

Meta Mito-Genomics (MMG):
the Next Generation Biodiversity
Monitoring Technology



Wang Wen-zhi

South China DNA Barcoding Center
Kunming Institute of Zoology, CAS

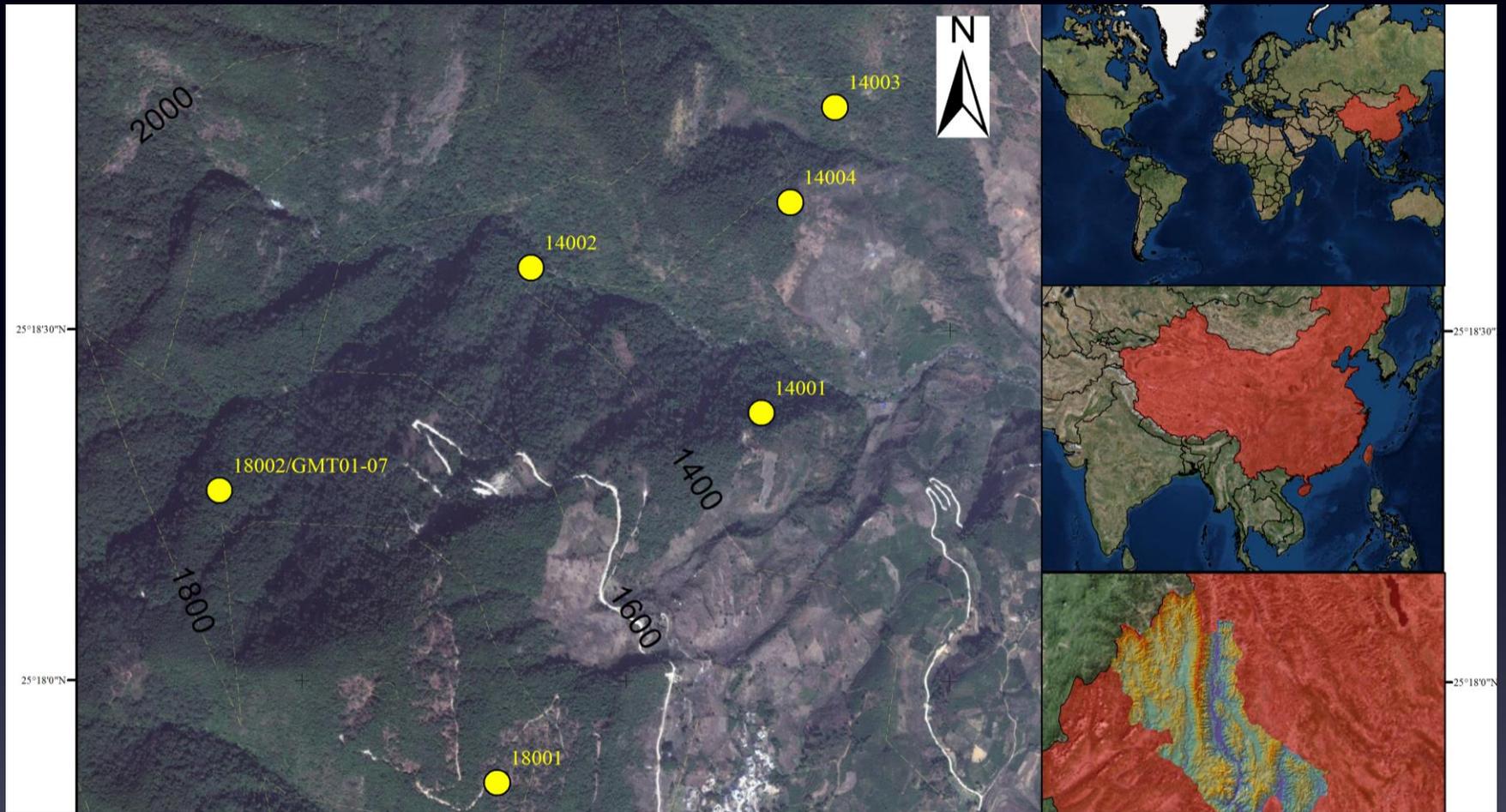
Outline

	Past/now	Now/future	The next generation
Field work	<p>Manually Collection</p> 	<p>Malaise Traps</p> 	Malaise Traps still.
Lab	<p>Soring and Taxidermy</p> 	<p>Meta-barcoding</p> 	MMG
Data analysis	Counting and Comparing	Alignment and Data mining against GenBank/BOLD	Mitogenome assembly, Data analysis against BOLD/ Dictionary , and Counting

