

Prof. Dr. Boas Pucker (Plant Biotechnology and Bioinformatics)

Availability of slides

- All materials are freely available (CC BY) - after the lectures:
 - StudIP: **GE31/MM12**
 - GitHub: <https://github.com/bpucker/teaching>
- Questions: Feel free to ask at any time
- Feedback, comments, or questions: [b.pucker\[a\]tu-braunschweig.de](mailto:b.pucker@tu-braunschweig.de)



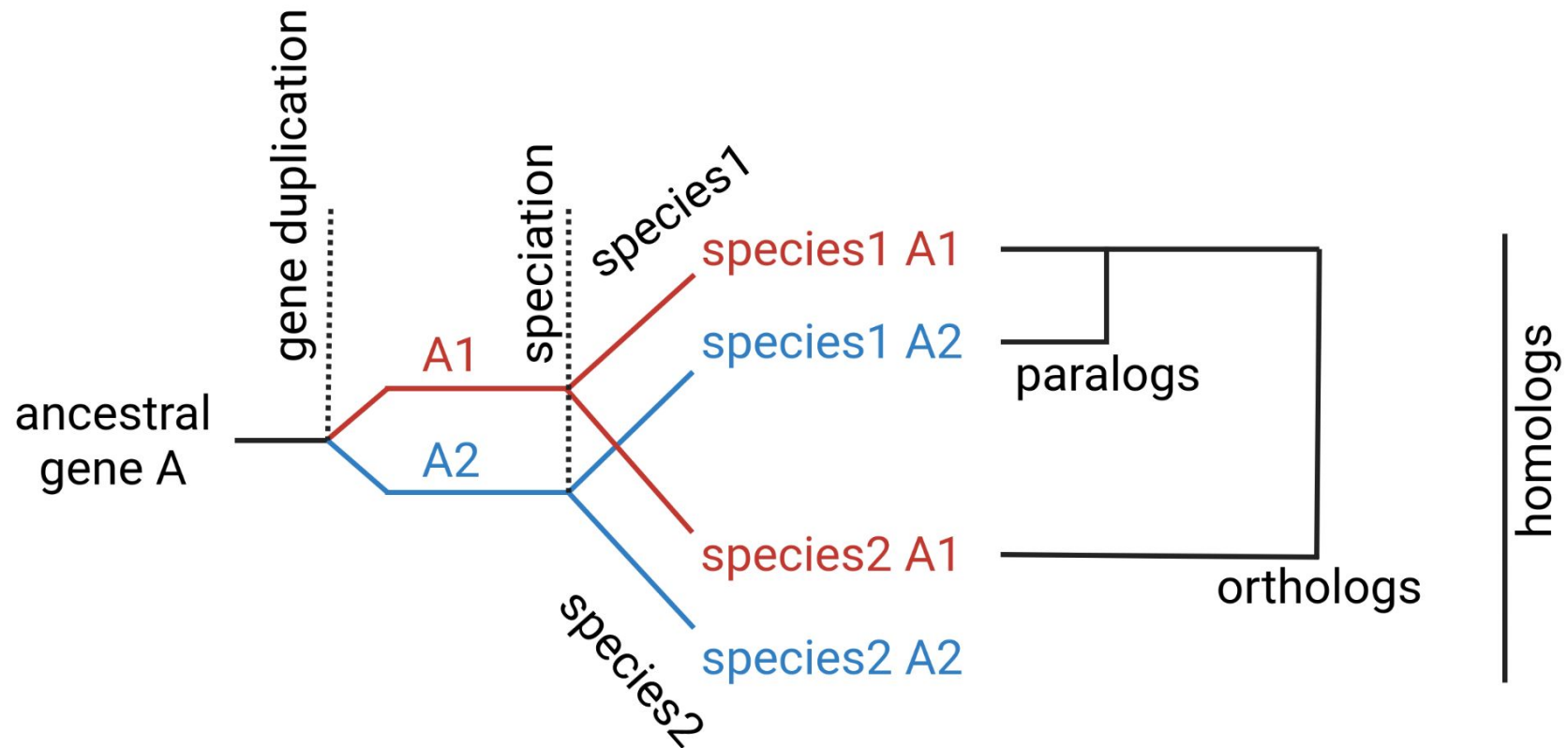
My figures and content can be re-used in accordance with CC BY 4.0, but this might not apply to all images/logos. Some figure were constructed using bioRender.com.

“Nothing in biology makes sense except in the light of evolution”
(who said this?)

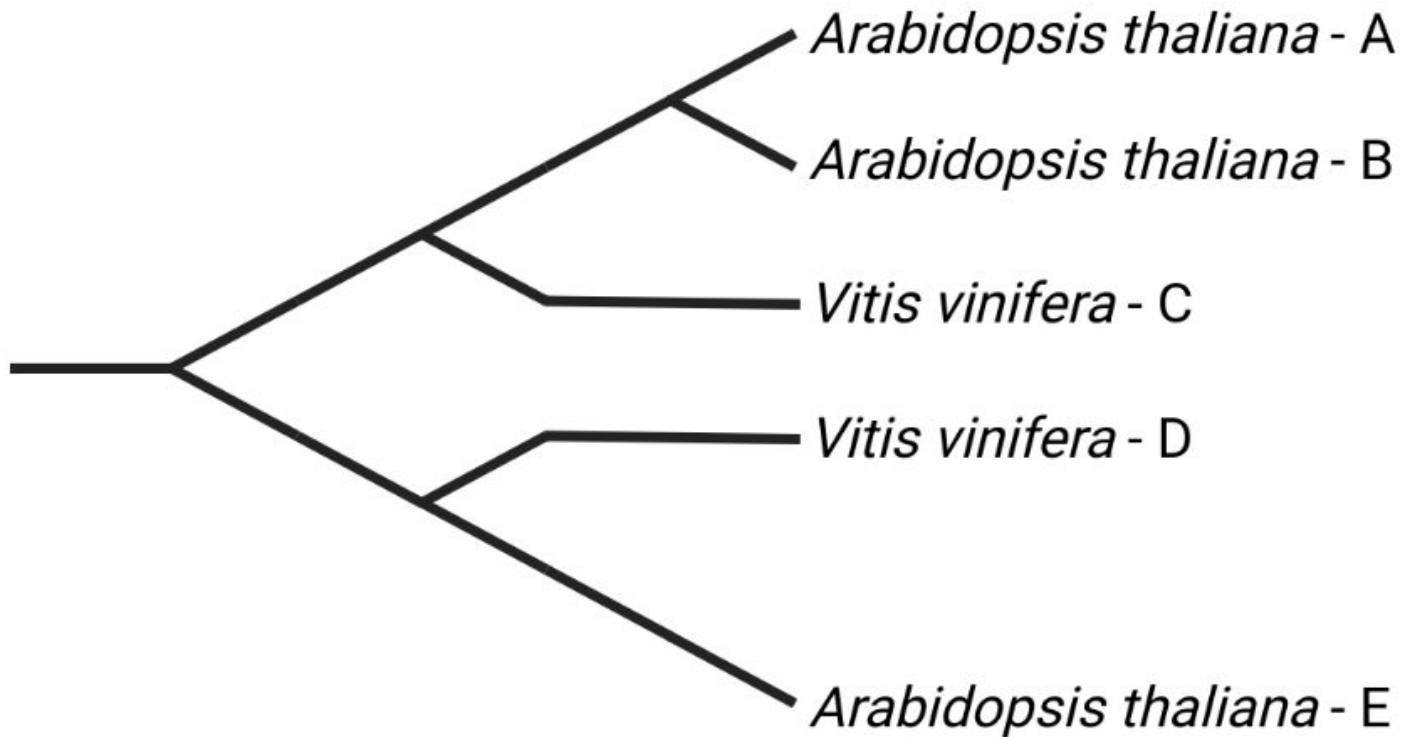
Evolutionary genomics

- Paralogous/orthologs
- OrthoGroup analysis with OrthoFinder (some evolution basics)
- Homeologs

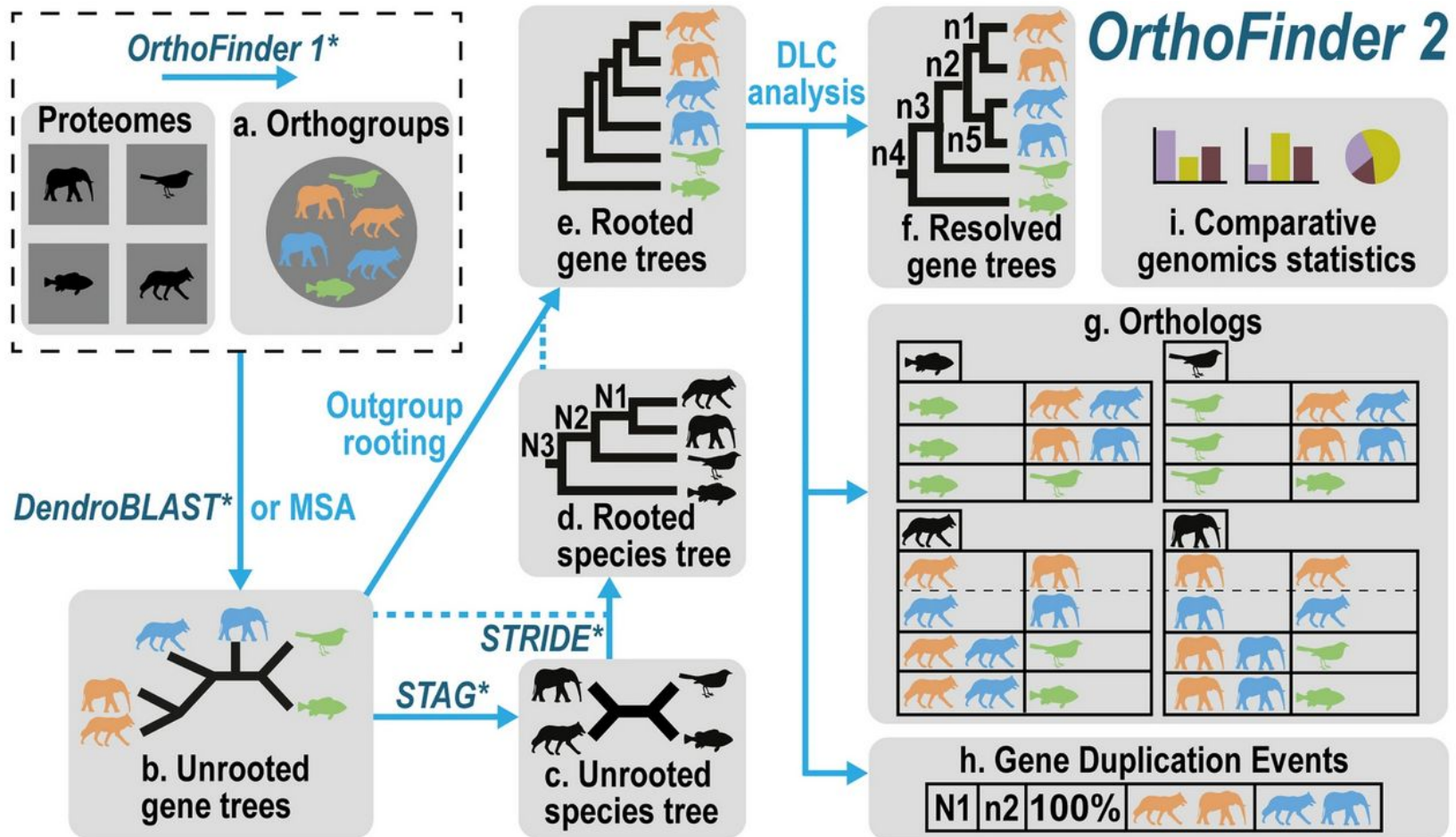
Paralogs & orthologs



