This interesting study targets the phylogenetic relationships and phylogeography of Sri Lankan cyprinids of the genus Pethia. I enjoyed reading the manuscript and have only some fairly minor comments:
1. line 130: add a reference for the general-lineage concept
2. lines 136-140: Keep in mind that in cases like yours the concatenated tree topology is mainly determined by the mitochondrial data (due to a typically higher substitution rate of cytb than rag1)
3. lines 222-225: pairwise distances based on the concatenated data are of only limited use. Better provide these data separately for the two markers (e.g. in the SI).
4. lines 685-686: "These were then evaluated using PhyML 3.0 [65] in the PartitionFinder 2 package. " ???? I don't understand this. Are you sure PhyML 3.0 is now part of the PartitionFinder 2 package? I didn't know that ... Actually, this whole sentence is not needed and you might omit it.
5. Discussion: The molecular specie delimitation methods you employed are known to perform differently. Some methods have a tendency for over- others for undersplitting. It might be good to briefly (in a few words/sentences) discuss this issue in your discussion (or did I overlook it?).
6. Any chance for doing a time-calibrated tree? This would greatly help to put your patterns of diversification in a temporal context.
7. Some minor language polishing is needed.