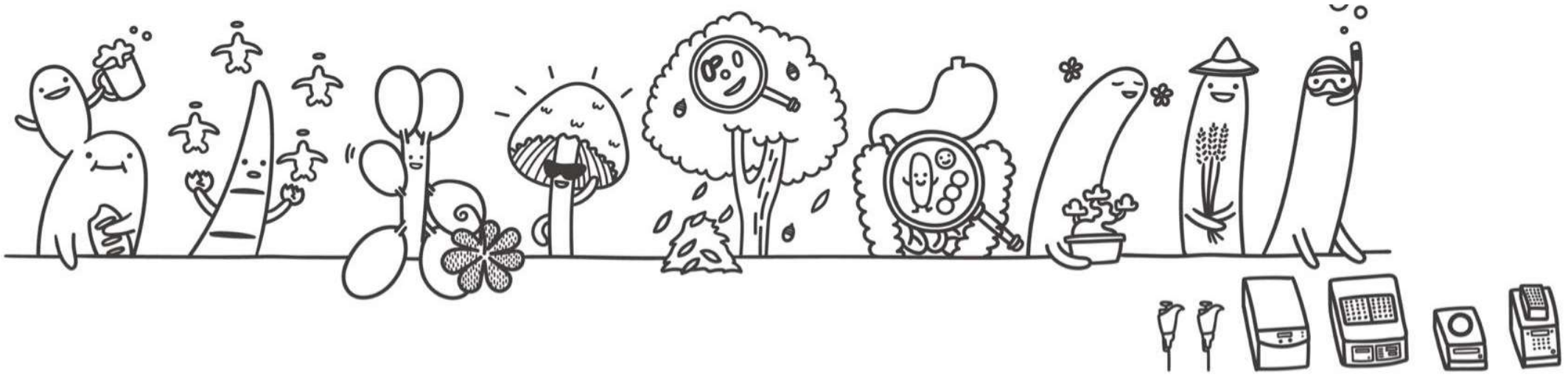
Extensive sampling of *Saccharomyces cerevisiae* in Taiwan reveals ecology and evolution of pre-domesticated lineages



Isheng Jason Tsai

Biodiversity Research Center, Academia Sinica, Taiwan

2022 PAS-AS meeting

Research organisms: Fungi and nematodes

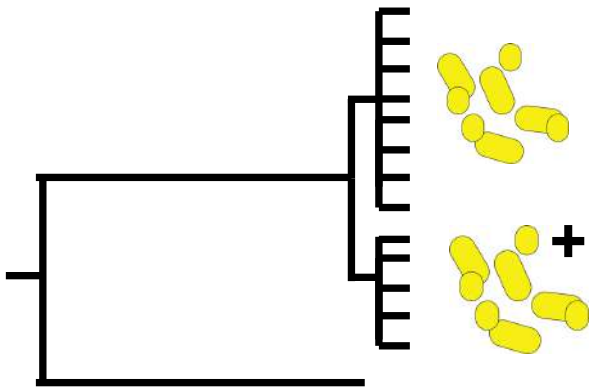
Fungi
Saccharomyces cerevisiae
Fusarium solani
Acrodontium crateriforme
bioluminescent *Mycena*

Microbiome and mycobiomes

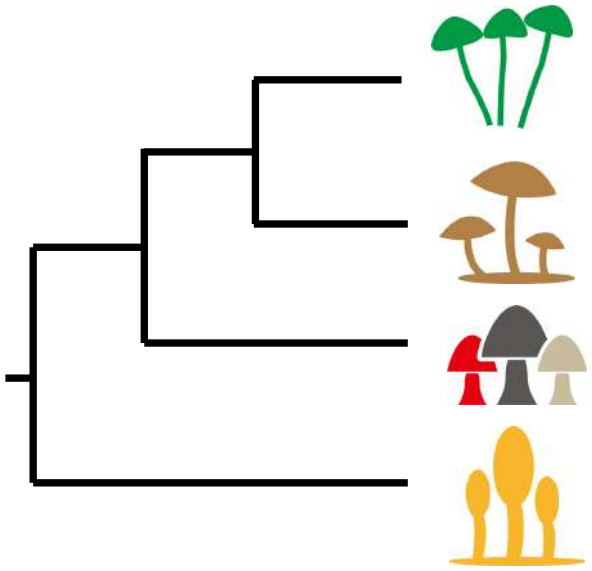
Nematodes
Bursaphelenchus xylophilus
Aphelenchoides besseyi
Marine free-living nematodes

Approaches

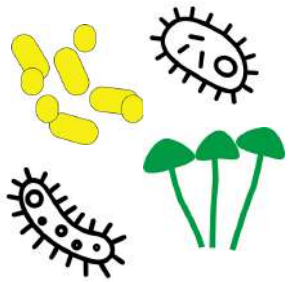
Population genomics



Comparative genomics/transcriptomics

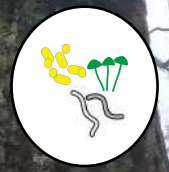


Metagenomics/ metatranscriptomics

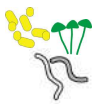


million years ago

Can we understand the whole picture (who, where, how species live, interact and evolve)?

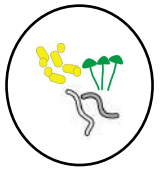


Ring-cupped Oak forest (~2300m, Nantou County, Taiwan)



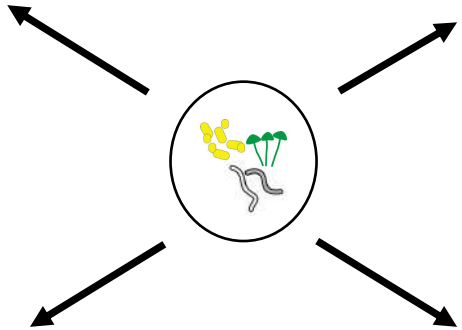
tiny fraction!