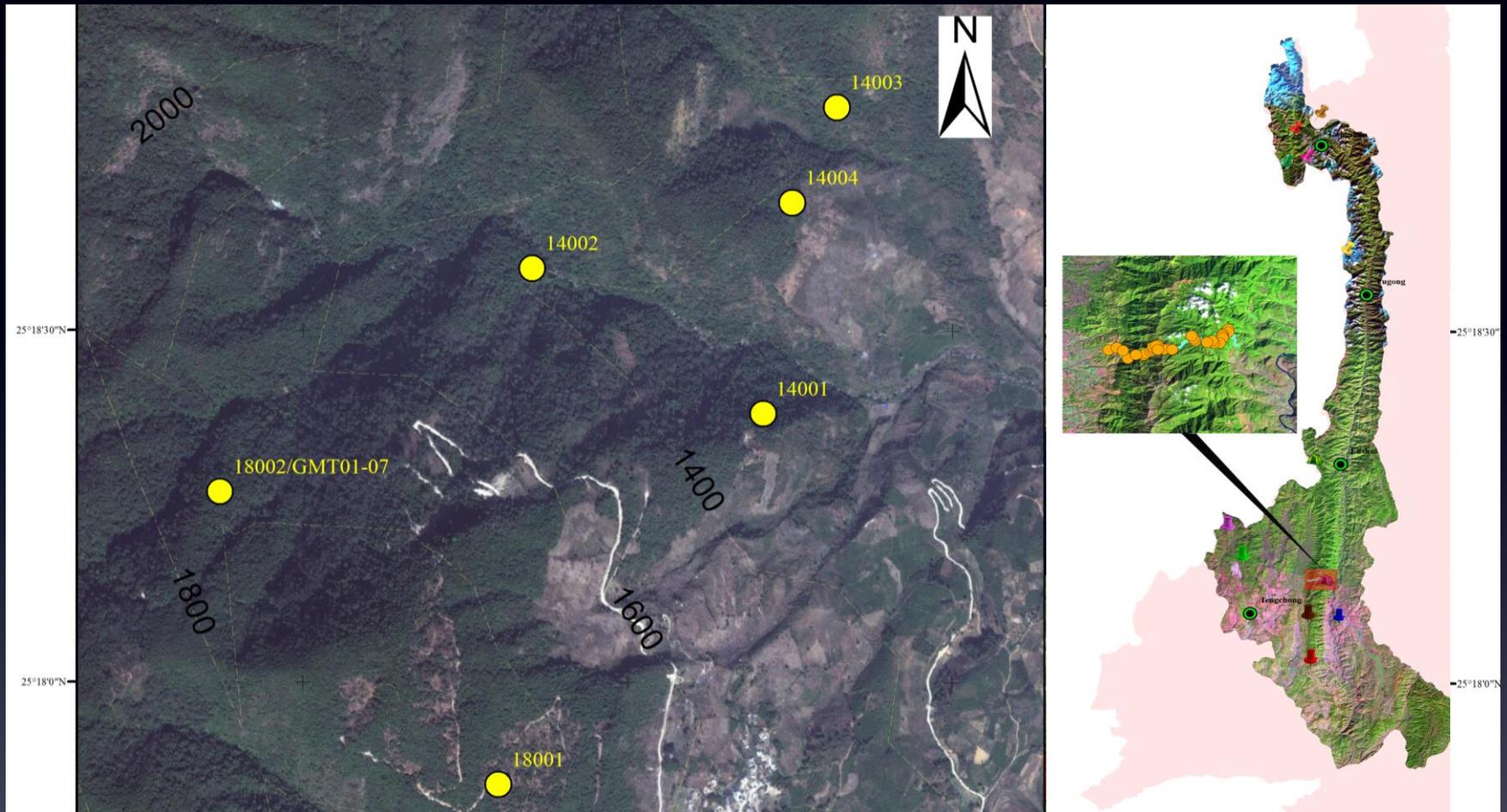
Collection using Malaise Traps

	Features	Advantage	Extra Benefits
1	Automatics	Better statistics power, Less labor cost	Education (Primary School) and Citizen Interaction.
2	Continuous	Time series	
3	Easily set up	Better way to collect unique and rare spp. Better way to set up in Spatial series (like altitude, Vegetation types) .	Local community maintain and expand sites.

The Baihualing Site in Gaoligong Mt. (Top)

