *mSphere*, 8(5).

2020

2. **Influence of gene position on the expression divergence of oxidative response genes in intraspecific yeast**

Huang, Y. H., Hsieh, D. K. & Sung, H. M. (2020). *Journal of Evolutionary Biology*, 33(4), 505–511.

2019

3. **Microbial volatile compounds-induced cytotoxicity in the yeast *Saccharomyces cerevisiae*: The role of MAPK signaling and proteasome regulatory pathway**

Wu, P. H., Ho, Y. L., Ho, T. S., Chang, C. H., Ye, J. C., Wang, C. H., Sung, H. M., Huang, H. J. & Liu, C. C. (2019). *Chemosphere*, 233, 786–795.

2017

4. **Bostrycin production by agro-industrial residues and its potential for food processing**

Huang, Y. H., Yang, W. J., Cheng, C. Y., Sung, H. M. & Lin, S. F. (2017). *Food Science and Biotechnology*, 26(3), 715–721.

2015

5. **Ecological genomics in *Xanthomonas*: The nature of genetic adaptation with homologous recombination and host shifts**

Huang, C. L., Pu, P. H., Huang, H. J., Sung, H. M., Liaw, H. J., Chen, Y. M., Chen, C. M., Huang, M. B., Osada, N., Gojobori, T., Pai, T. W., Chen, Y. T., Hwang, C. C. & Chiang, T. Y. (2015). *BMC Genomics*, 16(1), 188.

6. **Highly diversified fungi are associated with the achlorophyllous orchid *Gastrodia flavilabella***

Liu, T., Li, C. M., Han, Y. L., Chiang, T. Y., Chiang, Y. C. & Sung, H. M. (2015). *BMC Genomics*, 16(1), 185.

2014

7. **Polymorphic microsatellite loci isolated from *Cervus unicolor* (Cervidae) show inbreeding in a domesticated population of Taiwan Sambar deer**

Lin, D. Y., Chiang, T. Y., Huang, C. C., Lin, H. D., Tzeng, S. J., Kang, S. R., Sung, H. M. & Wu, M. C. (2014). *Genetics and Molecular Research*, 13(2), 3967–3971.

2013

8. **Identifying cis-regulatory changes involved in the evolution of aerobic fermentation in yeasts**

Lin, Z., Wang, T. Y., Tsai, B. S., Wu, F. T., Yu, F. J., Tseng, Y. J., Sung, H. M. & Li, W. H. (2013). *Genome Biology and Evolution*, 5(6), 1065–1078.

9. **Systematic screening of glycosylation- and trafficking-associated gene**

knockouts in *Saccharomyces cerevisiae* identifies mutants with improved heterologous exocellulase activity and host secretion

Wang, T. Y., Huang, C. J., Chen, H. L., Ho, P. C., Ke, H. M., Cho, H. Y., Ruan, S. K., Hung, K. Y., Wang, I. L., Cai, Y. W., Sung, H. M., Li, W. H. & Shih, M. C. (2013). *BMC Biotechnology*, 13, 71.

2012

10. Effects of cis and trans regulatory variations on the expression divergence of heat shock response genes between yeast strains

Li, C. M., Tzeng, J. N. & Sung, H. M. (2012). *Gene*, 506(1), 93–97.

2011

11. Functional characterization of cellulases identified from the cow rumen fungus *Neocallimastix patriciarum* W5 by transcriptomic and secretomic analyses

Wang, T. Y., Chen, H. L., Lu, M. Y. J., Chen, Y. C., Sung, H. M., Mao, C. T., Cho, H. Y., Ke, H. M., Hwa, T. Y., Ruan, S. K., Hung, K. Y., Chen, C. K., Li, J. Y., Wu, Y. C., Chen, Y. H., Chou, S. P., Tsai, Y. W., Chu, T. C., Shih, C. C. A., Li, W. H. et al. (2011). *Biotechnology for Biofuels*, 4, 24.

2010

12. Natural selection on cis and trans regulation in yeasts

Emerson, J. J., Hsieh, L. C., Sung, H. M., Wang, T. Y., Huang, C. J., Lu, H. H. S., Lu, M. Y. J., Wu, S. H. & Li, W. H. (2010). *Genome Research*, 20(6), 826–836.

