

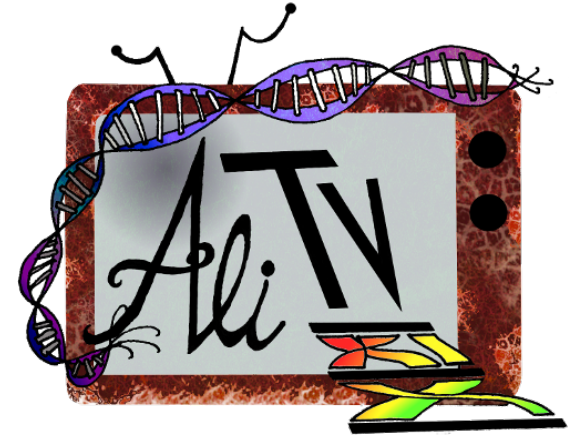
AliTV - Alignment Toolbox and Visualization

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Abstract: One of the main tasks in current genomics is comparing complete genomes of different organisms. For this task specialized whole genome alignment programs have been developed. Yet results of established tools are not easily comprehensible as they often consist of large tables of coordinates. In contrast graphical representations of alignments vastly improve the perceivability by humans. Thus different tools are available to visualize whole genome alignments. However the created images are static and therefore can not easily be adjusted to do further analyses. Here we present AliTV with its outstanding feature of interactive visualization of whole genome alignments. It thereby facilitates the comparative analysis of whole genomes, one of the bottle necks in modern biology. AliTV is freely available at <http://bioinf-wuerzburg.github.io/AliTV/>

1) Biological Question



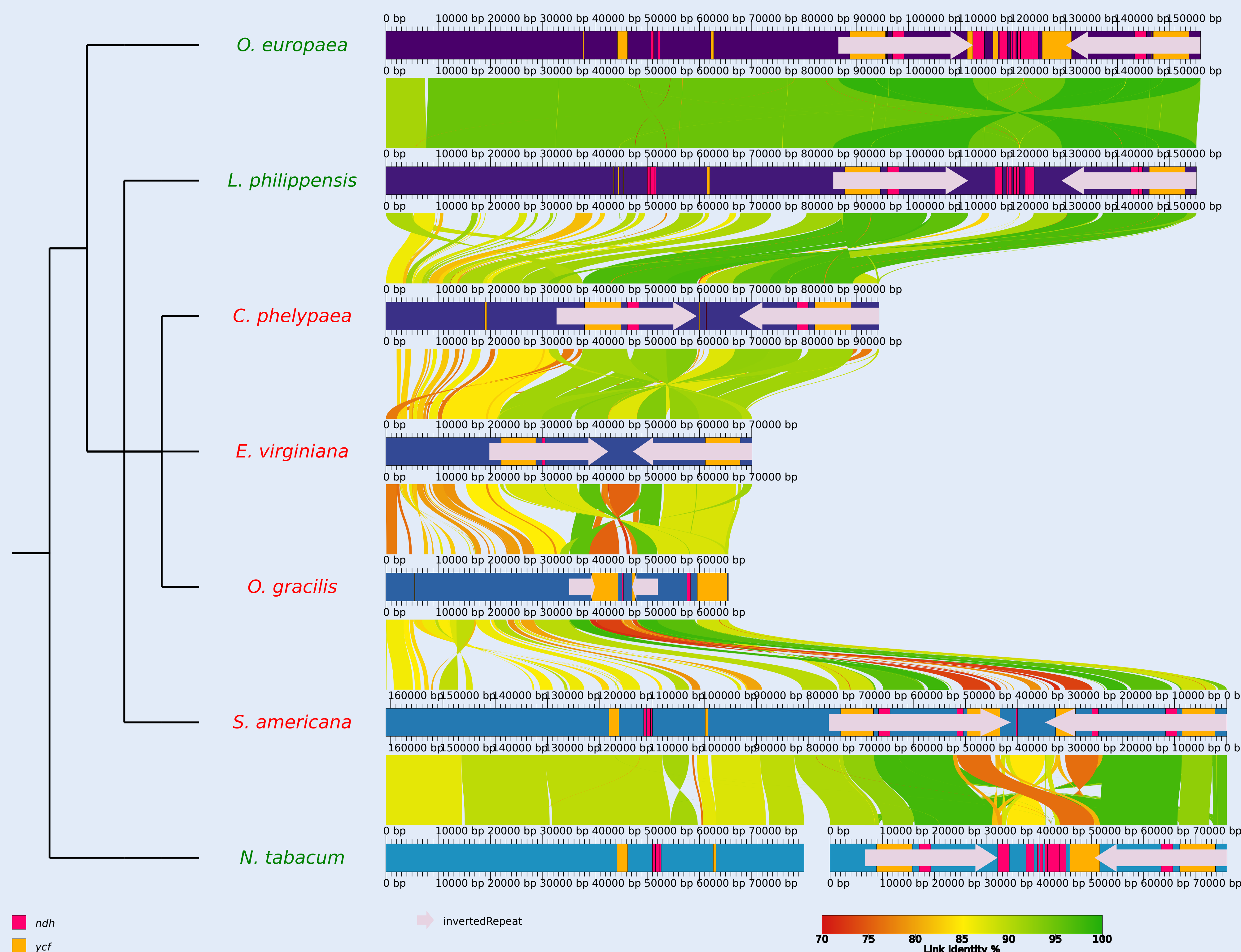
Do chloroplast genomes of **non-parasitic** and **parasitic** plants differ?

2) Preparation



AliTV requires annotated sequences. Those can be retrieved from public databases or generated by sequencing, assembly and gene prediction [5-8].

3) Analysis



Comparative genomics via whole genome alignment. AliTV provides interactive visualization and analysis (<https://goo.gl/Q2LqJZ>)

4) Results & Discussion

Genome sizes vary by a factor of two. Nucleotide sequences are different. Some regions are rearranged. There are less *ndh* genes in the chloroplasts of parasitic plants.

Those observations can be used to refine hypotheses (e.g. *ndh* genes are not necessary in chloroplasts of parasitic plants) and design further experiments for their testing.

Perspective

AliTV has no limitation to small genomes. Therefore also microbial, animal or plant genomes can be analyzed. And publication ready figures can be produced.

Moreover other applications for AliTV are imaginable, e.g. the evaluation of assemblies.



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