



Convergent adaptation at multiple genomic levels among mangrove

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Introduction

- Sequencing multiple species that share the same ecological niche may be a new frontier of genomic studies.
- Woody plant species that colonized the global tropical coasts, collectively referred to as mangroves, are ideal for convergence studies.
- We sequenced the genomes/transcriptomes of 16 species belonging in three major mangrove clades.
- Mangroves support rich biodiversity and high levels of productivity, supplying seafood at capacities large enough to feed millions of people (IUCN).



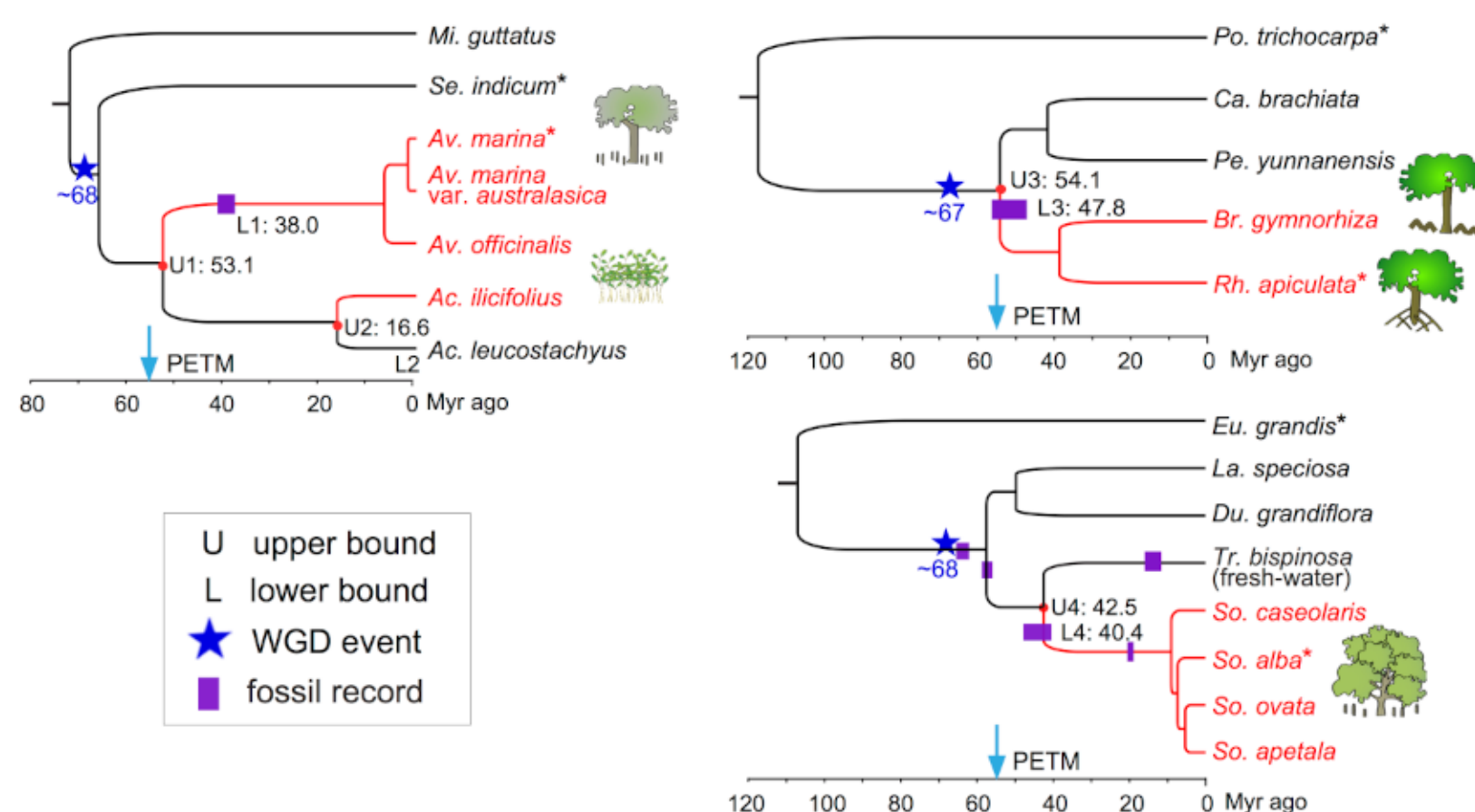
Avicennia
Avicennia marina
A. m. v. australasica
A. m. v. eucalyptifolia

Rhizophoreae
Rhizophora apiculata
R. stylosa
R. mucronata
R. mangle
Bruguiera gymnorhiza

