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Interactive comment on “Testing the spatial and temporal framework of speciation in an ancient lake species flock: the leech genus *Dina* (Hirudinea: Erpobdellidae) in Lake Ohrid” by S. Trajanovski et al.

Anonymous Referee #1

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This study presents analyses of phylogenetic relationships and genetic diversity of leeches with a main focus on *Dina*-species from lake Ohrid. The authors found that the *Dina*-species from Ohrid represent a monophyletic group that probably originated by intralacustrine diversification. Furthermore a genetic subdivision of individuals from spring and lake populations became apparent. Molecular clock analyses revealed that the radiation of Lake Ohrid *Dina*-species flock starts approximately 2 Ma ago. This estimate closely matches estimates on the origin of lake Ohrid revealed by geological data. This is a very well written paper that provides interesting data for a less studied

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taxonomic group and significantly improves our understanding of evolution and diversification in lake Ohrid. The only shortcoming is that only one gene was analysed causing a lack of resolution of the basal phylogenetic relationships in the Erpobdellidae phylogenetic analysis. However because the main focus of the study lies on the diversification of the Ohrid Dina-species this missing resolution may be less important.

Specific comments:

1. Introduction: Not everyone is familiar with leeches. As far as possible the authors should at least add a few words about the biology and ecology of the Dina species.
2. Page 5018, 10: How many haplotypes have been found within the 109 sequenced individuals? How were these haplotypes distributed across the sampling sites?
3. Test for genetic structure, page 520, 16-24: More details are needed: How many individuals have been analysed within each group? How many haplotypes have been found within each group? Is it wise to arrange all springs into one group? Springs are isolated habitats and hence gene flow among springs may be strongly reduced.
4. Page 5023, 9-12 and page 5025: I do not understand why there is no significant difference in population structure between profundal and littoral although the authors state that these sites never share haplotypes?

Interactive comment on Biogeosciences Discuss., 7, 5011, 2010.

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