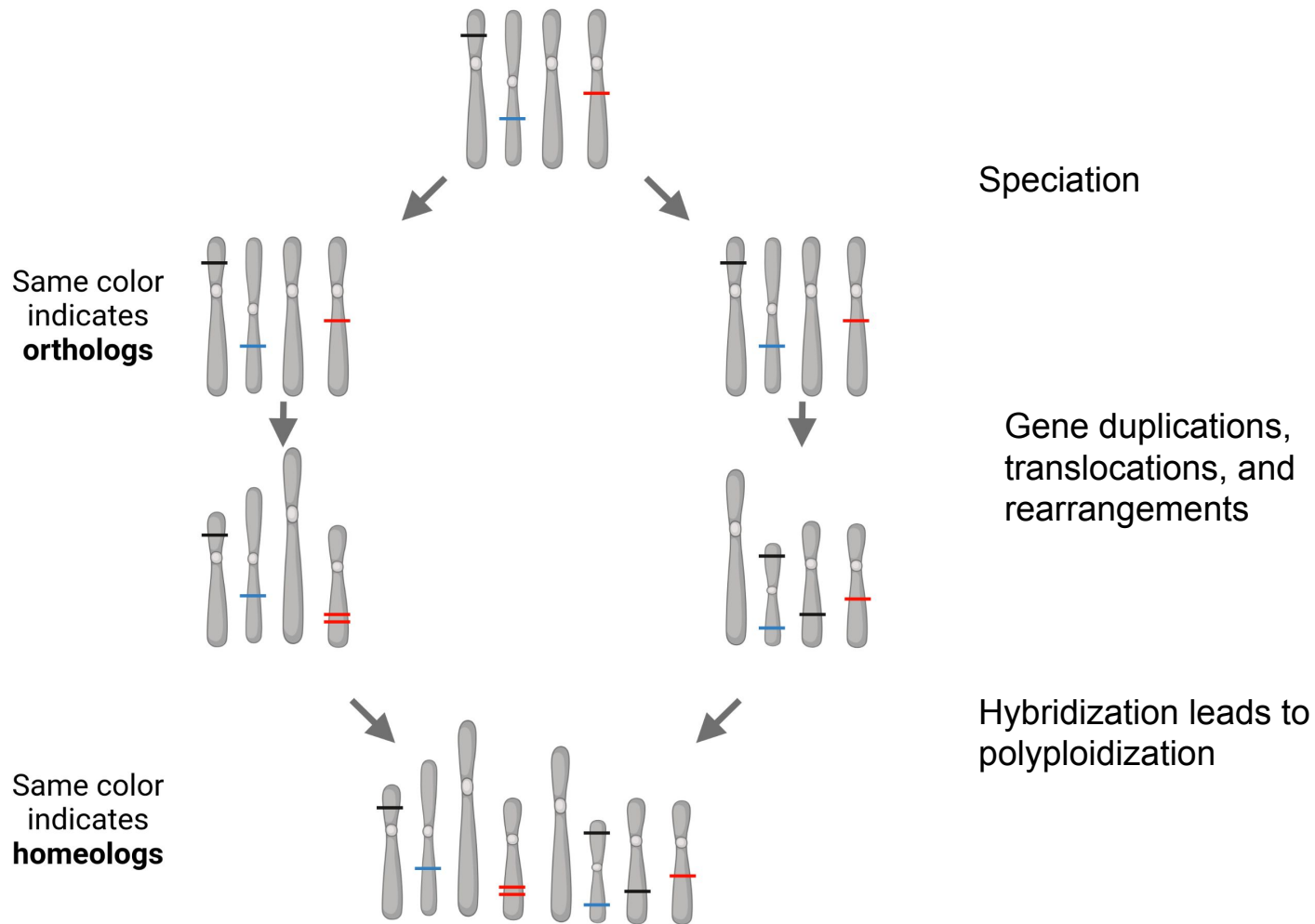
Which are orthologs/paralogs?



