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The relationship between ploidy, sex chromosomes, and sexual condition in *Syntrichia*

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Northern California Botanists
2024 Symposium
Bryophyte Session: Presenter 4
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Sunset Magazine


reddit.com/user/emeraldpity

Syntrichia

- A diverse genus of mosses, with ~100 named species
- A large number of dryland specialists
- Low rates of sexual reproduction, extreme female population bias common


USGS

Presentation Outline

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- Moss Reproduction

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- Sex Chromosomes

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- Polyploid Phylogenetics

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- Future Research

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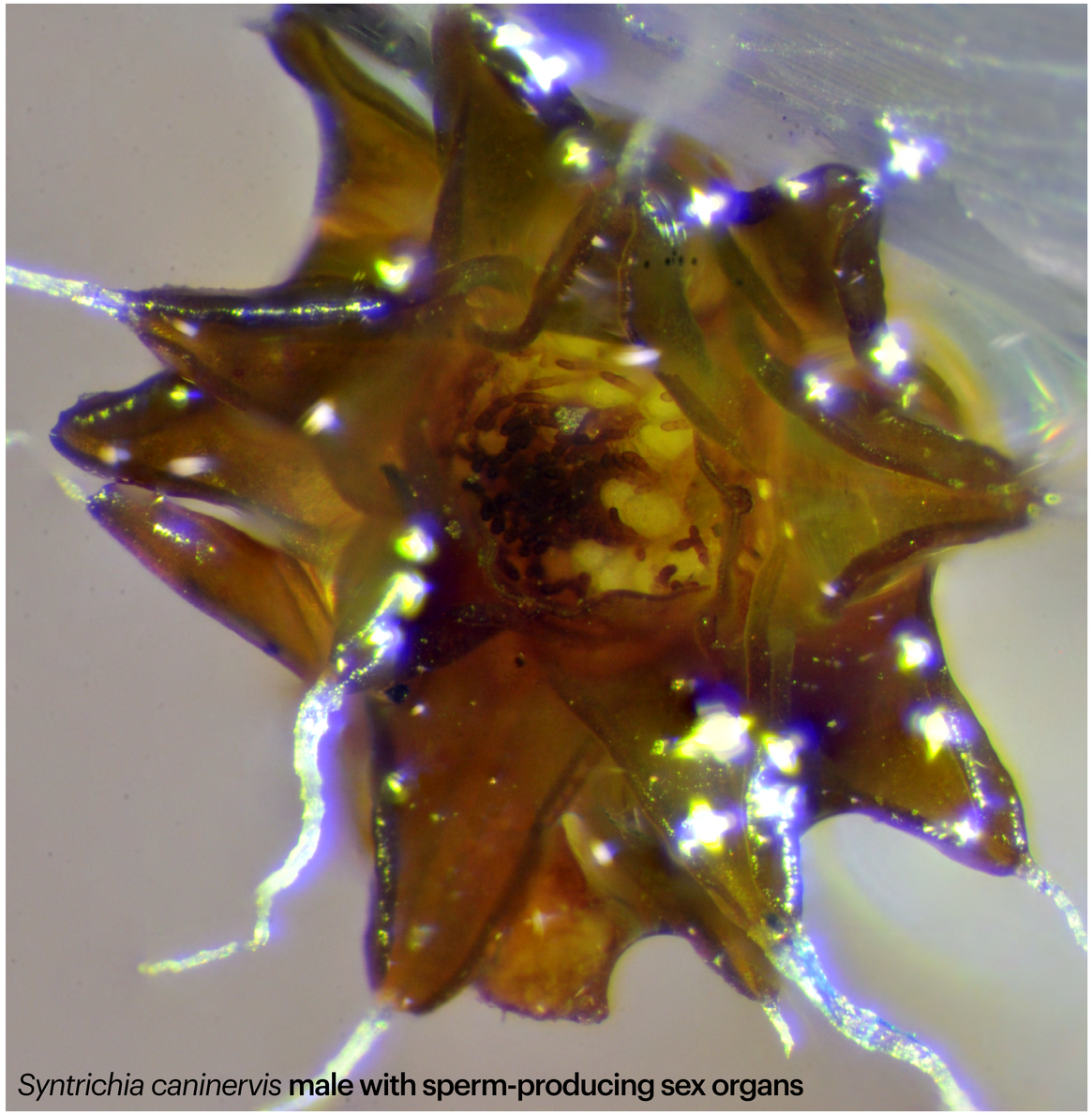
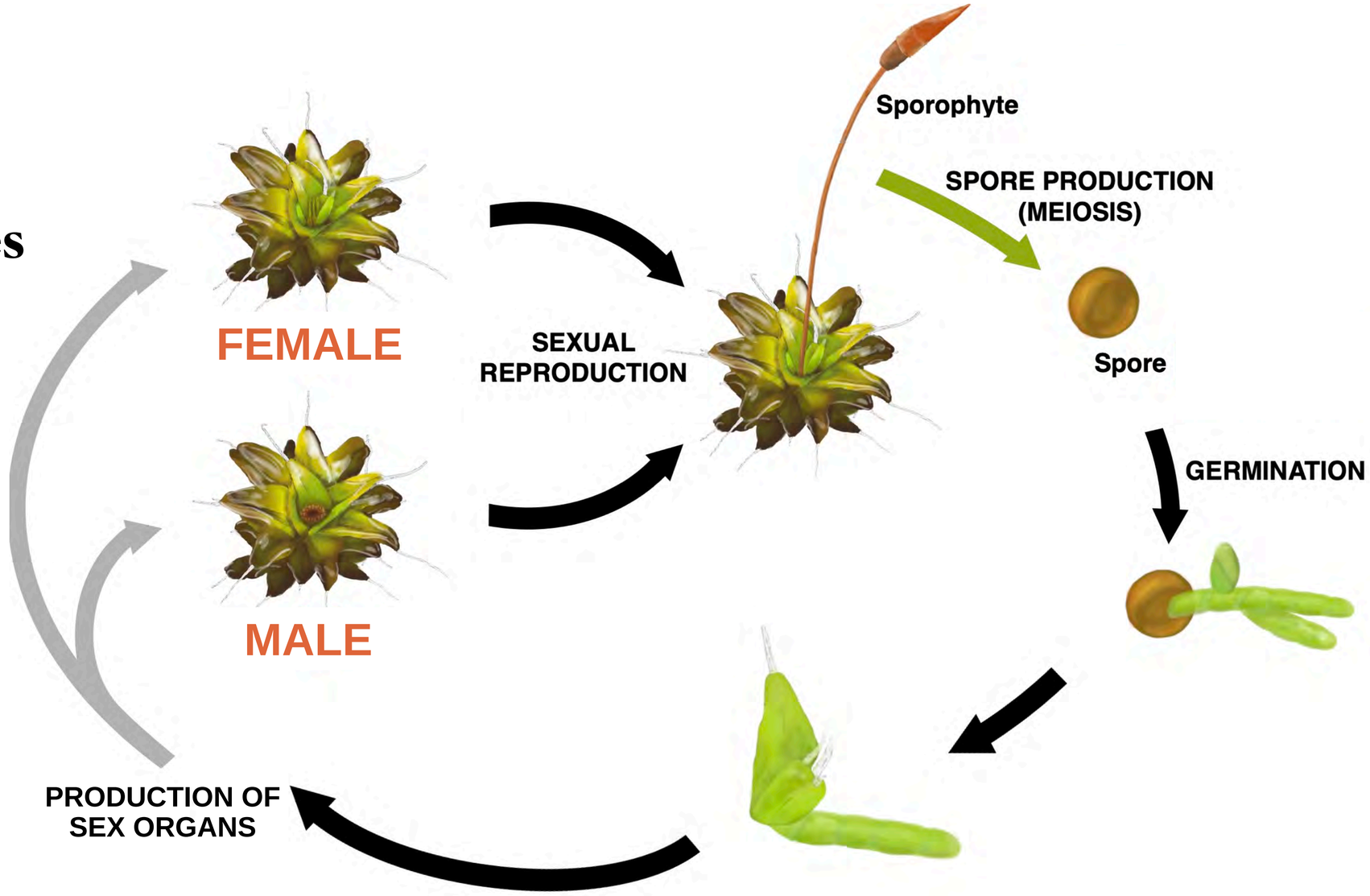
- Haploid-dominant, free-living gametophyte
- Spore-bearing and reproduce with swimming sperm



Syntrichia caninervis male with sperm-producing sex organs

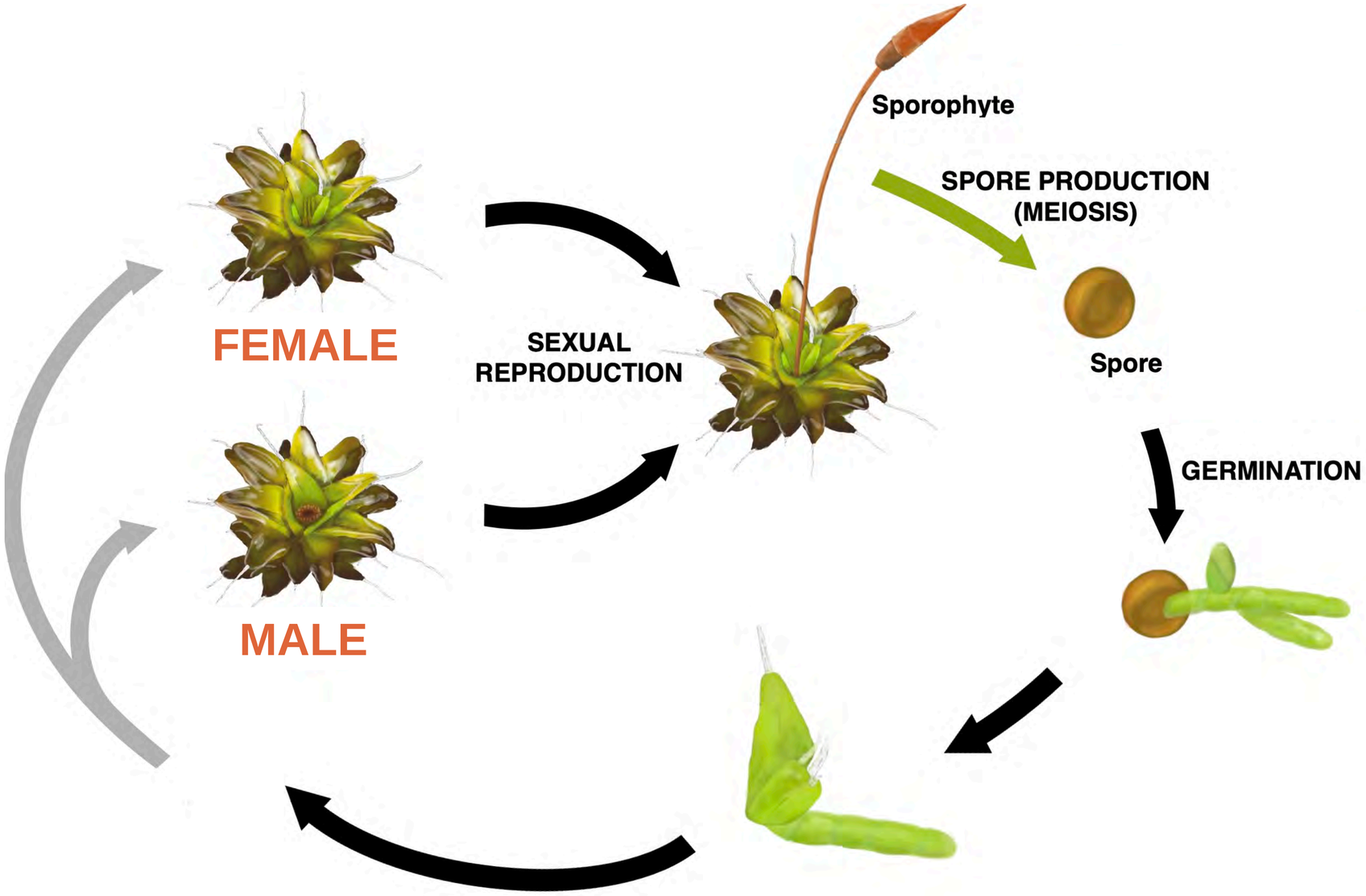
Most moss species (~60%) produce unisexual gametophytes



Moss Reproduction

Modified from: Ekwealor, JTB, SD Benjamin, JZ Jomsky, MA Bowker, LR Stark, DN McLetchie, BD Mishler, and KM Fisher (2022). Genotypic confirmation of a biased phenotypic sex ratio in a dryland moss using a novel RFLP technique *APPS*.

Bisexual gametophytes produce both sperm and egg



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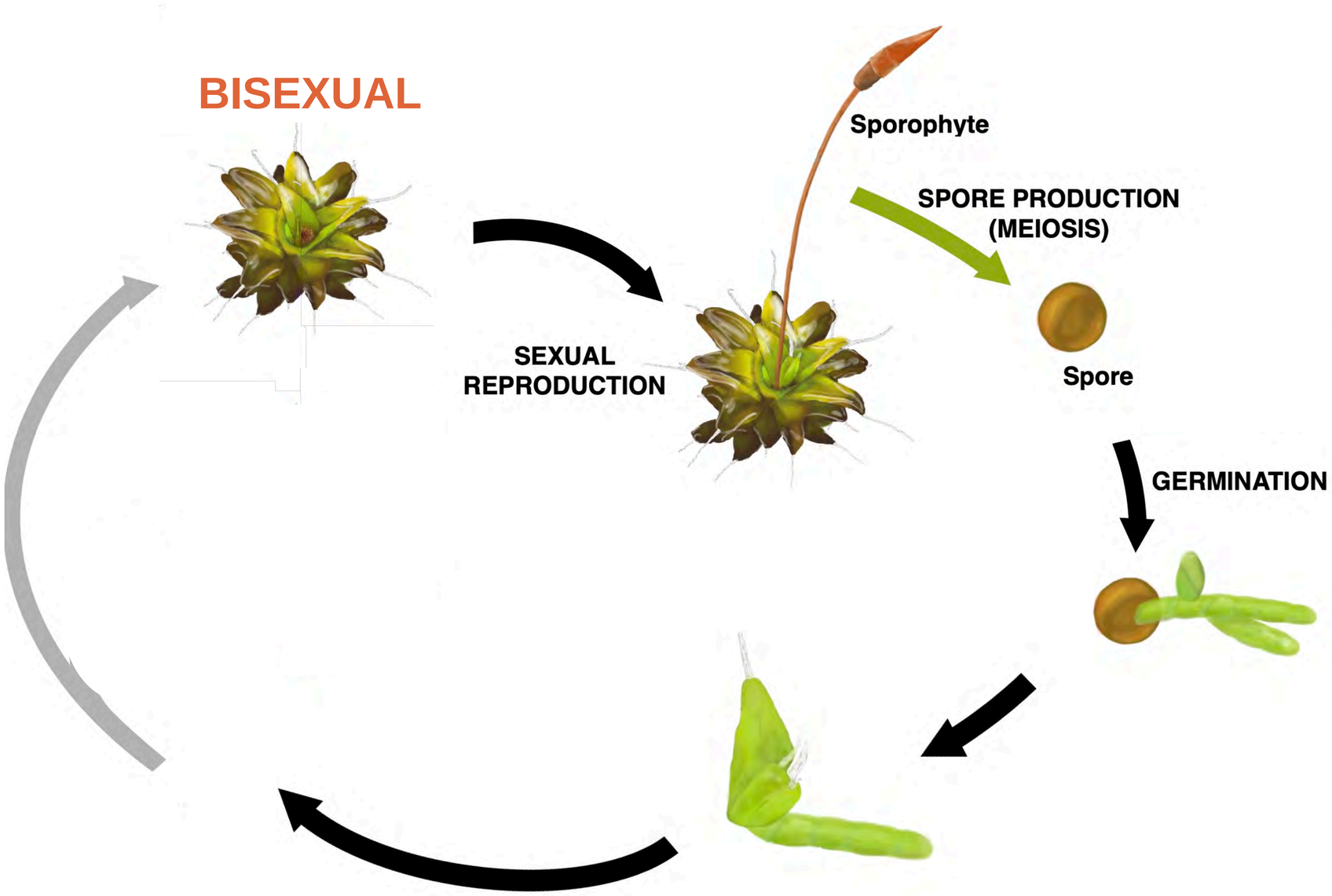
Bisexual gametophytes produce both sperm and egg

Many bisexual species can self, resulting in a sporophyte that is homozygous at all loci and spores that are clones of the parent



