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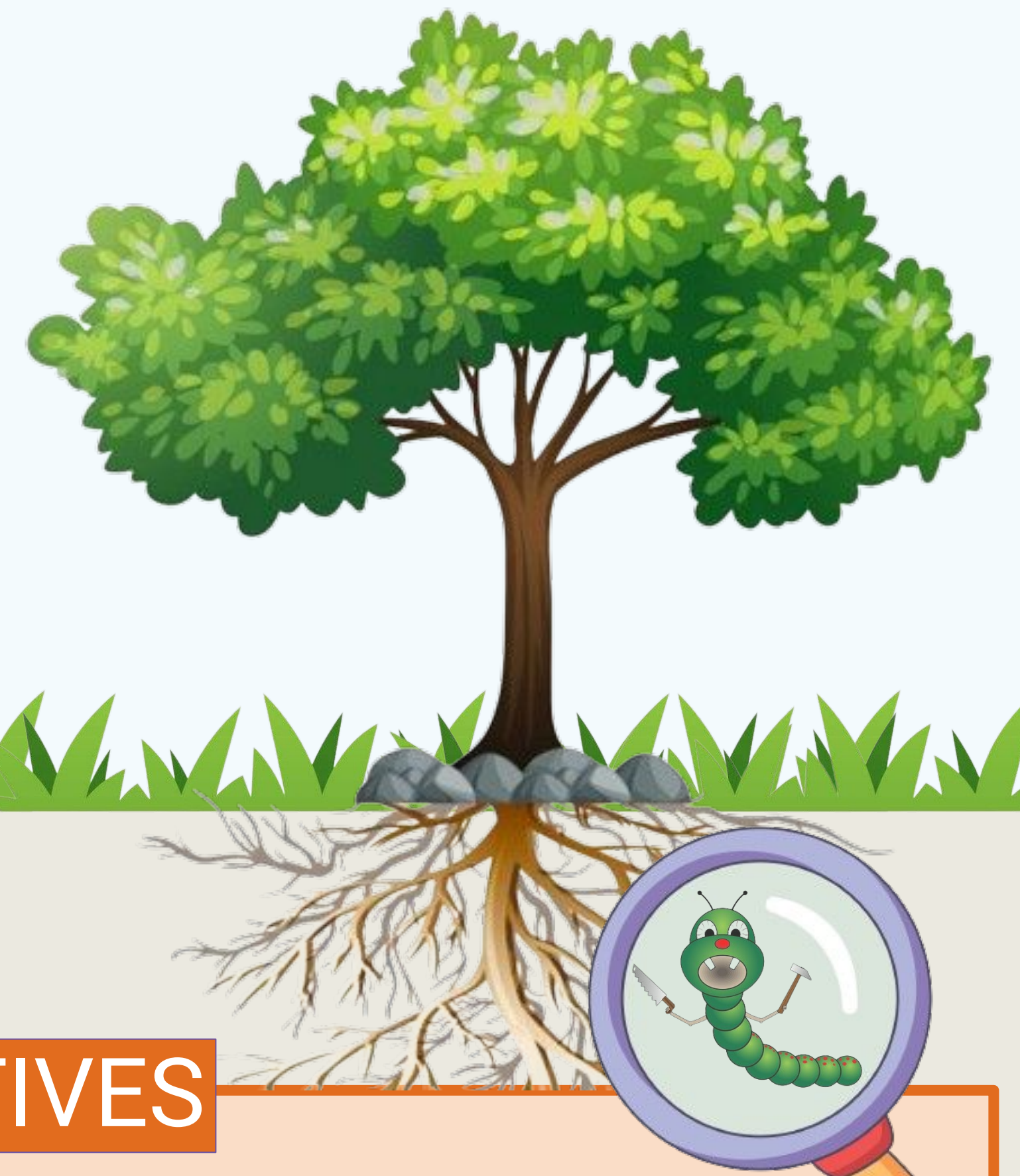
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ORPHAN GENES: THEIR IDENTIFICATION AND EVOLUTION IN PLANT PARASITIC NEMATODES

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INTRODUCTION

- Orphan genes are genes that have no identifiable homologs. They are systematically found in eukaryotic genomes, and represent up to 30% of the genes [1].
- The emergence of such genes is an important mechanism of functional acquisition during evolution. They may originate from duplication or horizontal transfer events followed by rapid divergence. Another possibility is that they may emerge from non-genic regions, which is known as *de novo gene birth* [2]. Hence, there is a debate on the real origin of orphan genes [3].
- The most common method for identifying orphan genes involves the search for homologues (identification of their absence). Then, their origin can be studied by syntenic approaches. However, these approaches cannot always distinguish between *de novo* genes and the ones that diverged significantly from their ancestor.

