



SSE

Divergence time is a good proxy for detecting phylogeographic concordance in montane system

Tao Wan^{1,2,3}, Huateng Huang², Jamie Oaks⁴, Lacey Knowles³

1. Shaanxi Normal University, China; 2. Kunming Institute of Zoology, Chinese Academy of Sciences; 3. Department of Ecology and Evolutionary Biology, University of Michigan; 4. Department of Biological Sciences, Auburn University

1. Background

Shared phylogeographic pattern among co-distributed species could shed light to how local biodiversity evolved and when ecological community had assembled.

Low latitude mountains are important biodiversity hotspots. Topographical and ecological complexity in montane system facilitate assembly-wide divergence and effectively reduce secondary contact, which provides an ideal model to test the potent trajectories in shaping concordant phylogeographic patterns.

"Outdated" single-locus sequences from multiple co-distributed taxa could be expedient for exploring diversification of sparsely studied area.

Hierarchical Bayesian Computation can accommodate stochastic processes associated with the gene coalescence, which promotes the statistical inference of the concordance criterion.

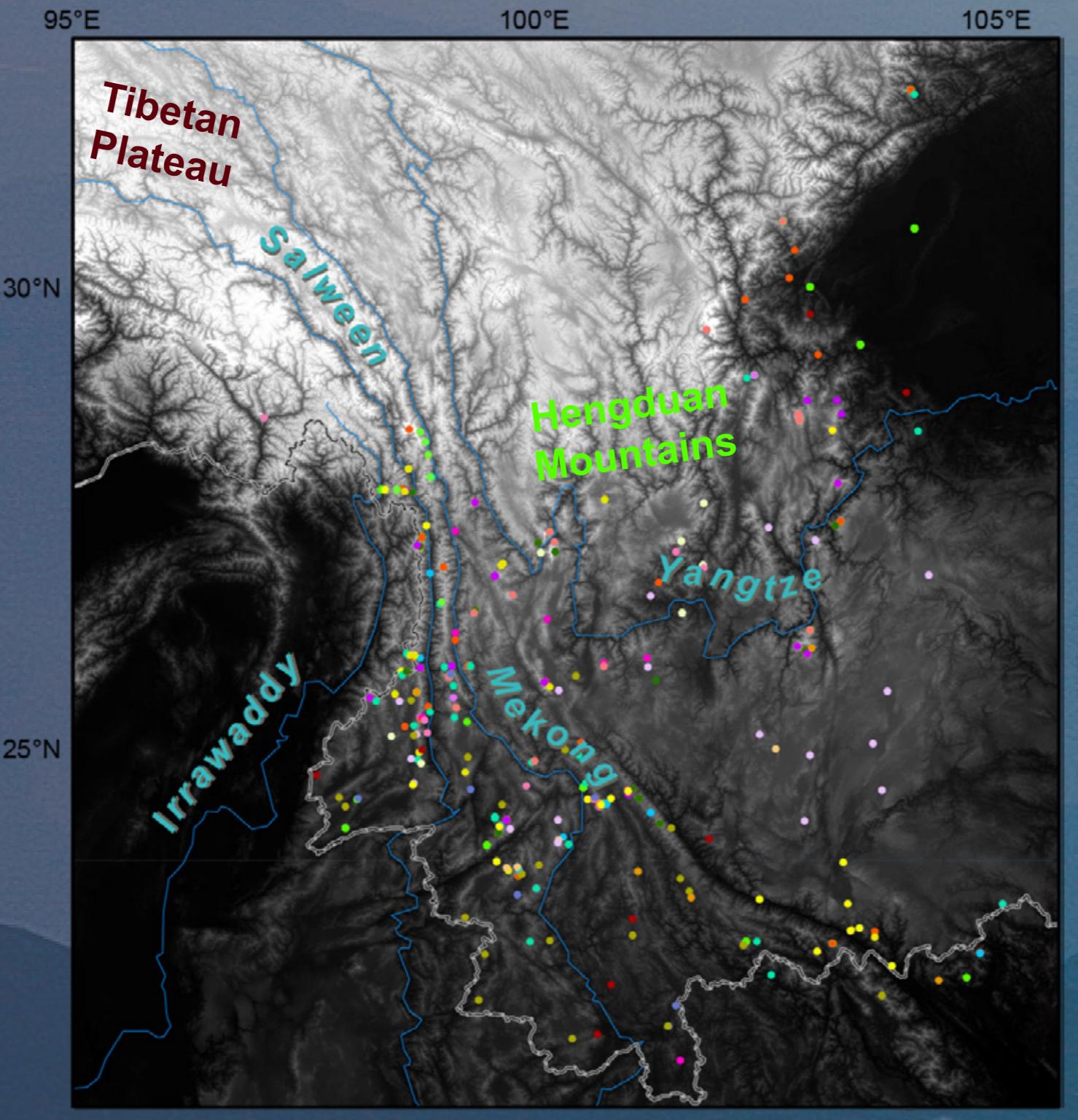
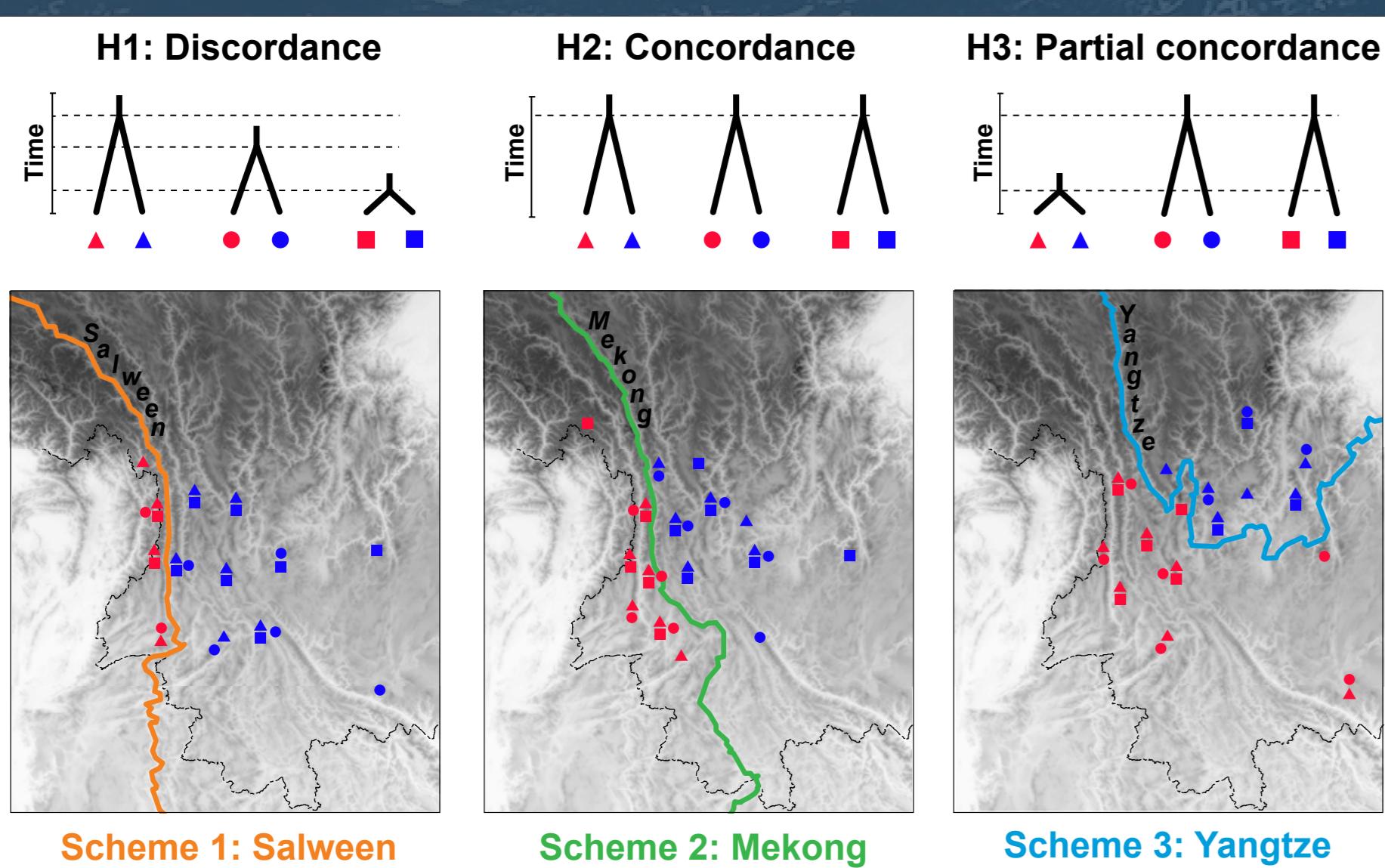


Fig. 1 Topography and major rivers in the Mountains of Southwest China *sensu lato*. The multiple parallel ridge-valley and sky island landscape is considered as a vital basis for the allopatric isolation. Pale indicates high elevation and black indicates low altitude places. Each colored dot represents a georeferenced sample location with sequences data available. Same color shows one taxon.