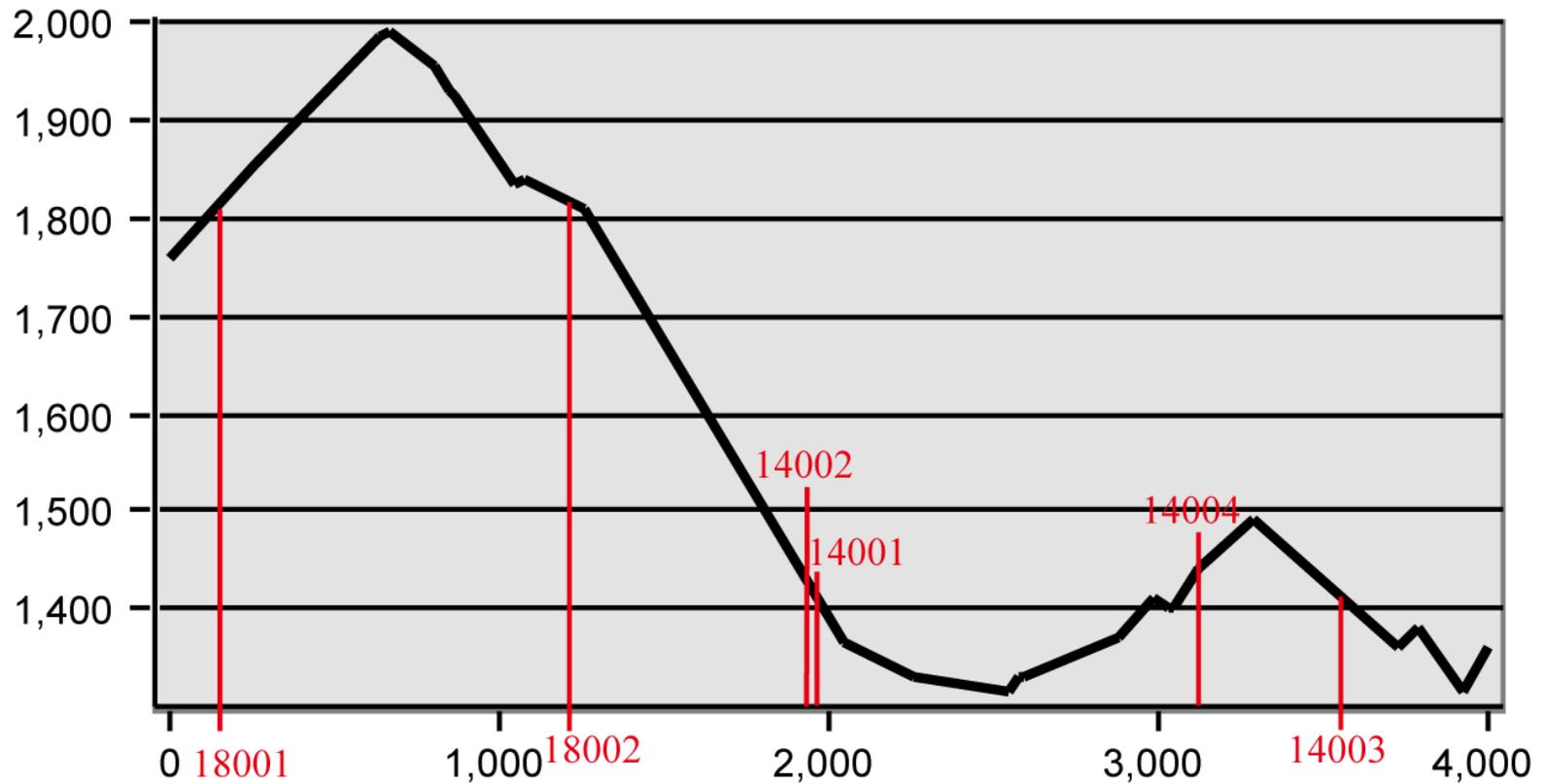


The Baihualing Site in Gaoligong Mt. (Top)



The Baihualing Site in Gaoligong Mt. (Cutout)

Profile of Baihualing Site



The Baihualing Site in Gaoligong Mt. (Traps)



140032 (northeast)

