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

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19 September 2018
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
- Lab Analysis
- Data Analysis
- Result

6/5/2019
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).
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

6/5/2019
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