



Genetic Population Structure of *Amblygaster sirm* in Southeast Asian Region

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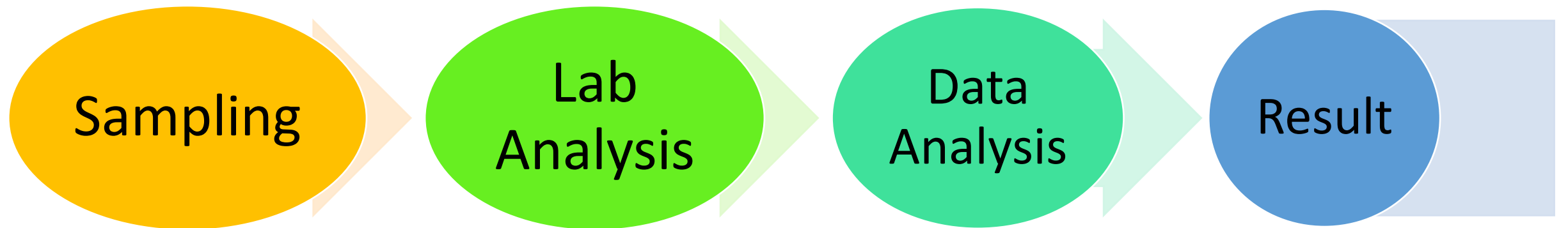
Introduction

- CEM in 2014 had agreed to choose *Amblygaster sirm* as the targeted species for genetic population study and mtDNA cytochrome *b* as the genetic marker.