OBJECTIVES

- We developed a bioinformatics pipeline to identify orphan genes and investigate their emergence dynamics and possible *de novo* origin.
- The biological purpose is to apply the built pipeline to the genus *Meloidogyne* of root-knot nematodes, which cause a huge global crop loss. The species of this genus secrete parasitism effector, proteins, many of which are encoded by genes having no identifiable homologues [4].

METHOD & RESULTS

PIPELINE

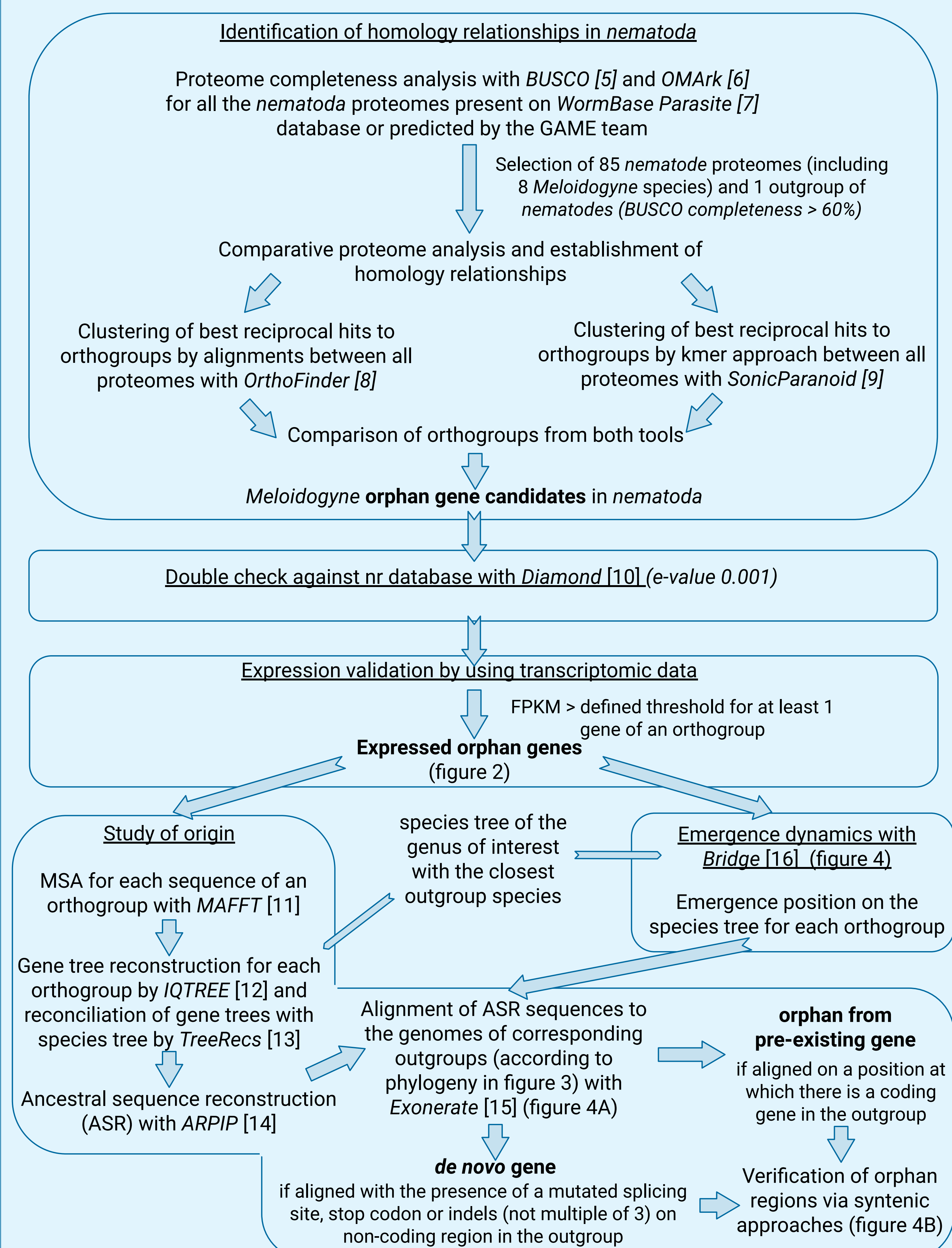


Figure 1: Developed bioinformatics pipeline to identify orphan genes and to study their evolution in *Meloidogyne*.