2. Hypothesis

In each of the three phylogeographic schemes, three hypotheses were compared: **H1** predicts several pairs of taxa sharing a phylogeographic structure yet have random divergence history; **H2** infers there is one deterministic divergence shaped one phylogeographic pattern in the community; **H3** assesses more than one prevailing events that have fundamentally structured the phylogeography of the community (Fig. 2). Besides, we also test the null hypothesis that assume synchronous diversification in the MSC animal community, with the main purpose to estimate the divergence time of each population pairs in the community.



3. Methods & Materials

Because of the statistical weakness of using single-locus data to infer the likelihood of shared history, we compared the ABC method (e.g. dpp-msbayes, Oaks 2014) with a new full-likelihood Bayesian method (*Ecoevolity*, Oaks 2019) and then determine which approach is more capable.

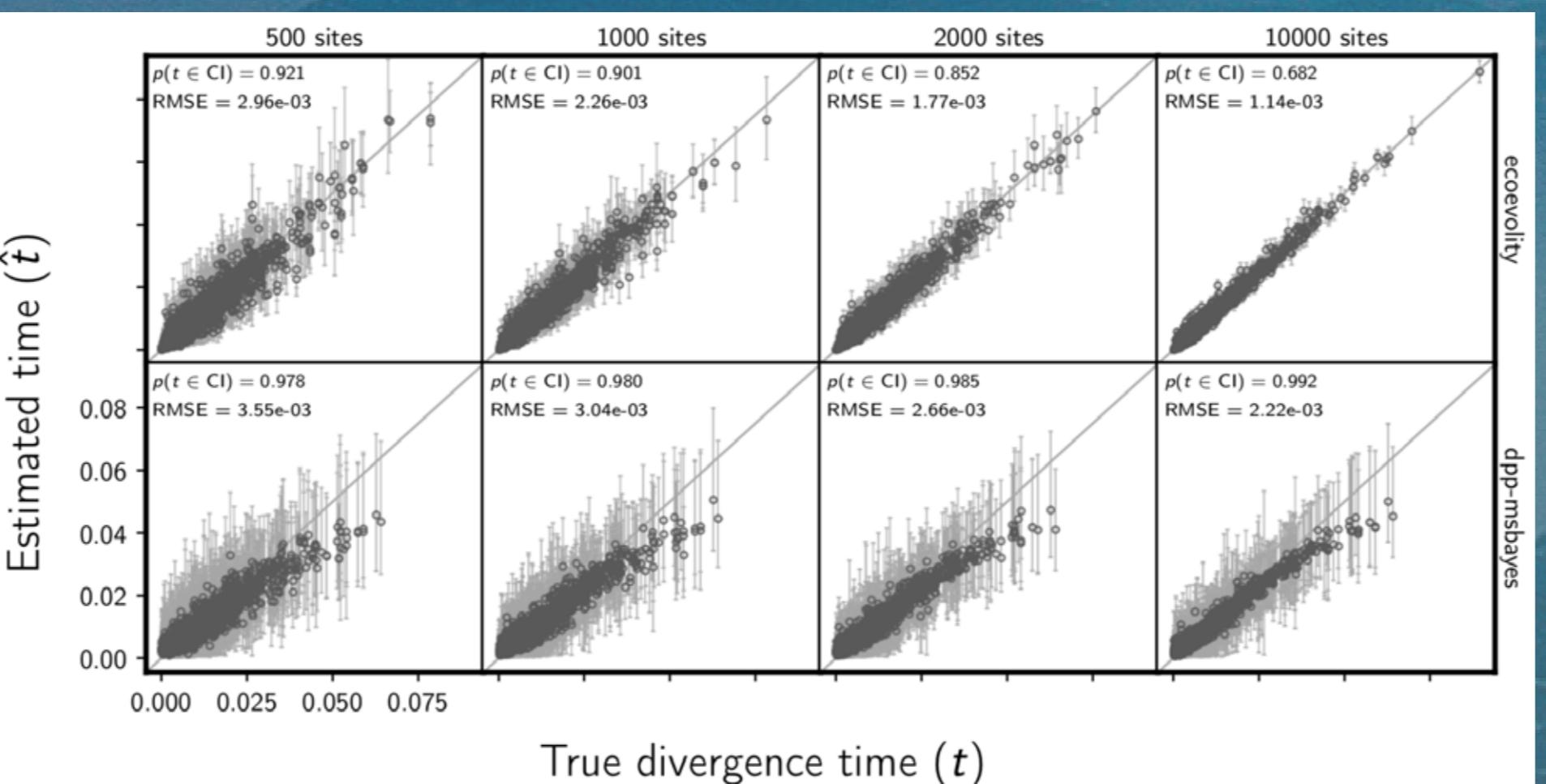


Fig. 3 Comparing the ability of full-likelihood method (ecoevolity) and ABC (dpp-msbayes) to estimate divergence times (in units of expected substitutions per site) given a locus of length 500, 1000, 2000, and 10,000 sites.

