

Symportal, what gives?

Hume et al., 2019

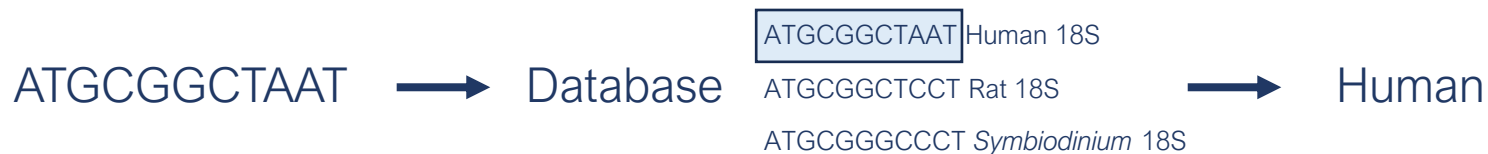


Brief intro to metabarcoding (reiteration)

- Metabarcoding is getting the sequences of a universal gene (barcode) from a community (2 or more organisms)



- Universal gene/universal gene marker = gene found in most living organisms which can provide taxonomy information
 - 16S, 18S, ITS2

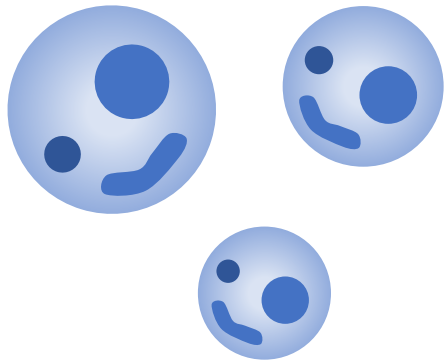


Symportal

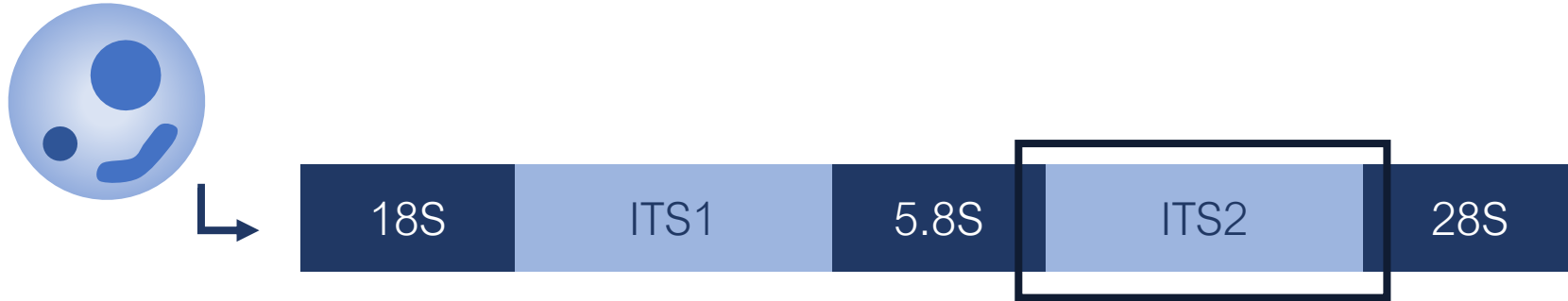
- A framework for resolving putative taxa of Symbiodiniaceae using NGS data of the **ITS2 amplicon**



What gives?



What gives?

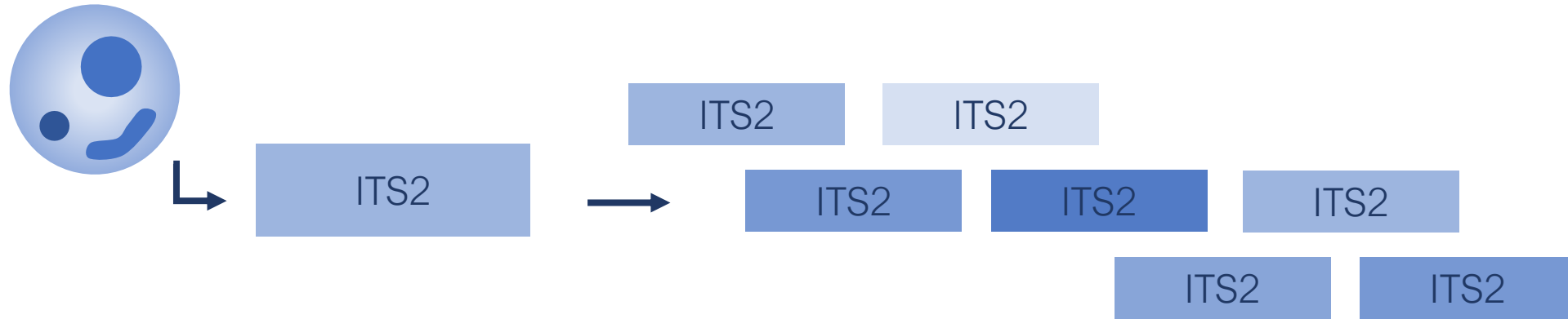


* 16S of bacteria (1-17 copies) and archaea (1-4 copies) has fewer copies

- ITS2 in Symbiodiniaceae can be hundreds to thousands;



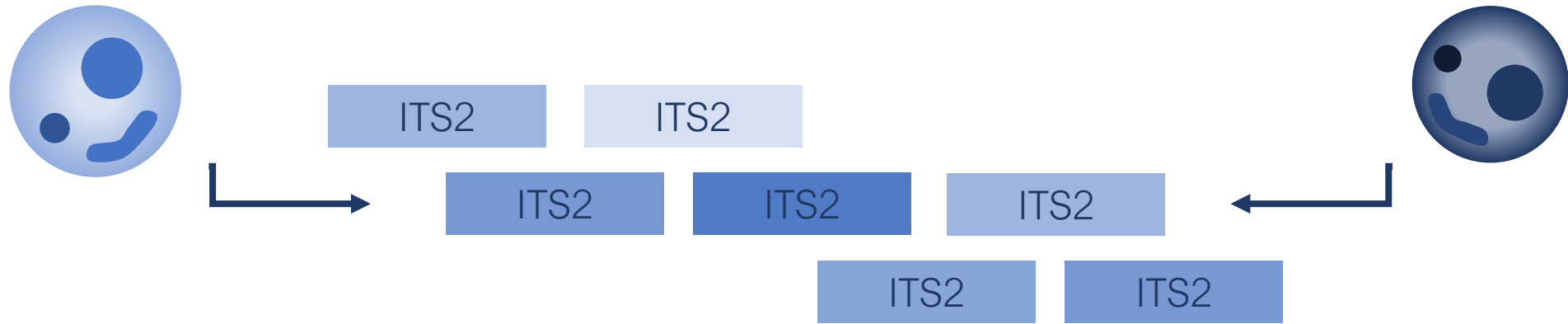
What gives?



- ITS2 in Symbiodiniaceae can be hundreds to thousands;
- and have high sequence variations (intragenomic diversity)
 - Presence of an ITS2 sequence is hard to correlate with actual abundance
 - No single ITS2 sequence correspond to one Symbiodiniaceae type/species



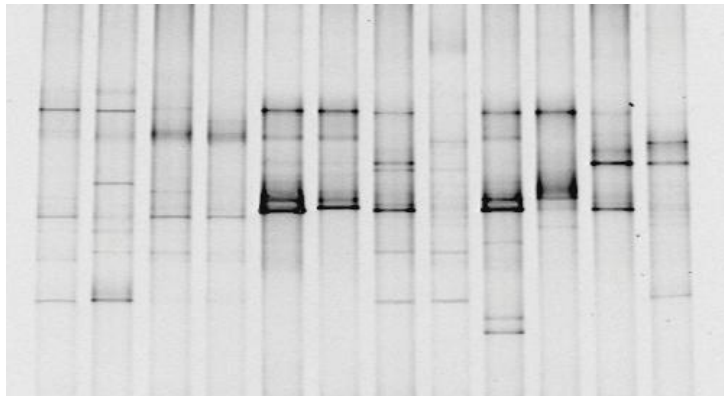
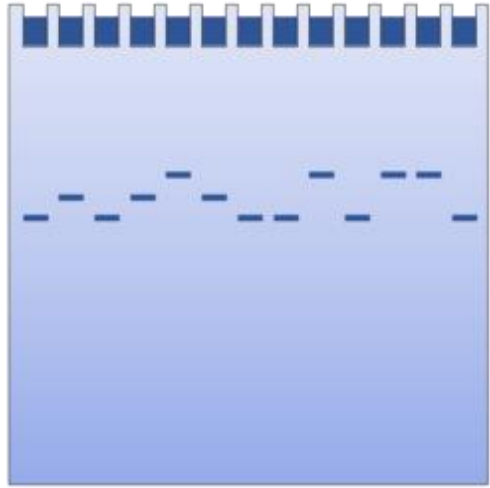
What gives?



- Also, multiple Symbiodiniaceae types could be harbored in a host with several ITS2 sequences that could sometimes be similar and could underestimate diversity (intergenomic diversity)



Why use?



Denaturing gel electrophoresis (DGGE)

- Molecular fingerprinting of communities based on denaturation characteristics of a sequence
- Low-throughput
- Low sensitivity
- Cannot distinguish putative Symbiodiniaceae strains from a common genus



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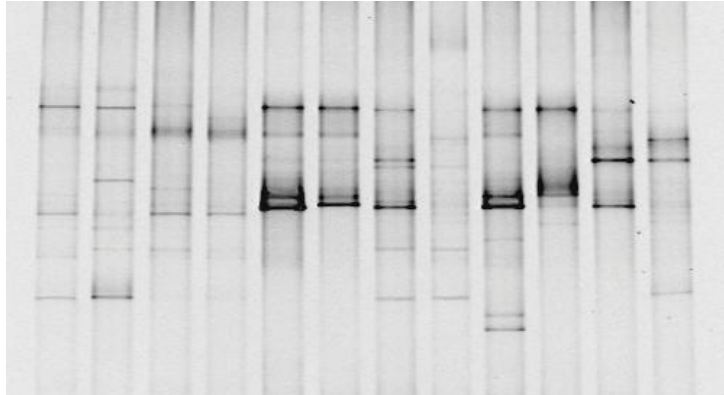


Symportal

- Community-wide identification of Symbiodiniaceae based on NGS
- High-throughput
- High sensitivity
- Can distinguish putative Symbiodiniaceae strains from a common genus

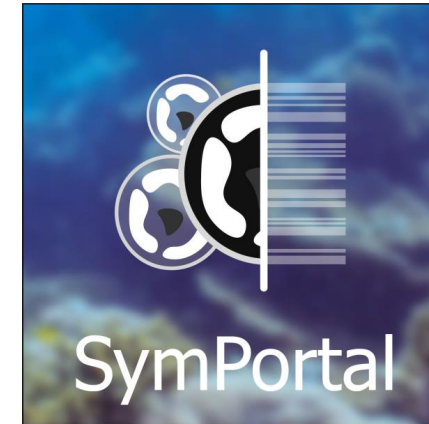


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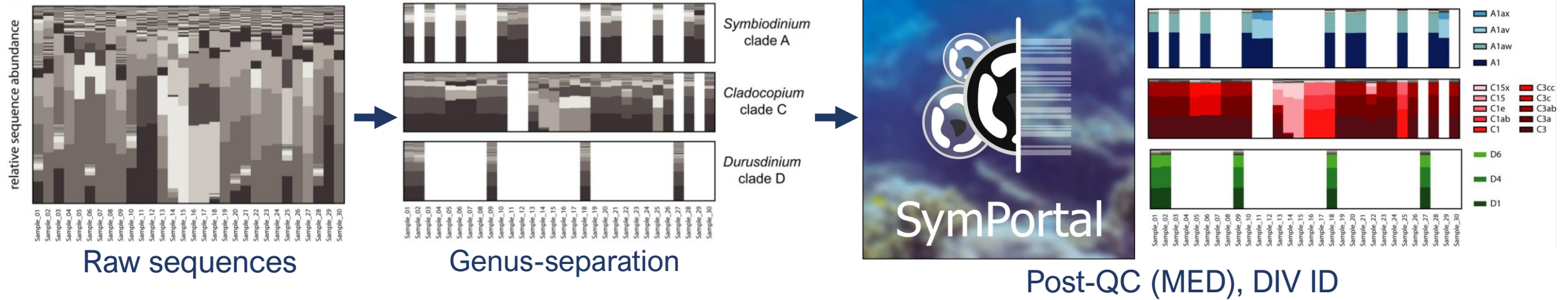


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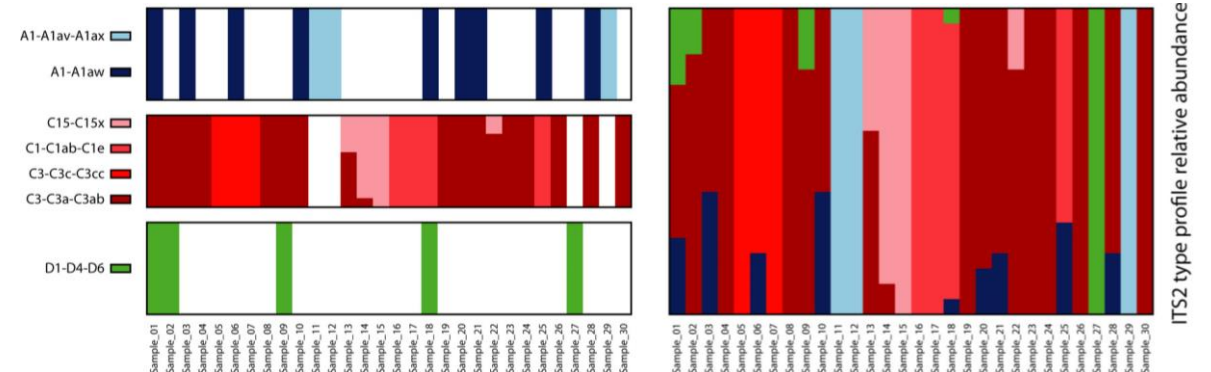
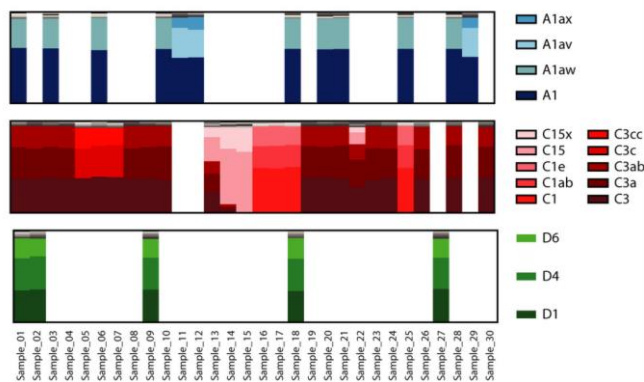
How?



How?



Post-QC, MED, DIV ID

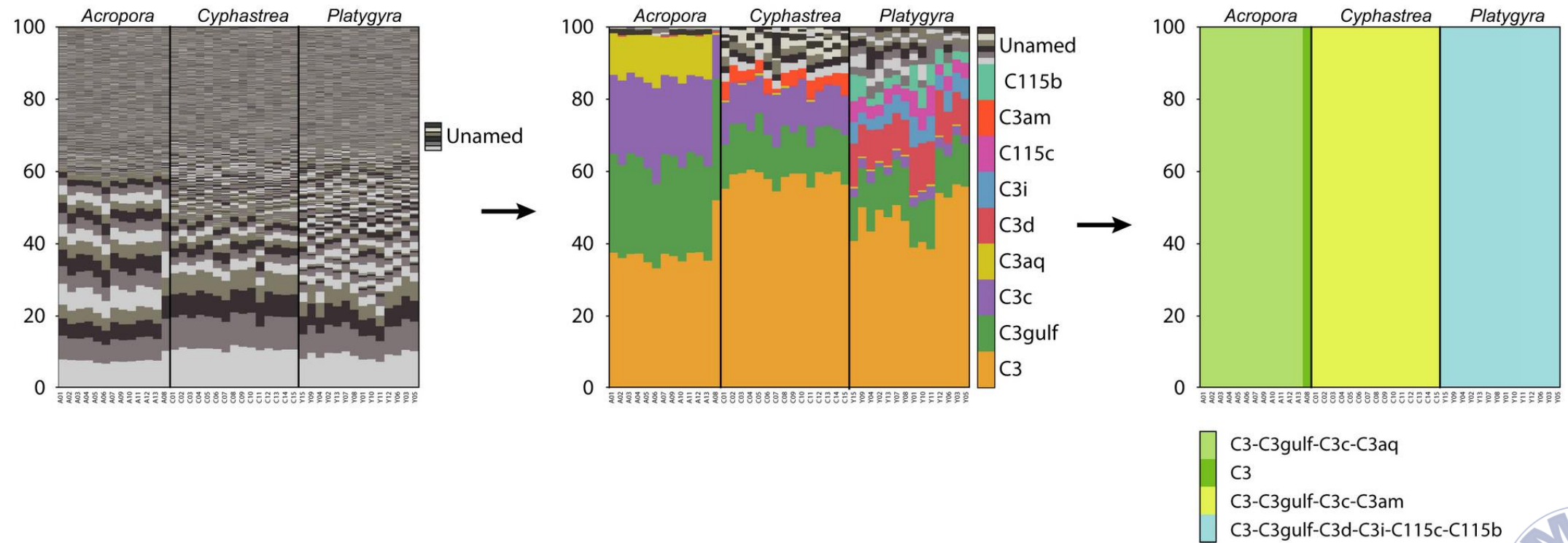


ITS2 type profile prediction



How?

Example



How?

Traditional example