Unknown domain



Understanding of model organisms /
disease orientated species

Strategy: study the ecology and evolution of siblings to model organisms



Goal

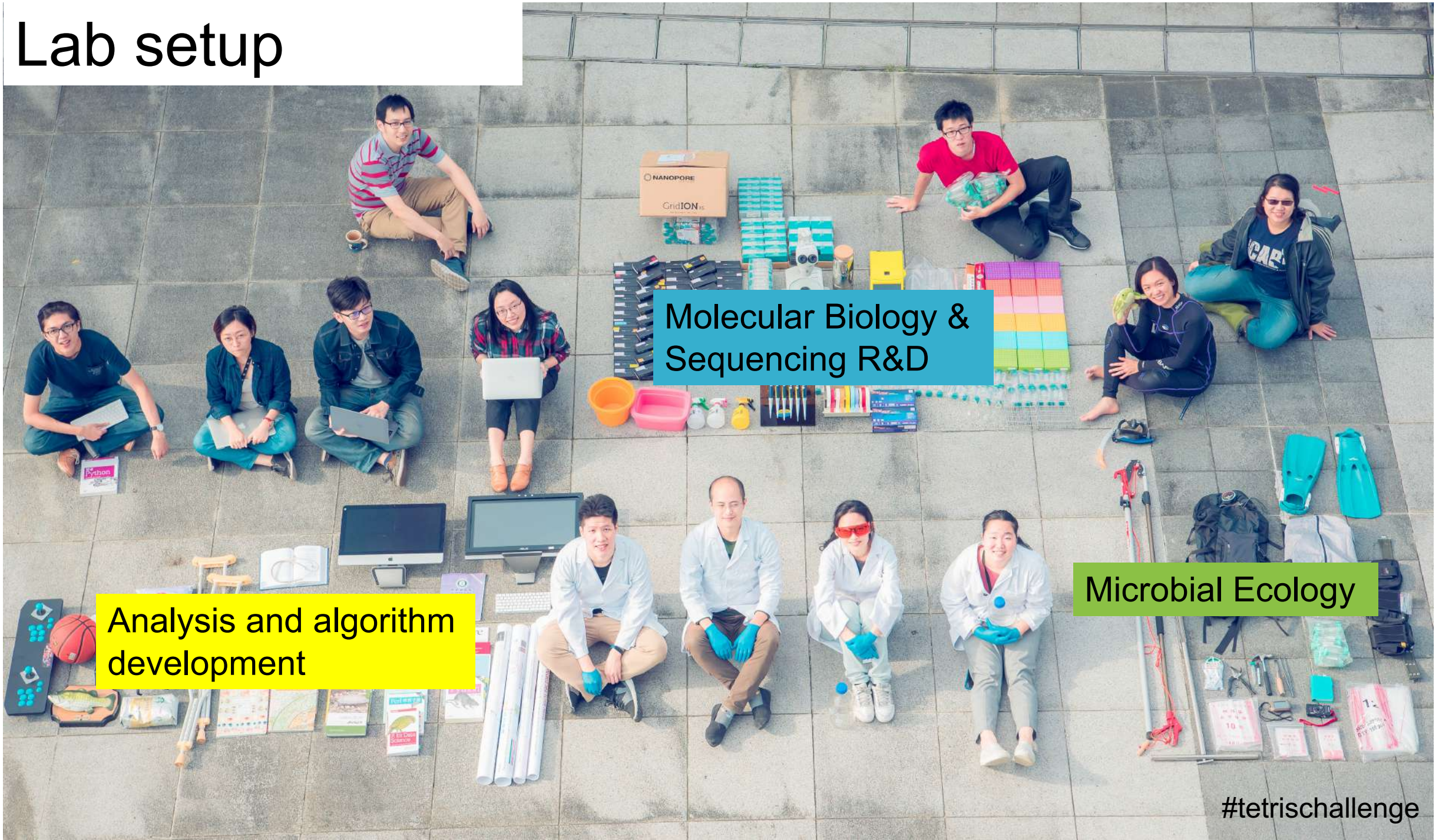
Extensive traits and tools

Research in model organism → Knowledge

Natural environment + Wild collections ↗

Establish new models in ecology;
Formulate questions from nature

Lab setup


NANOPORE
GridION
Molecular Biology & Sequencing R&D
Analysis and algorithm development
Microbial Ecology
#tetrischallenge

Deep sampling of ancestral genetic diversity reveals *Saccharomyces cerevisiae* pre-domestication life histories