RESULTS

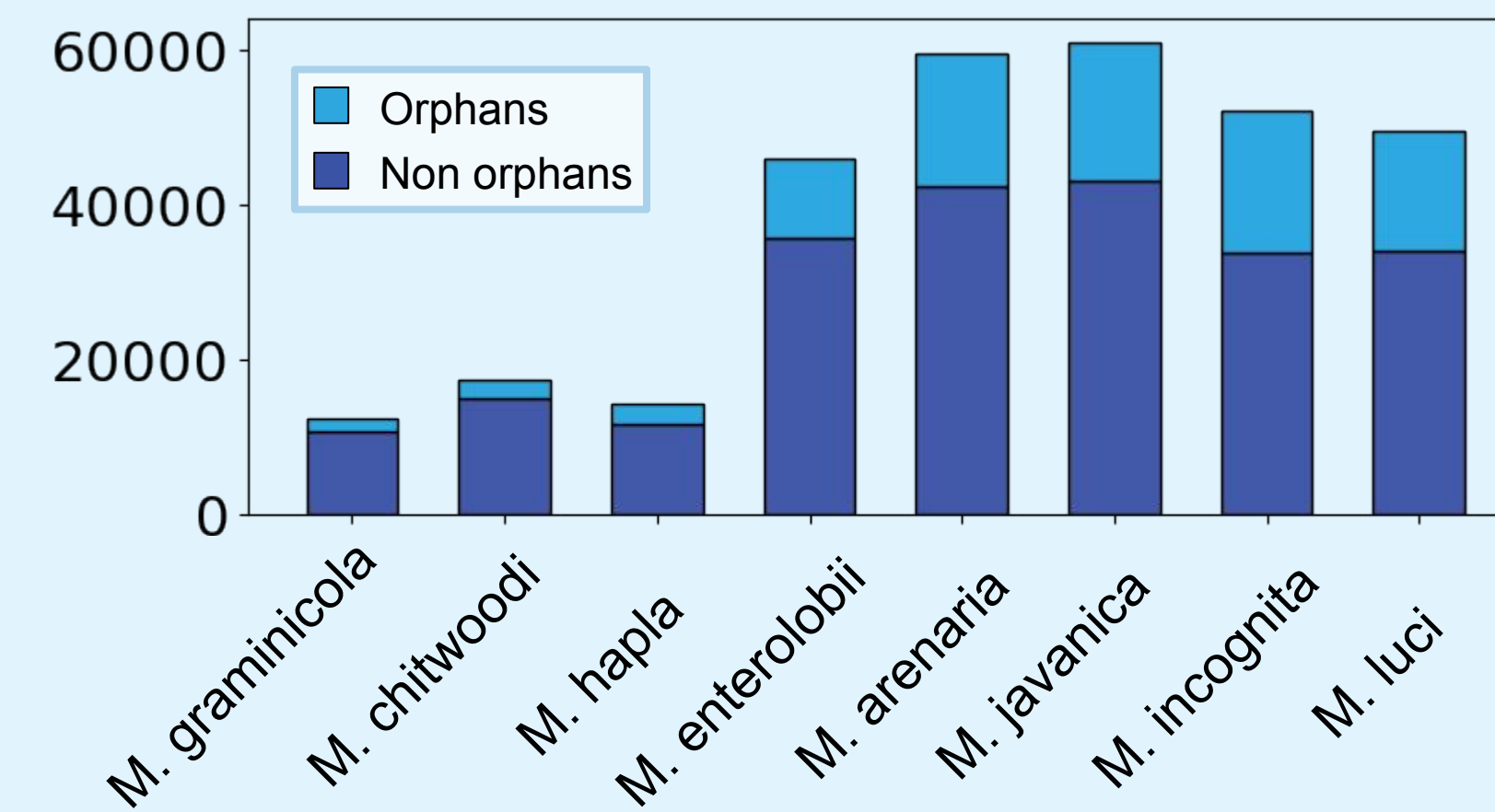


Figure 2: Number of orphan and non-orphan genes for 8 *Meloidogyne* species studied. Barplot representing the number of orphan genes identified for each of the 8 *Meloidogyne* species. Each bar corresponds to the total number of genes of each species. Light blue represents orphans and dark blue represents non-orphan genes.



Figure 3: Species tree of *Meloidogyne* species with their closest outgroup species *P. penetrans*. Species tree with 8 *Meloidogyne* species corresponding to three different clades (represented at the right of the species) of *Meloidogyne* genus along with *P. penetrans*, which is the closest outgroup to this genus. Each ancestral node is represented by a dot. Number of orphan orthogroups emerged in each node is given by a value next to it.