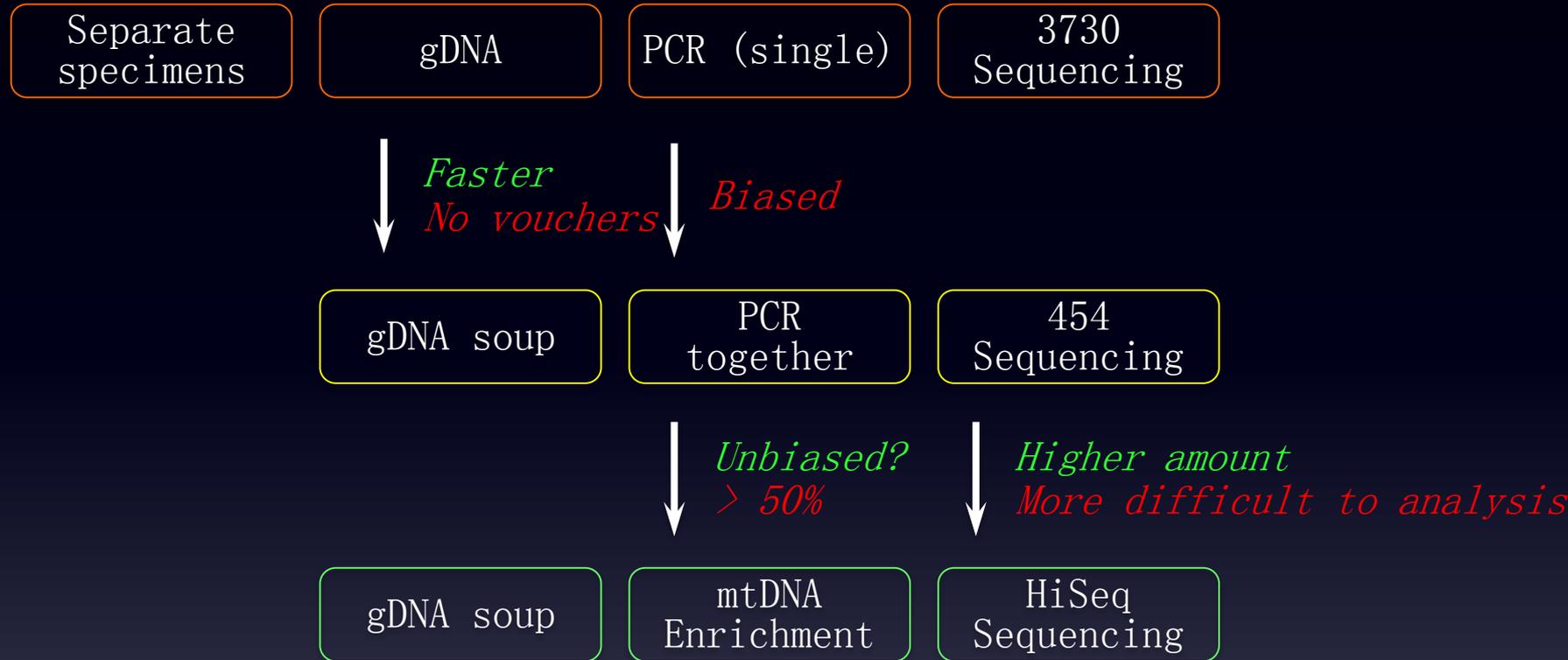


140031 (southwest)

“Bottle Mountain Bottle Sea” – So many specimens!