Sonneratia
S. alba
S. caseolaris

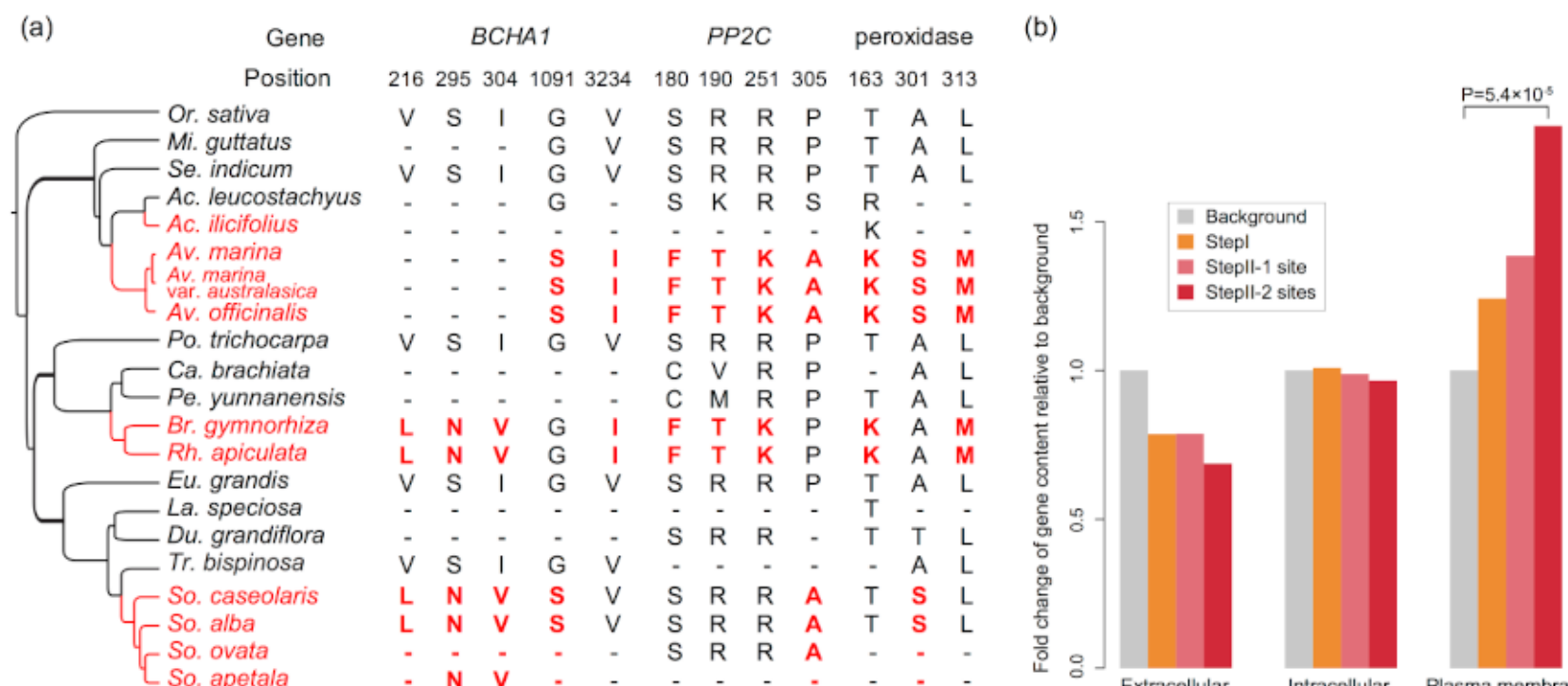
Results

1. Independent and concurrent emergence of mangroves



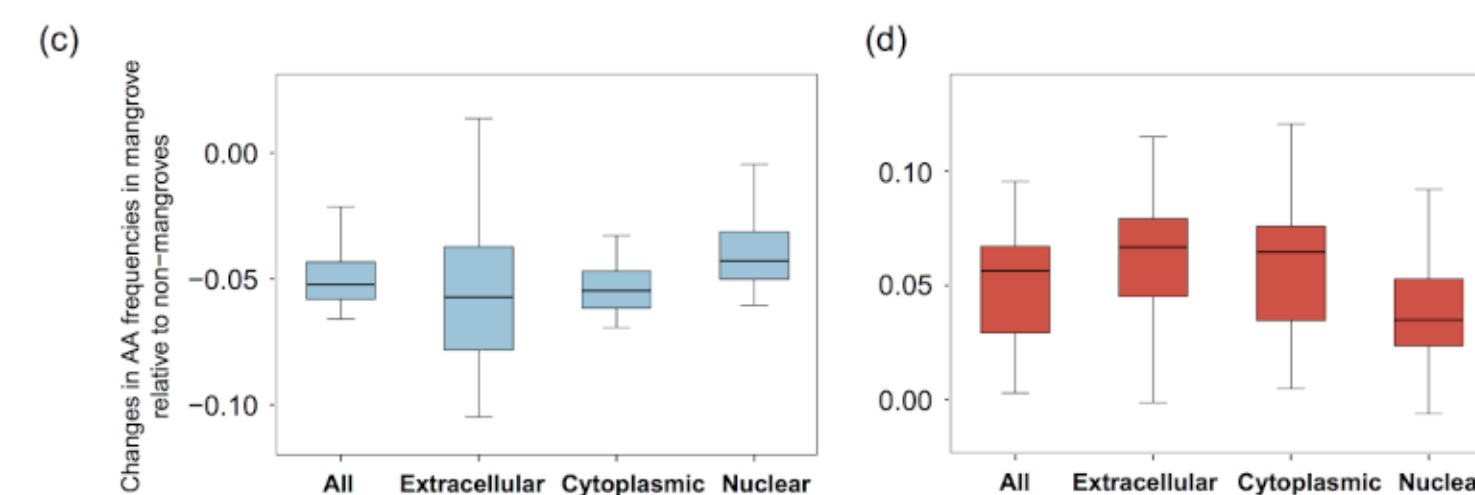
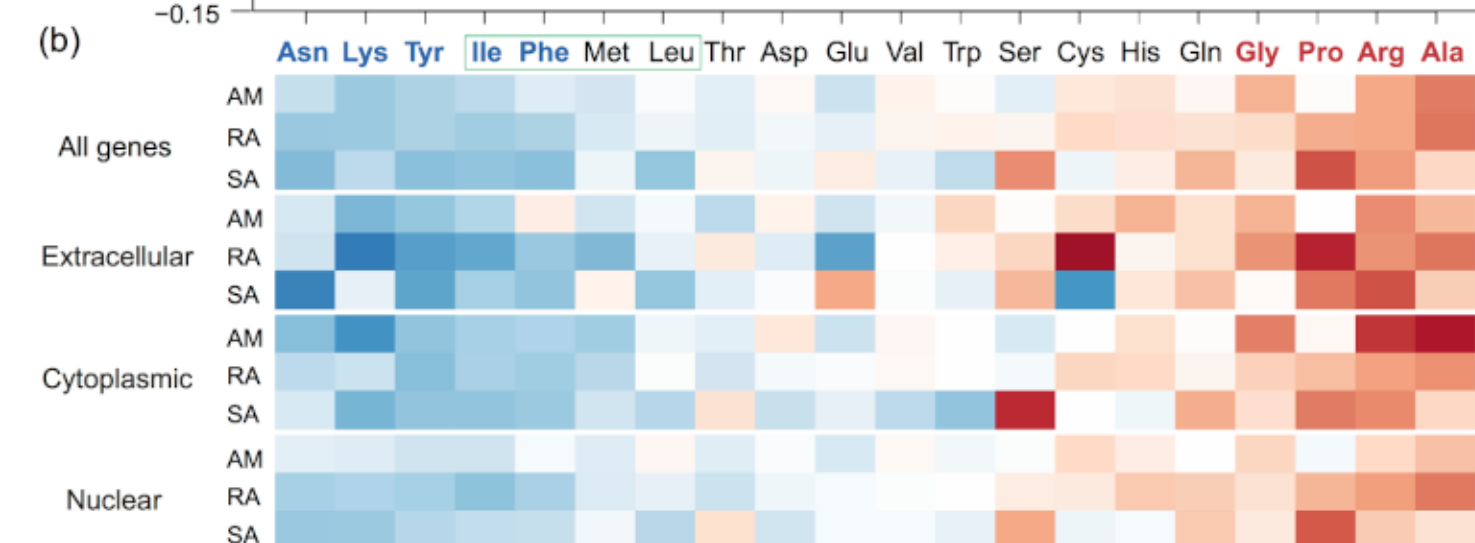