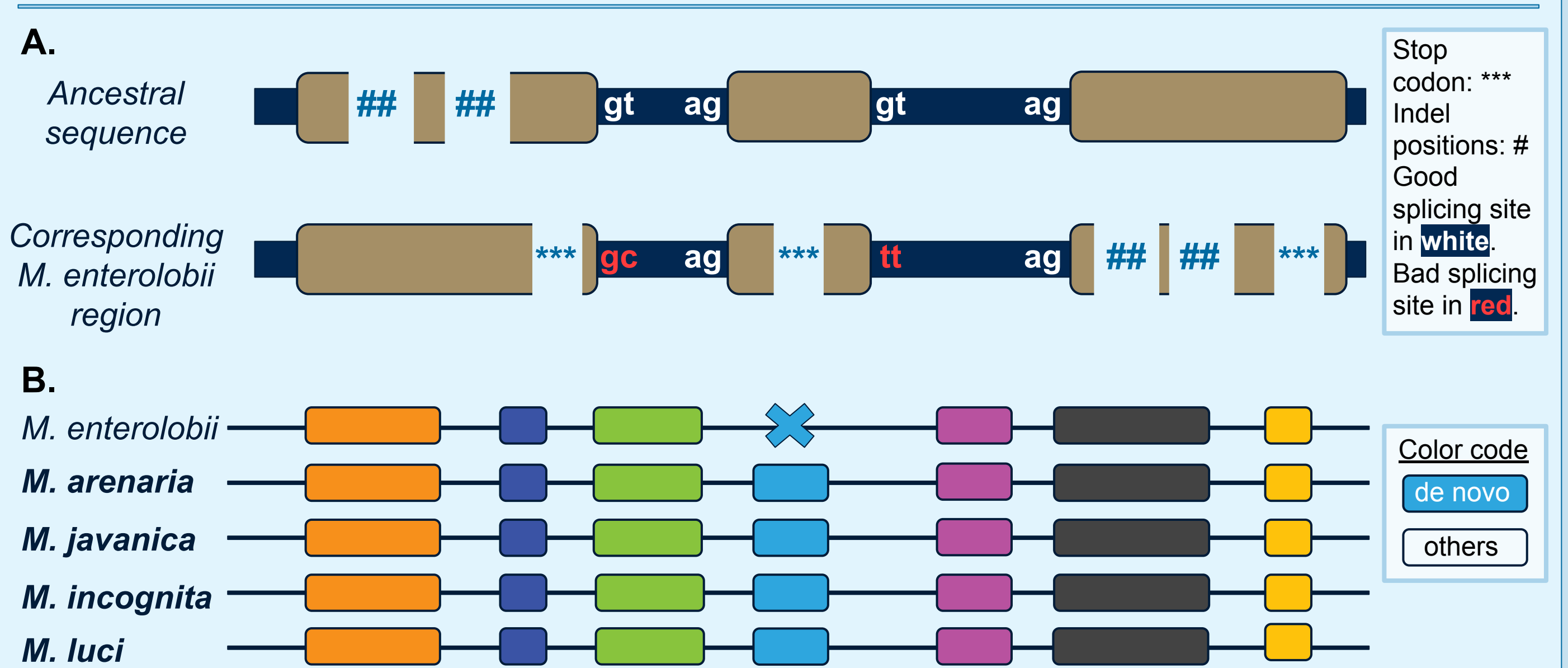


Figure 4: Example of a *de novo* gene birth that emerged inside the clade I. A. Alignment of the reconstructed ancestral sequence of an example orthogroup common to all members of clade I except for *M. enterolobii* to the genome of *M. enterolobii* by Exonerate [15]. Brown represents exons and dark blue represents introns. Stop codons are represented by ***. Insertion-deletion positions (not a multiple of 3) are represented by #. Good splicing sites are in white, mutated ones in red. B. Verification of the syntenic conservation of the identified *de novo* gene. For the position where ancestral sequence aligns to *M. enterolobii*, closest 3 genes in both directions are studied to determine the conservation of the region. Lines corresponds to introns and boxes corresponds to genes. Blue boxes corresponds to the *de novo* gene and blue cross is where it aligns on *M. enterolobii*. The color code indicates where the same genes align on different species.

CONCLUSION & DISCUSSION

- This study introduces a pipeline that combines homology, transcriptomics, and ancestral sequence reconstruction to identify and investigate the origin of orphan genes. This makes it possible to correctly distinguish between orphan genes that have diverged from pre-existing genes and those that have emerged *de novo*. To date, results indicate that 24% of *Meloidogyne* genomes consist of orphan genes. At least 7% of these are the result of *de novo gene birth*. Yet, it should be kept in mind that the results depend highly on the quality of genomes in disposition.
- Despite the fact that some effectors in *Meloidogyne* are coded by non-homologous genes, there is still no connection between the orphan genes and their functions in *Meloidogyne*. Thus, we are exploring structural approaches to better characterize these gene-structure-functions associations.

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