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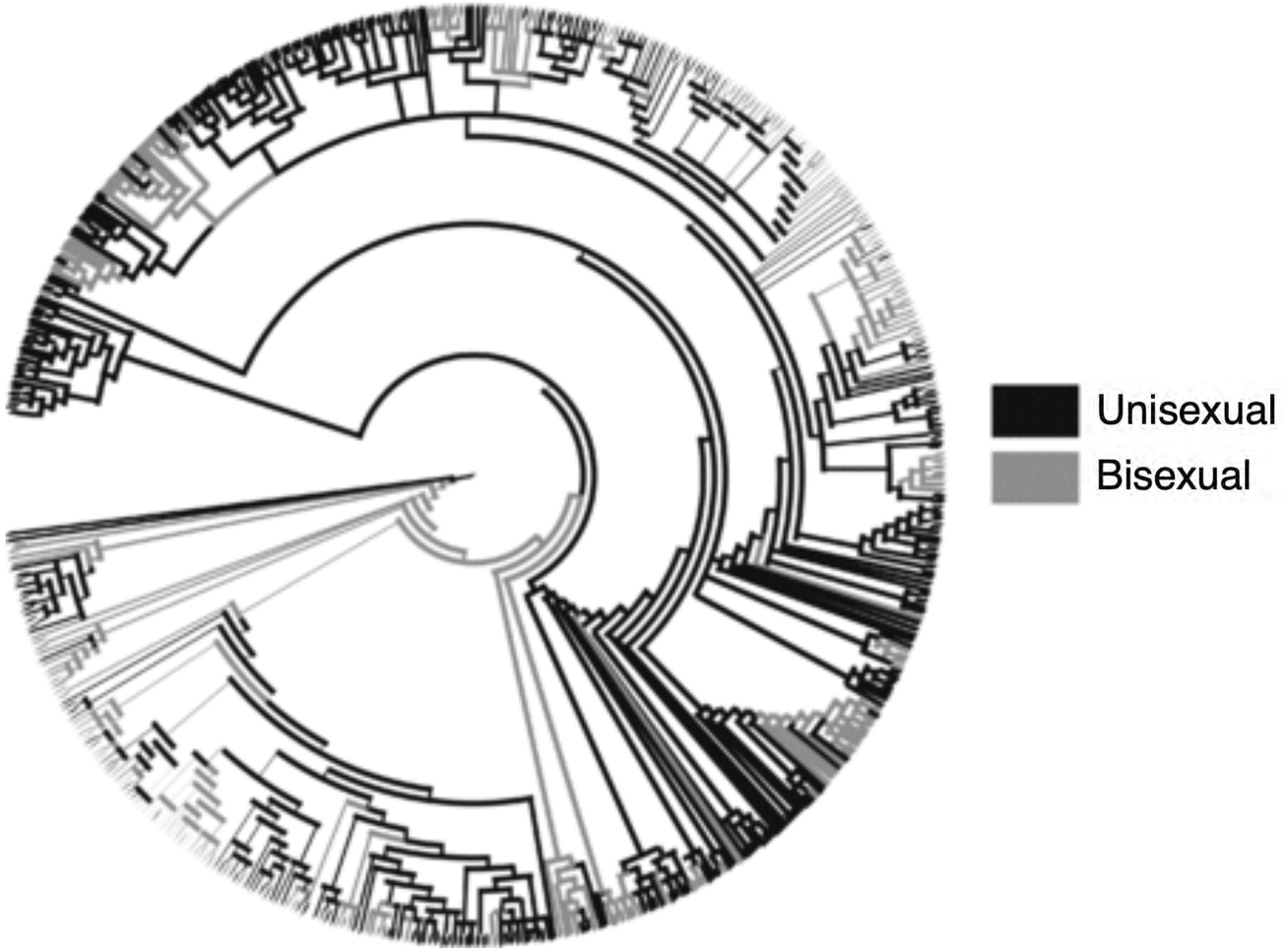
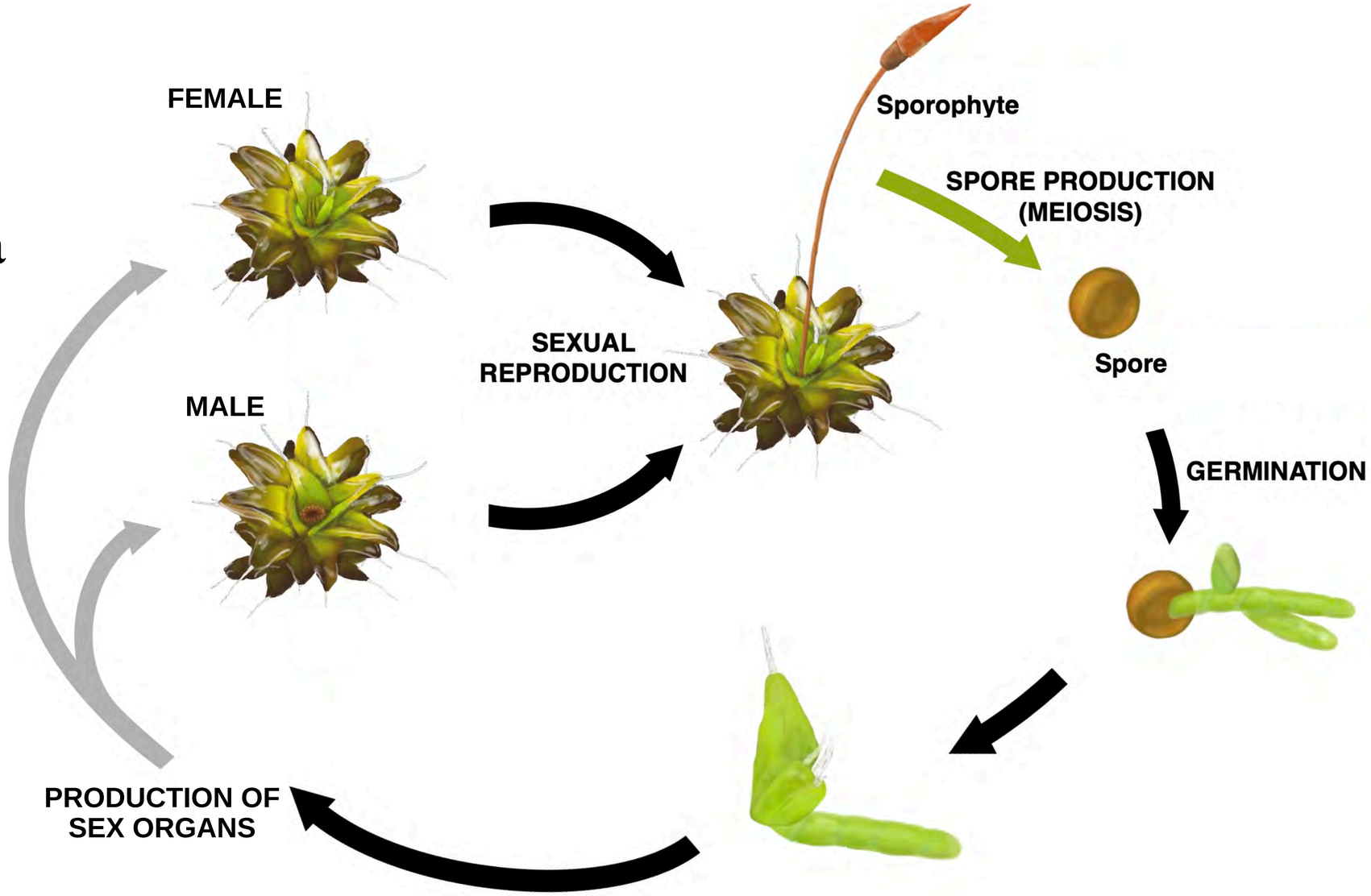


Evolutionary transitions in sexual condition

- McDaniel (2013) et al. found least 133 transitions between unisexuality and bisexuality in mosses
  - Rate of bisexuality to unisexuality was 2x higher than the reverse
  - Net diversification rates higher in bisexual lineages

Modified from: McDaniel, SF, J Atwood, and JG Burleigh (2013). Recurrent evolution of dioecy in bryophytes. *Evolution*.

Sex determination occurs in the haploid gametophyte stage via a single sex chromosome



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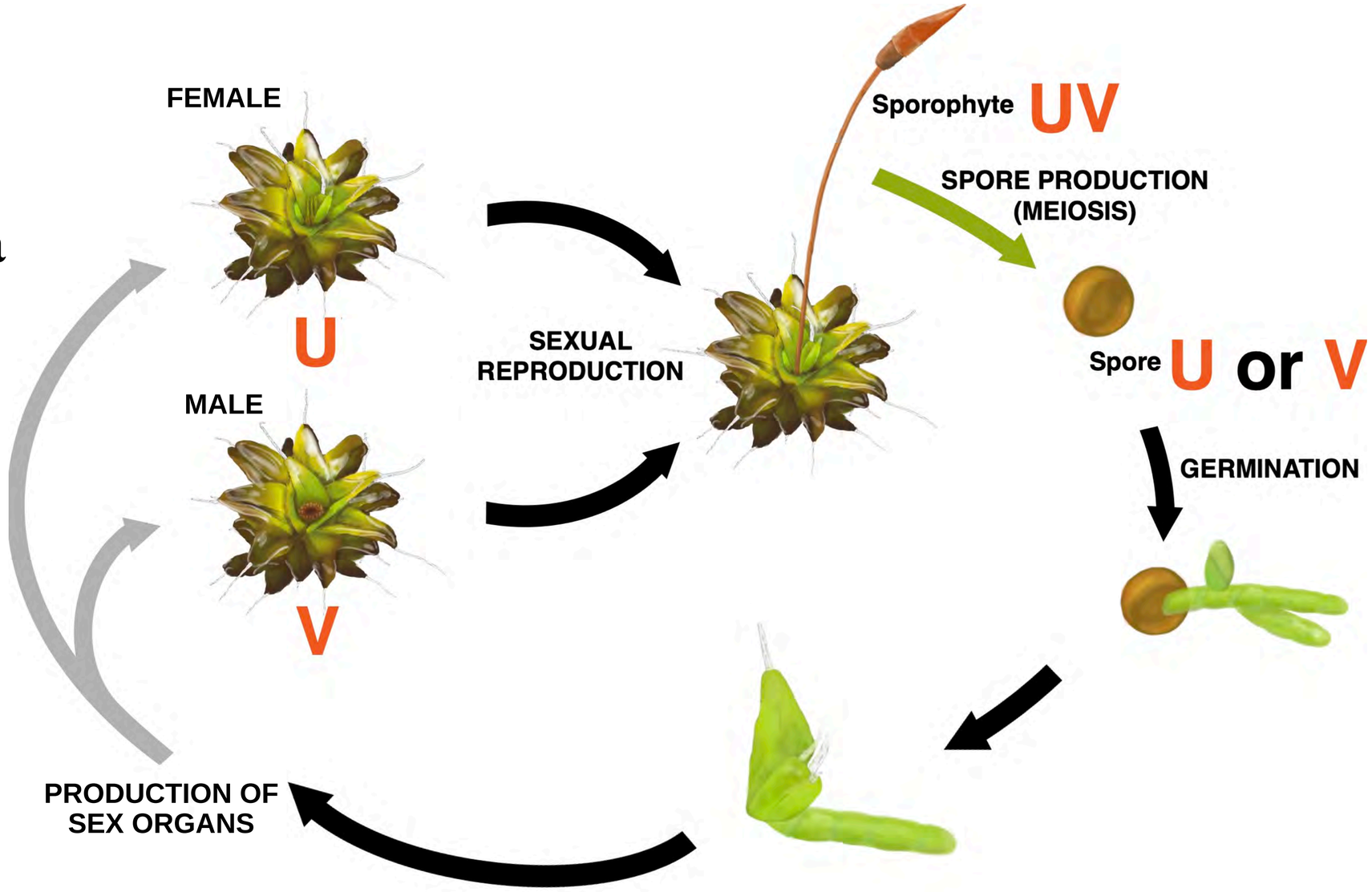

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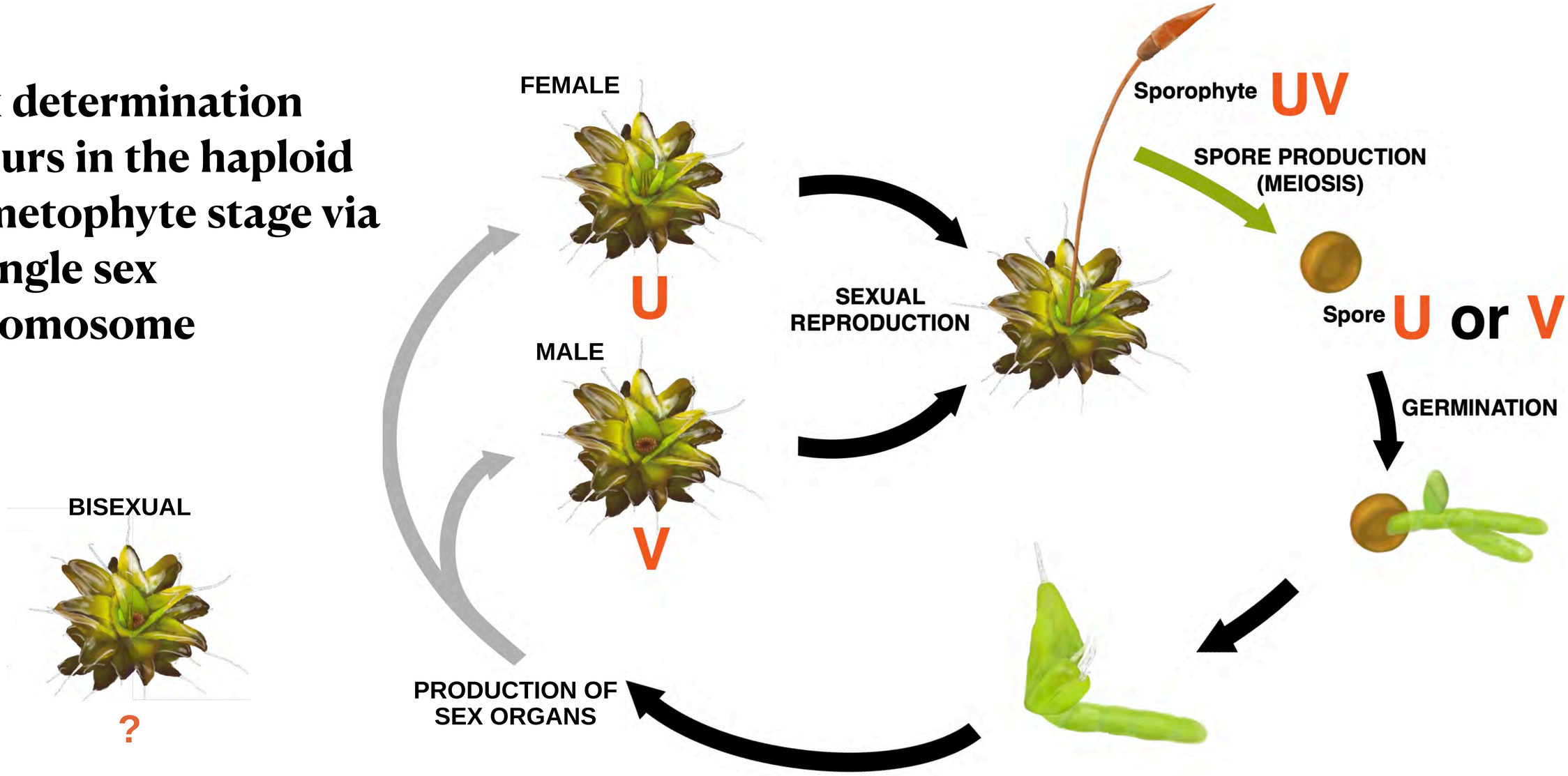

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How does **bisexuality** evolve?

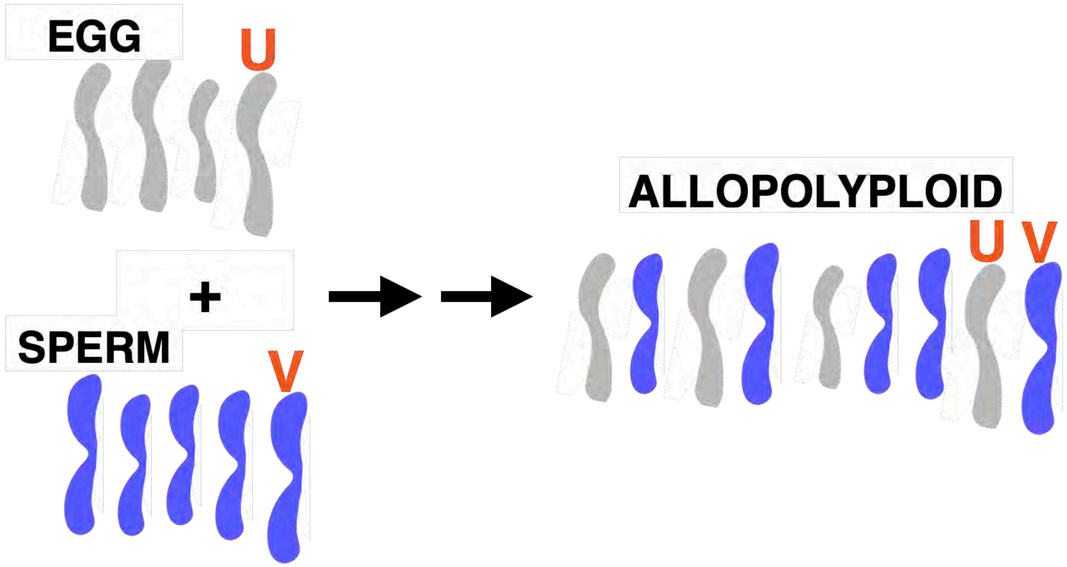
Hypothesis

Hypothesis

UV?