Data of 24 Southwestern China terrestrial species (14 small mammals, 10 birds, 6 amphibians & reptiles) were repurposed, 6 new-derived small mammal dataset were combined.

Divergence time were estimated independently in each species using traditional methods (e.g. Beast, BPP), but also overall implemented in hierarchical Bayesian model.

According to the phylogeographic assignment, each species were divided into pair(s) of taxon and then submitted to 3 hierarchical models. The likelihood of concordance were inferred in the models.

5. Discussion

1. Balance the cons and pros of using single-locus data in comparative phylogeography; shift the paradigm from the abiotic oriented to the biotic oriented (Papadopoulou & Knowles, 2016).
2. Why partial concordant pattern among the montane community of Southwestern China important?
3. The role of ridge-rivers and what should know in the next.

References

- Oaks, J. R. (2014). An Improved Approximate-Bayesian Model-choice Method for Estimating Shared Evolutionary History. *BMC Evolutionary Biology* 14:150.
 Oaks, J. R. (2019). Full Bayesian Comparative Phylogeography from Genomic Data. *Systematic Biology* 68(3):371–395.
 Papadopoulou A. & Knowles L. (2016). Toward a paradigm shift in comparative phylogeography driven by trait-based hypotheses. *PNAS* 113 (29):8018–8024.

4. Results

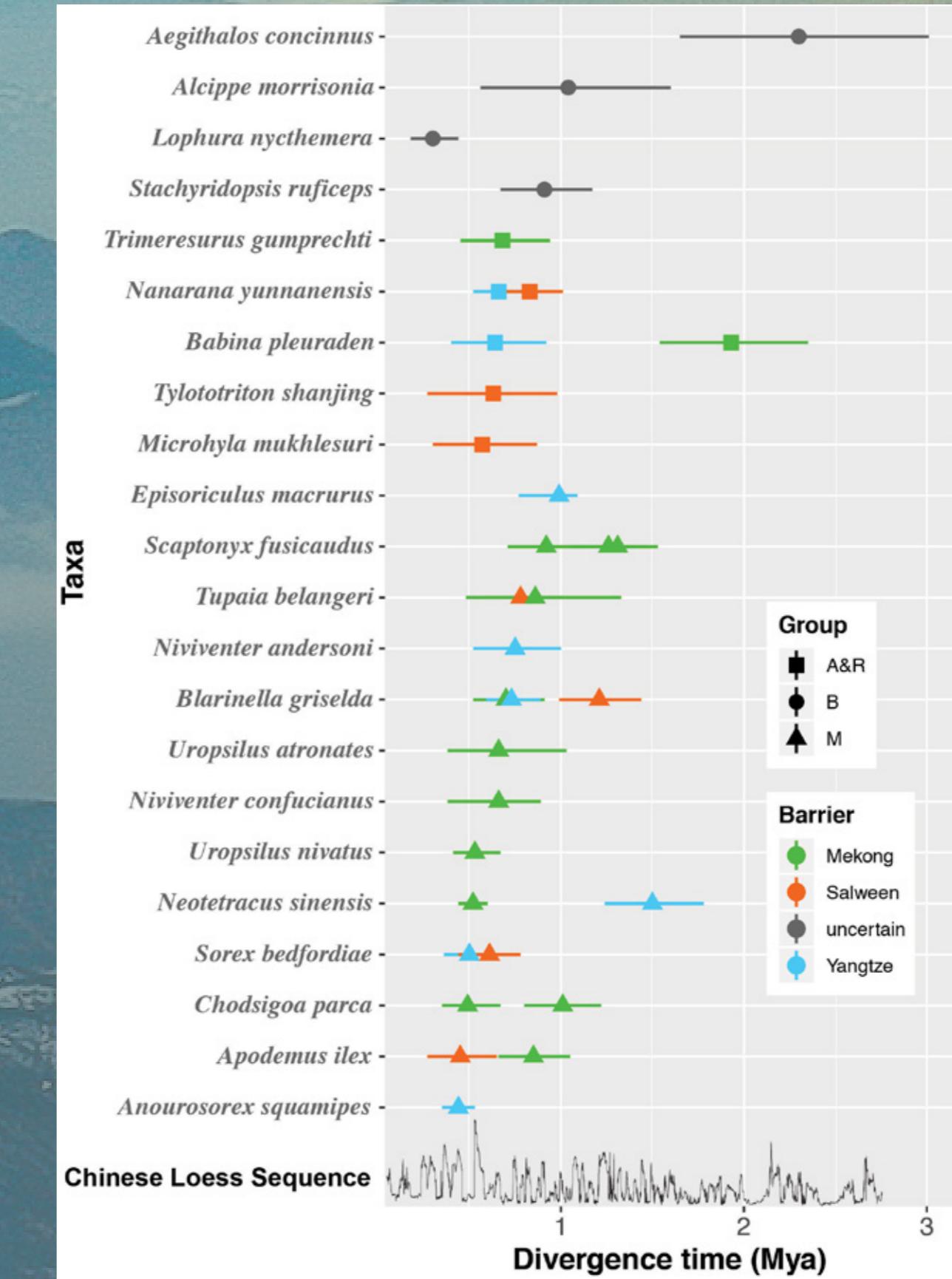


Fig. 4 Divergence time (mean and 95% CI) of 33 pairs of taxa that across riverine barriers. The time was estimated in BPP and convert into real time. Bottom plot shows the record of Chinese Loess Sequence in the Pleistocene, peaks represent Glaciations.