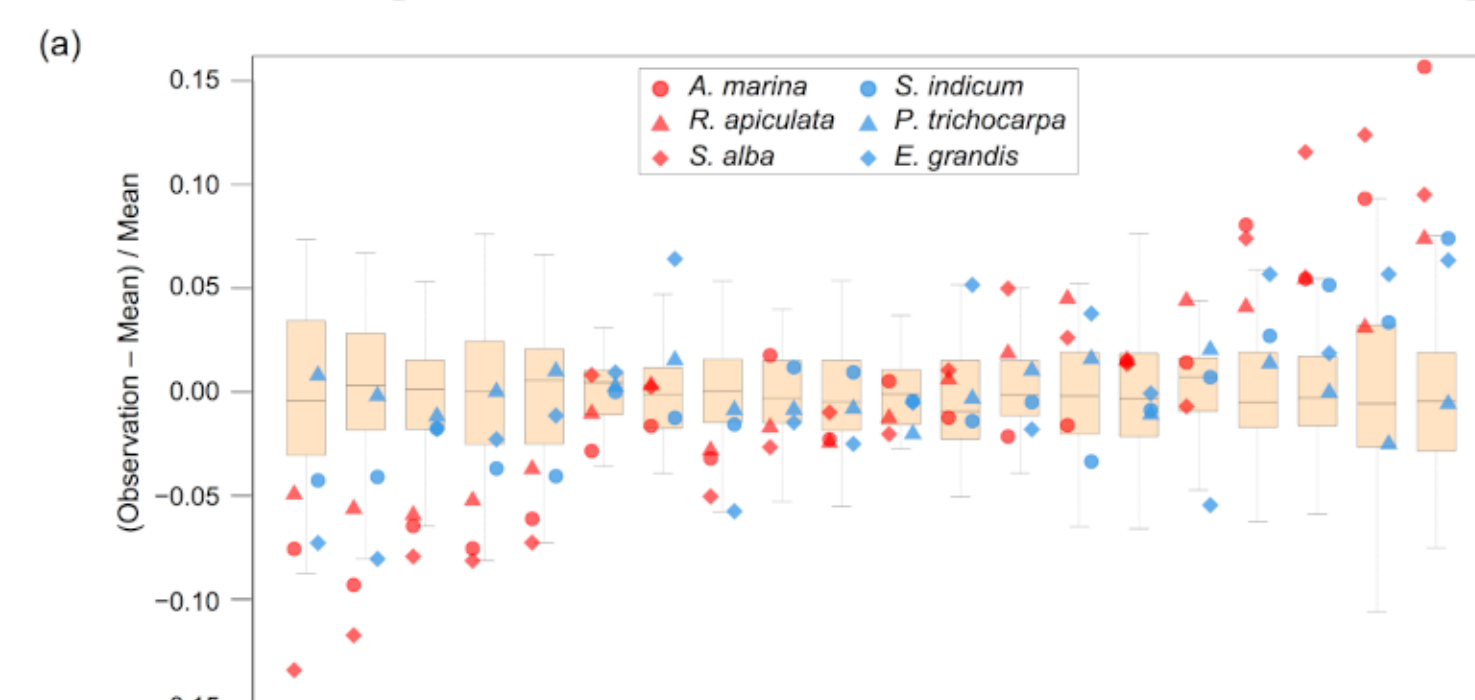
- The origins of the three major mangrove clades are clustered in the interval of 43-54 Myr ago. This interval roughly corresponds to a brief period of extreme global warming called the Paleocene-Eocene Thermal Maximum (PETM, blue arrows), ~55.5 Myr ago.
- Prior to colonization of the new habitats, the three mangrove clades independently experienced whole genome duplication (stars on branches).