13. Omics Applications to Biofuel Research

Wang, T. Y., Chen, H. L., Li, W. H., Sung, H. M. & Shih, M. C. (2010). In *Biocatalysis and Biomolecular Engineering*, John Wiley and Sons, pp. 265–276.

2009

14. Roles of trans and cis variation in yeast intraspecies evolution of gene expression

Sung, H. M., Wang, T. Y., Wang, D., Huang, Y. S., Wu, J. P., Tsai, H. K., Tzeng, J., Huang, C. J., Lee, Y. C., Yang, P., Hsu, J., Chang, T., Cho, C. Y., Weng, L. C., Lee, T. C., Chang, T. H., Li, W. H. & Shih, M. C. (2009). *Molecular Biology and Evolution*, 26(11), 2533–2538.

2008

15. Roles of cis- and trans-changes in the regulatory evolution of genes in the gluconeogenic pathway in yeast

Chang, Y. W., Robert Liu, F. G., Yu, N., Sung, H. M., Yang, P., Wang, D., Huang, C. J., Shih, M. C. & Li, W. H. (2008). *Molecular Biology and Evolution*, 25(9), 1863–1875.

2007

16. Expression evolution in yeast genes of single-input modules is mainly due to changes in trans-acting factors

Wang, D., Sung, H. M., Wang, T. Y., Huang, C. J., Yang, P., Chang, T., Wang, Y. C., Tseng, D. L., Wu, J. P., Lee, T. C., Shih, M. C. & Li, W. H. (2007). *Genome Research*, 17(8), 1161–1169.

17. **Patterns of internal gene duplication in the course of metazoan evolution**

Chen, C. C., Li, W. H. & Sung, H. M. (2007). *Gene*, 396(1), 59–65.

2006

18. **Novel role of *mfd*: Effects on stationary-phase mutagenesis in *Bacillus subtilis***

Ross, C., Pybus, C., Pedraza-Reyes, M., Sung, H. M., Yasbin, R. E. & Robleto, E. (2006). *Journal of Bacteriology*, 188(21), 7512–7520.

2003

19. **Roles of YqjH and YqjW, homologs of the *Escherichia coli* UmuC/DinB or Y superfamily of DNA polymerases, in stationary-phase mutagenesis and UV-induced mutagenesis of *Bacillus subtilis***

Sung, H. M., Yeaman, G., Ross, C. A. & Yasbin, R. E. (2003). *Journal of Bacteriology*, 185(7), 2153–2160.

2002

20. **Adaptive, or stationary-phase, mutagenesis, a component of bacterial differentiation in *Bacillus subtilis***

Sung, H. M. & Yasbin, R. E. (2002). *Journal of Bacteriology*, 184(20), 5641–5653.

2001

21. **Characterization of O6-methylguanine-DNA-methyltransferase (O6-MGMT) activity in *Xiphophorus* fishes**

Walter, R. B., Sung, H. M., Intano, G. W. & Walter, C. A. (2001). *Mutation Research - Genetic Toxicology and Environmental Mutagenesis*, 493(1–2), 11–22.

2000

22. **Transient growth requirement in *Bacillus subtilis* following the cessation of exponential growth**

Sung, H. M. & Yasbin, R. E. (2000). *Applied and Environmental Microbiology*, 66(3), 1220–1222.

1997

23. **Molecular phylogeny of extant gymnosperms and seed plant evolution: Analysis of nuclear 18S rRNA sequences**

Chaw, S. M., Zharkikh, A., Sung, H. M., Lau, T. C. & Li, W. H. (1997). *Molecular Biology and Evolution*, 14(1), 56–68.

1995

24. **The phylogenetic positions of the conifer genera *Amentotaxus*, *Phyllocladus*, and *Nageia* inferred from 18S rRNA sequences**

Chaw, S. M., Sung, H. M., Long, H., Zharkikh, A. & Li, W. H. (1995). *Journal of Molecular Evolution*, 41(2), 224–230.