Hypothesis

Allopolyploids have both maternal and paternal progenitors, so are expected to have both U and V chromosomes



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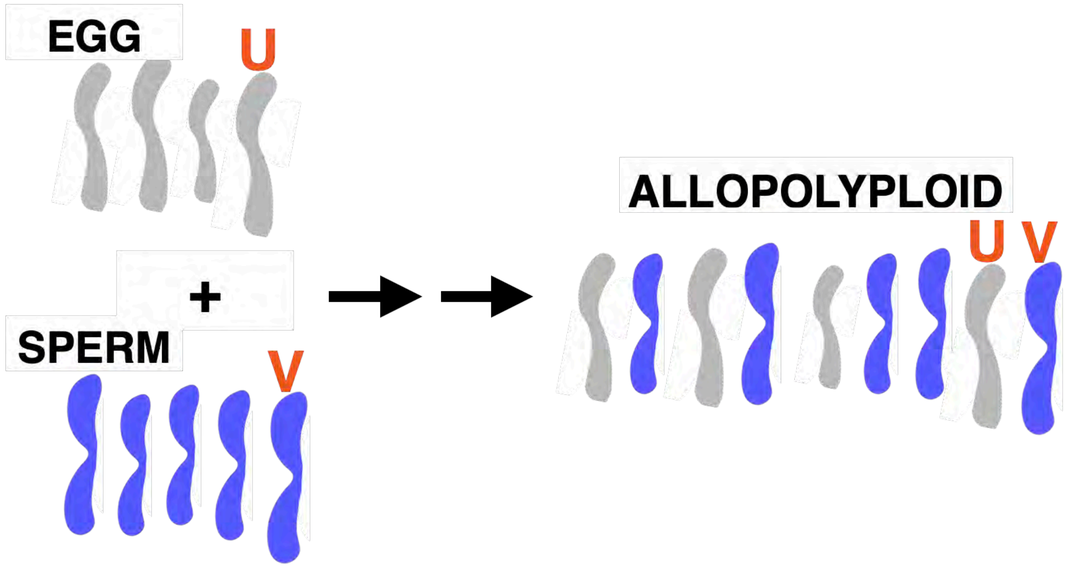

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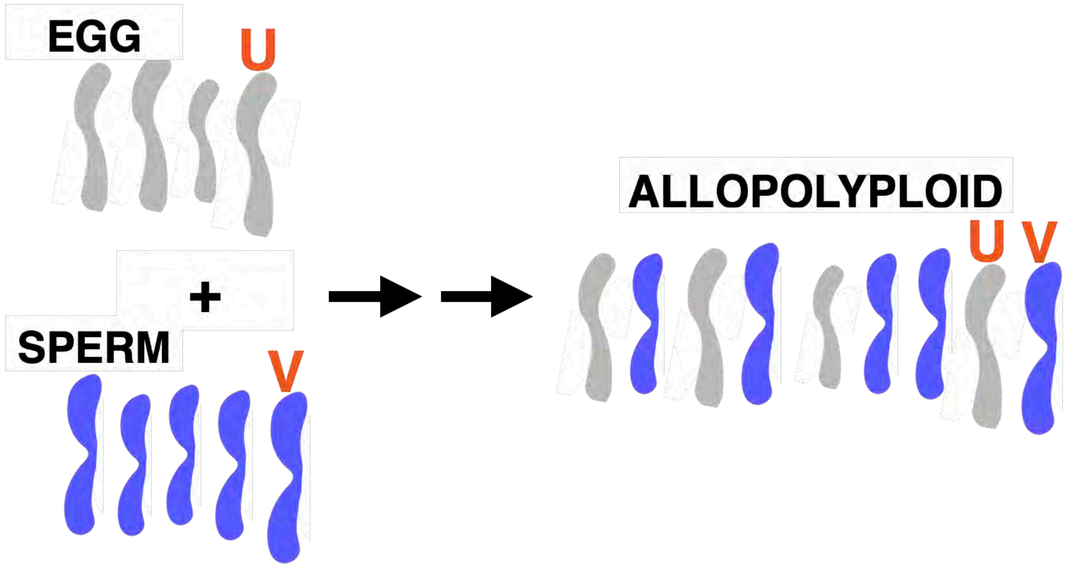

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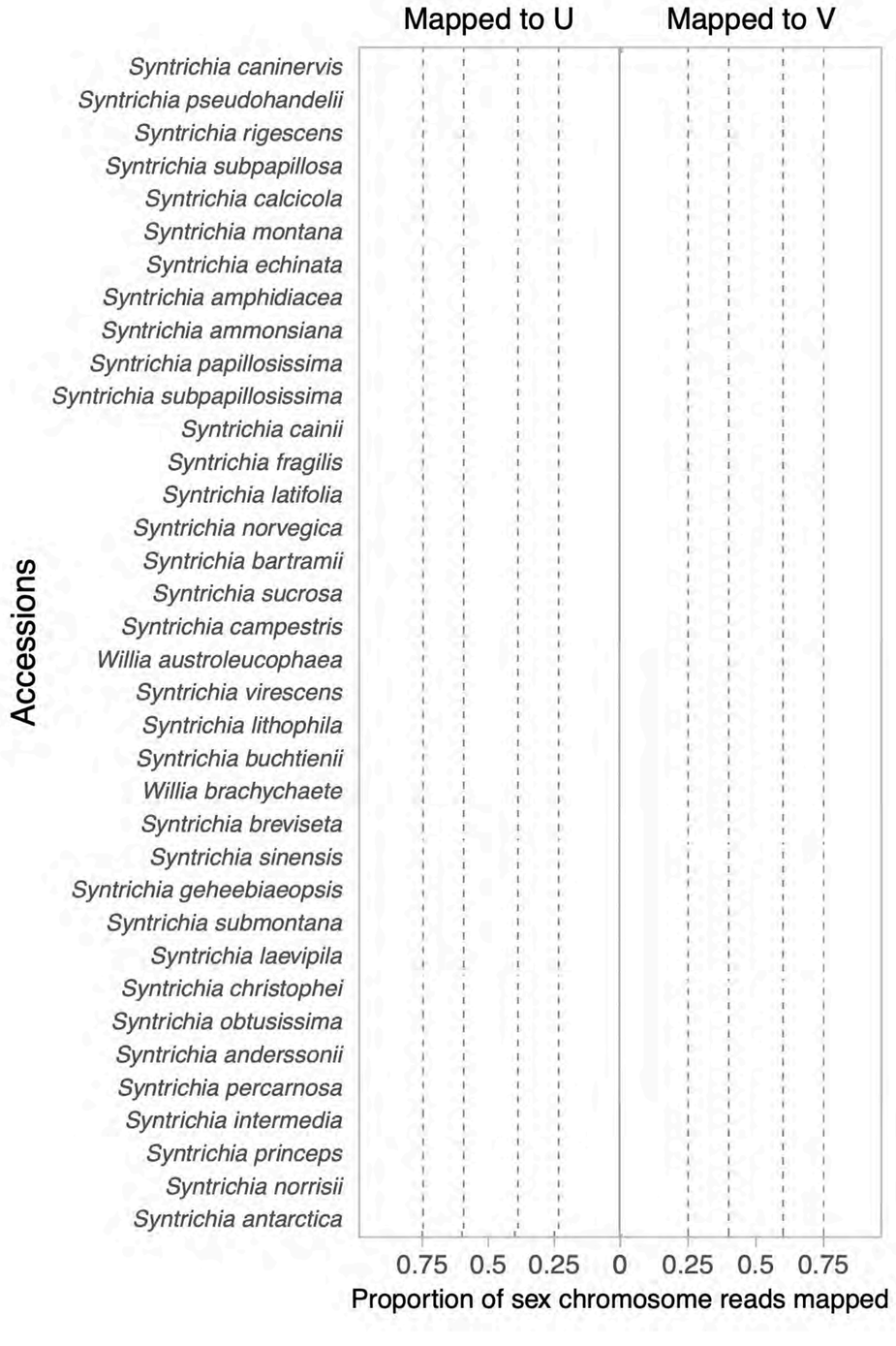
UV gametophytes may be bisexual

Inferring sex chromosomes



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Inferring sex chromosomes

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- Mapped reads to two reference genomes:

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- Mapped reads to two reference genomes:
  - Female (U) *S. caninervis* (Silva et al. 2020)
  - Male (V) *S. ruralis* (Zhang et al. in press)
- Counted reads that differentially mapped to U and V

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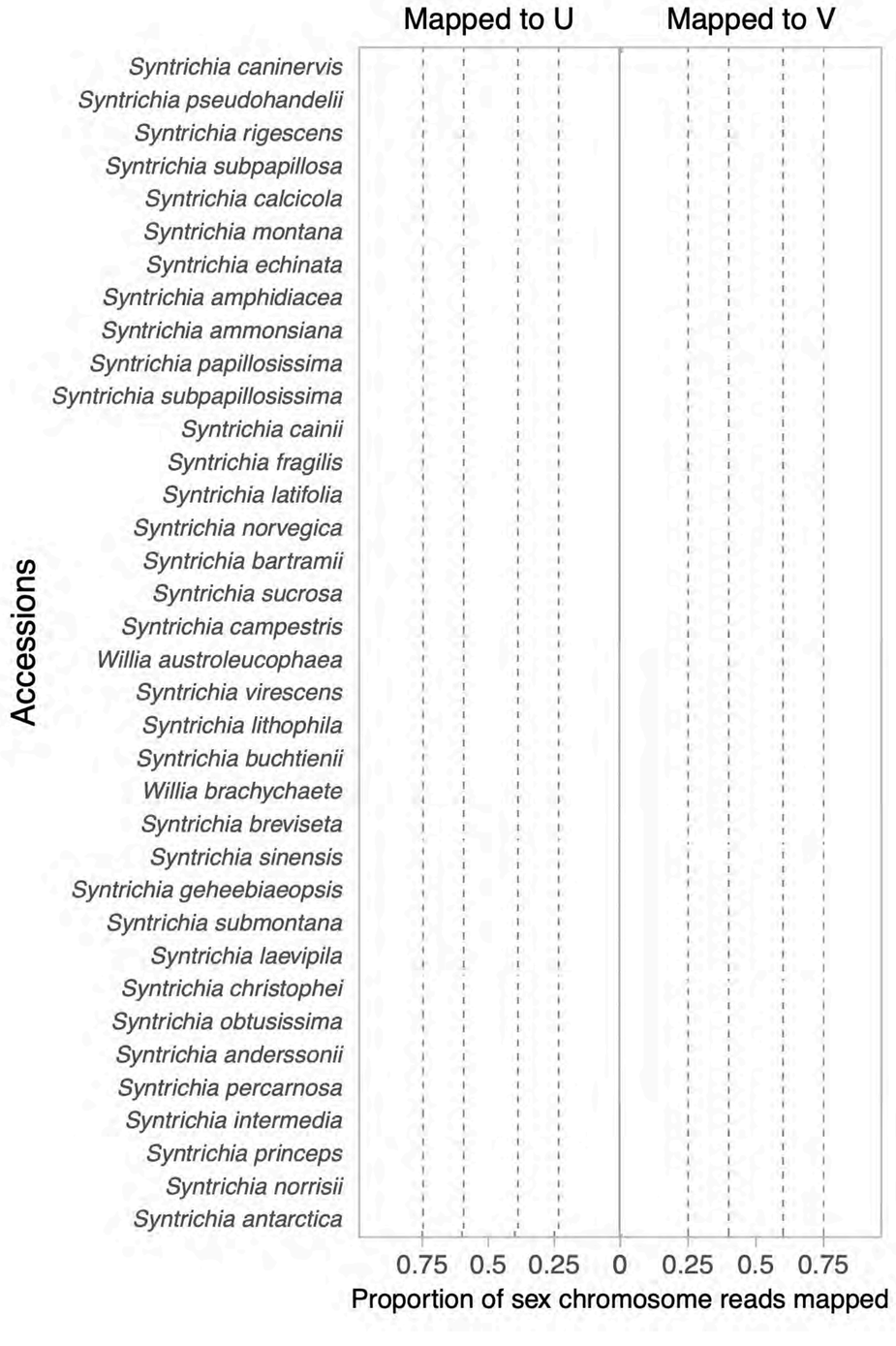

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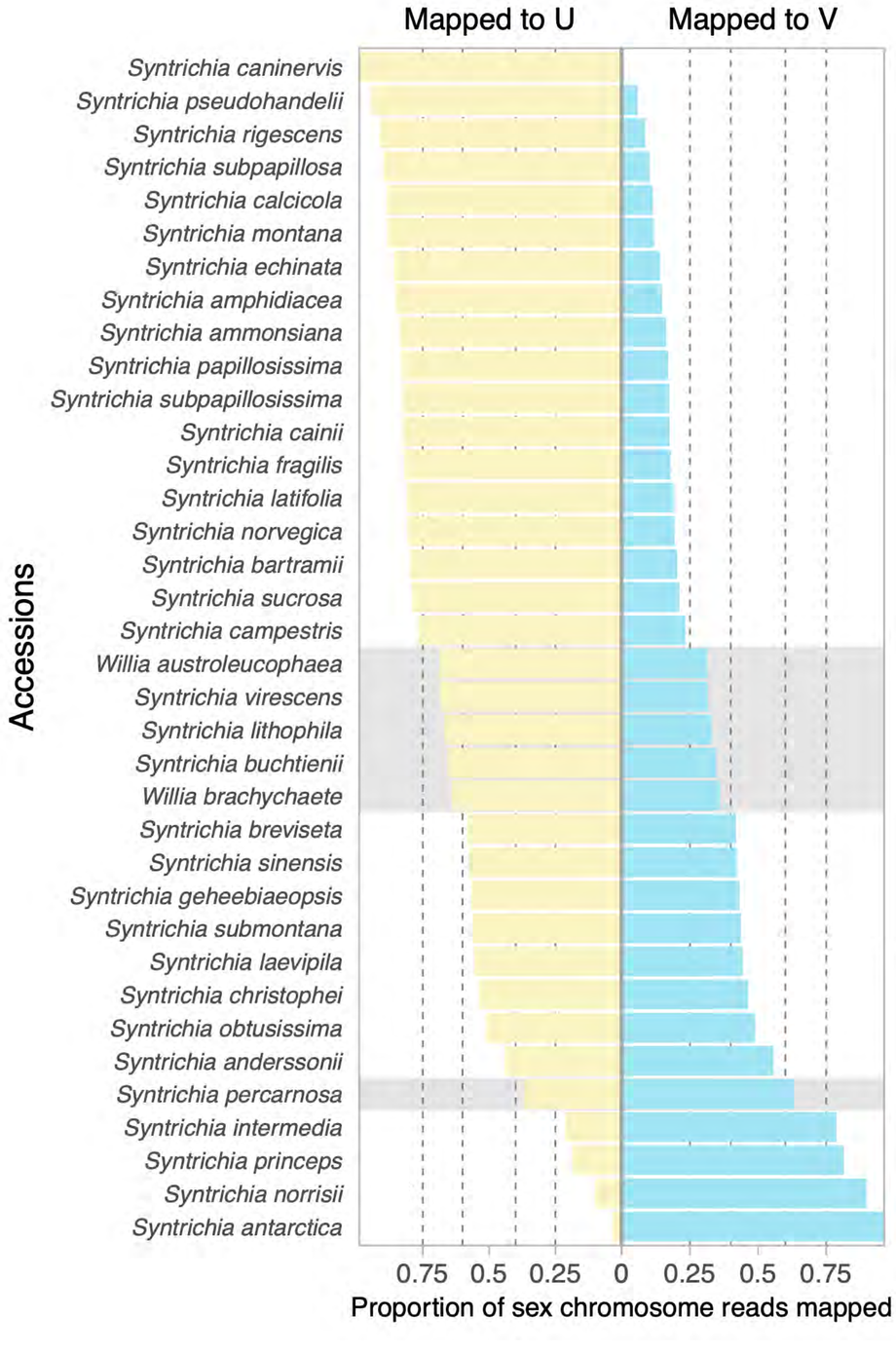

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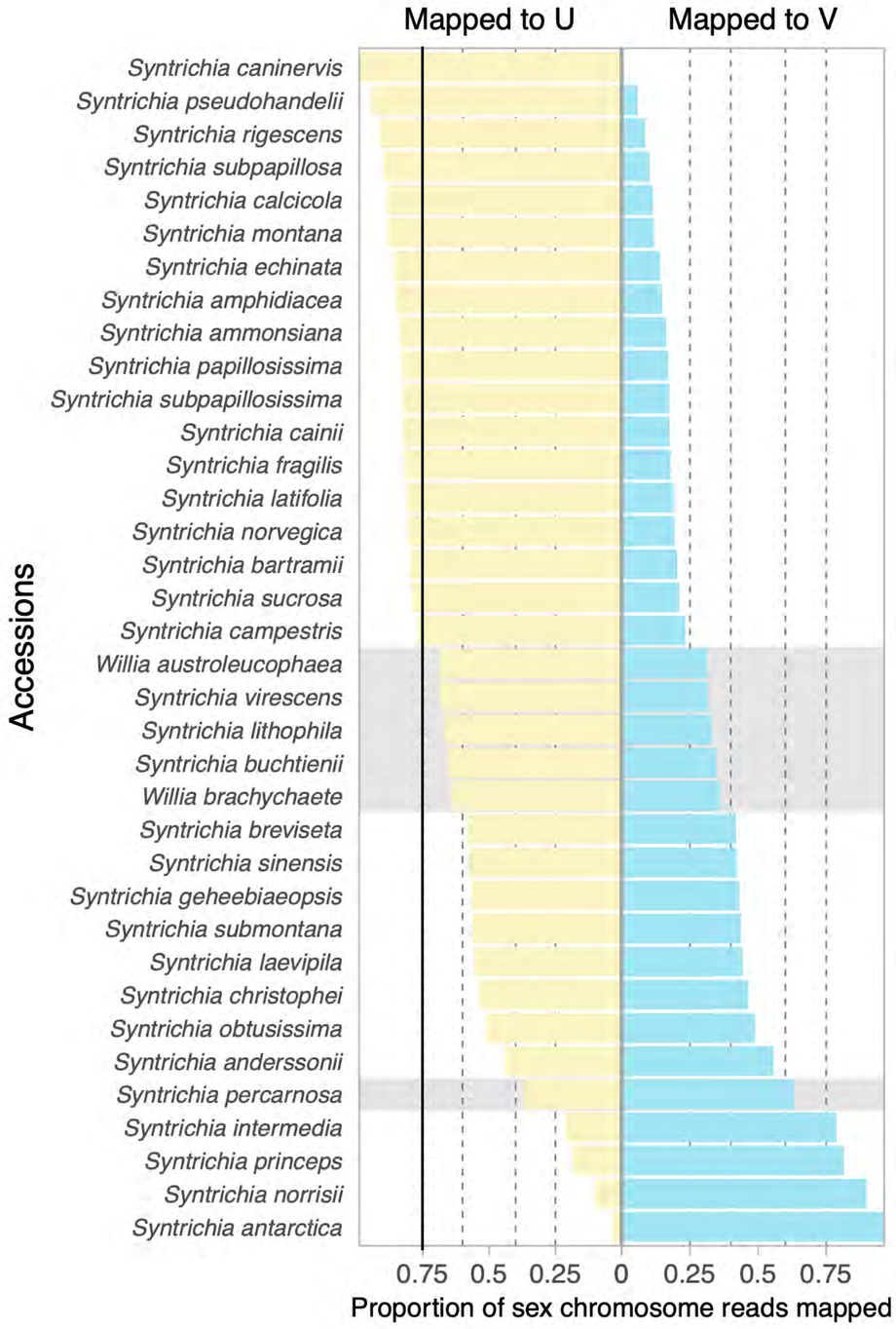