2. Convergent evolution at amino acid sites



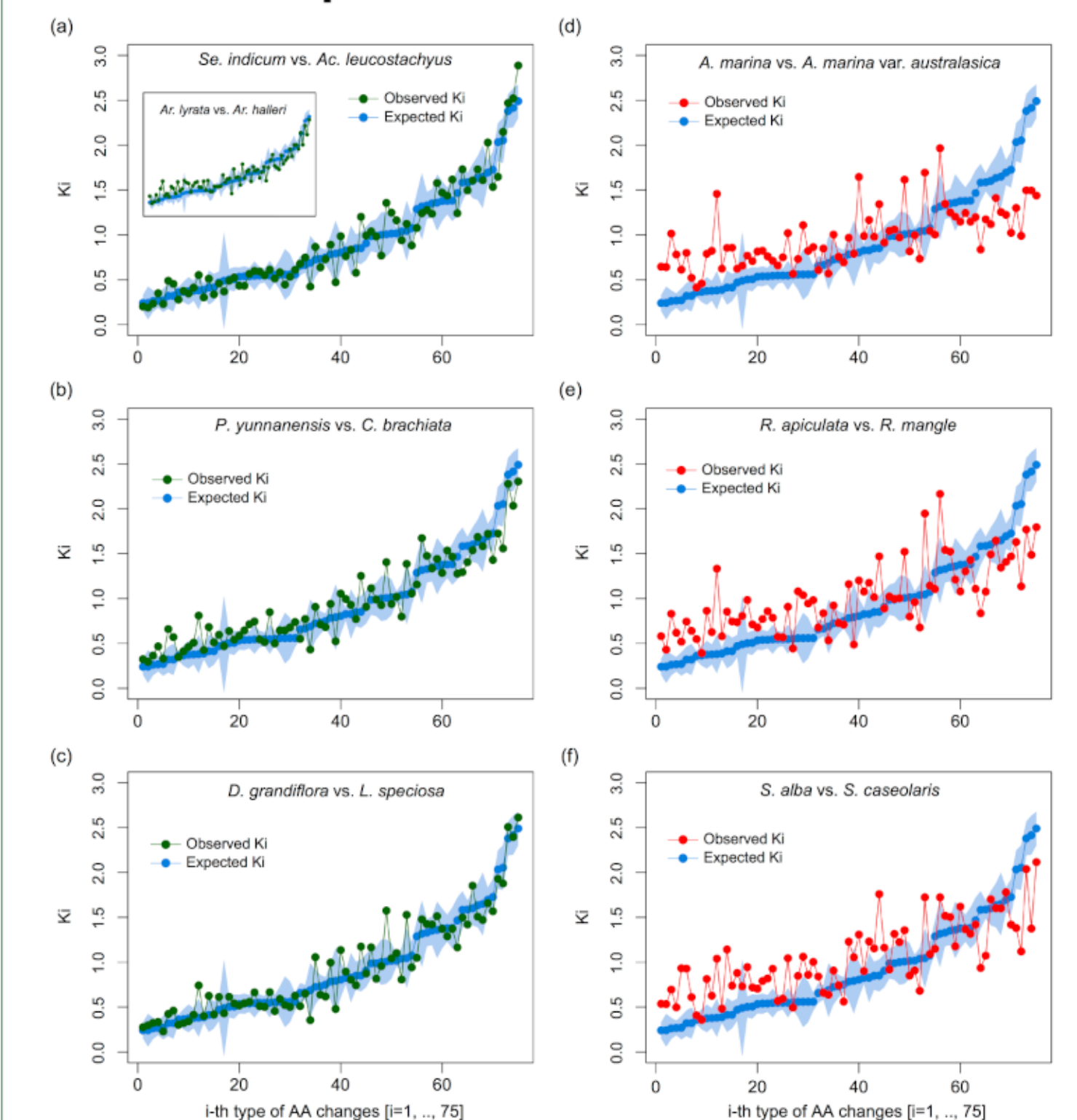
- CCS method (Xu et al. 2017 MBE) was first applied to confirm the higher level of convergence in mangroves than controls (inland relatives).
- Using the full phylogeny of 21 species, we identified 73 convergent genes with high confidence. Genes of the “ubiquitin mediated proteolysis” pathway are enriched in the sets.
- Three mangrove convergent genes have ≥ 3 convergent sites and are associated with salinity tolerance.
- Proteins of convergence are enriched on plasma membrane.

3. Convergent evolution in amino acid usage



- Comparing with 54 other dicotyledonous plants, AA usages in mangroves are consistently the outliers. There are four AAs overused (red font) and five AAs underused (green font) in three mangroves.
- For the nine most significantly changed AAs, the degree of change is highest in the extracellular and lowest in the nuclear location. This pattern indicates the degree of deviation in AA usage to correspond with the local salinity level.

4. The evolutionary mechanism of convergence observed between closely related species



- There are 75 pairs of AAs that substitute with 1-bp change. The rank and relative magnitude of these substitution rates (Ki's) are nearly constant across species (Tang et al. 2004 MBE).
- In non-mangroves, the observed Ki's agree well with the expected values.
- In mangroves, the observed Ki's deviate strongly from the expected Ki's.

Conclusions

- Implementing a CCS+ model, we identified 73 highly confidential convergent genes. Products of the convergent genes tend to be on the plasma membrane associated with salinity tolerance.
- Convergence is more often manifested at a higher level than at amino acid (AA) sites. Relative to > 50 plant species, mangroves strongly prefer 4 amino acids (AAs) and avoid 5 others across the genome.
- AA substitutions between mangrove species strongly reflect these tendencies.
- The selection of taxa, the number of species and, in particular, the empirical control are all crucial for detecting genome-wide convergence.