OrthoFinder2



Homeologs



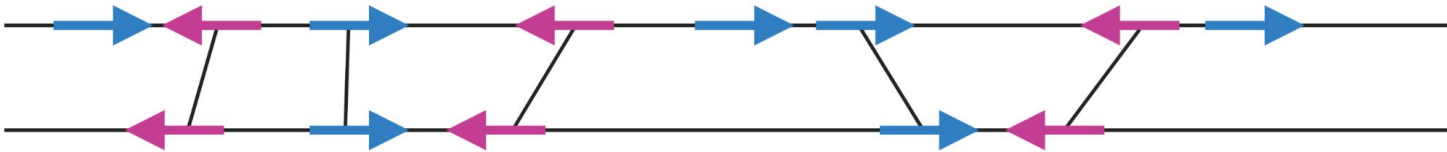
Glover et al., 2016: 10.1016/j.tplants.2016.02.005

Comparative genomics

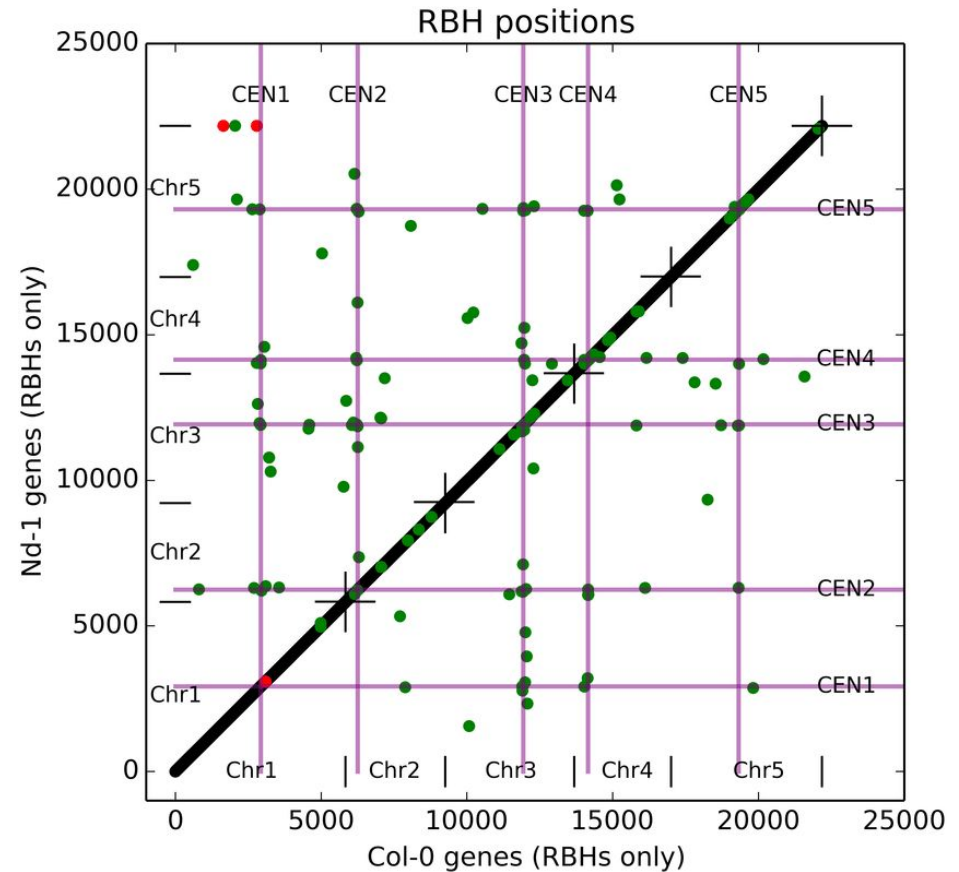