- Based from the previous result and also presented in CEM 2016, **no significant or homogenous structure** of *Amblygaster sirm* in **4 locations in South China Sea** (Kudat, Kuantan, Muara and Songkhla).

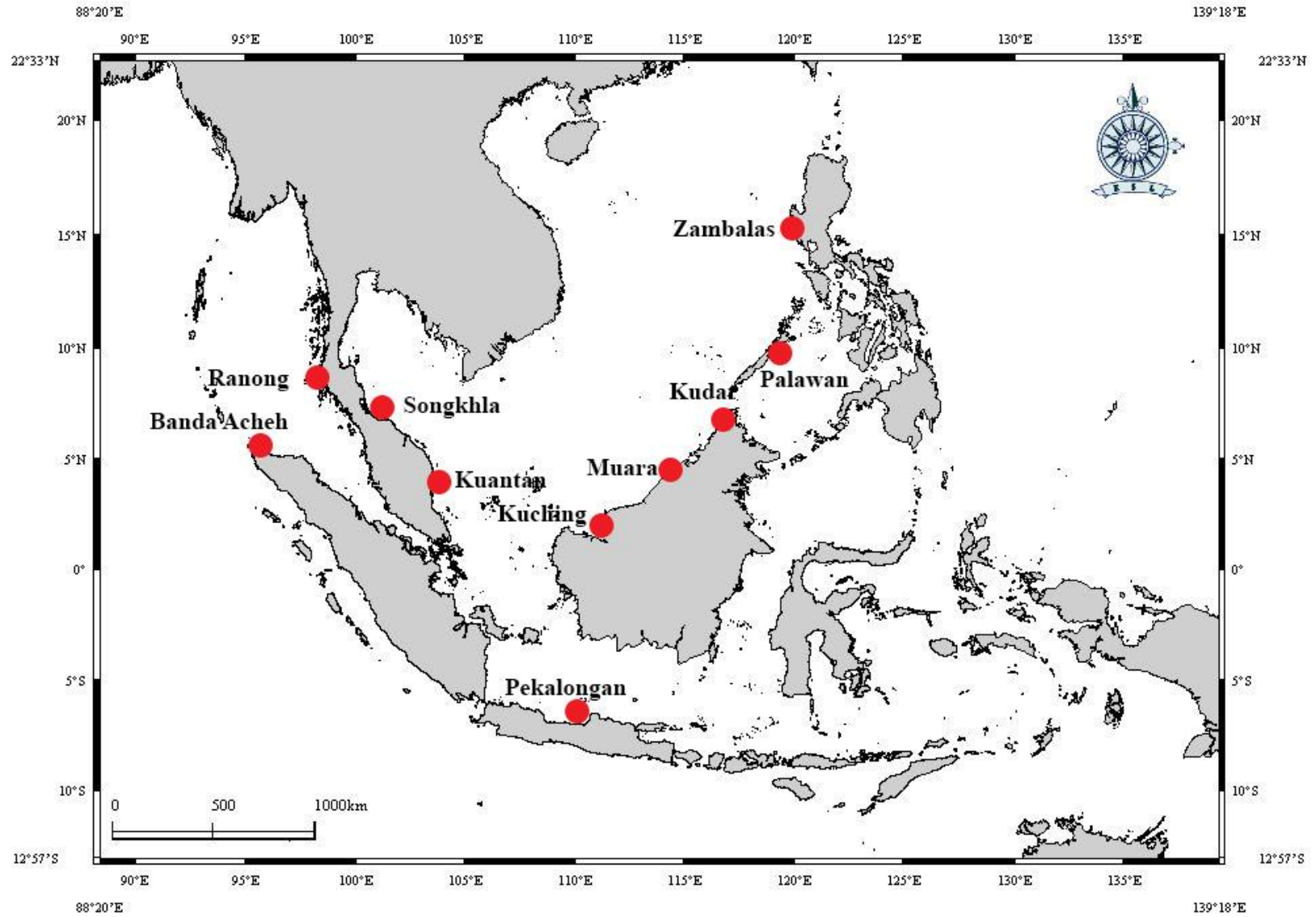
However...

