National Taiwan University and Academia Sinica Joint Program Office

TOPIC

DECEMBER 2024

The NTU/AS Innovative Joint Program has been implemented for several years, and lots of PIs achieved excellent outcomes.

In this Issue, we have 3 articles sharing the recent research results in the field of "**Humanities**" and "**Life Science**".



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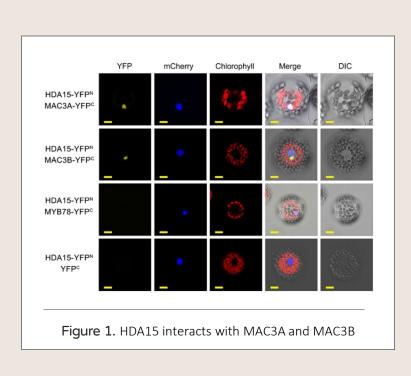
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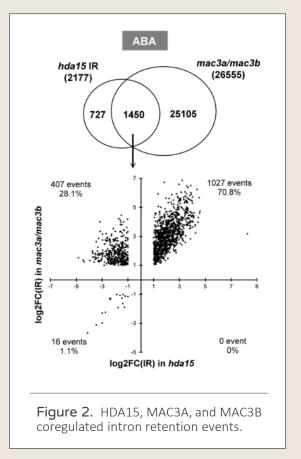
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HISTONE DEACETYLASE 15 and MOS4-Associated Complex subunits 3A/3B coregulate intron retention of ABA-responsive genes

Keqiang Wu¹, and Pao-Yang Chen²

Dr. Keqiang Wu's team of National Taiwan University collaborated with Dr. Pao-Yang Chen's team of Academia Sinica to study the epigenetic regulation mechanism of plant development and stress response. Through the mutant analysis, mass spectrometry analysis, proteomics and transcriptome studies carried out by the Wu's team, combined with bioinformatics analysis by the Chen's team, the molecular mechanism how the histone deacetylase HDA15 is involved in the abscisic acid (ABA) response in Arabidopsis was revealed.





Histone deacetylases (HDAs) play an important role in transcription regulation of multiple biological processes. In this study, the function of the histone deacetylase HDA15 in ABA responses was investigated. Immunopurification coupled with mass spectrometry-based proteomics was used to identify proteins interacting with HDA15 in Arabidopsis (Arabidopsis thaliana). HDA15 interacted with the core subunits of the MOS4-associated complex (MAC), MAC3A and MAC3B, with interaction between HDA15 and MAC3B enhanced by ABA. HDA15 and MAC3A/MAC3B mutants were ABA-insensitive during seed germination and hyposensitive to salinity. RNA sequencing analysis demonstrated that HDA15 and MAC3A/MAC3B co-regulate ABA-responsive intron retention (IR). Furthermore, HDA15 reduced the histone acetylation level of genomic regions near ABA-responsive IR sites and the association of MAC3B with ABA-responsive pre-mRNA was dependent on HDA15. These results indicate that HDA15 is involved in ABA responses by interacting with MAC3A/MAC3B to mediate splicing of introns. This collaboration research has been published in Plant Physiology, 2022, 190: 882–897. https://doi.org/10.1093/plphys/kiac271

Yi-Tsung Tu, Chia-Yang Chen, Yi-Sui Huang, Chung-Han Chang, Ming-Ren Yen, Jo-Wei Allison Hsieh, Pao-Yang Chen* and Keqiang Wu* (2022) HISTONE DEACETYLASE 15 and MOS4-associated complex subunits 3A/3B coregulate intron retention of ABA-responsive genes. Plant Physiology 190(1): 882-897. [citation: 14]

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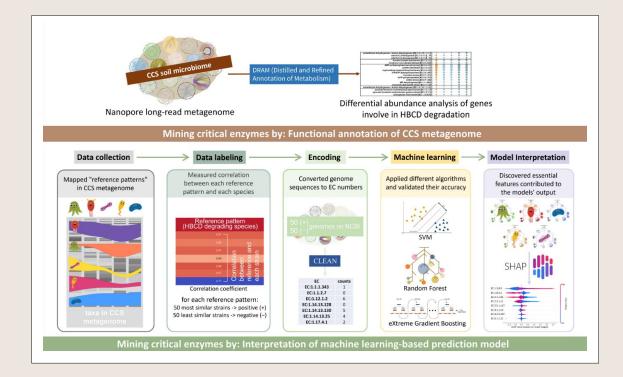
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Interpretation of Machine Learning-Based Prediction Models and Functional Metagenomic Approach to Identify Critical Genes in Hexabromocyclododecane Degradation

> Yu-Jie Lin¹, Ping-Heng Hsieh¹, Chun-Chia Mao¹, Yang-Hsin Shih², Shu-Hwa Chen³, and Chung-Yen Lin^{1, 4, 5*}

Hexabromocyclododecane (HBCD) is one of the persistent organic pollutants (POPs) and poses serious risks. Tackling HBCD contamination through microbial degradation is promising, but identifying the effective microbes and genes has been complex. A joint research team led by NTU Prof. Yang-Hsin Shih and Academia Sinica Prof. Chung-Yen Lin has made significant progress using metagenomics combined with machine learning to uncover key genes involved in HBCD breakdown. Yang-Hsin Shih's team discovered that Chiang Chun Soil, a representative soil series in Taiwan, efficiently degrades HBCD. Prof. Chung-Yen Lin then utilized the metagenomic dataset from Chiang Chun Soil and data from HBCD-degrading species identified in Prof. Yang-Hsin Shih's earlier studies to successfully identify critical and novel genes involved in HBCD degradation.



