

# A liberal Supertree approach to test the Ecdysozoa hypothesis

Gayle K. Philip<sup>1</sup>, Christopher J. Creevey<sup>1</sup>, James O. McInerney<sup>1</sup>

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## 1 Introduction.

Researchers have often been divided on the relationship of nematodes to arthropods and vertebrates. Traditionally, vertebrates and arthropods have been grouped together with nematodes occupying a basal position. This classic hypothesis, named “Coelomata” argues that vertebrates and arthropods are more closely related as they have a true body cavity (coelem), which nematodes lack. However, a recent hypothesis now joins the nematodes with the arthropods in a molting clade, the Ecdysozoa. Since the publication of the Ecdysozoa hypothesis, evidence has appeared both for and against it [1,2]. It was our aim to test these hypotheses through the construction of a supertree [3] from all the single gene families identified from all the available eukaryotic genomes.

## 2 Materials and Methods.

Our approach was to identify single gene, orthologous families containing a minimum of four members, from ten fully characterised eukaryotic genomes. The ten genomes consist of three vertebrates, two arthropods, one nematode, two yeasts, one apicomplexan and one plant species. Hypotheses of relationships for each gene family were re-constructed. The supertree software program Clann (<http://bioinf.may.ie/software/clann>) was then used to find the supertree that best described the relationships from all the source trees.

## 3 Discussion.

The tree that best described the relationships in the 780 source trees is shown in Figure 1. We recover this tree using a variety of methods and we have not been able to find a method that does not recover this tree.

In conclusion, it can be seen that our supertree supports the traditional Coelomata hypothesis with the vertebrates more closely related to the arthropods.

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<sup>1</sup> National University of Ireland, Maynooth, Co. Kildare, Ireland. E-mail: [gayle.k.philip@may.ie](mailto:gayle.k.philip@may.ie)

## 4 Figures.

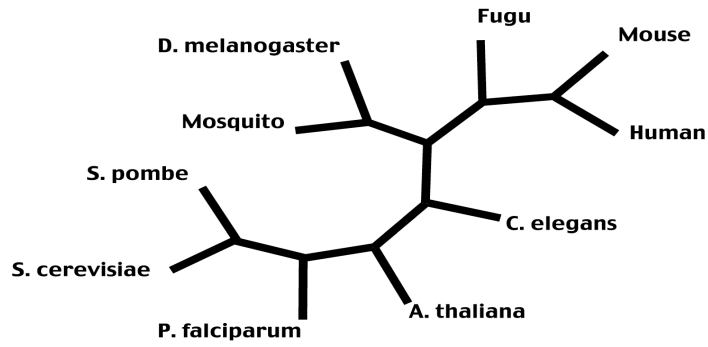


Figure 1. The supertree best describing the relationships in the 780 source trees.

## 5 References and bibliography

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