- From CEM 2017, the results based from both sides; South China Sea and Andaman Sea (particularly from Ranong) shows a genetic different from *Amblygaster sirm* inferred by mtDNA Cyt b gene.
- To confirm this result, additional data was taken and analysis was done using other gene (mtDNA COI) for comparison/confirmation.
- The current result was discussed among genetic experts during workshop in August 2018 at Langkawi, Malaysia.

Materials and Methods



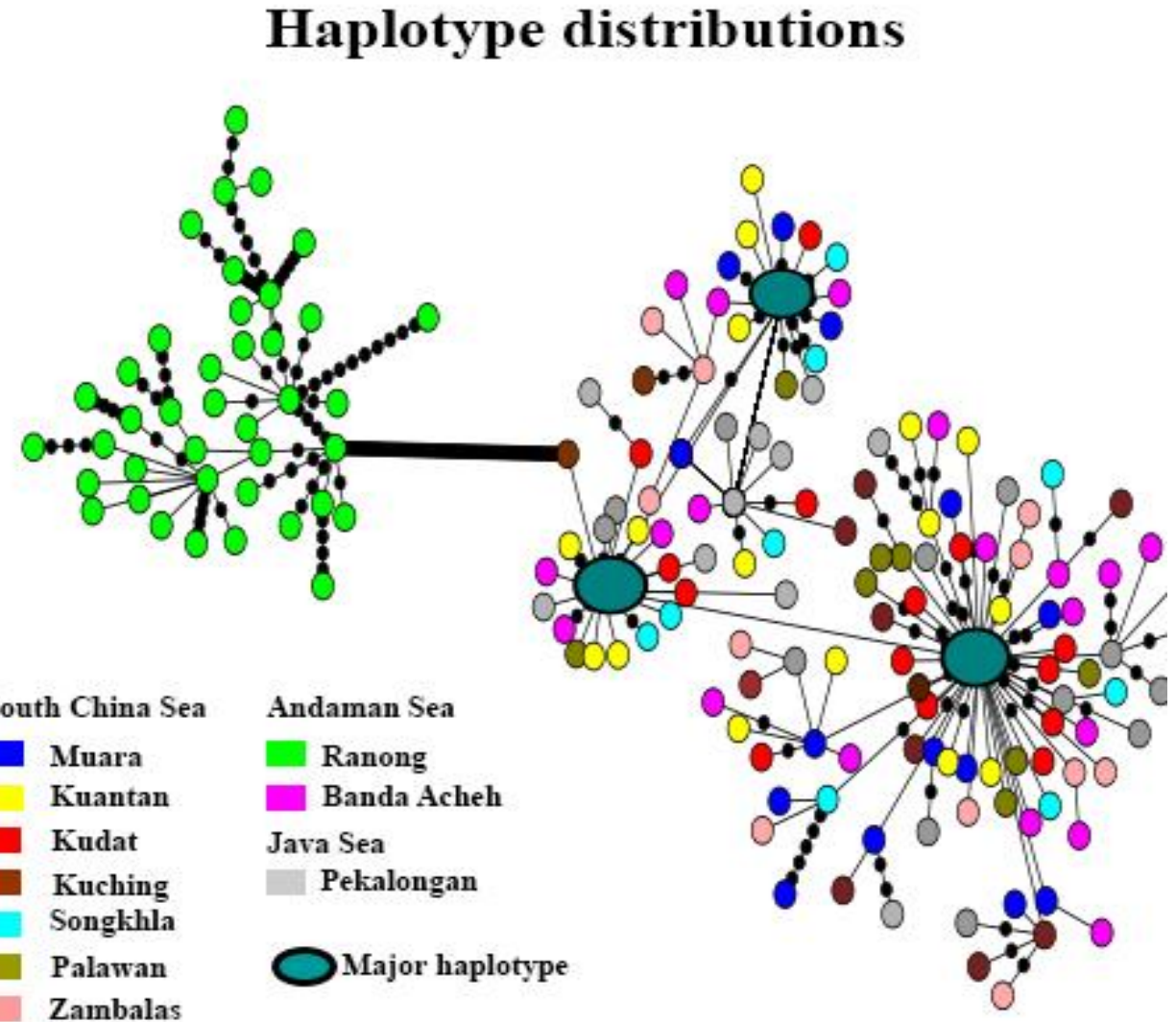
Sampling sites (Cyt b)



10 locations, 323 samples

Results (Cyt b)

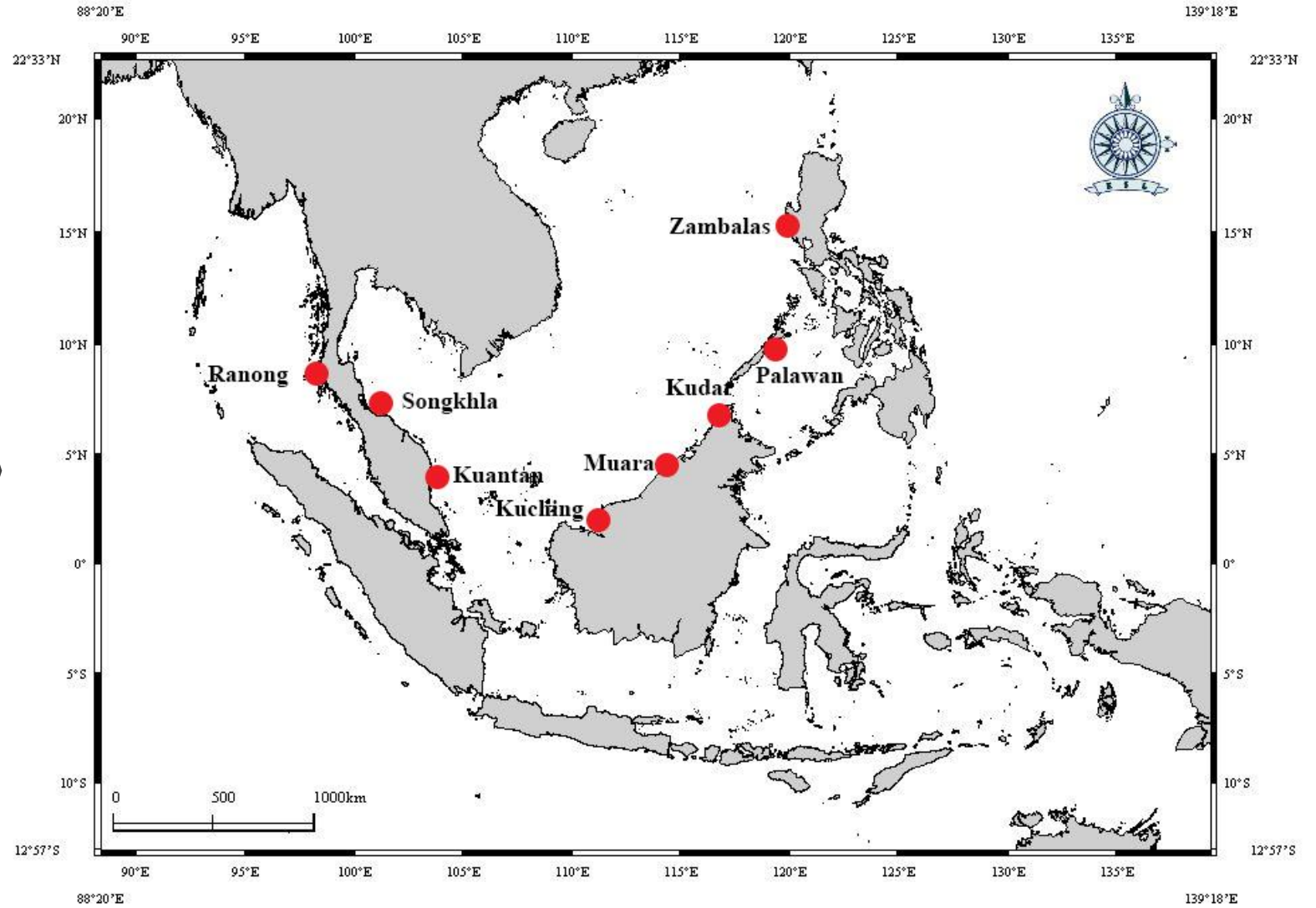
1. **TWO** groups of *Amblygaster sirm* with **HIGH** genetic distance between South China Sea (including Banda Aceh (southern Andaman Sea) and Ranong (northern Andaman Sea).



	<u>Muara</u>	<u>Kuching</u>	<u>Kudat</u>	<u>Kuantan</u>	<u>Palawan</u>	<u>Songkhla</u>	<u>Zambalas</u>	<u>Pekalongan</u>	<u>Banda Aceh</u>	<u>Ranong</u>
<u>Muara</u>	0.030									
<u>Kuching</u>	0.003	0.004								
<u>Kudat</u>	0.003	0.003	0.002							
<u>Kuantan</u>	0.003	0.003	0.002	0.003						
<u>Palawan</u>	0.003	0.003	0.003	0.003	0.003					
<u>Songkhla</u>	0.003	0.003	0.003	0.003	0.003	0.003				
<u>Zambalas</u>	0.003	0.003	0.003	0.003	0.003	0.003	0.003			
<u>Pekalongan</u>	0.004	0.004	0.003	0.003	0.003	0.003	0.004	0.004		
<u>Banda Aceh</u>	0.003	0.004	0.003	0.003	0.003	0.003	0.003	0.004	0.004	
<u>Ranong</u>	0.071	0.071	0.070	0.070	0.071	0.071	0.071	0.071	0.071	0.007

Genetic differentiation (distance) shows **very high divergence (~7%)** between Ranong and other locations.

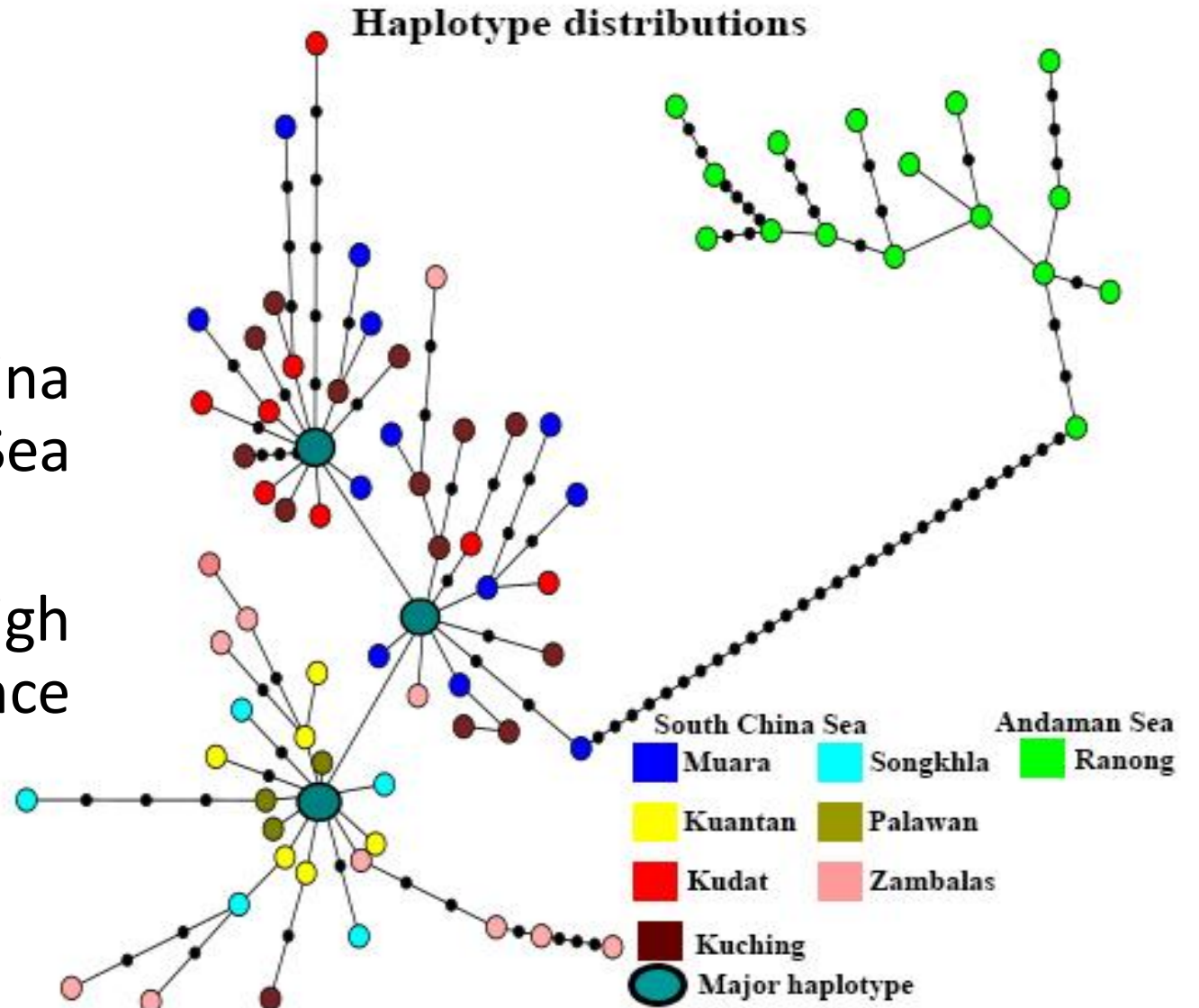
Sampling sites (COI)



8 locations, 138 samples

Results (COI)

1. **TWO** groups for South China Sea and Andaman Sea (Ranong).
2. Same result as Cyt b with high genetic distance/divergence (~5%).



Amblygaster sirm (morphology)