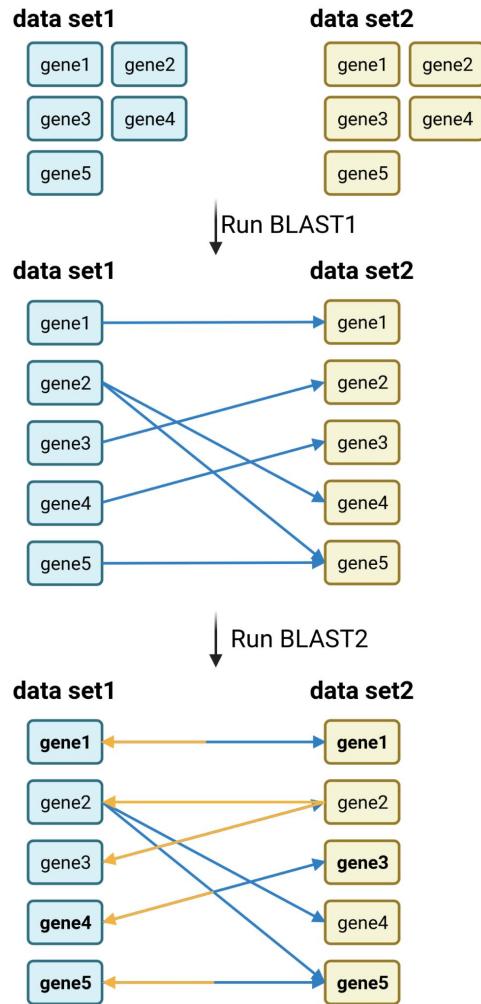
- Compare genome sizes
- Compare chromosome numbers
- Compare gene sets
- Compare gene positions & chromosome structures