Tracy Lee

Cold Spring Harbor Laboratory

bioRχiv

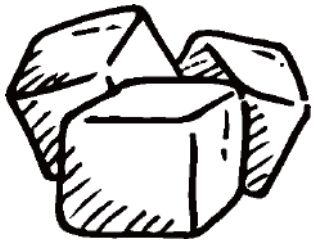
THE PREPRINT SERVER FOR BIOLOGY

https://www.biorxiv.org/content/10.1101/2021.09.07.459046v1

S. cerevisiae as arguably one of the most domesticated (researched) species for its fermentation ability

yeast

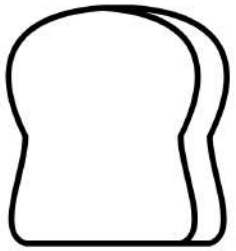
+



sugar

fermentation

CO_2



-OH

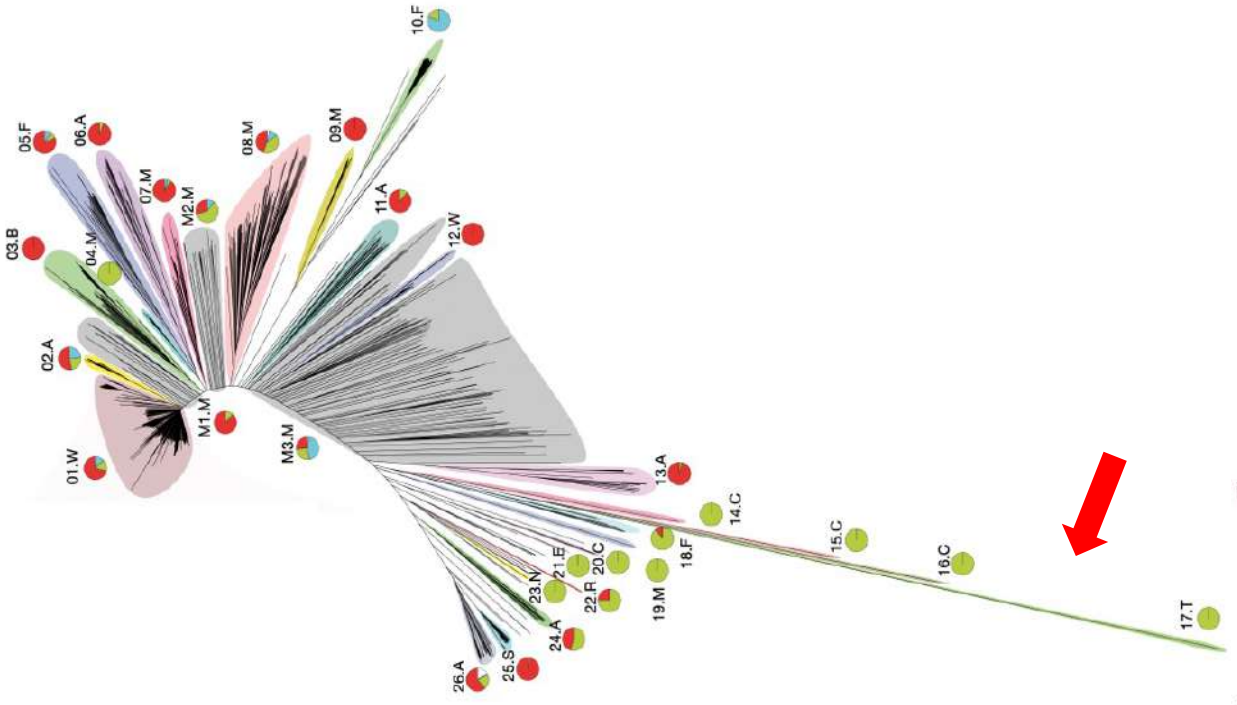
(low) Energy

Outstanding questions

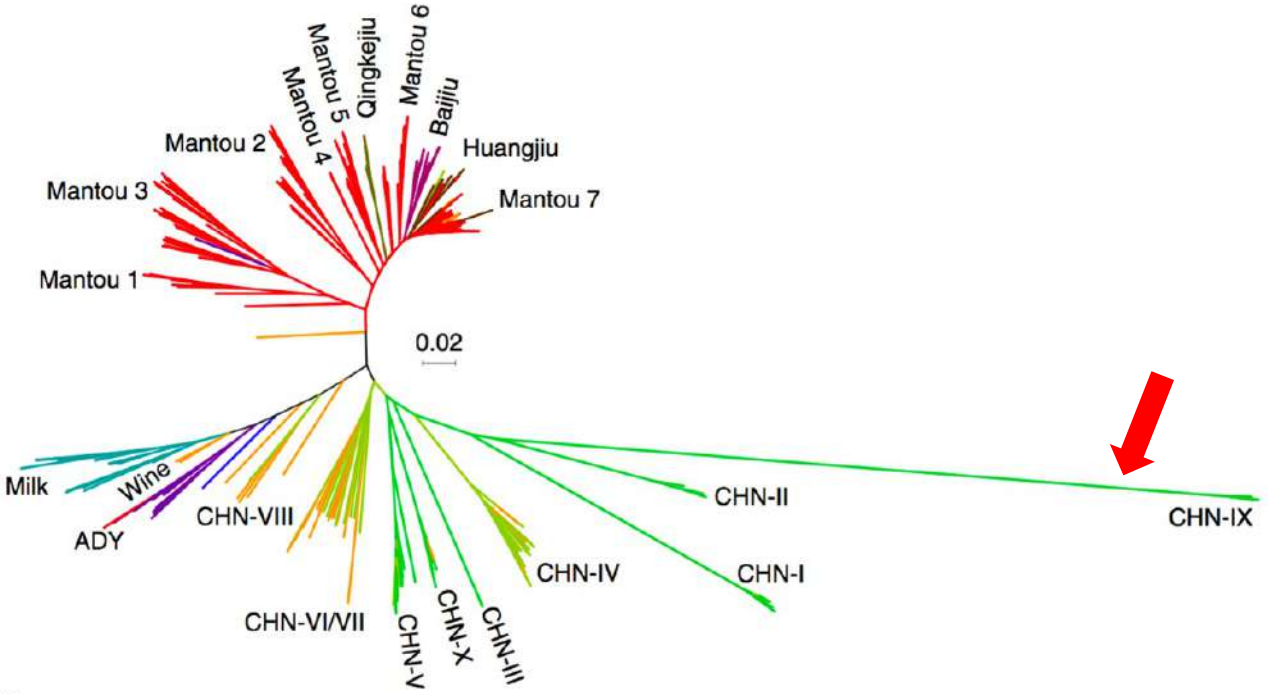
1. geographic origin of *S. cerevisiae*

A far east origin of *S. cerevisiae*

1,011 isolates



266 isolates



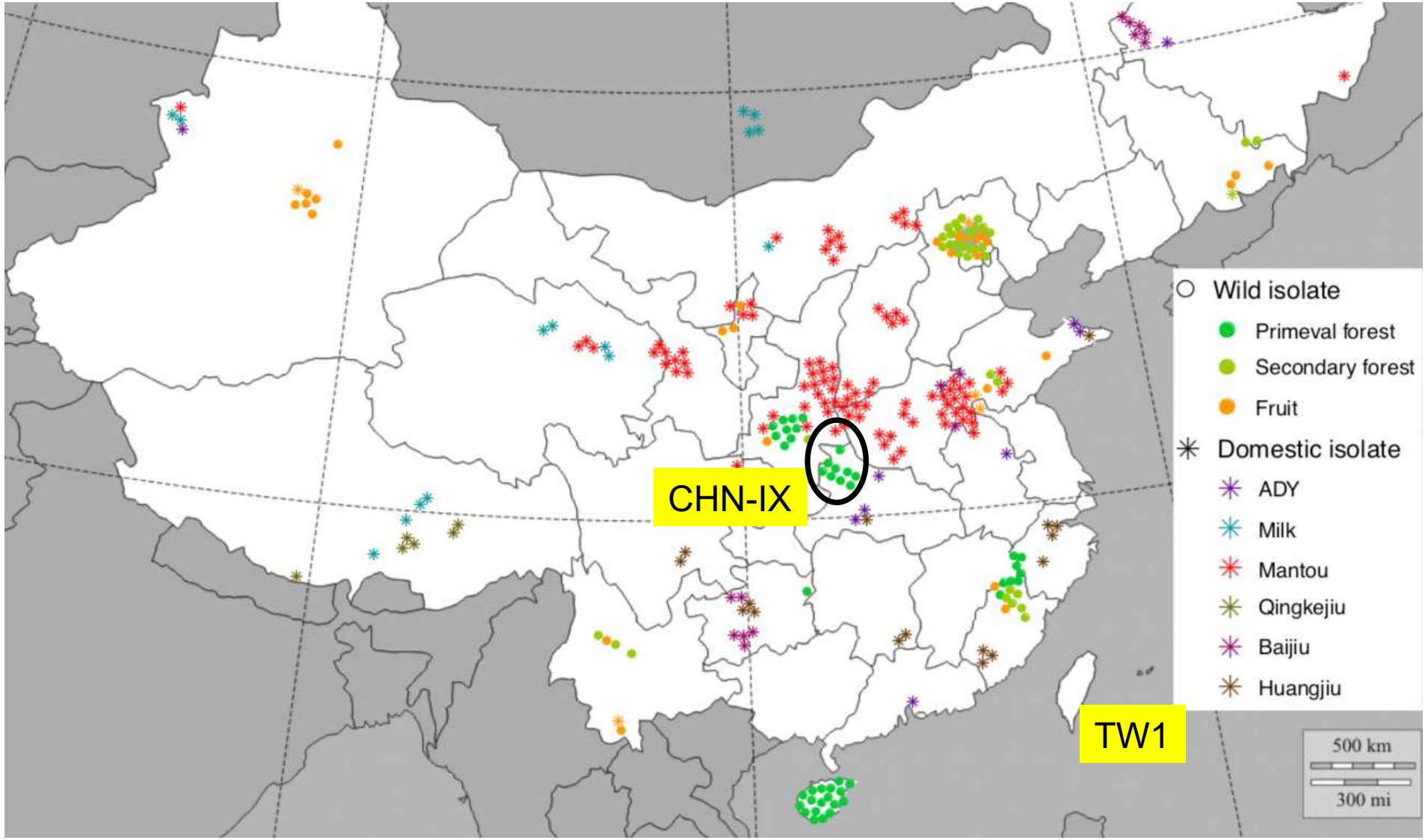
"The **Taiwanese wild lineage** represents the most divergent population that has yet been described"