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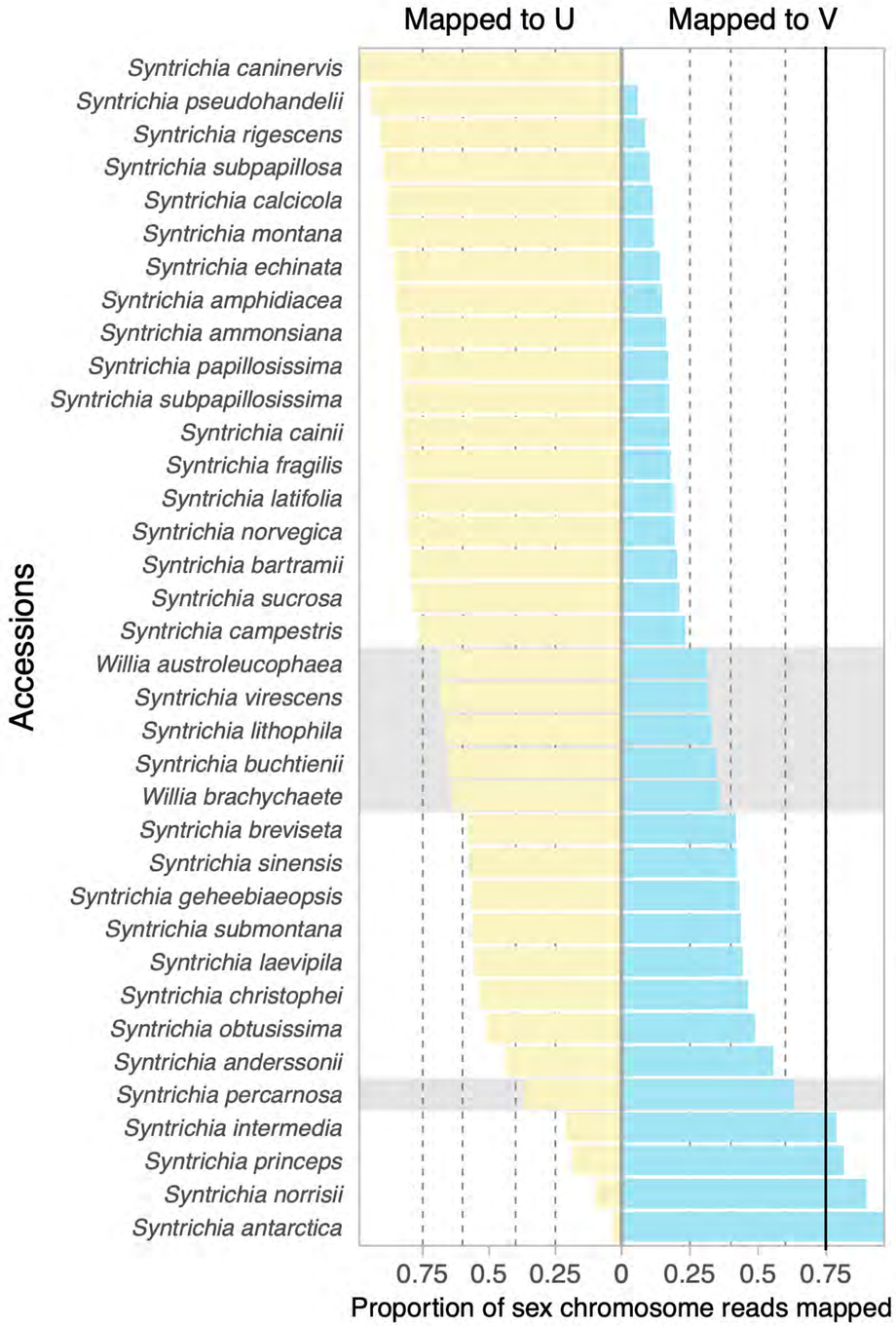

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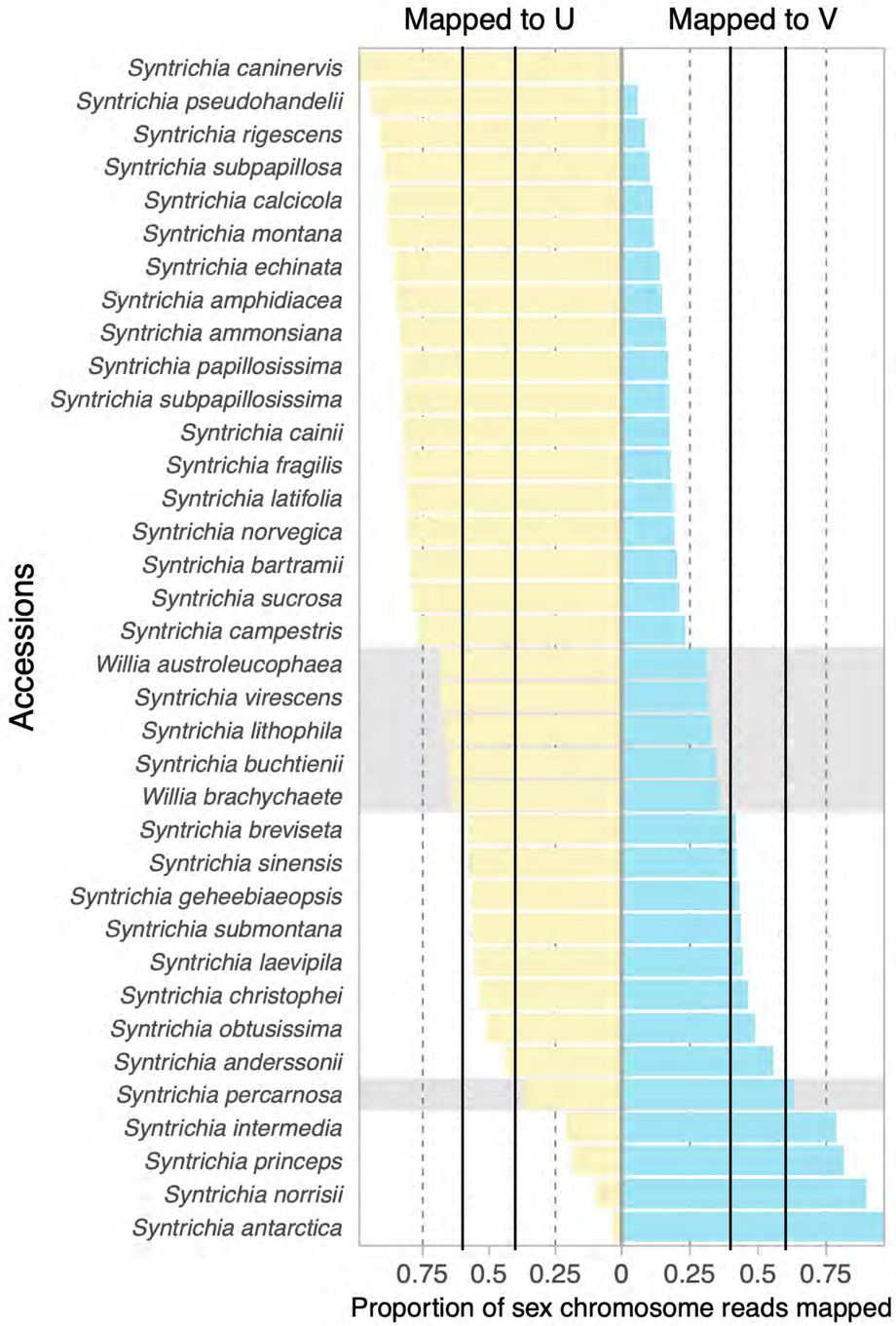

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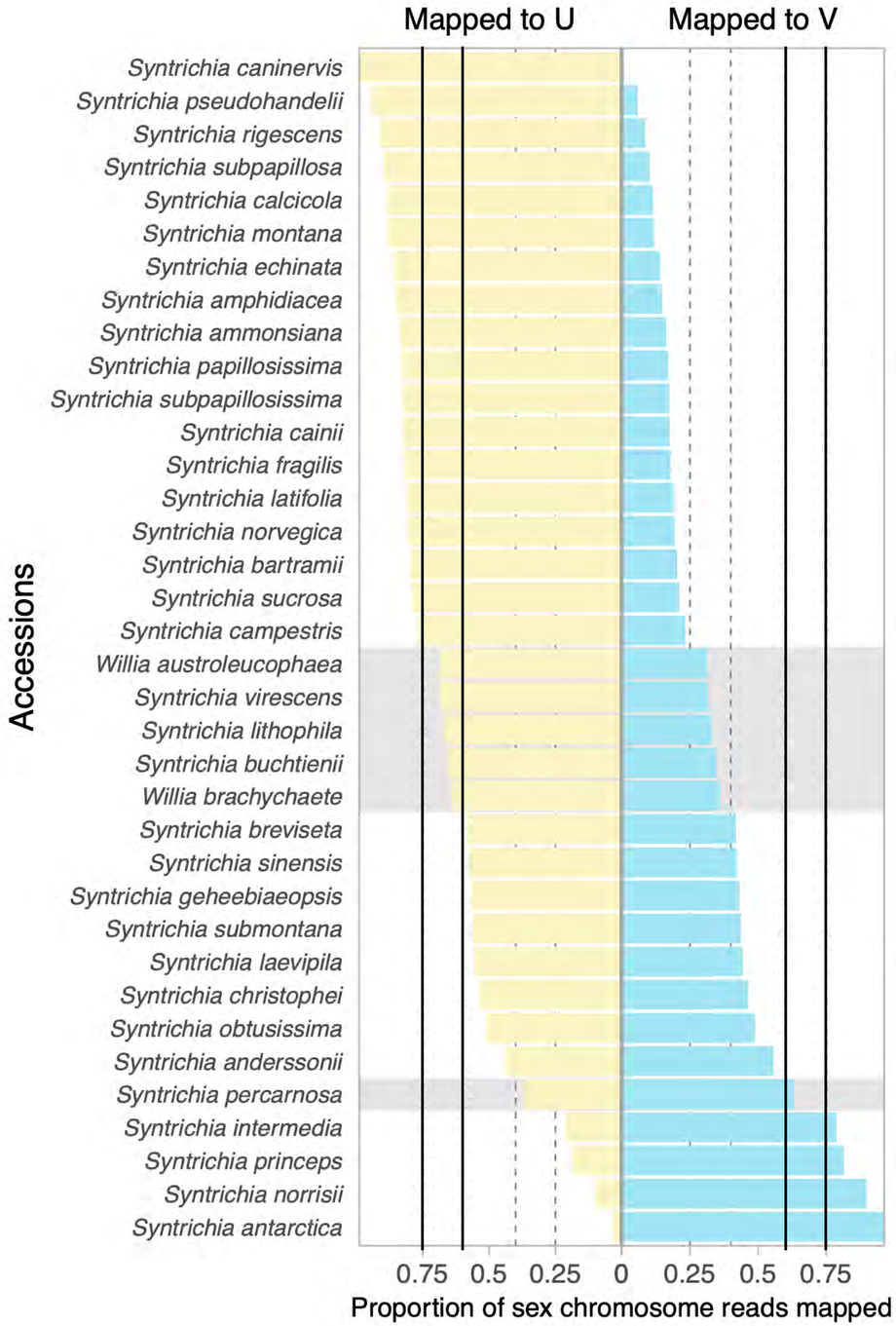

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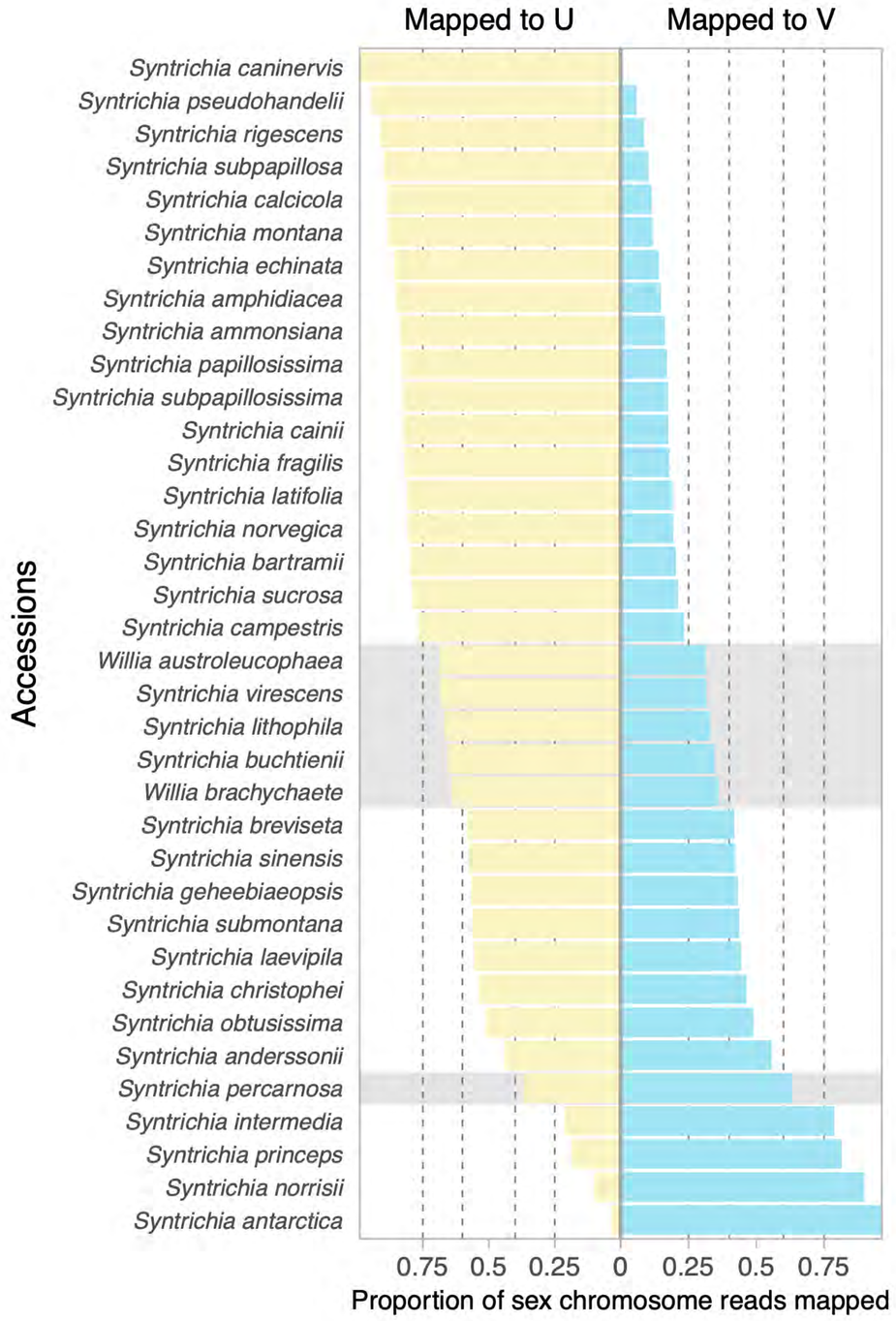

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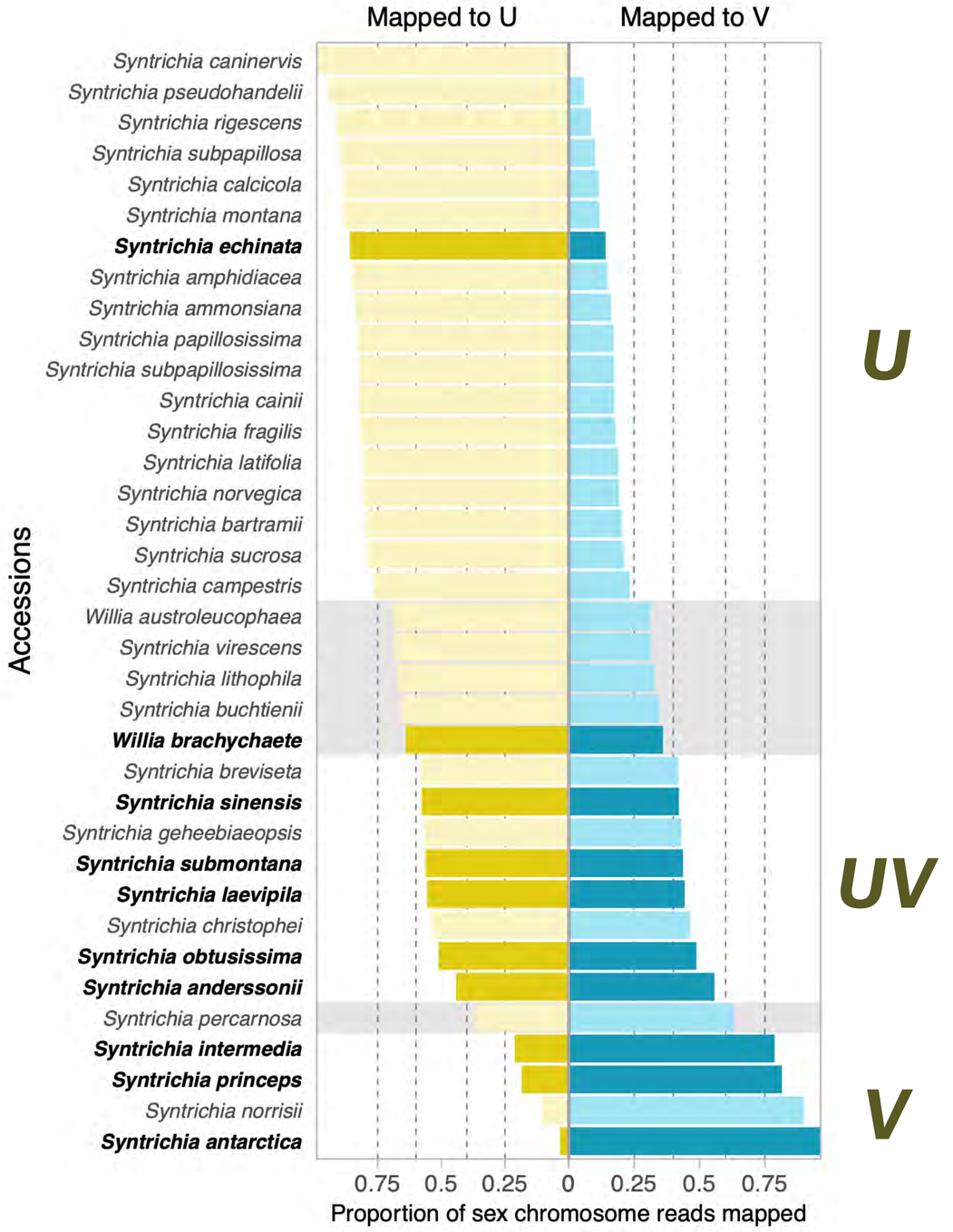

