Background information to accompany poster:

High throughput mitogenomics for Lepidopteran phylogenetics

- One of the targeted species (*Micropterix calthella; Micropterigoide*) was excluded from phylogenetic analysis as it was deemed to divergent (Fig 1).

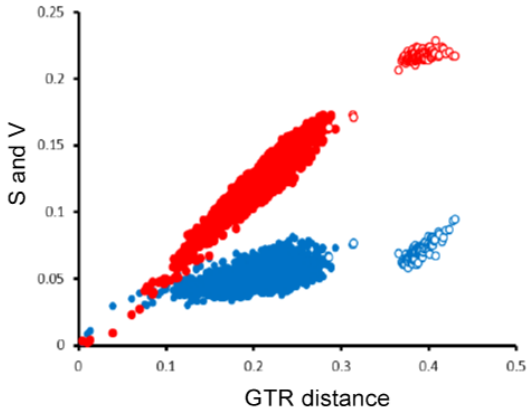

Fig 1: Saturation plot for all species. Open circles depict pairwise comparisons with *Micropterix calthella* Calculations were performed using DAMBE (Xia, 2000).

- The final alignment was recoded to generate four different data matrices for phylogenetic analyses. PartitionFinder (Lanfear et al., 2012) was used to select partition schemes and models for each of the four datasets (Fig 2). Schemes used: 1) no recoding (all positions retained), 2) all degenerate sites recoded to IUPAC code, 3) first codon RY coded third codon position removed, 4) translated to amino acids.

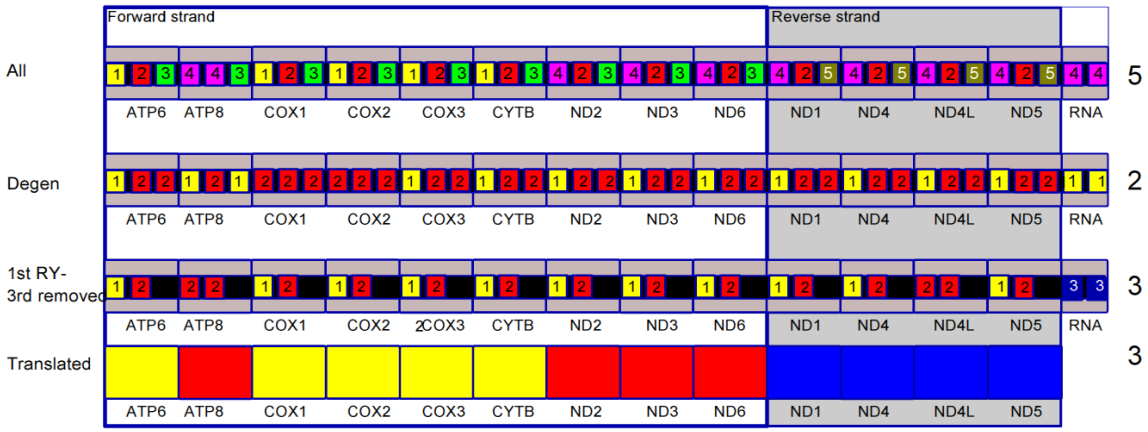

Fig 2) Partition schemes used for each of the four datasets. Each gene is divided by codon position. Numbers on the right indicate the total number of partitions.

- Phylogenetic analyses were performed using a Bayesian framework (MrBayes; Huelsenbeck, J. P. and F. Ronquist. 2001). The four topologies that were obtained are all highly comparable (Fig 3).

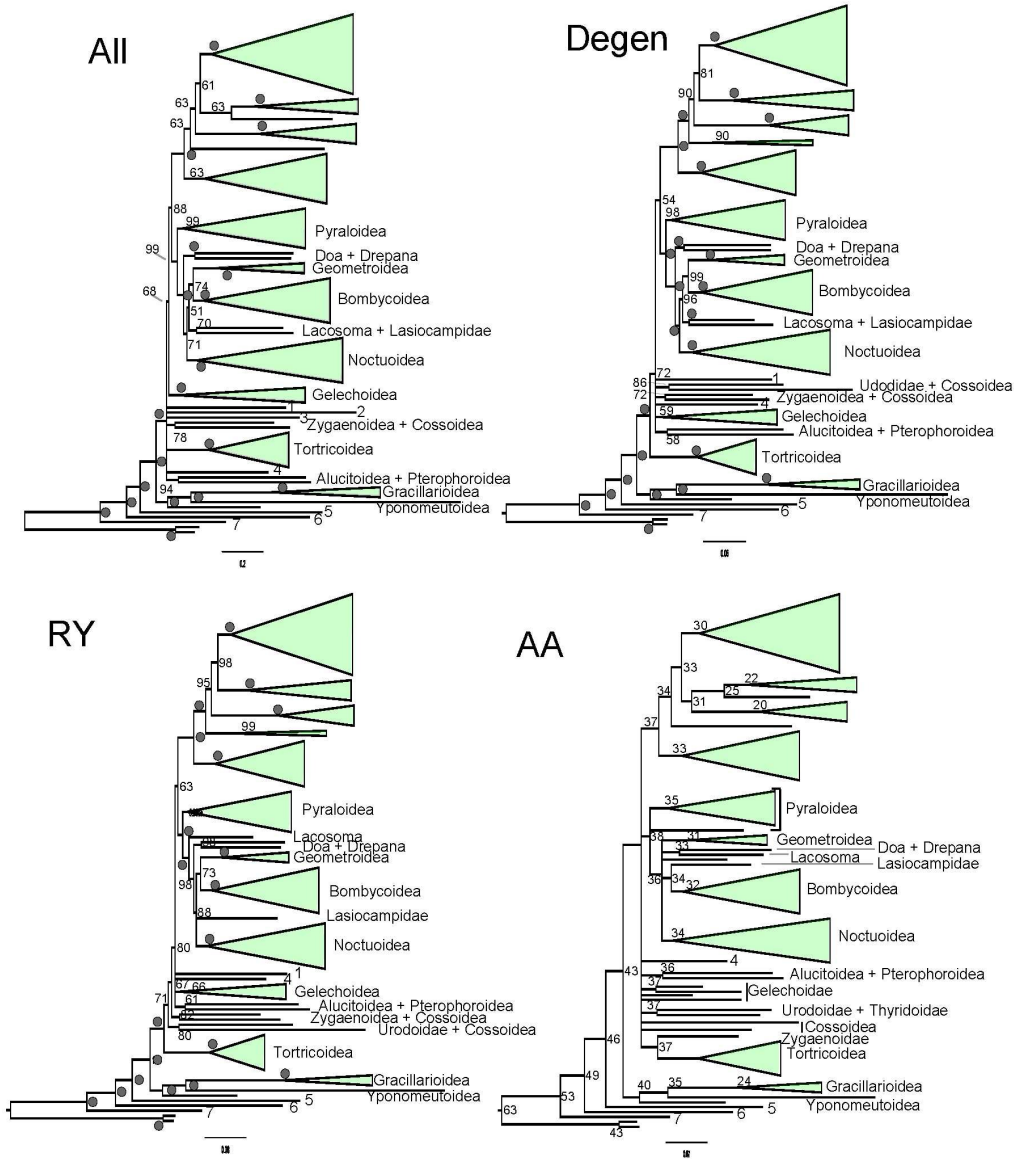

Figure 3:The phylogenetic hypotheses that were obtained for each of the four datasets. All analyses included 13 protein coding and two rRNA genes (except for the AA analysis, which included protein coding genes only). Values at nodes give posterior probabilities. Grey dots indicate posterior probability of 1.