Barcoding, meta-barcoding and MMG



Barcoding, meta-barcoding and MMG



↓ *Faster*
↓ *No vouchers* ↓ *Biased*



↓ *Unbiased? > 50%* ↓ *Higher amount*
More difficult to analysis

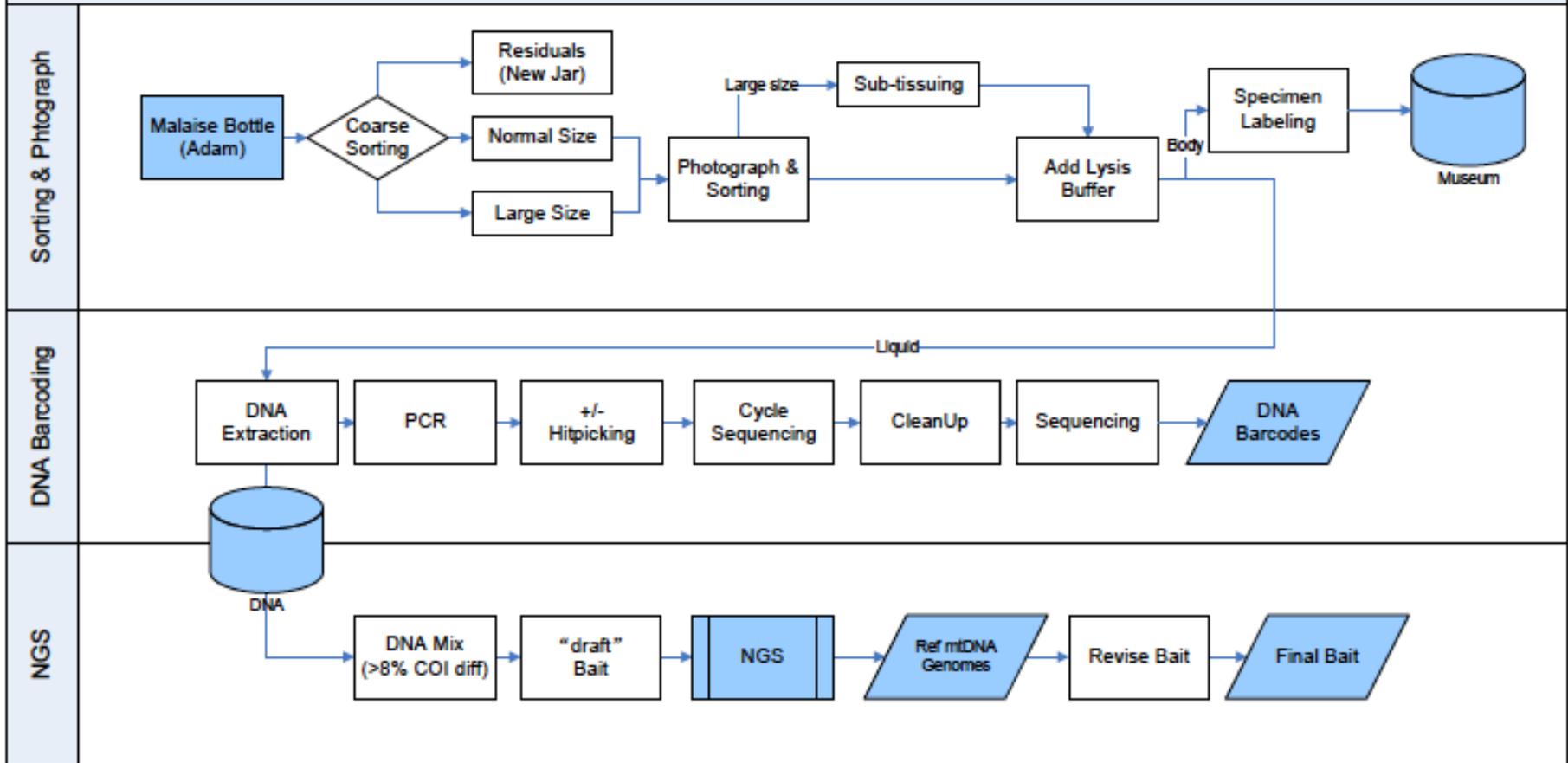


$N(\text{reads}) = f(\text{species})$