Kuala Terengganu, Malaysia



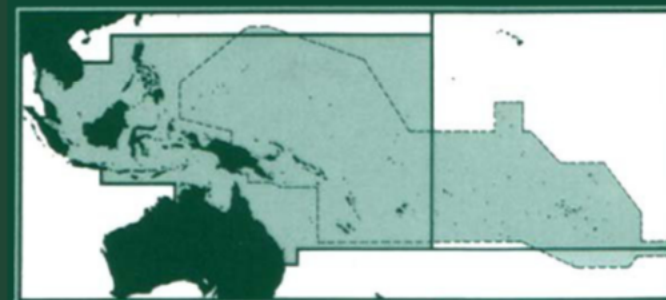
Ranong, Thailand



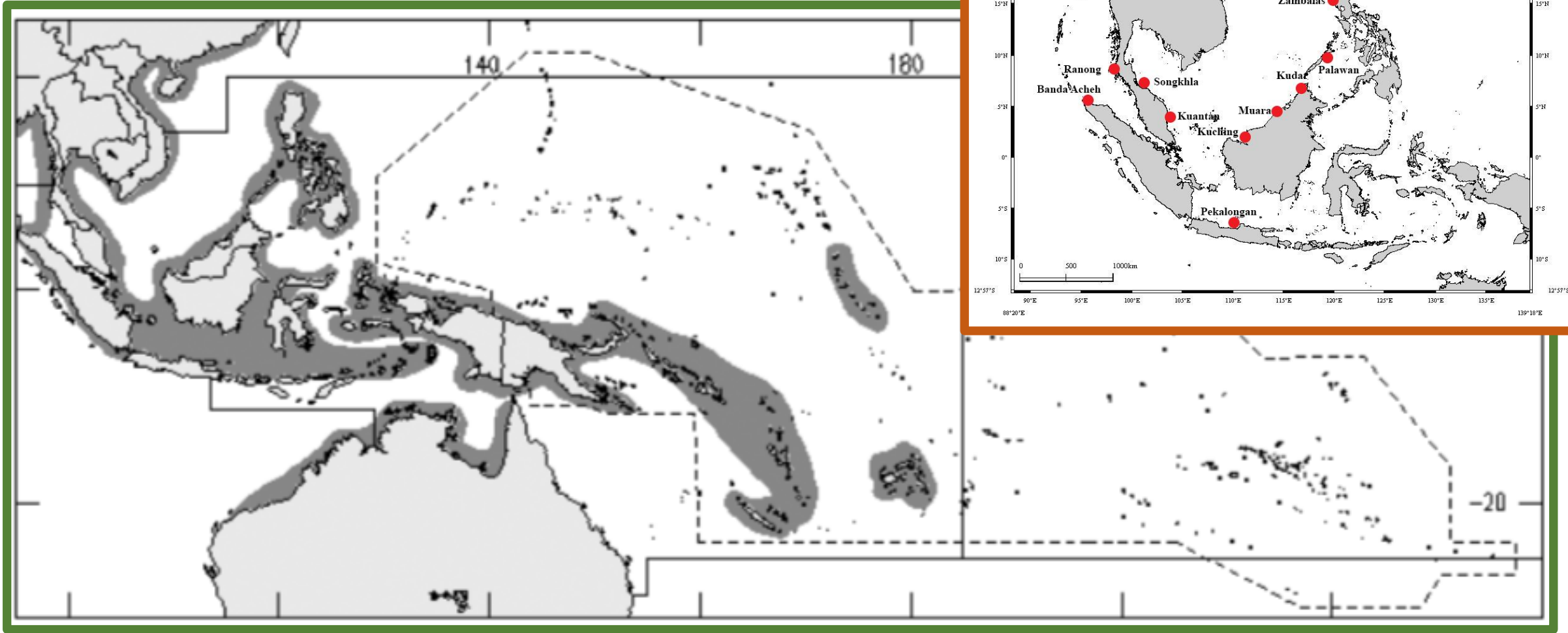
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This lead to the assumptions (from the workshop in August, 2018)

- Two different stocks of *Amblygaster sirm* between Ranong (**northern Andaman Sea**) and South China Sea (including **southern Andaman Sea**)- not agreed by genetic experts due to the genetic distance was very high.
- Different species/existing of sub-species. Possibility of expansion of genetic content but not in morphology.

Contribution factors/recommendations

- There are many factors that could have attributed to the existence of the sub-species or taxon such as;
 - i. Hybrid
 - ii. Faster rate of genetic evolution
 - iii. Discovery of new or cryptic species

Recommendations

- Future studies should include nuclear DNA such as microsatellites and RAG to provide paternal origin information.
- Additional samples from Bay of Bengal could also verify the current results.
- A more detailed morphological investigations is also crucial to identify any subtle differences between the two clades.
- A larger geographical coverage is essential for the Andaman Sea (northern).

Conclusion

Both the DNA markers used in this study revealed two highly genetic divergent stocks; Ranong vs the rest of the populations (South China Sea and Andaman Sea (southern part)). It is recommended that these stocks should be independently managed.

**Thank
You**

