

The Phylogeny of Staphylinidae (Rove Beetles) from Whole Mitochondrial Genomes

April 5, 2024

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1 Keywords

Phylogeny, Rove Beetles, Staphylinidae, Diversification, Phylogenetic Tree, Mito-Genomes, Basal Relationships

2 Introduction

Staphylinidae (Rove Beetles) is the most species rich family of the diverse Coleopteran order. Staphylinidae consists of many subfamilies including the highly diverse Staphylininae, Paederinae, and Aleocharinae. Molecular phylogenetic studies of the family Staphylinidae have continued throughout the 21st Century, with the most accurate and successful analysis' making use of Bayesian and Maximum Likelihood methods for tree building [1]. The development of modern sequencing techniques and an increased abundance of genetic data is a burden on traditional phylogenetic methods lacking computational power to process many and large sequences.

Thus, this project will overcome this challenge through the use of machine learning clustering algorithms to help create a phylogenetic 'backbone' for traditional phylogenetic methods to take place consequently. The outcome of this project will ultimately provide an efficient and automated pipeline that will take sequences as input, and output an accurate tree based on the aforementioned methods. This project will also aim to make sense of the diversification of Staphylinidae on a geographical basis. Nuclear or mitogenomes can be used in this analysis, however, mitogenomes are useful due to their relatively high evolutionary rate and their lack of genetic recombination - thus numerous phylogenetic signals [2].

3 Methods

To construct an accurate phylogenetic tree using the mitogenomes of 1000 Staphylinidae species from around the world. Clustering (machine learning) methods will first be implemented to create a backbone, reference tree which can consequently be refined and added to, using traditional phylogenetic methods. k-means clustering can be applied to sequence similarity metrics (based on pairwise sequence comparisons, i.e. Damerau-Levenshtein Distance) to identify 'clusters' of similar species. Iterative k-means clustering

will be implemented to determine the most suitable clusters (potentially according to a silhouette coefficient score). Consequently, the ‘centroid’ species will be chosen from each cluster for traditional phylogenetic tree construction. Once this backbone is made, the remaining species in each cluster can be added to their respective centroid to refine the tree. The tree will then be used to place existing (meta)barcode sequences for a phylogenetic framework and reference system. All methods are likely to be carried out using Python and R.

4 Timeline

MSc Project Timeline					
	Apr	May	Jun	Jul	Aug
Lit Review & Intro					
Sequence Clustering					
Tree Completion					
Interpret tree					
Write-up					

5 Budget

1TB Hard Drive for **£100** required for storing large amounts of mitogenomic data. **HPC Computing Time** may be required for tree building or machine learning tasks but **cost unknown**. **Travel fee (c£50)** for commuting to the Natural History Museum via Transport for London.

References

- [1] Vladimir I. Gusarov. *Phylogeny of the Family Staphylinidae Based on Molecular Data: A Review*, pages 7–25. Springer International Publishing, Cham, 2018.
- [2] Xin-yan Lu, Quan-fu Zhang, Dan-dan Jiang, Ya-fang Liu, Bin Chen, Shuang-ping Yang, Zong-ti Shao, Hang Jiang, Jian Wang, Yi-hao Fang, Chun-hong Du, and Xing Yang. Complete mitogenomes and phylogenetic relationships of *haemaphysalis nepalensis* and *haemaphysalis yeni*. *Frontiers in Veterinary Science*, 9, November 2022.