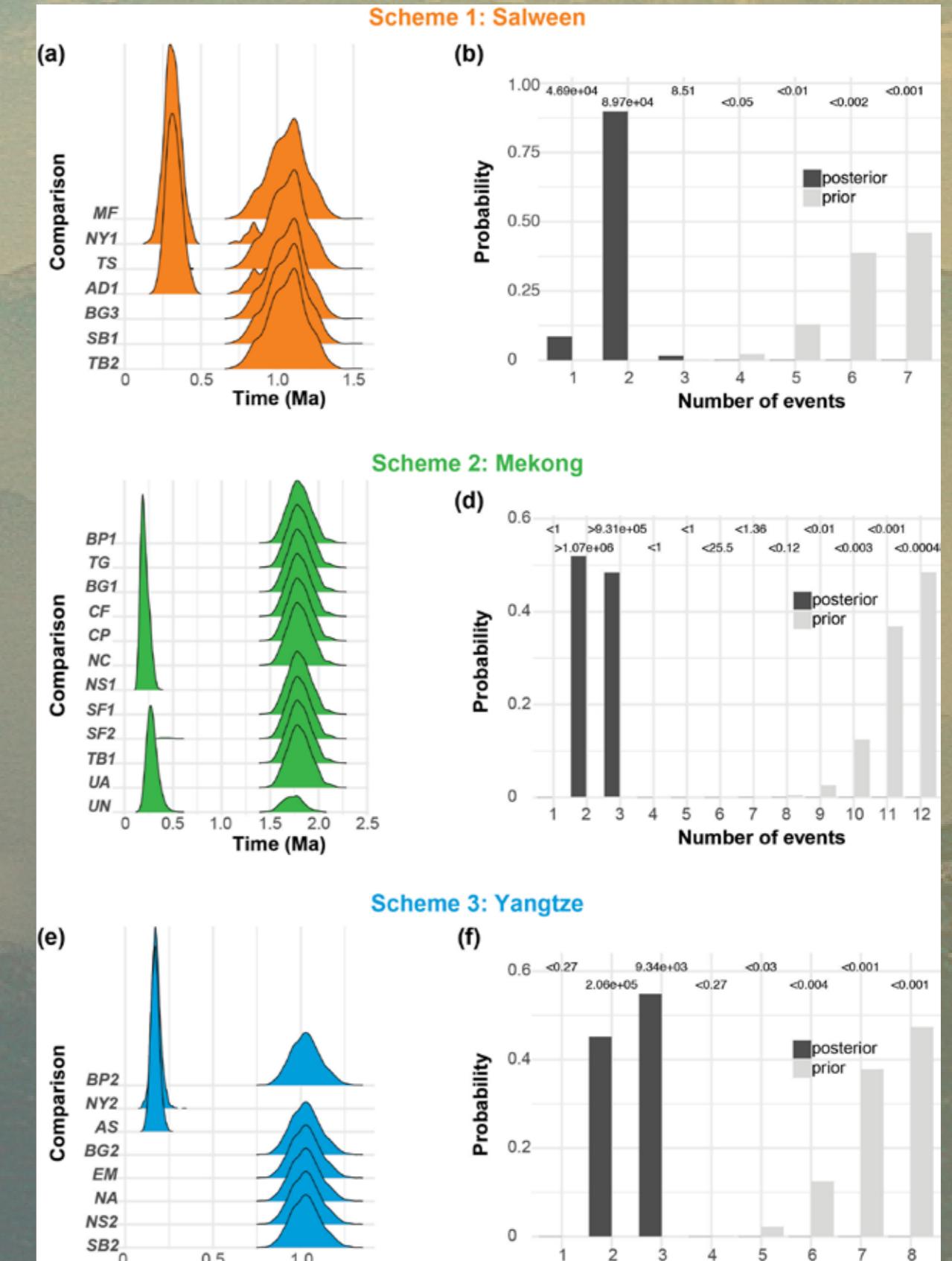


Fig. 5 Comparative phylogeographic test implemented by full-likelihood Bayesian computation. (a), (c), (e) shows approximate marginal posterior densities of divergence times for each taxon from different scheme. (b), (d), (f) shows prior and posterior probabilities of numbers of divergence events from scheme 1, 2, 3, respectively.

Table 1. Statistical inference of phylogeographic hypotheses

	H1-Discordance	H2-Concordance	H3-Partial Concordance	
	Best events ($\Psi > 3$)	Best events ($\Psi = 1$)	Best model	Best events
Salween	cumulative PP ($\Psi > 3$) = 0.015; 2lnBF* = 4.19	PP = 0.08; 2lnBF > 22.72	$\Psi = 2$ (PP = 0.76; 2lnBF > 30.02)	$\Psi = 2$ (PP = 0.91; 2lnBF = 23.55)
Mekong	cumulative PP ($\Psi > 3$) ≈ 0; 2lnBF* < 6.49	PP < 0.0004; 2lnBF < 0	$\Psi = 3$ (PP = 0.48; 2lnBF > 27.49)	$\Psi = 2$ (PP = 0.52; 2lnBF > 27.82)
Yangtze	cumulative PP ($\Psi > 3$) ≈ 0; 2lnBF* < -2.62	PP < 0.001; 2lnBF < -2.62	$\Psi = 3$ (PP = 0.55; 2lnBF > 28)	$\Psi = 2$ (PP = 0.55; 2lnBF = 18.28)

*: the highest 2lnBF value among all $\Psi > 3$ events

6. Conclusions

Our study turned the aimless investigation that explore the synchronous divergence in a ecological community into seek whether the divergence times is a surrogate to phylogeographic concordance. The result suggested that the phylogeographic structure is strongly in accordance with limited pulses of diversification in the Mountains of Southwest China. Albeit the lack of the strict concordance undermines the interpretative power, the climatic and/or geologic events in the Early Pleistocene have extensive impact on phylogeographic diversity of the local fauna. This result could invoke following concern on the biological conservation of the area.



Thank Knowles Lab for providing critical suggestions and UM-LSA for the computational resources.

wantsy@gmail.com
 @Tao_UUan