The study highlighted critical findings, including specific genes associated with degradation efficiency. Machine learning models identified two genes - EC 1.8.3.2 (thiol

oxidase) and EC 4.1.1.43 (phenylpyruvate decarboxylase)- linked to reduced degradation. Conversely, EC 2.7.1.83 (pseudouridine kinase) was positively correlated with improved degradation. Although the exact enzymes identified varied between methods, the overall metabolic pathways were closely aligned. This alignment suggests that while functional annotations focus on increased gene abundance, machine learning can highlight genes supporting and hindering HBCD degradation.

As the first study to apply machine learning to metagenomic data to understand xenobiotic biodegradation, these results offer a comprehensive view of microbial dynamics. The insights gained from this study will help develop more effective strategies for cleaning up HBCD contamination, enhancing our ability to address this persistent environmental issue.

The related paper from this research has been submitted and is currently under revision. For more data, code and other information, please access our GitHub site.

- Li, Y.-J., Chuang, C.-H., Cheng, W.-C., Chen, S.-H., Chen, W.-L., Lin, Y.-J., Lin, C.-Y., & Shih, Y.-H. (2022). A metagenomics study of hexabromocyclododecane degradation with a soil microbial community. *Journal of Hazardous Materials*, 430, 128465. https://doi.org/10.1016/j.jhazmat.2022.128465
- Lin, Y.-J., Hsieh, P.-H., Mao, C.-C., Shih, Y.-H., Chen, S.-H., Lin, C.-Y. (2024) Interpretation of Machine Learning-Based Prediction Models and Functional Metagenomic Approach to Identify Critical Genes in HBCD Degradation. Journal of Hazardous Materials. (under revision)
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Analyzing the Complex Interactions between the Politics and Religions in China and Eurasia

Yang Fu¹, and Ling-Wei Kung²

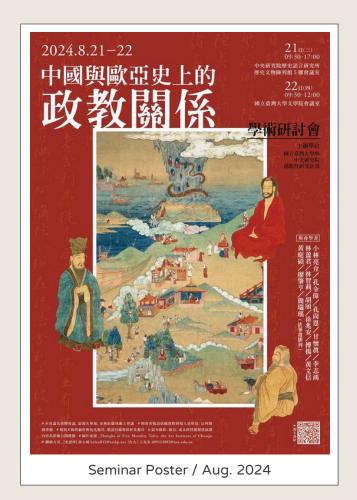
In traditional China, religions and politics were closely intertwined. From the pre-Buddhist rituals and beliefs in ghosts and spirits, to the profound impact of Buddhism's sweep through China, to the stimulation of multiple religions and regional traditions, the significance of the interaction between the politics and religions in China's history is evident. However, compared to its historical significance, there is still much room for further research. Focusing on the relationship between the politics and religions before the eighteenth century, this project attempts to present new findings, advance future research, and build a dynamic research team.





The PIs and members of the project have made significant achievements in organizing academic activities and building research teams. In carrying out the project, the members have published a number of papers in A&HCH and THCI core journals in the humanities, as well as a number of book chapters and academic conference papers. Three outputs are especially noteworthy :

First, Ling-wei Kung (IHP, Academia Sinica) hosts a reading session on the *Tongdian*, and produces a series of textual collation and research papers in a detailed and systematic manner. This activity is expected to provide a better text for research and studies on the *Tongdian*, and to establish a platform for closer exchanges between NTU students and experts from Academia Sinica and beyond, so as to nurture young research talents.



Second, Yang Fu (History, NTU) will edit and publish a collection of essays on the relationship between the politics and religions in medieval and early modern China. This collection emphasizes that in order to deeply explore the relationship between the politics and religions in Chinese history, apart from the elaboration of ideas and doctrines, it is also necessary to analyze it in terms of "state and ritual" and "beliefs and society".

Third, Huai-chen Kan (History, NTU) publishes a monograph, The Birth of the All under Heaven. It suggests that the idea of the All under Heaven was by nature a state religion. In the long process of its development, the concept of deities based on shamanism contributed

NEWSLETTER NO. 3

contributed to a new religion based on rituals. The social changes in the pre-Qin period, interpretations of classics in the Han, and contacts between China and exterior cultures, moreover, had shaped the Confucian state with strong religious connotations, which had far-reaching effects.

Overall, this project has achieved significant results in terms of both the individual achievements of the PIs and team members and the exchange of talents and resources between NTU and Academia Sinica, and has clearly demonstrated that the interplay between the politics and religions is a topic of huge research potential inviting further studies.

For details of the research outcomes, please see the National Taiwan University and Academia Sinica Joint Program Office website.

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