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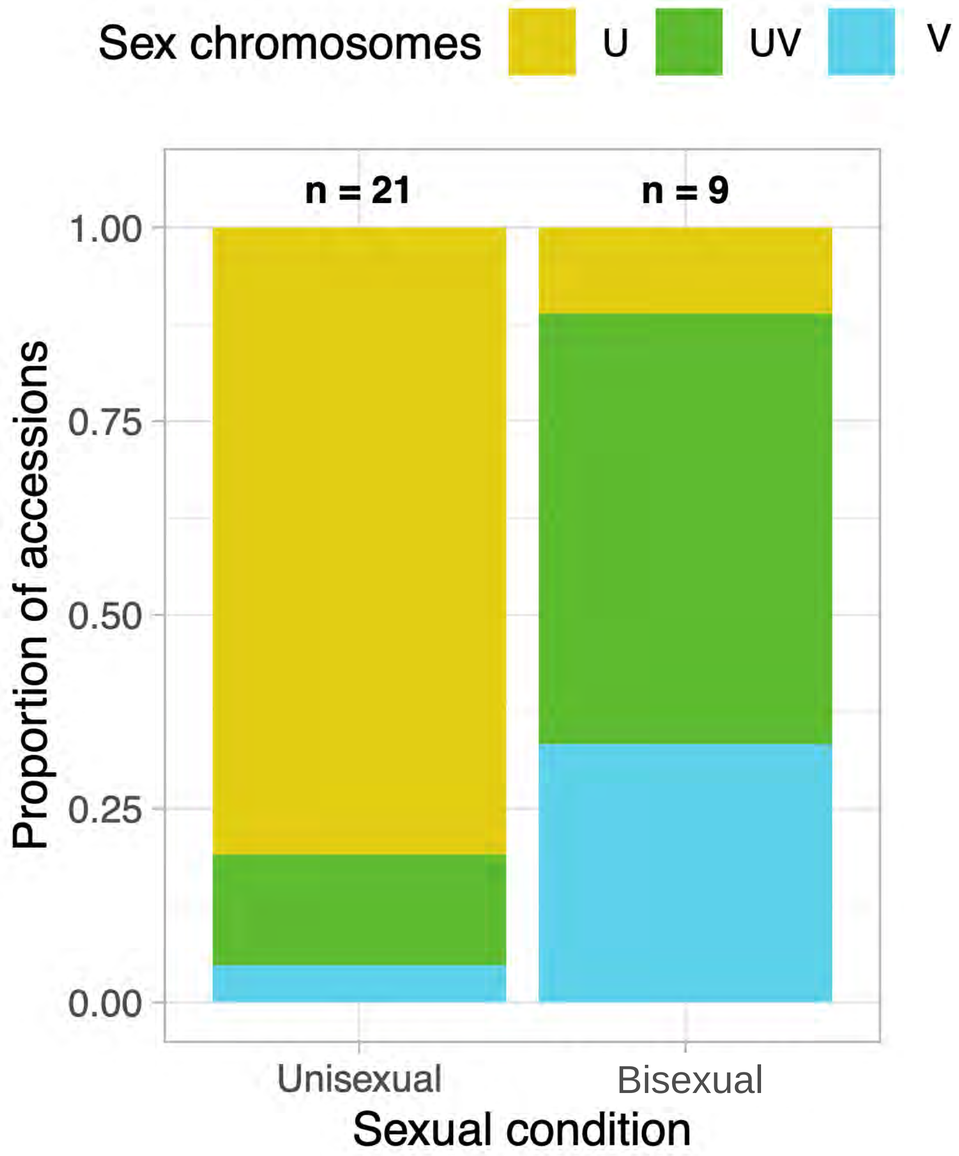

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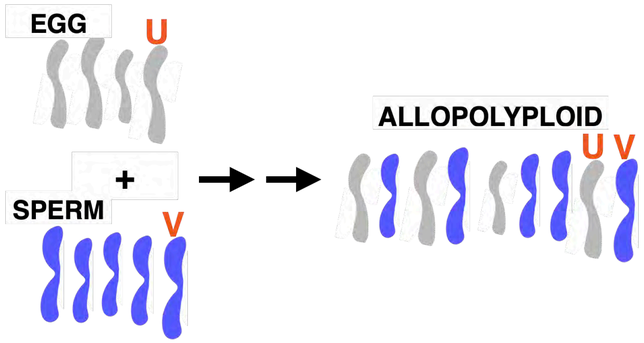

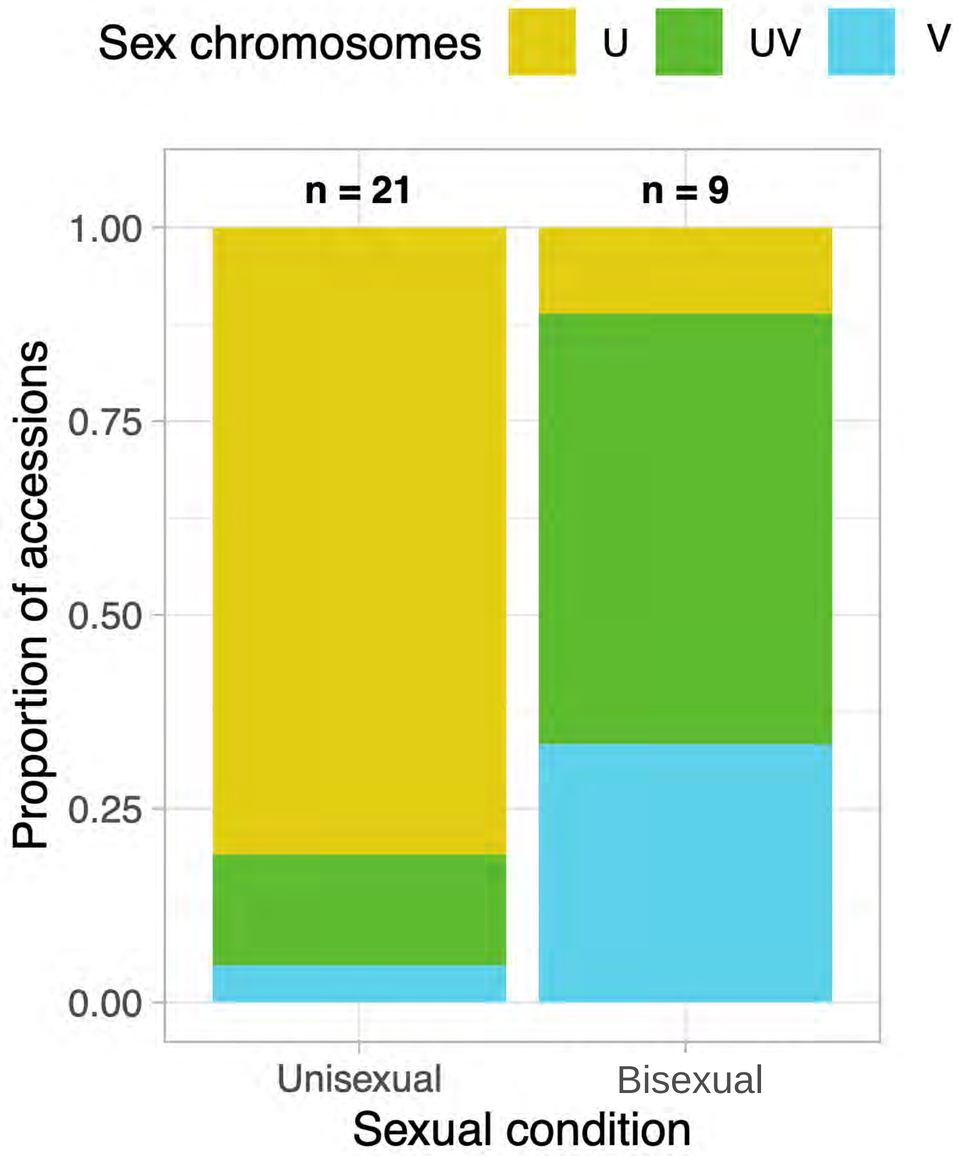

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Polyploid Phylogenetics

Possible polyploidy in *Syntrichia*

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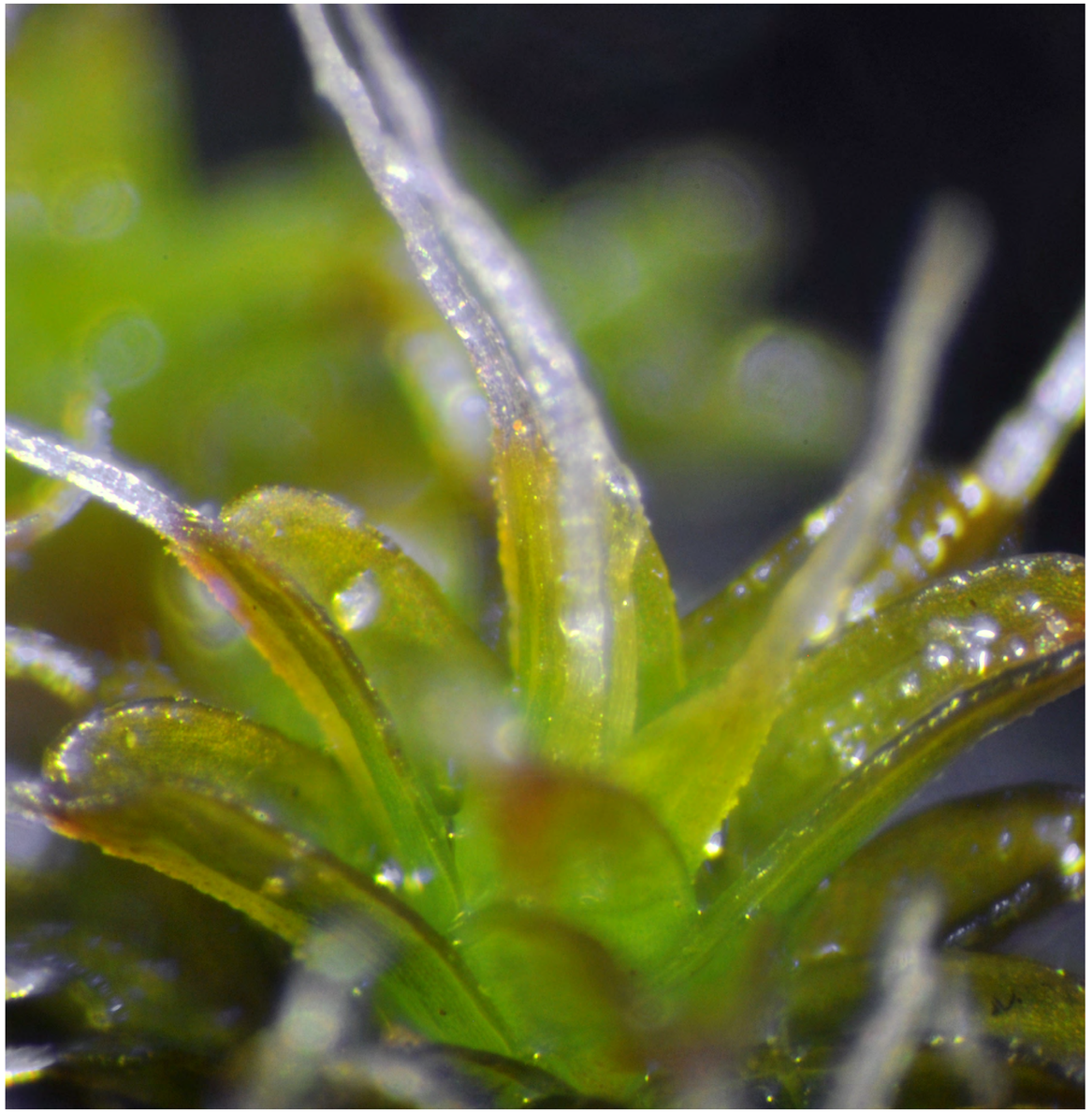

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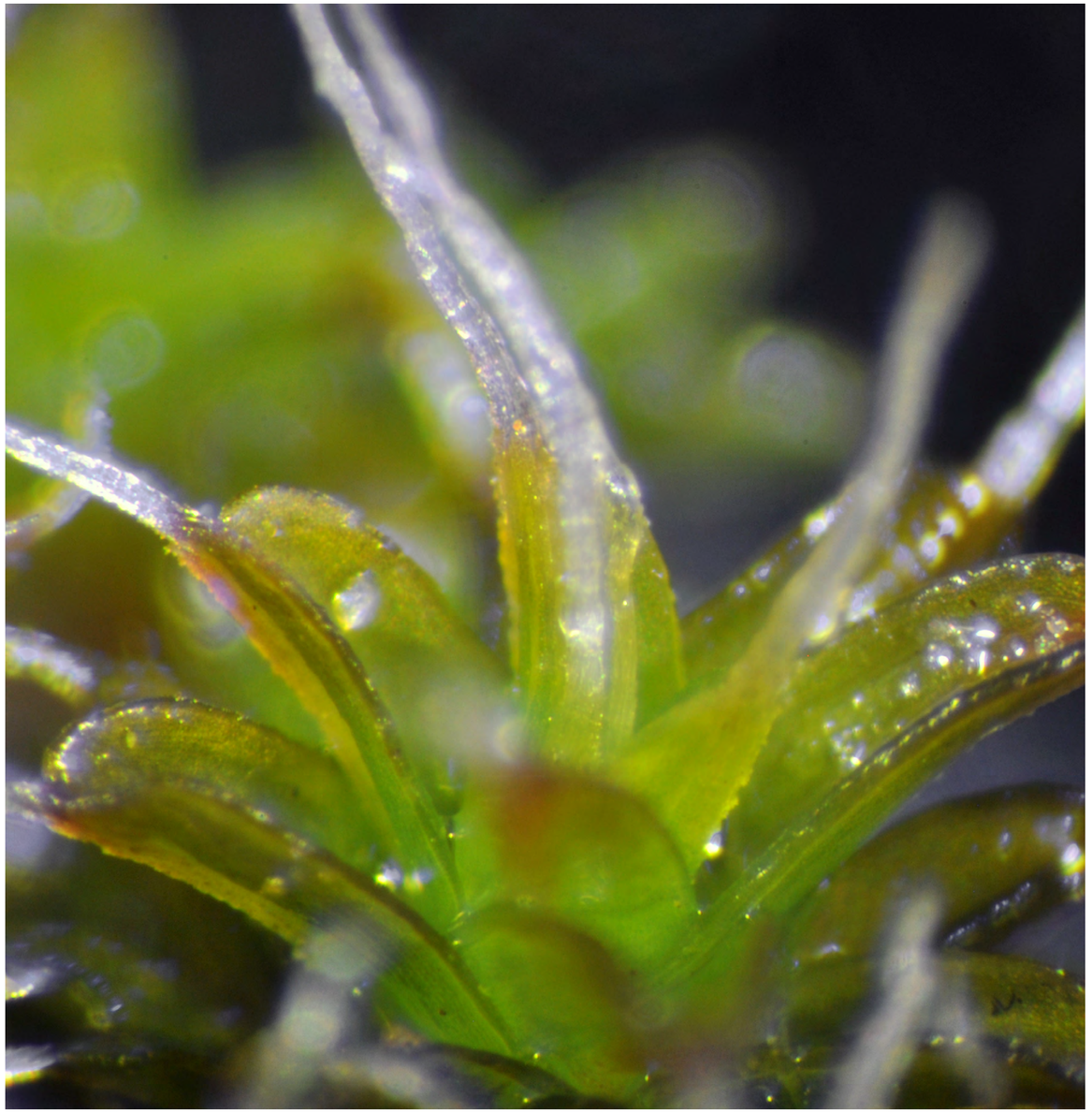

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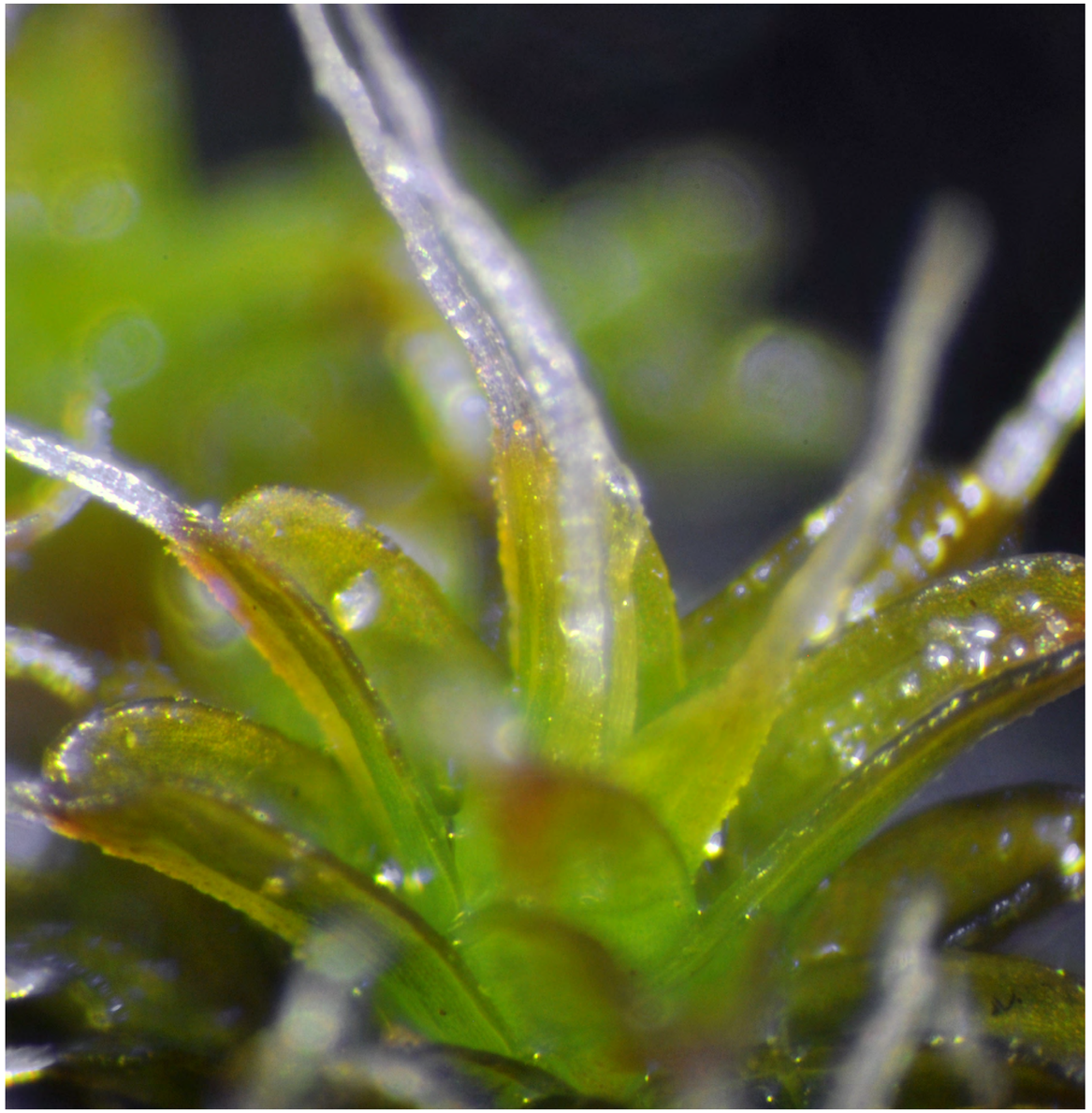
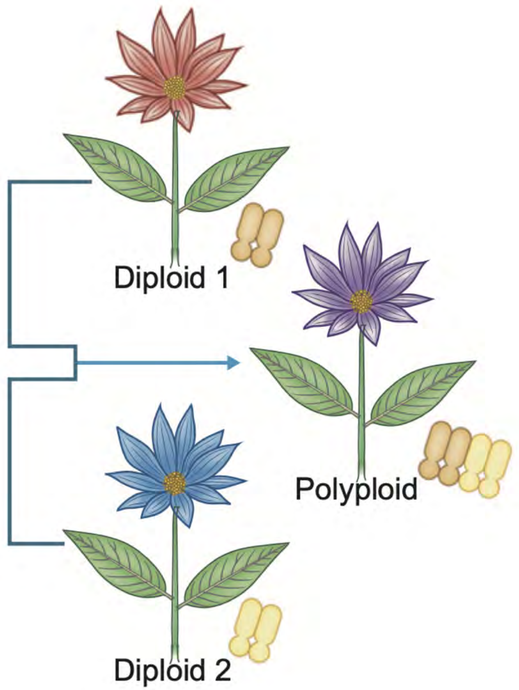
- Many intra-specific chromosome series in the genus (n = ~12, 24, 36, etc.; Fritsch 1991)





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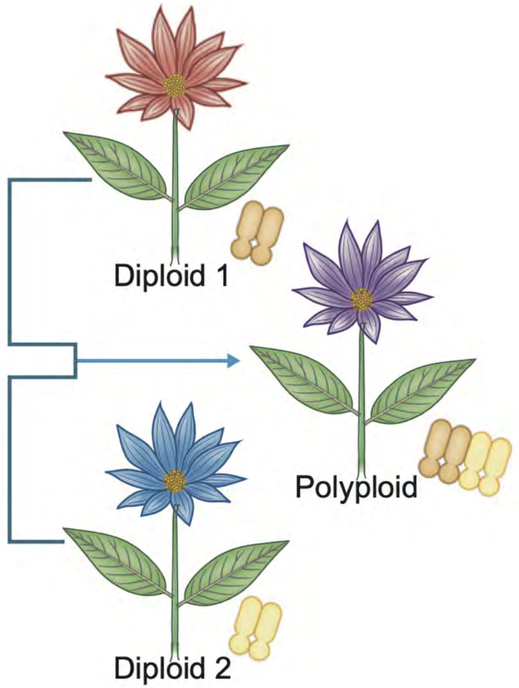
Hybridization + Polyploidization

= Allopolyploidy



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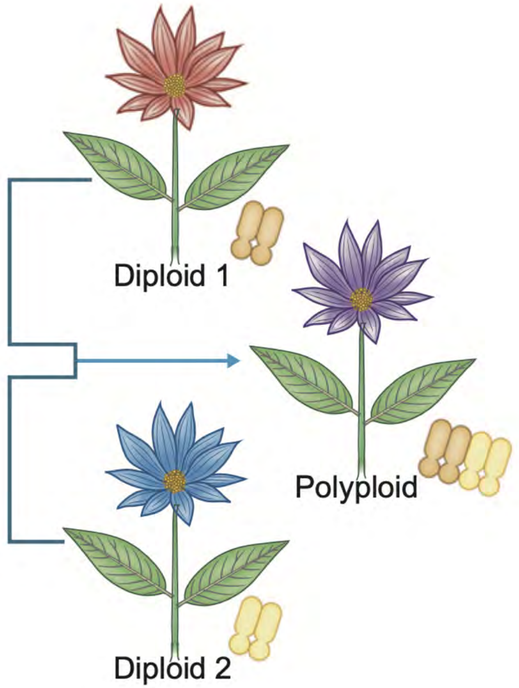

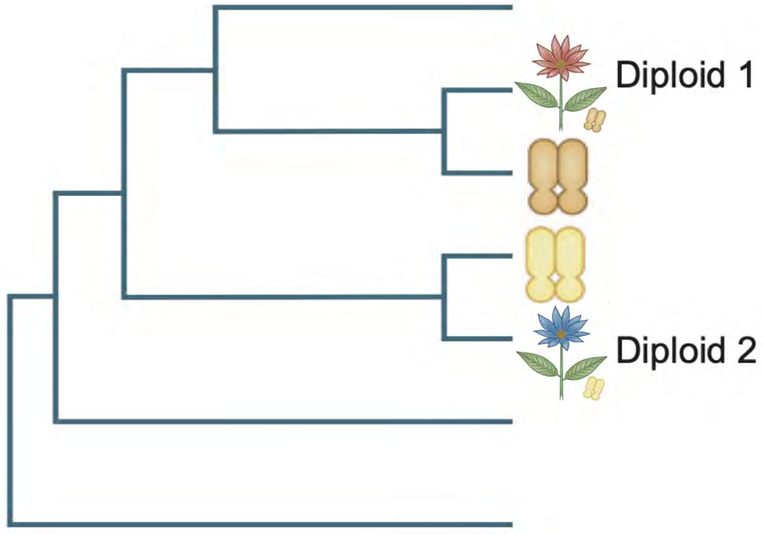

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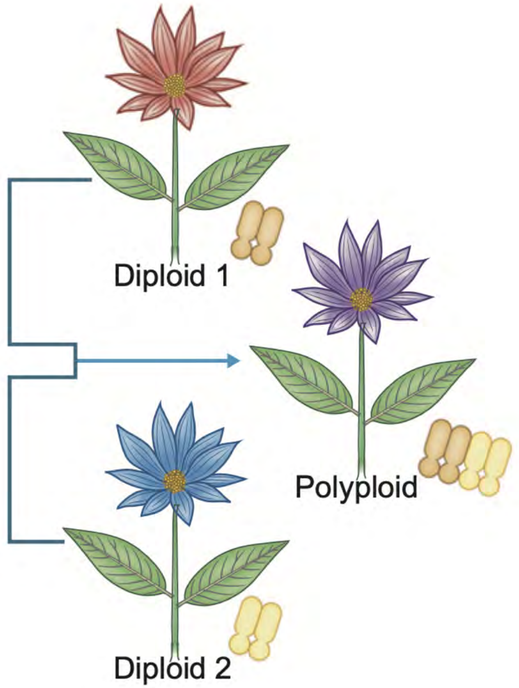
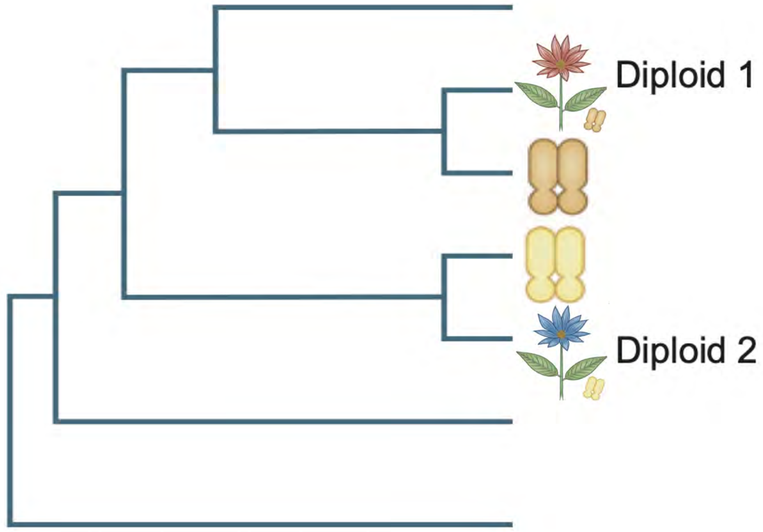


Multree

1 tip per subgenome



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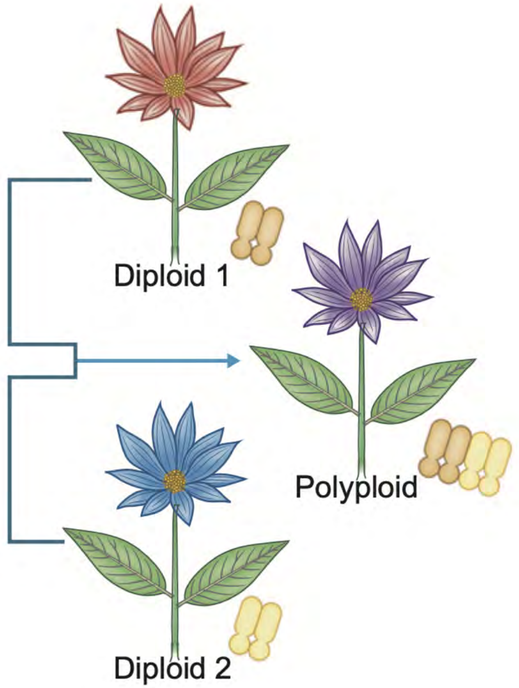

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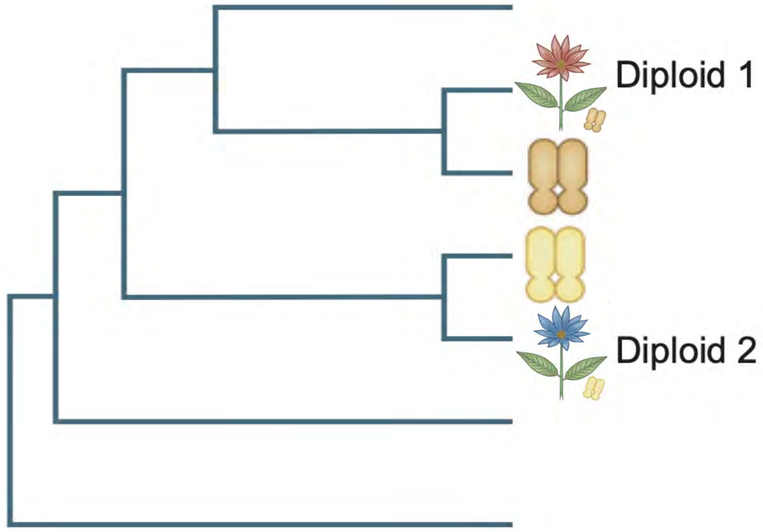

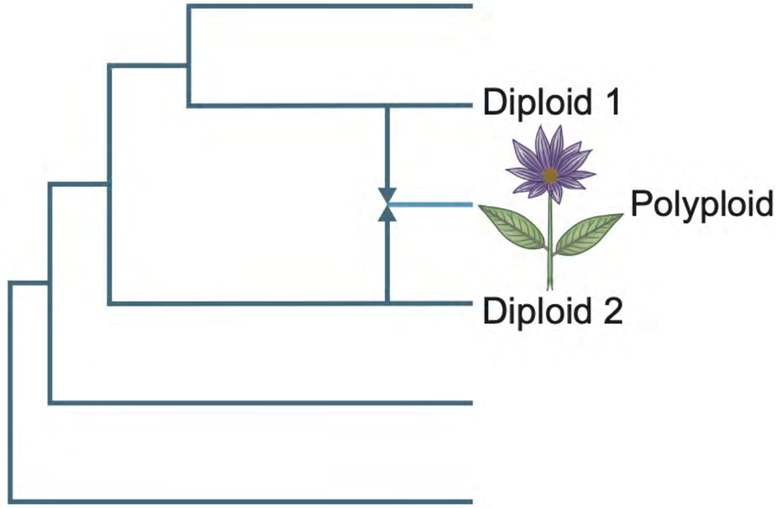

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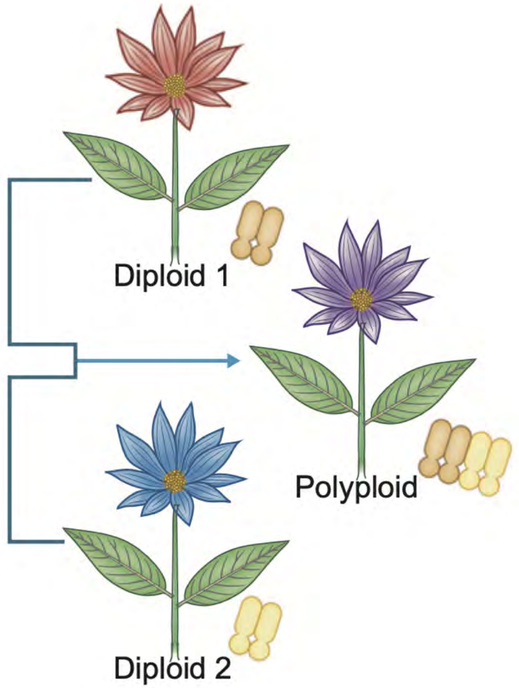

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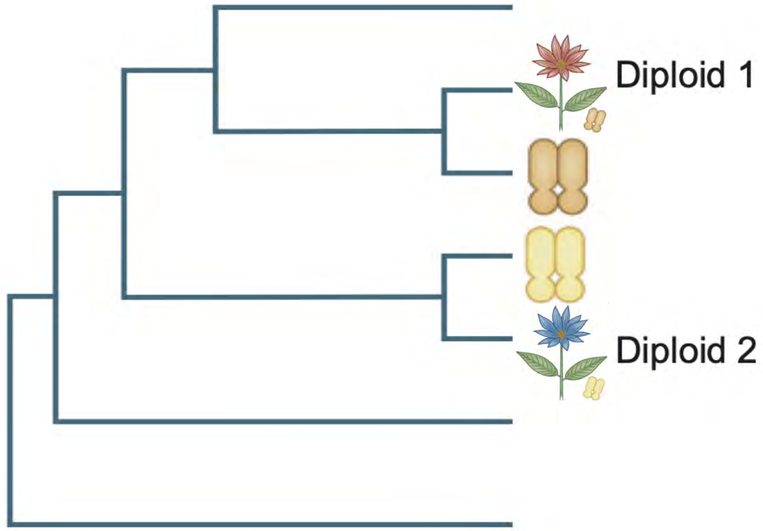
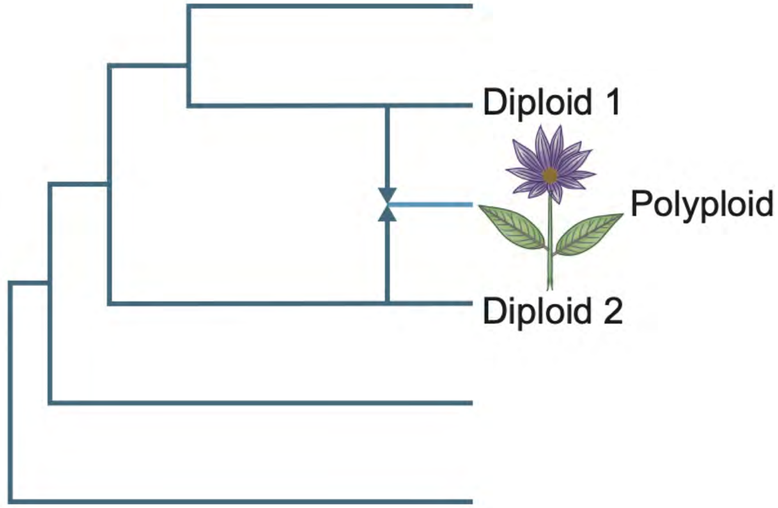


Network

1 tip per species/ individual



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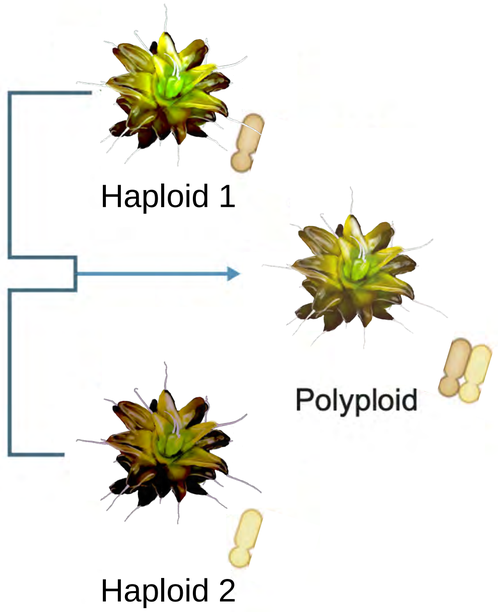
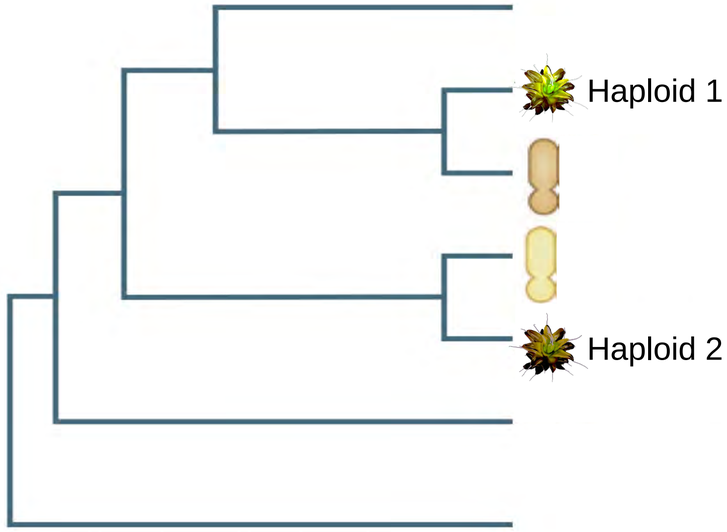


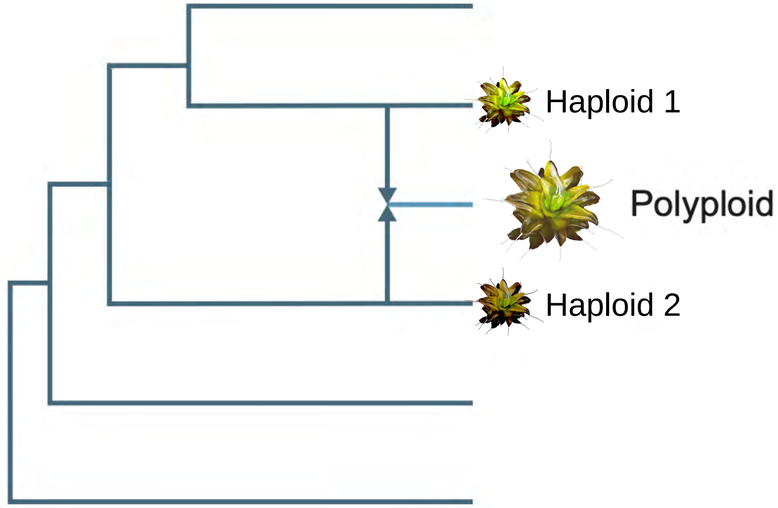
Multree

1 tip per subgenome



Network

1 tip per species/ individual



Modified from: Rothfels, CJ. 2021. Tansley insight: Polyploid phylogenetics. *New Phytologist*.

Approach

Ekwealor, JTB, S. Roy, J. Brinda, C. Anajemba, R. Dikow, J. Jauregui-Lazo, B. Mishler, M. Oliver, and C. Rothfels, et al. In prep.

Approach

- HybSeq/Target Capture; GoFlag probe set (Breinholt et al. 2021)
  - 80 accessions of *Syntrichia* + outgroups

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  - 80 accessions of *Syntrichia* + outgroups
  - *de novo* assembly of raw reads with strict parameters in `SPAdes` (Bankevich et al. 2012)
  - Manual selection and curation of alignments
- Identified **8** potential polyploids to investigate
  - Based on presence of >1 sequence per locus
- Phase gene copies and build tree with `HOMOLOGIZER` (Freyman et al. 2023) in `RevBayes` (Höhna et al. 2016)

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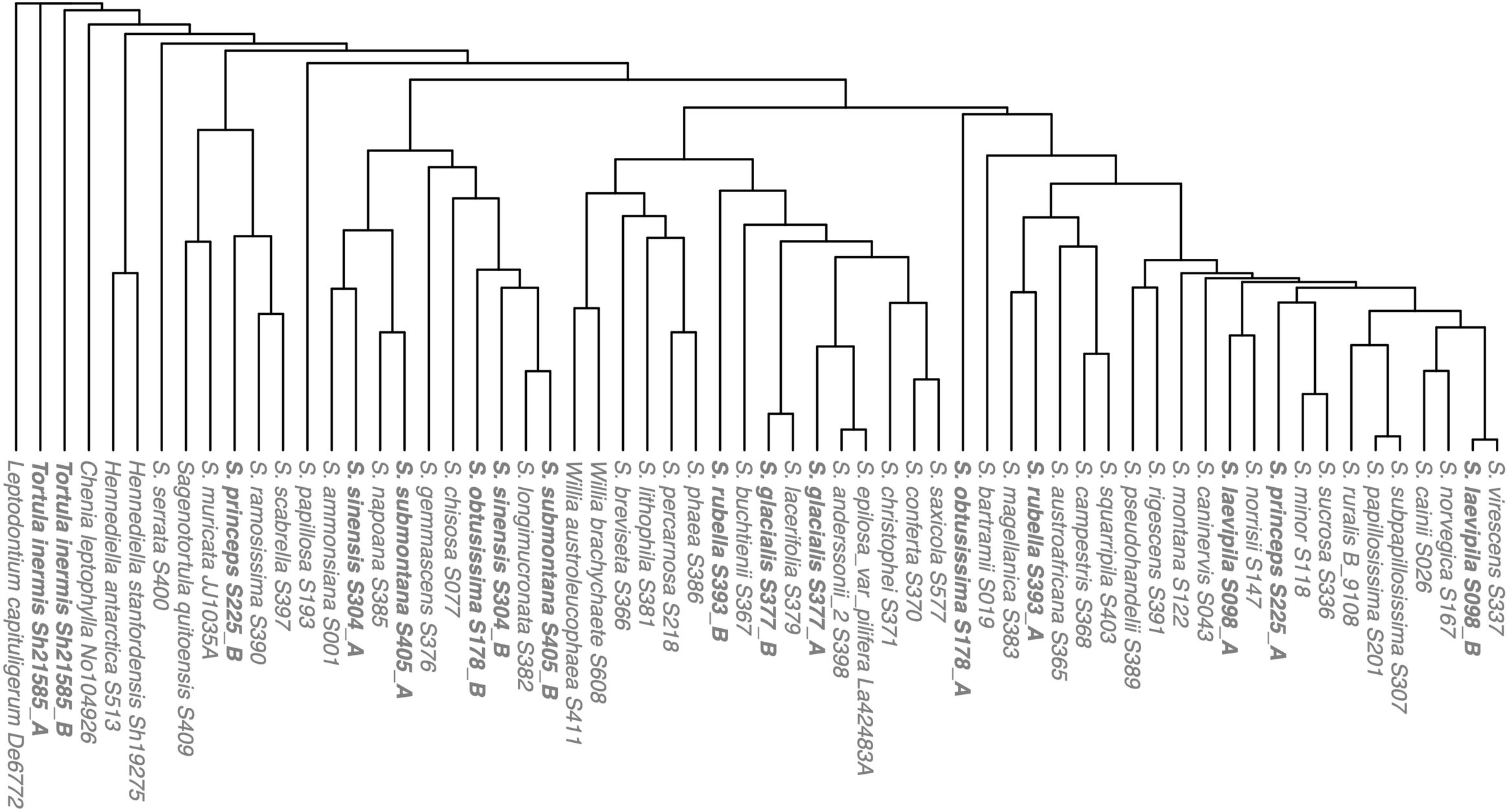

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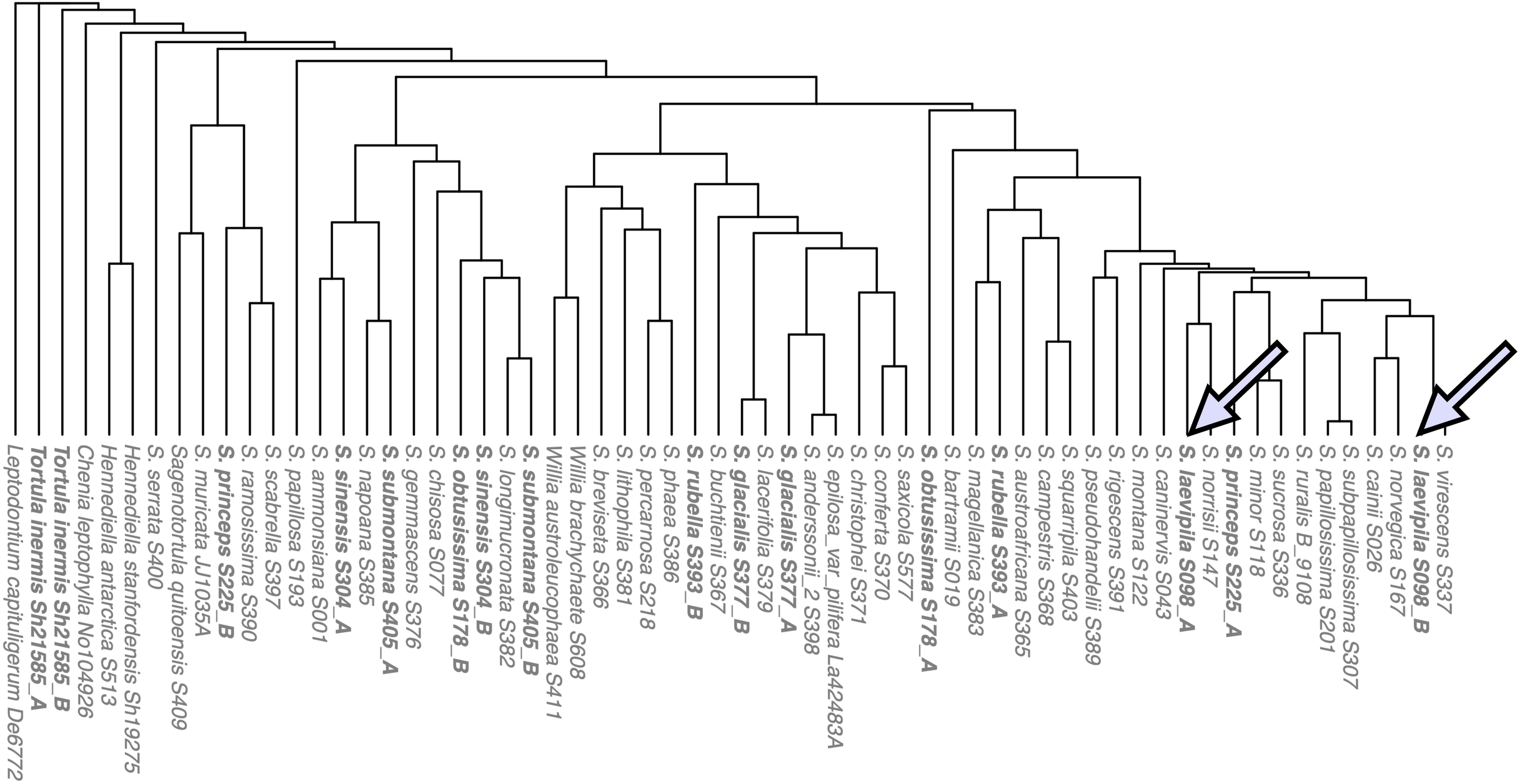

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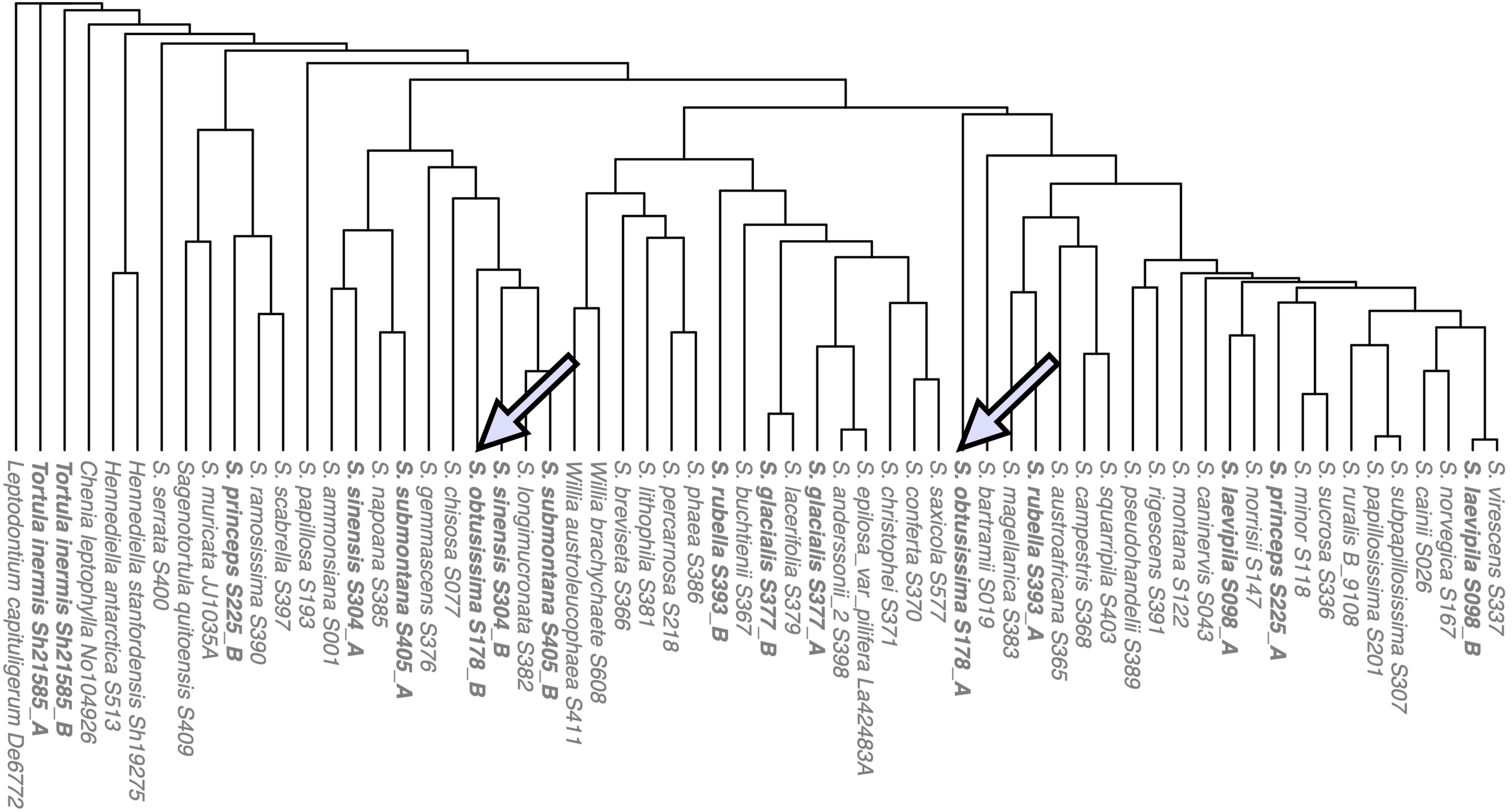

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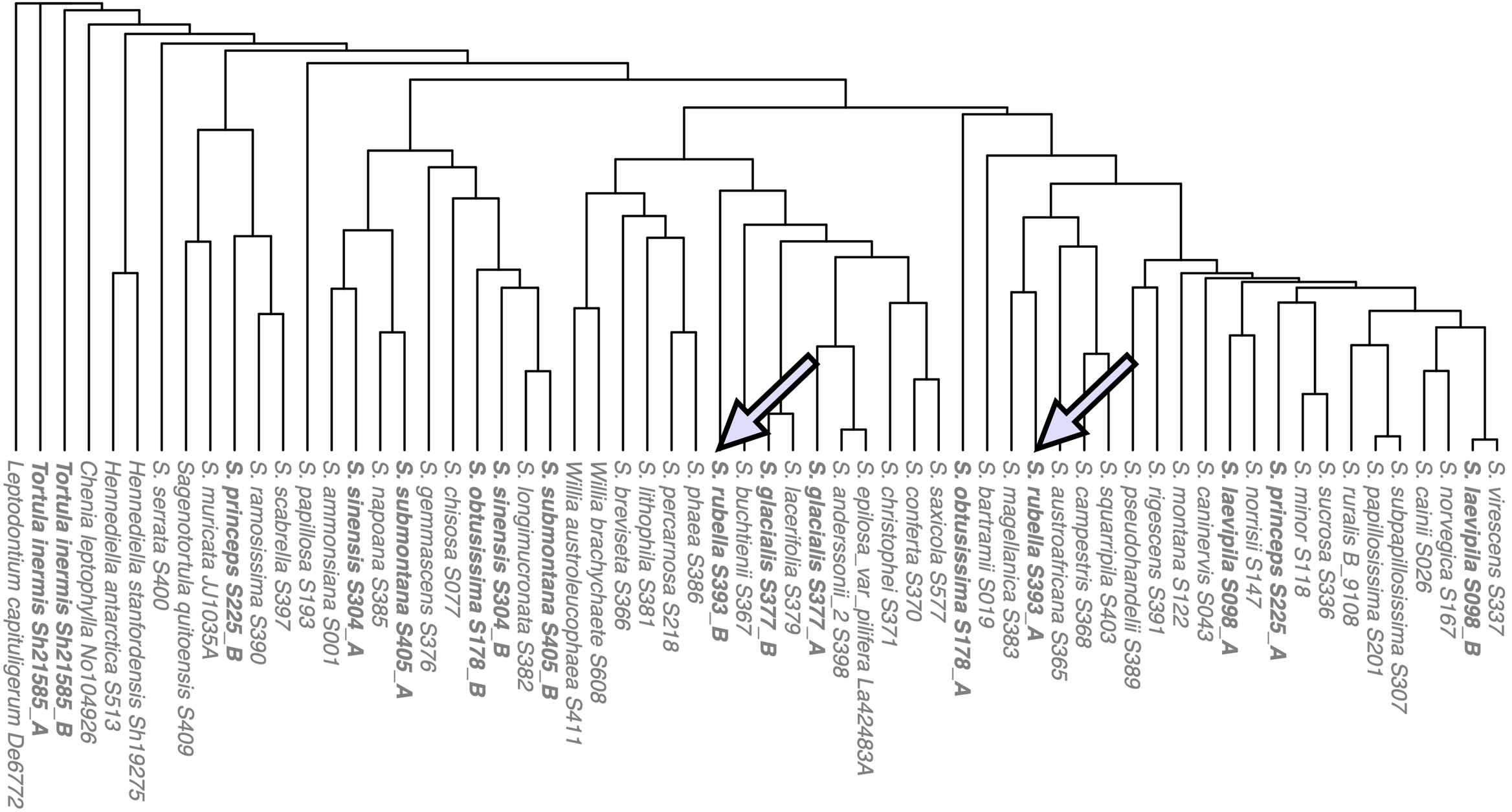