Peter *et al.,* (2018) Nature

"CHN-IX contains isolates from a subtropical **primeval forest located in central China** and represents the most basal lineage of *S. cerevisiae*"

Duan *et al.,* (2018) Nature Communications

S. cerevisiae lineages displaying a disjunct distribution



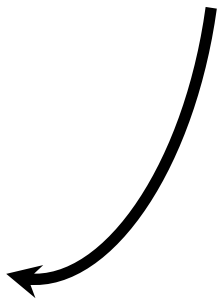
Duan *et al* (2018) ; Peter *et al* (2018)

Outstanding questions

1. geographic origin of *S. cerevisiae*

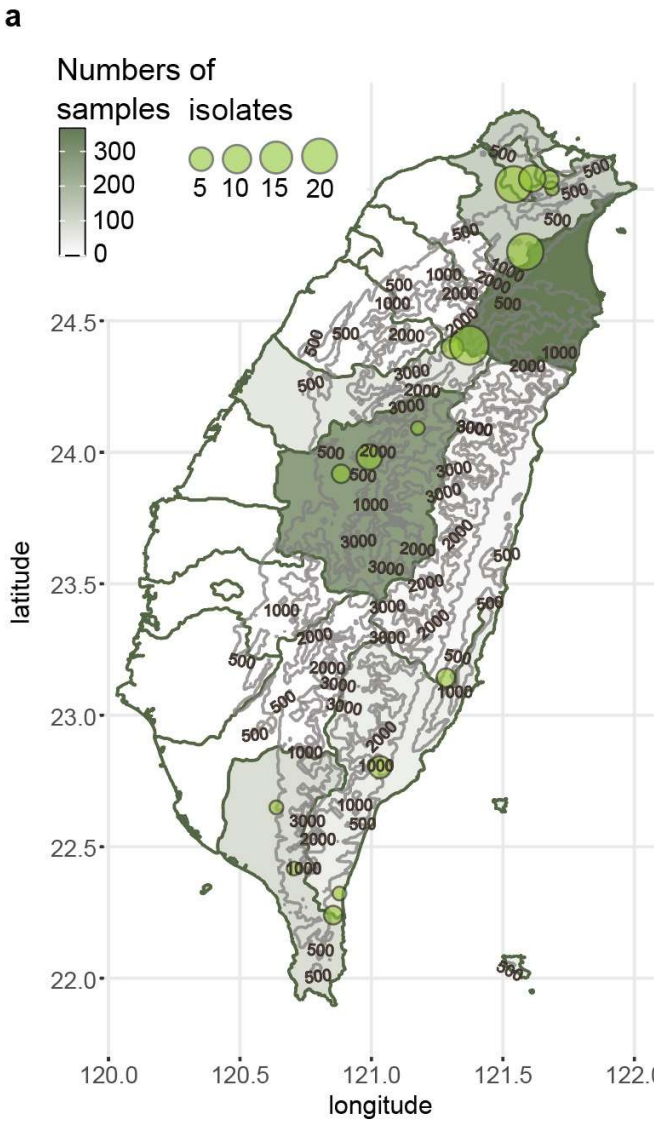
East Asia

2. ecology of *S. cerevisiae* in nature



3. biogeography of *S. cerevisiae*

Sampling and isolating *Saccharomyces* since 2016



Flowers of Fagaceae

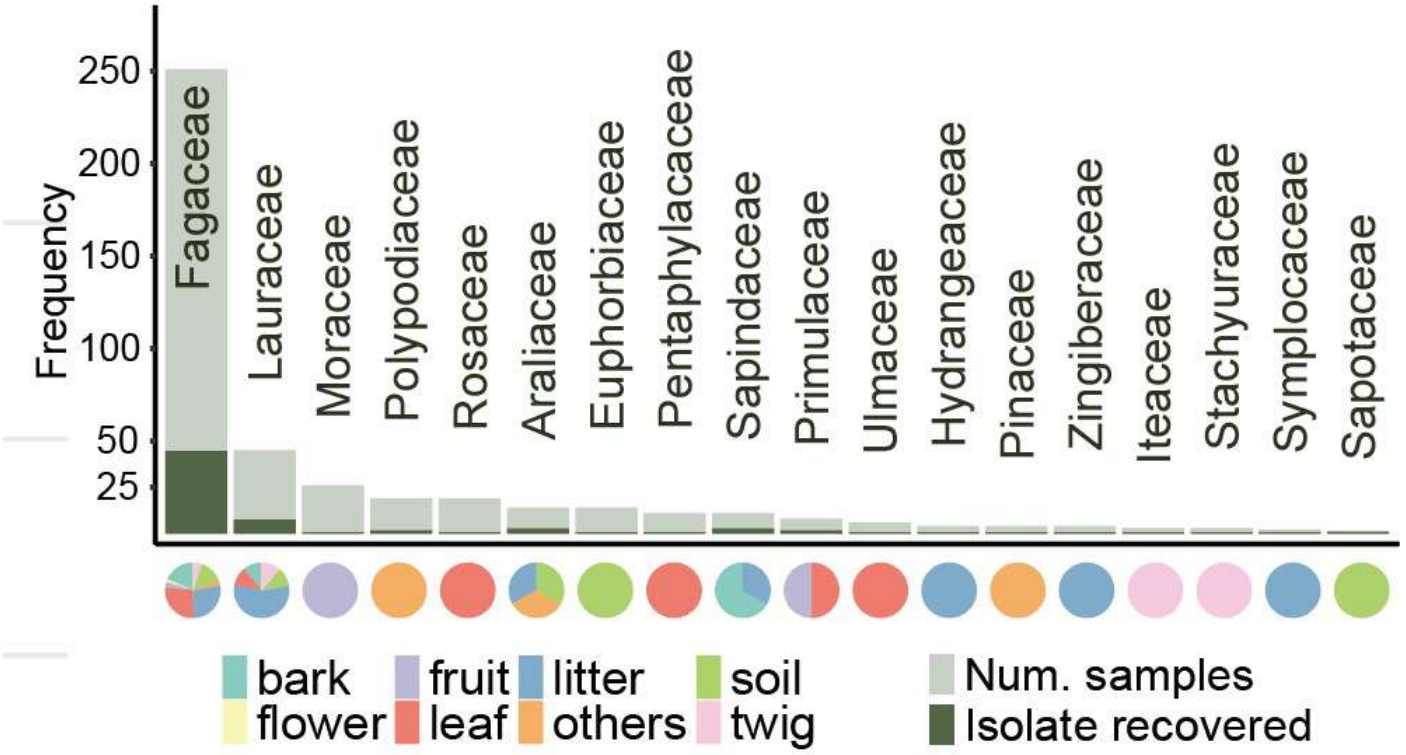
National park paths

Quercus

公路旁

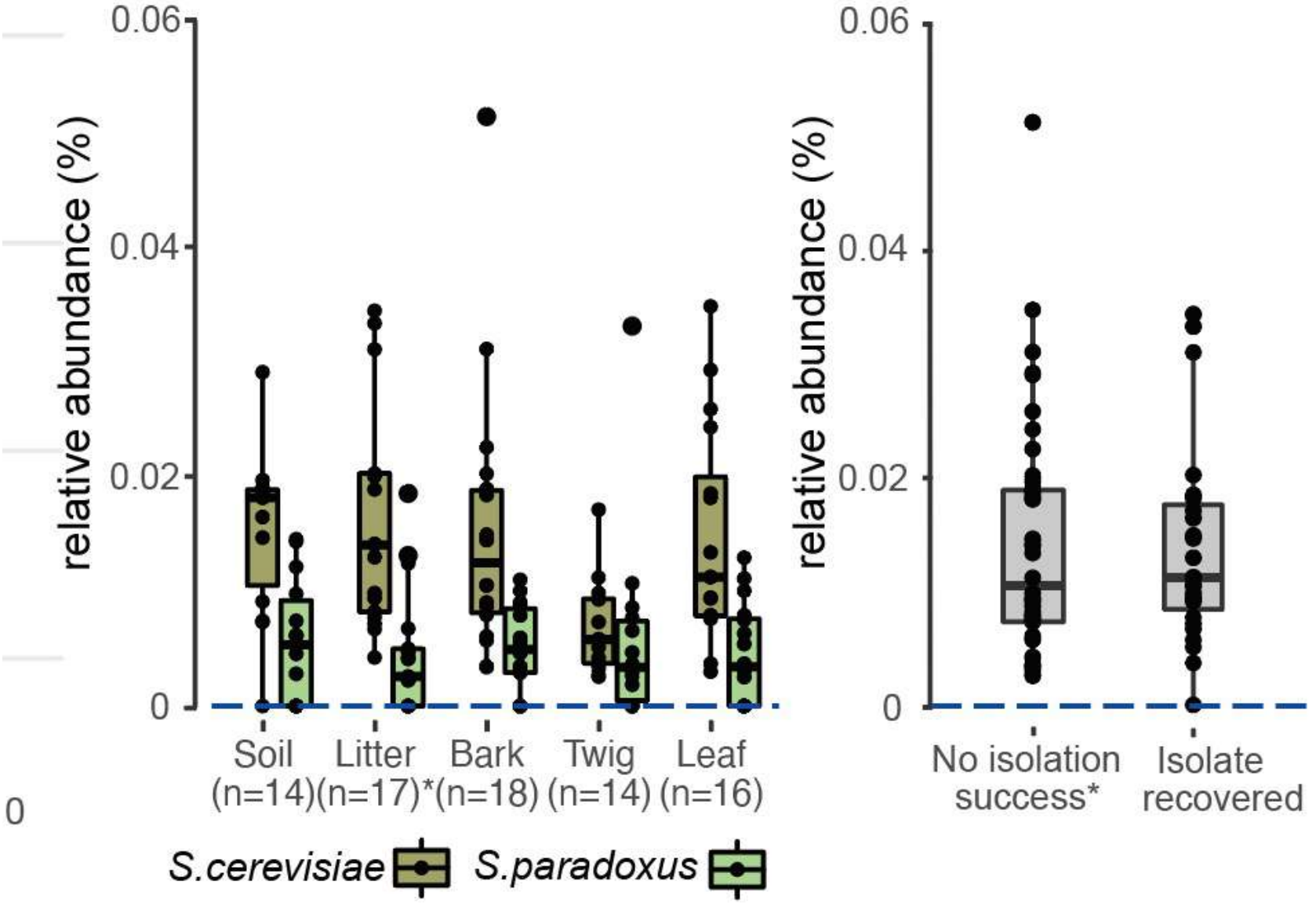
Amenity trees

Deep sampling and isolation of *S. cerevisiae* in Taiwan.

