

A mitogenomic approach to resolve the phylogeny of Afrotropical hoverflies (Syrphidae)

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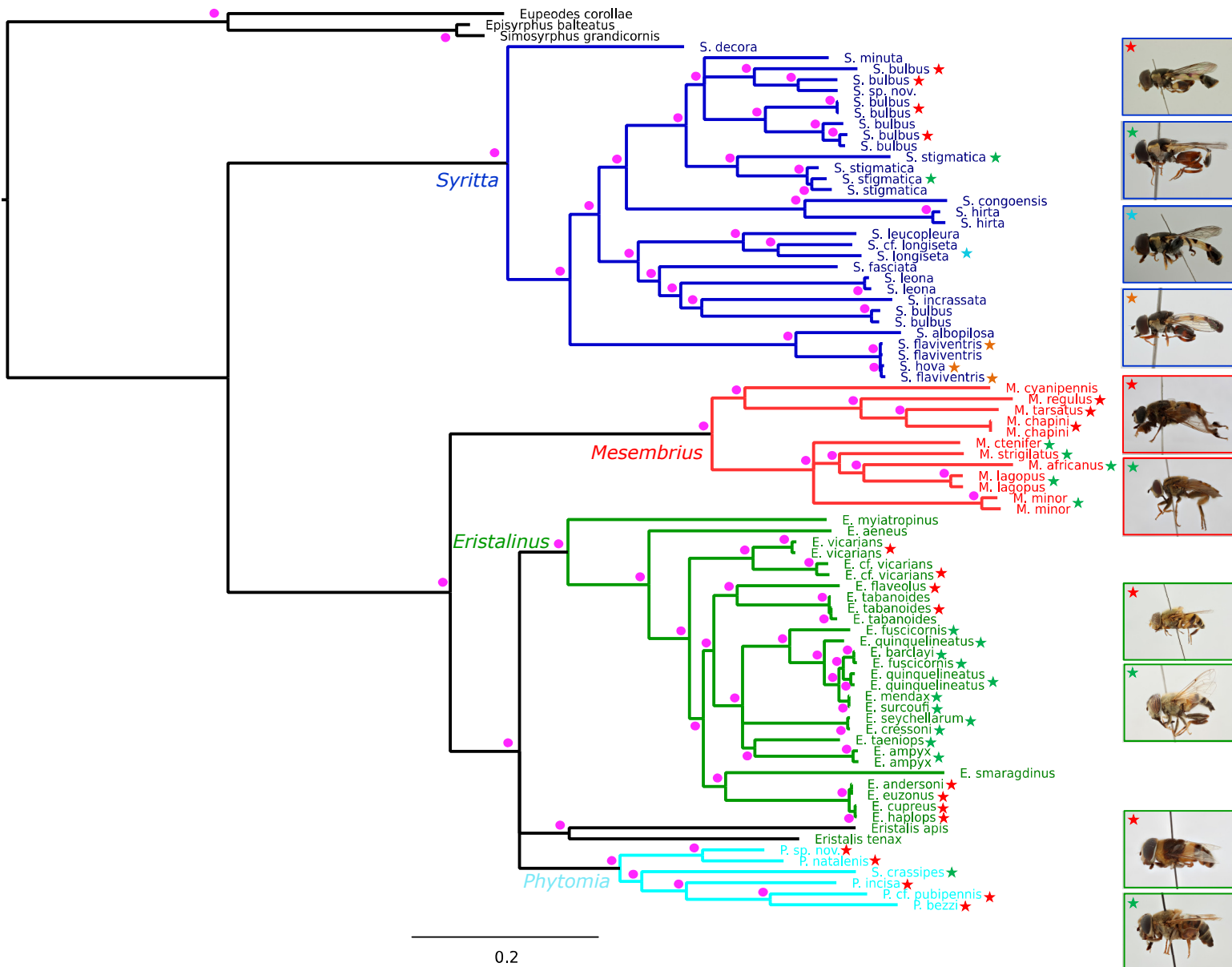
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Introduction – Materials – Methods

Syrphidae (hoverflies or flower flies) is a diverse family with >600 species in the Afrotropics. Phylogenetic relationships among species have not been studied so far. Here, we present the results of a phylogenetic reconstruction using whole mitochondrial DNA (mtDNA) sequences of 79 specimens, (mostly) of the genera *Syritta*, *Mesembrius*, *Eristalinus* and *Phytomia* (subfamily Eristalinae). Genomic libraries were sequenced on an Illumina MiSeq platform. *De novo* assembly was based on the Geneious assembler (<https://www.geneious.com>) with reference mapping in Geneious R10 mapper and its plugin BBMap. The concatenated alignment (13,535 bp) was subjected to PartitionFinder and Bayesian tree reconstruction (50x10⁶ iterations, default priors/parameters, sampling every 5000 generations, burnin = 50%) was used to obtain a phylogenetic tree. Bayesian posterior probabilities (>0.98 = ●) were plotted at the nodes.



Results – Conclusions

Phylogenetic analysis of whole mtDNA sequences of Afrotropical Syrphidae (Eristalinae) results in phylogenetic hypothesis with high support and suggests:

- in *Syritta*: cryptic diversity in several morphospecies [e.g., *S. bulbus* (★), *S. stigmatica* (★), *S. longiseta* (★)] or absence of phylogenetic divergence [e.g., *S. hova* and *S. flaviventris*: (★)];
- in *Mesembrius*: reciprocal monophyly of species groups with strong (★) and minor (★) sexual morphological dimorphism;
- in *Eristalinus*: confirm previous hypothesis with respect to phylogenetic relationships among subgenera [e.g., *Eristalodes* (★) renders *Eristalinus* s.s. (★) paraphyletic];
- in *Phytomia* (★): new phylogenetic hypothesis with respect to morphologically closely related general [i.e., *Simoides* (★)].

The technique thus seems a powerful, fast and relatively cheap method to assist in phylogenetic and taxonomic research field of Afrotropical Syrphidae.

This research is sponsored by:

