Model selection and presenting a convincing argument

An example question:

Does the evolutionary transition from "aquatic eggs + aquatic tadpoles" to "terrestrial eggs + terrestrial tadpoles" always proceed through an intermediate stage?[1]

[1] see Gomez-Mestre et al. (2012)

A LRT approach

Estimate the phylogeny of frogs.

1. calculate the log-likelihood for a model that asserts that this transition happens at some instantaneous rate, $\hat{\mu}$.
2. calculate the log-likelihood for a model that asserts that this transition never happens instantaneously ($\mu = 0$).
3. conduct a likelihood-ratio test.

Problem

Maddison et al. (2007) introduced the "BiSSE" model to protect against a certain artifact in comparative analyses:

If some character state leads to altered diversification rates, then estimating character histories while ignoring diversification rates can lead to biased estimates of rates of character change.

For example:
If a state causes high extinction rates, then it will be rare. A naive analysis will infer that the state rarely arises.
For a BiSSE type model[2] you need to estimate diversification rates for each state.

[2] there are now many BiSSE-like models - see work by Rich FitzJohn, Emma Goldberg, and others

Results of a test

A Likelihood ratio test found that the BiSSE (multiple diversification rates) model does **not** have a significantly better fit than a 1 diversification rate model.
(AIC and BIC agree with this)

To answer the original question:
Should we:

1. Test $\hat{\mu}$ vs $\mu = 0$ assuming there is 1 diversification rate, OR
2. Test $\hat{\mu}$ vs $\mu = 0$ while allowing for multiple diversification rates (in the style of BiSSE) ?

AIC tells you what model is expected to have the highest predictive power.

The LRT tells you if you can reject a simpler model.

The BIC should correctly identify the true model, if it is in the set of models.

None of them tell you which model to use to produce the most convincing argument.

Answering the original questions with the BiSSE model enabled would let us make the argument:

> "Even if we allow for the possibility that the character states affect diversification rates, we find evidence that $\mu \neq 0 \ldots$"

Omitting the BiSSE model lets us make this argument:

> "There is not much evidence for character-dependent diversifcation rates. If we assume character states do not affect diversification rates, we find evidence that $\mu \neq 0 \ldots$"

This is a weaker argument.

References

Gomez-Mestre, I., Pyron, R. A., and Wiens, J. J. (2012). Phylogenetic analyses reveal unexpected patterns in the evolution of reproductive modes in frogs. *Evolution*, 66(12):3687–3700.

Maddison, W. P., Midford, P. E., and Otto, S. P. (2007). Estimating a binary character's effect on speciation and extinction. *Systematic Biology*, 56(5):701–710.