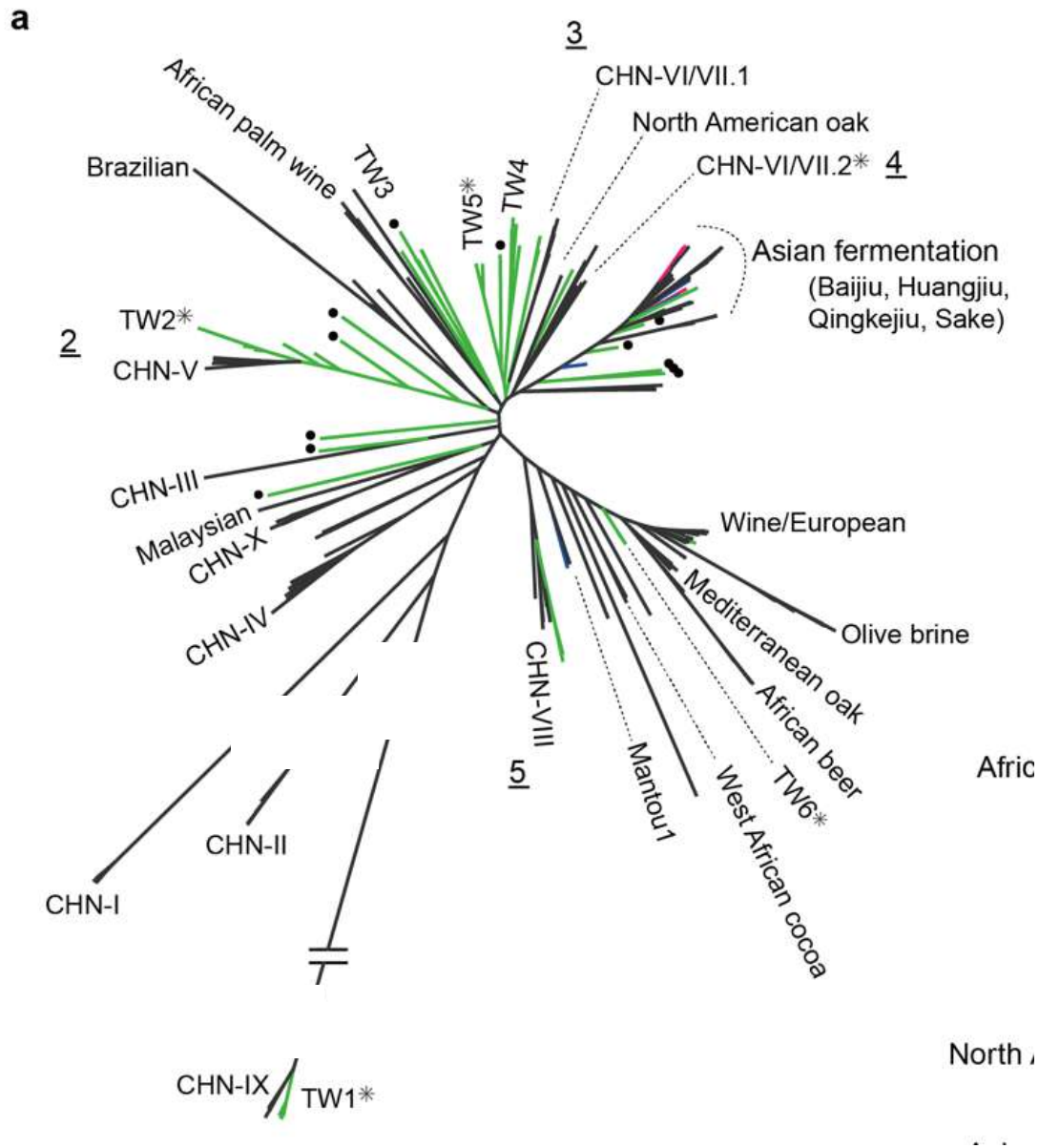


Isolation rates of *S. cerevisiae* per sample and per tree host was **1.9** and **10.8%**, respectively

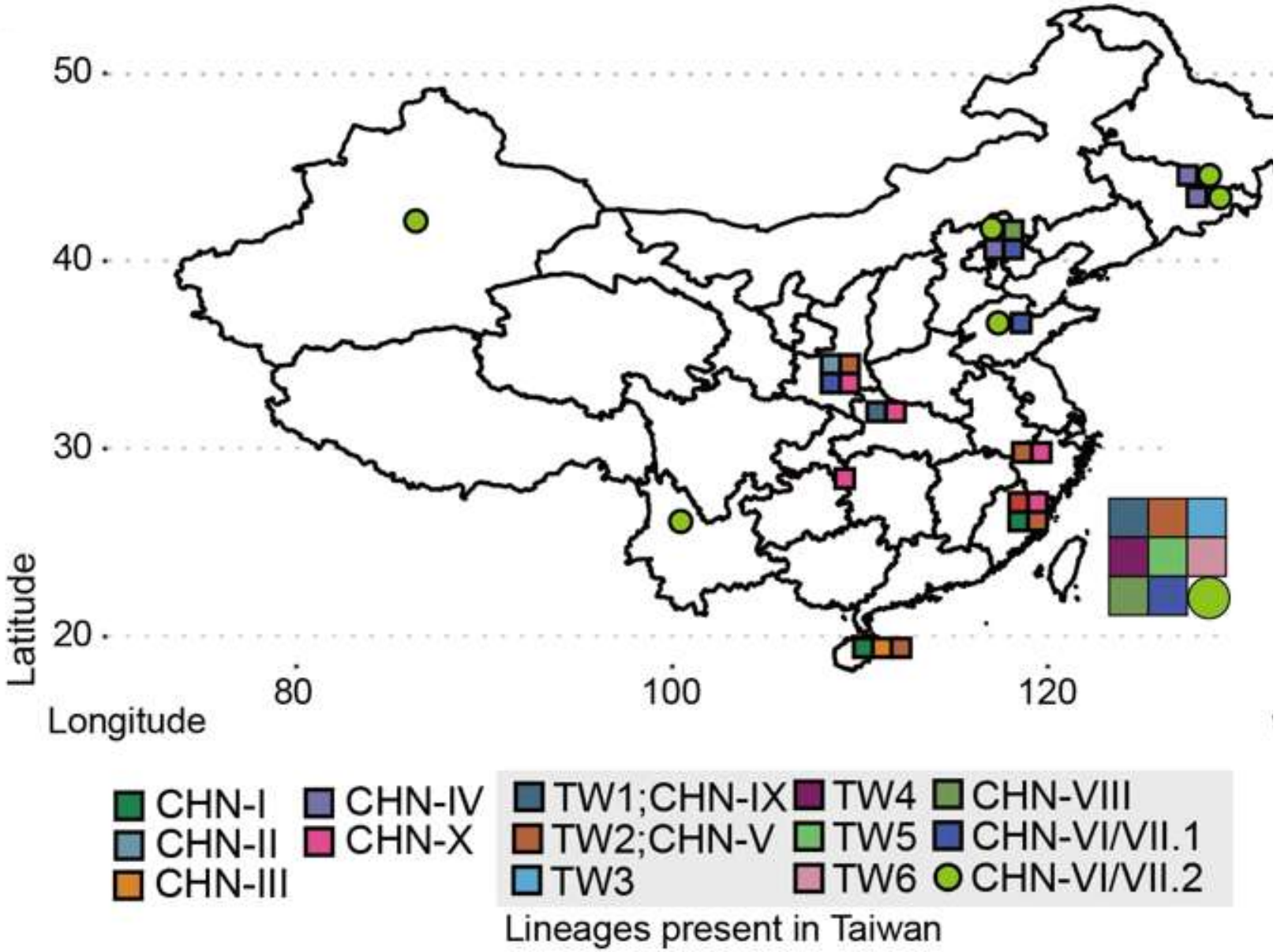
Deep sampling and isolation of *S. cerevisiae* in Taiwan.