Synteny

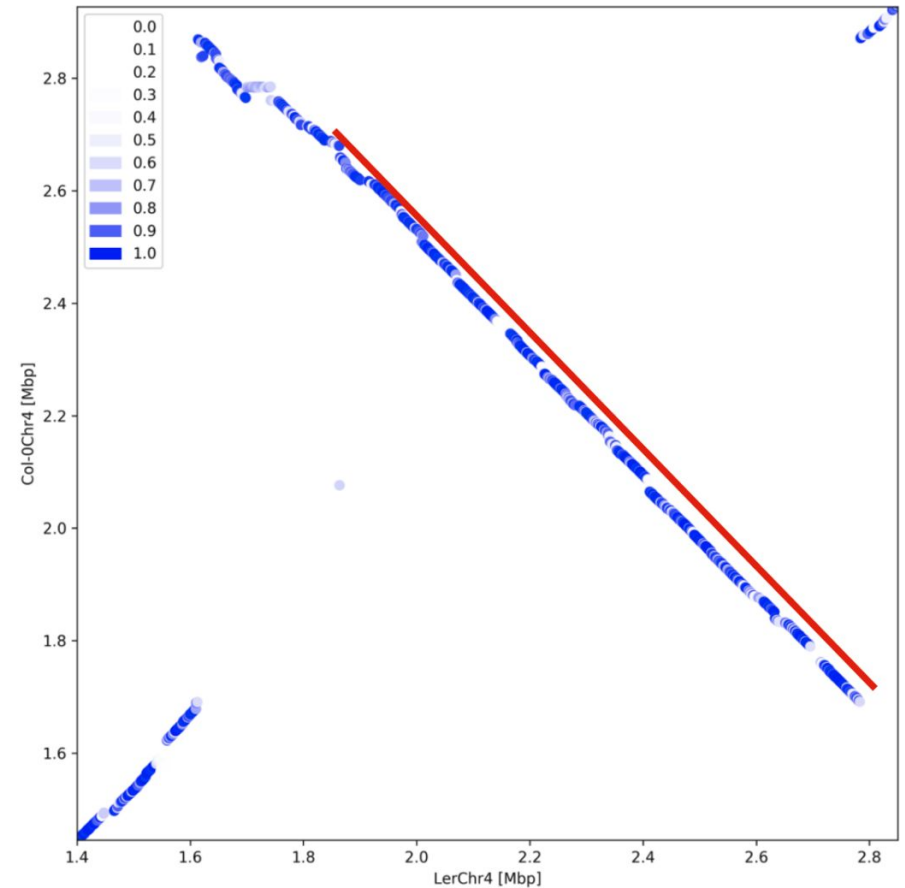
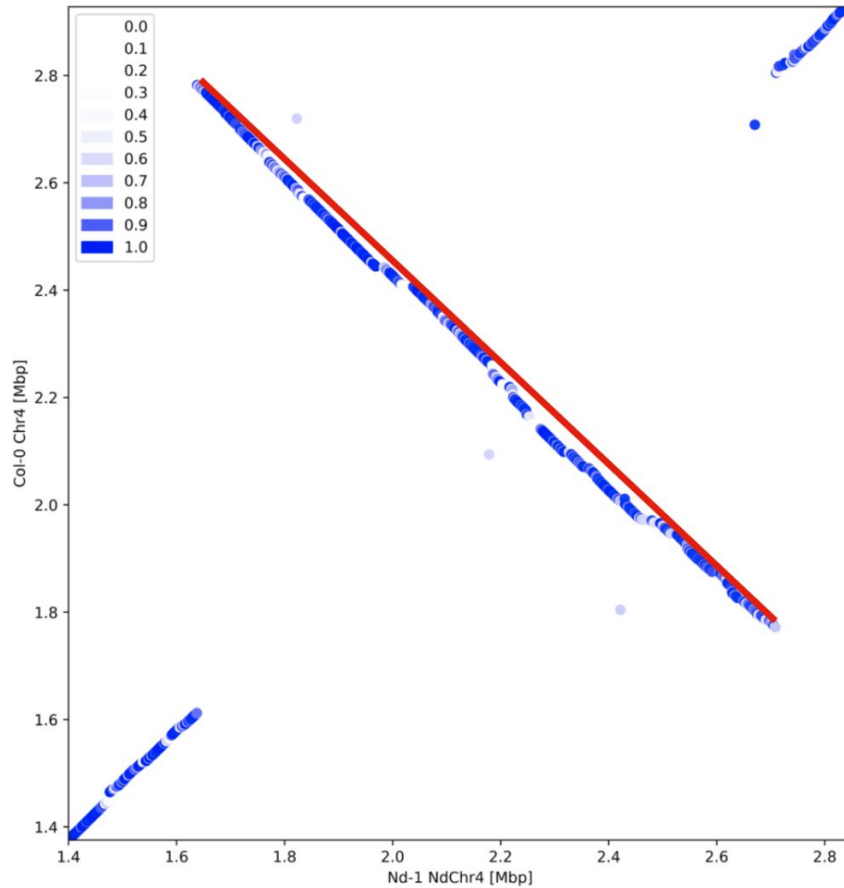
Synteny = Same order of genes in different genomes



Reciprocal Best BLAST hits (RBHs)