mitogenome dictionary

Revised Bait

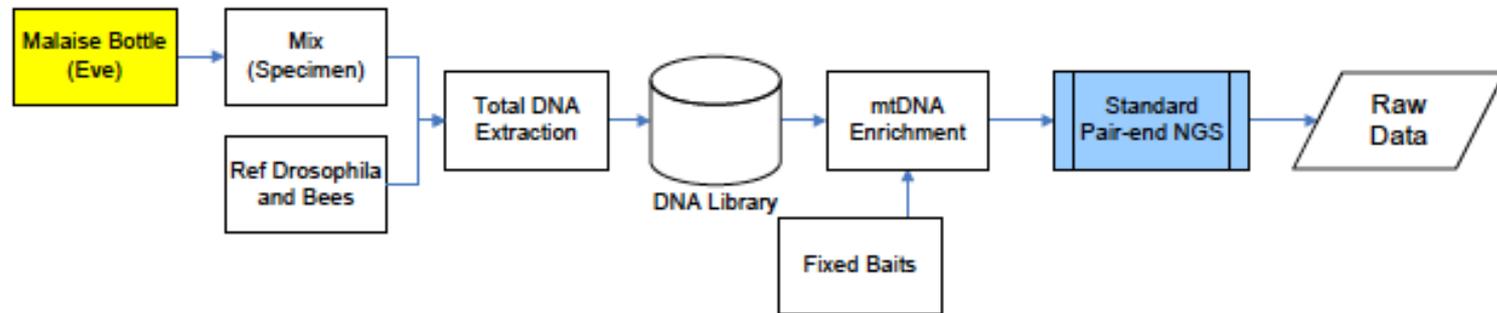
Adam



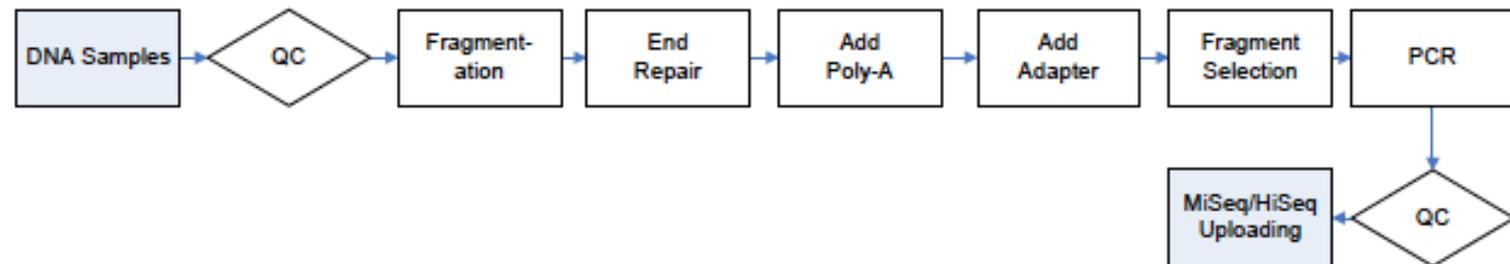
50g GITC;
5.3 mL 1M Tris-HCl;
5.3 mL 0.2M EDTA (pH 7.5);
10.6 mL Sarkosyl;
1 mL beta-mercaptoethanol;
=> 50 mL ddH2O