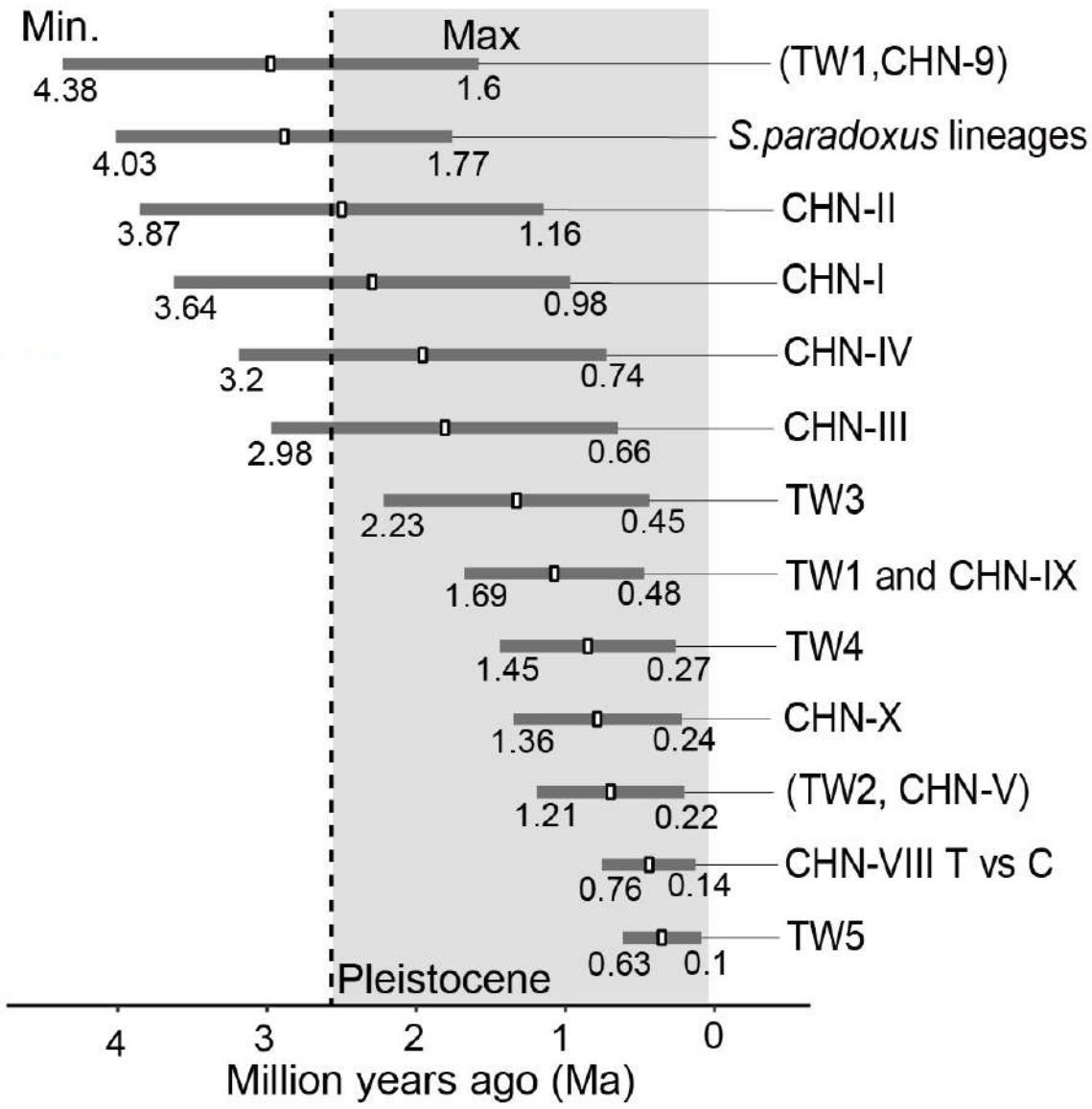
A maximum likelihood phylogeny based on 808,864 SNPs segregating in 340 isolates