Dot plots



Pucker et al., 2019: 10.1371/journal.pone.0216233

JCVI/MCscan

① Extraction of mRNA sequences based on genomic positions of genes

species1 

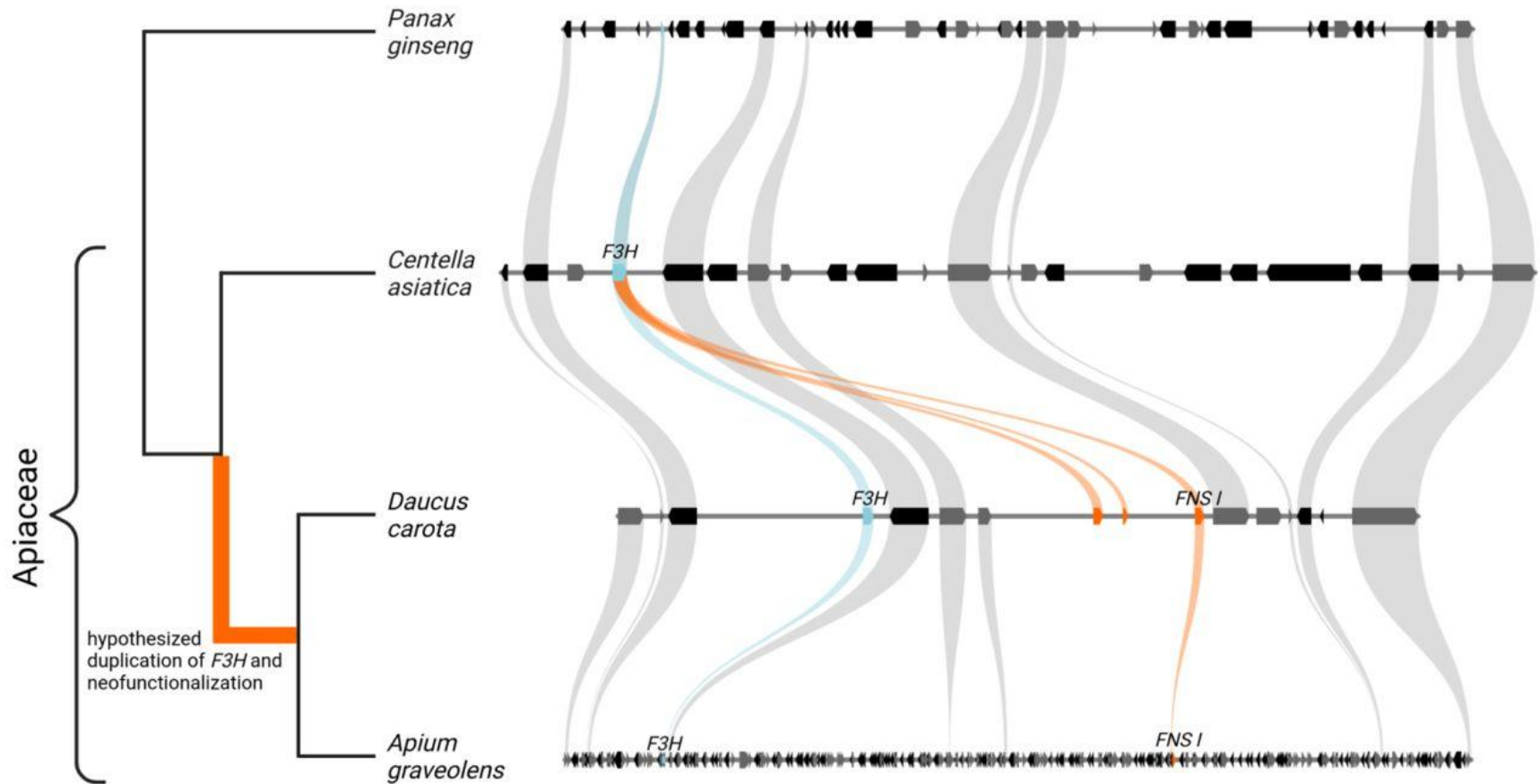
② Comparison of concatenated mRNA sequences via BLAST

species2 

③ Identification of syntenic blocks



Evolution of FNS I in the Apiaceae



Pucker & Iorizzo, 2022: 10.1101/2022.02.16.480750

Time for questions!

Questions

1. What are paralogs/orthologs?
2. What is synteny?
3. Which methods can be used to analyze synteny?
4. Which pattern indicates an inversion in a dot plot?
- 5.