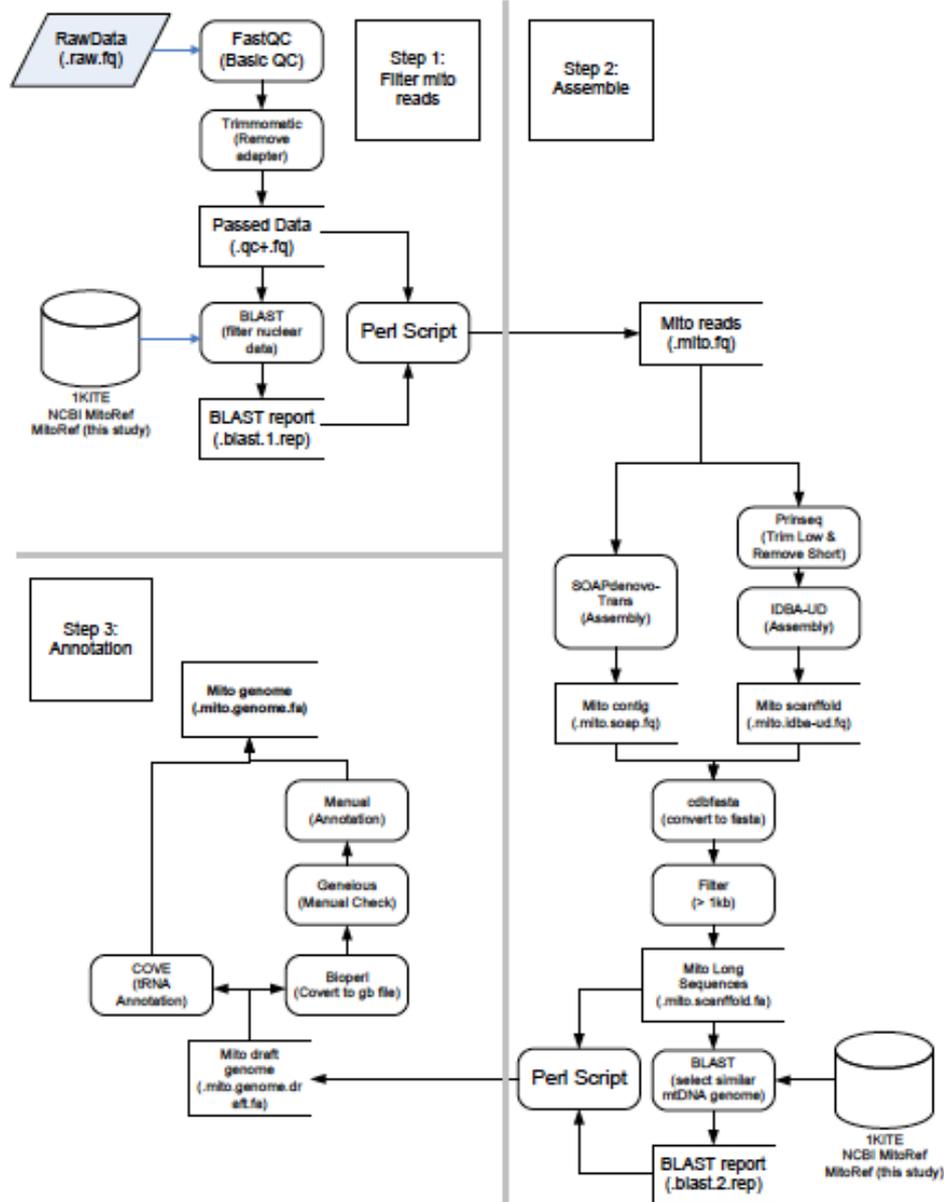
DNA
Extraction
Buffer

MMG



NGS





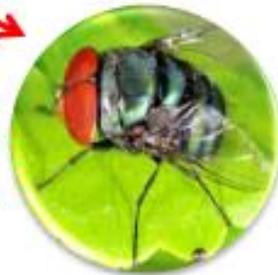
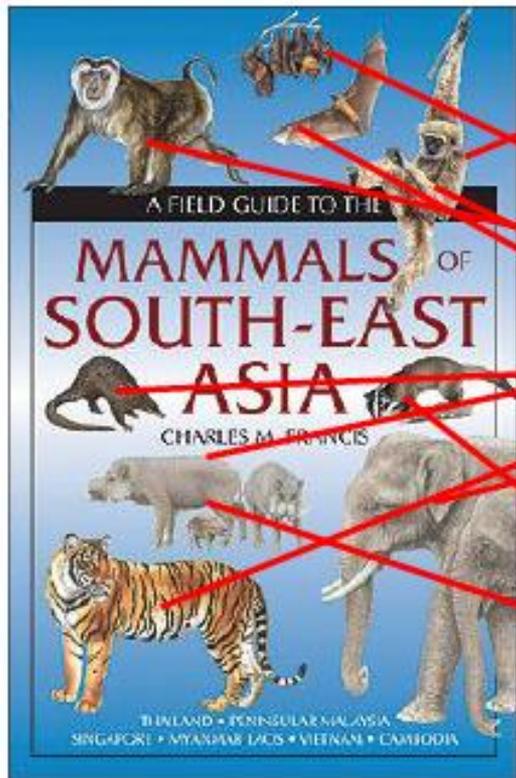
$$N(\text{reads}) = n(\text{sp}) \cdot \text{bodysize}(\text{sp}) \cdot \delta(*)$$

1. The **body size** of the species is a NORMAL distribution with average body size and variation.
2. **gDNA** is the DIRECT RATIO of the **body size**.
3. Non-PCR MMG with the (near-)unbiased bait mtDNA enrichment solution make **mtDNA** is a constant ratio of the **gDNA**.
4. apart from the sequencing bias, the total number of reads which could be mapping to one species can be the estimation of the number of this species (biomass).
5. Inner species marker controls the sequencing bias

Conclusion

- Malaise trap is a **SAMPLE** of the biodiversity of the site of that given time range (population).
- MMG provides a solution to monitoring the biodiversity (species number, biomass, genetic variations w/ the species) at a certain space-time point.

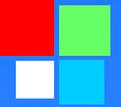
New approaches



+ DNA barcoding
Short DNA sequences that
allow **species recognition**

Acknowledgment

- My Crews: LI Zong-xv, CHEN Xing, LIU Liu.
- Several groups in the State Key Lab of Genetic Resources and Evolution
 - Environment Conservation and Ecology Center (Douglas Yu, JI Yin-qiu, WANG Xiao-yang et al.)
 - ZHANG Ya-ping' s group
 - JIANG Xue-long' s group
- Gaoligong Mt. Administration Bureau
- MOST and NSFC



Thank you!