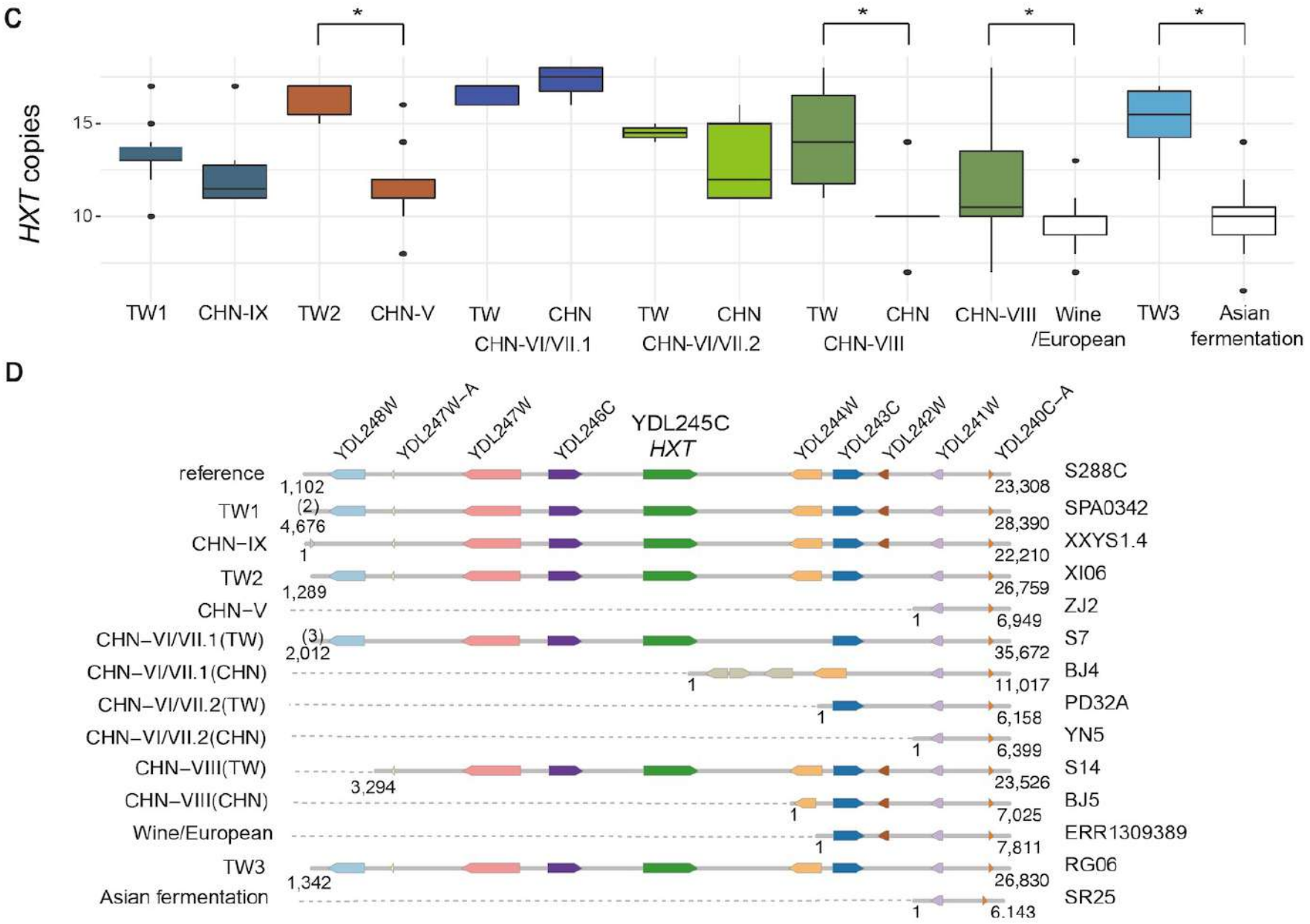
Biogeography of *S. cerevisiae*



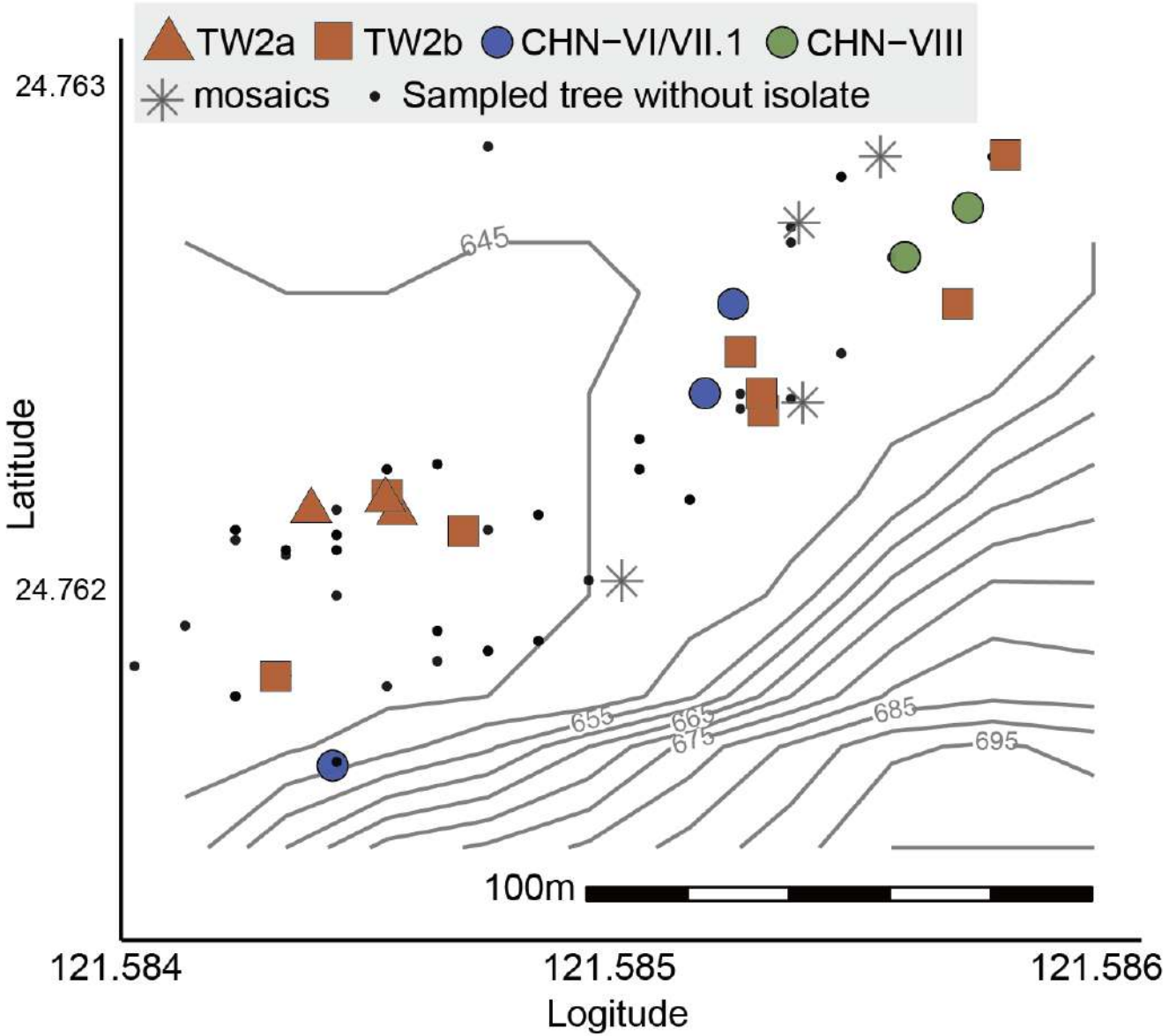
CHN/Taiwan isolates diverged during the Pleistocene



CHN/Taiwan undergo independent evolutionary scenarios

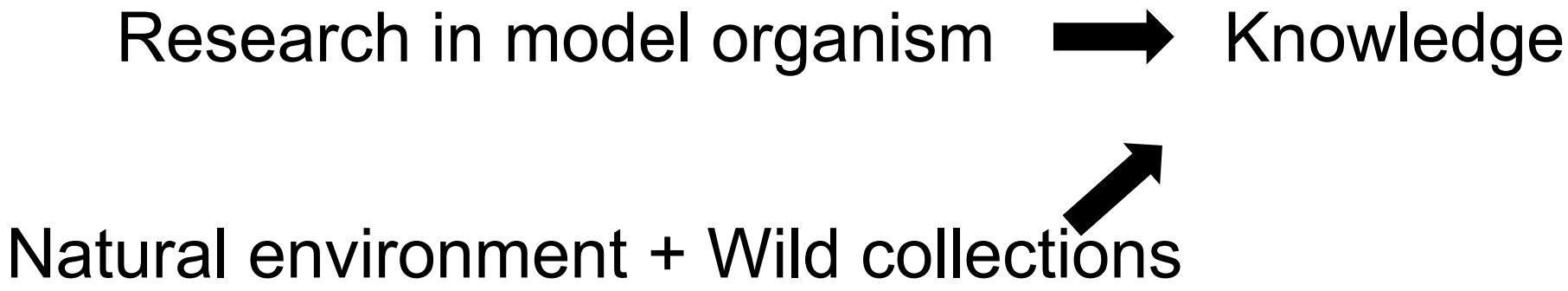


Patterns of genetic variations and geographical distribution in *S. cerevisiae*



Summary

Extensive traits and tools



Establish *S. cerevisiae* as the new model in microbial ecology; Formulate questions from nature

Acknowledgement

Deep sampling of ancestral genetic diversity reveals *Saccharomyces cerevisiae* pre-domestication life histories

Tracy J. Lee, Yu-Ching Liu, Wei-An Liu, Yu-Fei Lin, Hsin-Han Lee, Huei-Mien Ke, Jen-Pen Huang, Mei-Yeh Jade Lu, Chia-Lun Hsieh, Kuo-Fang Chung, Gianni Liti, Isheng Jason Tsai

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