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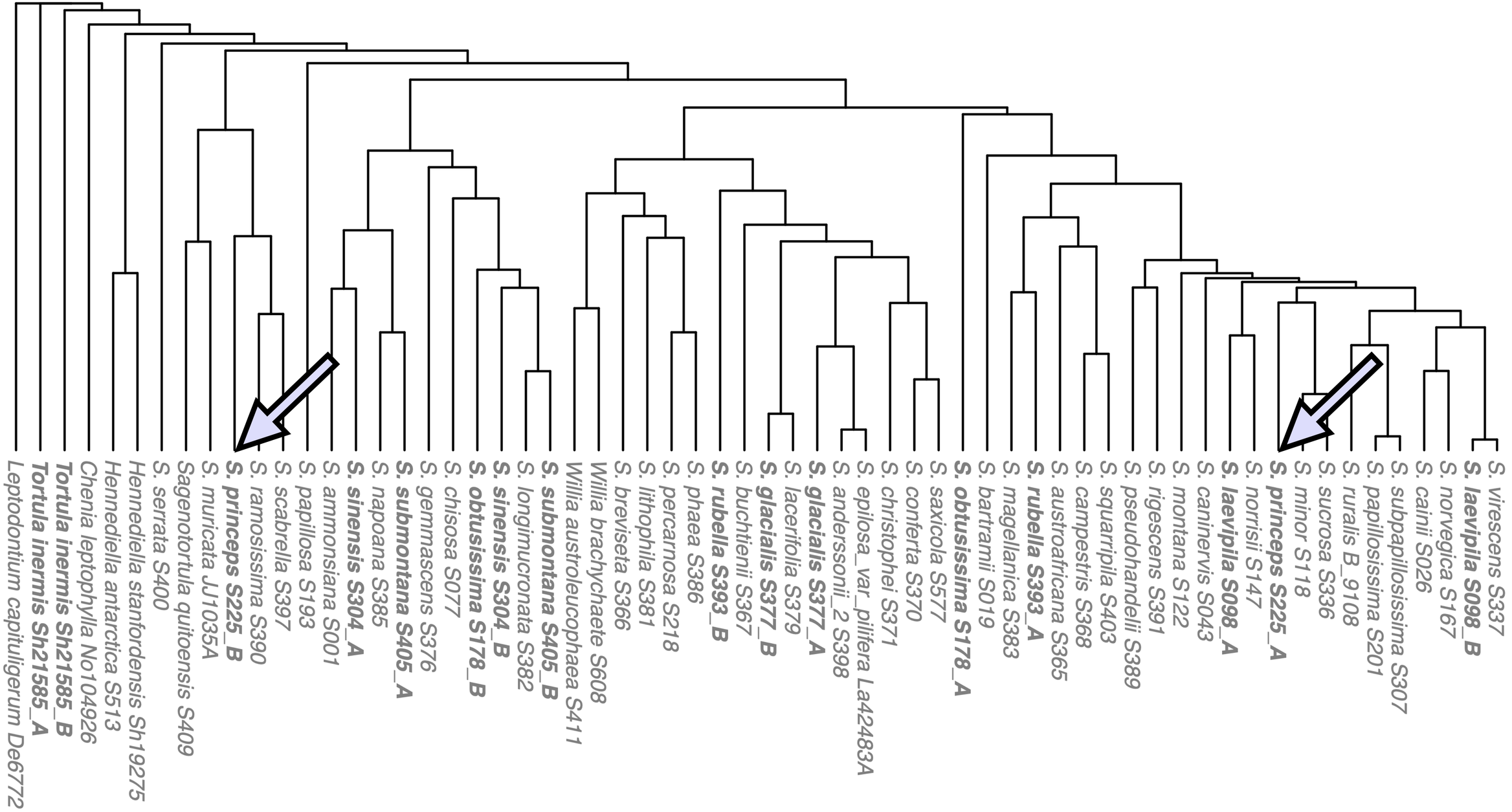

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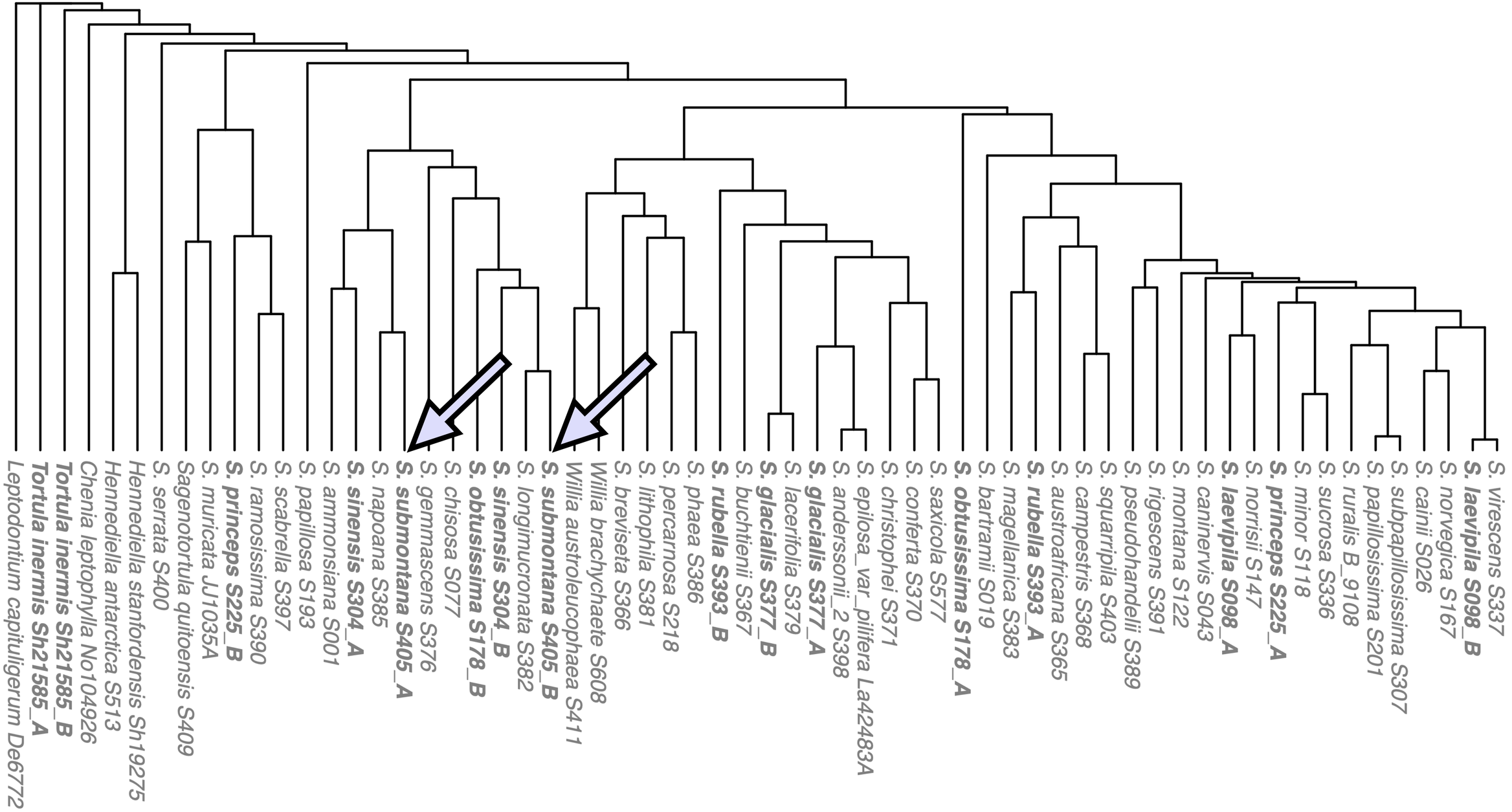

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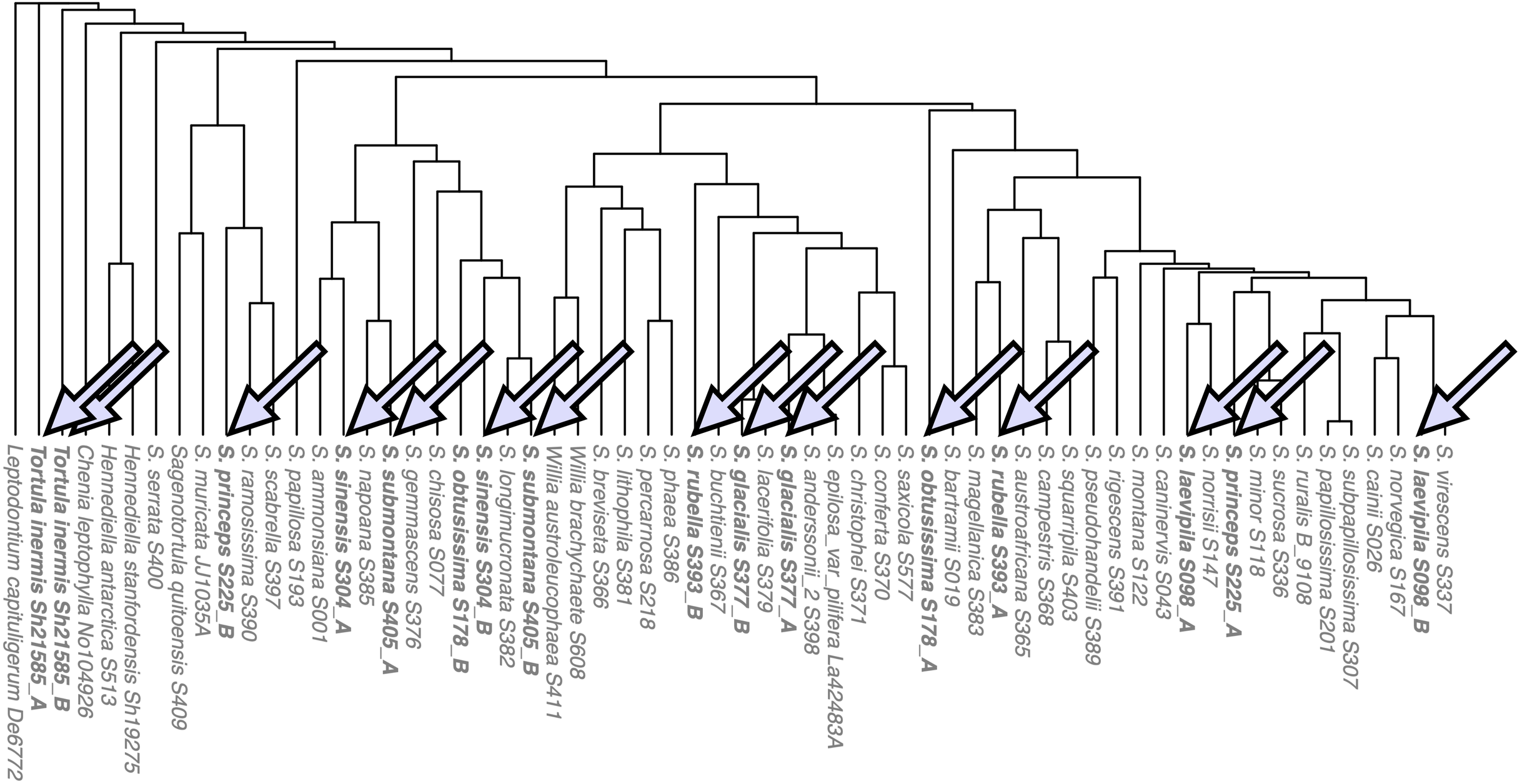

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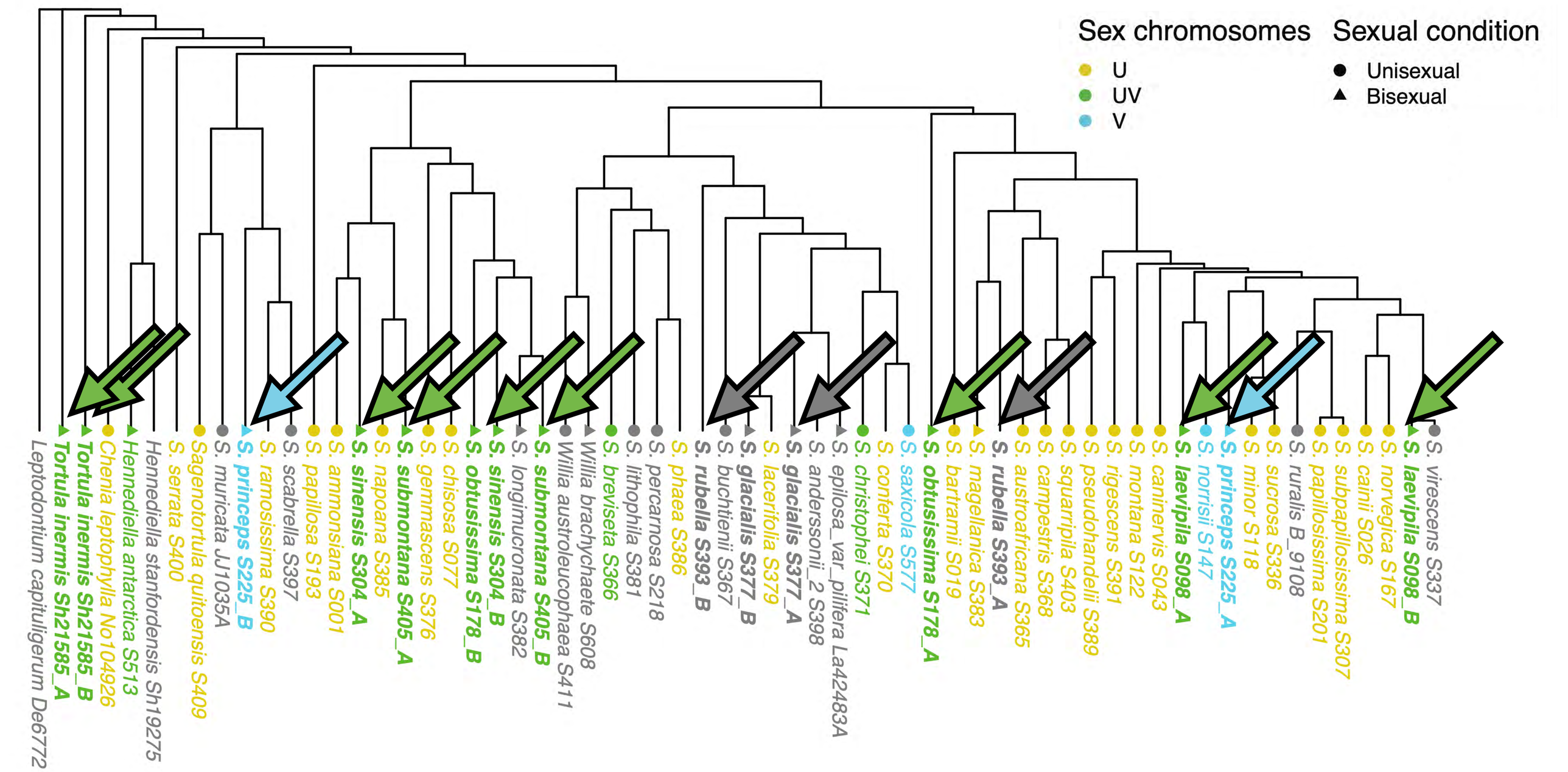

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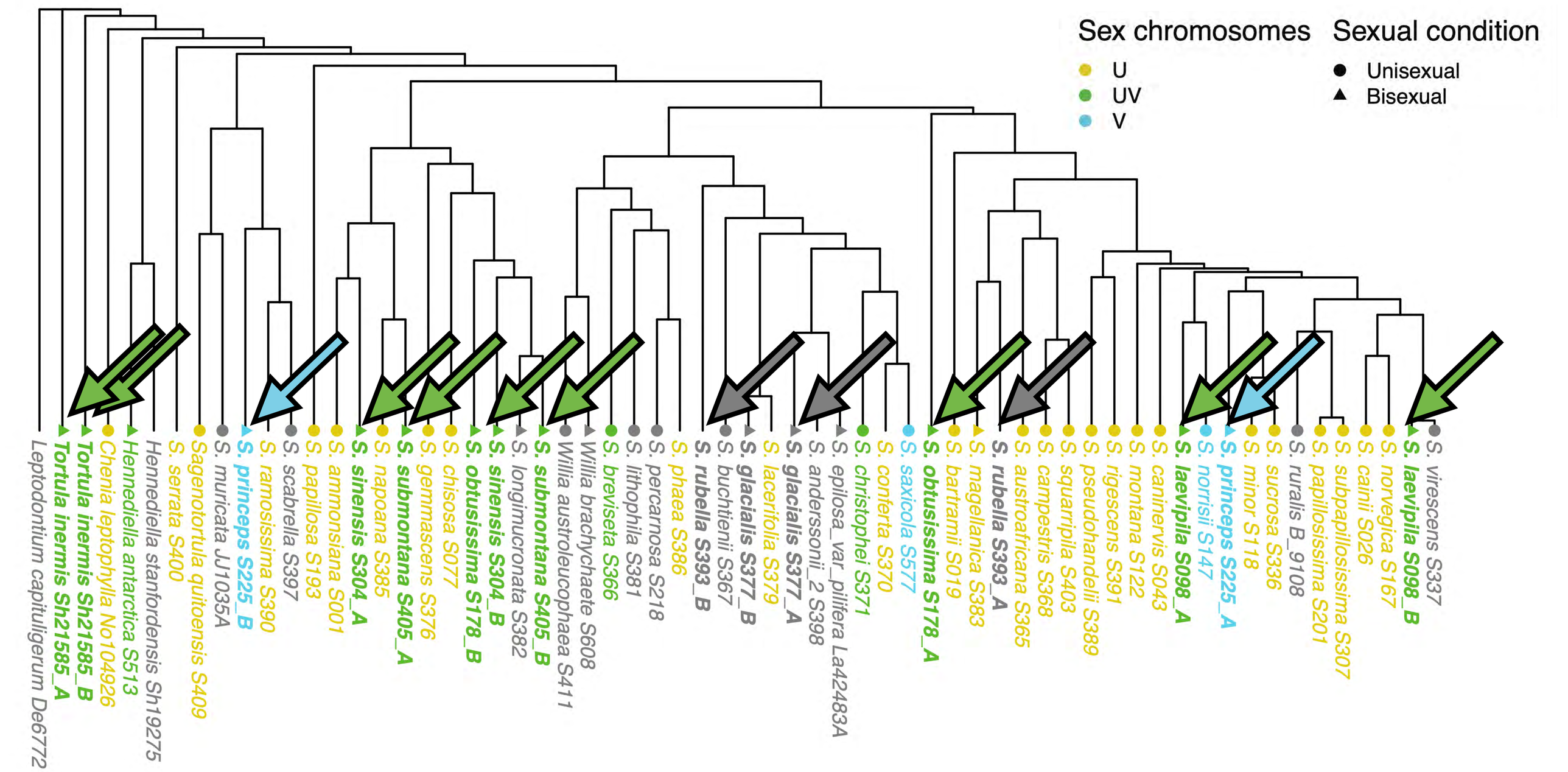

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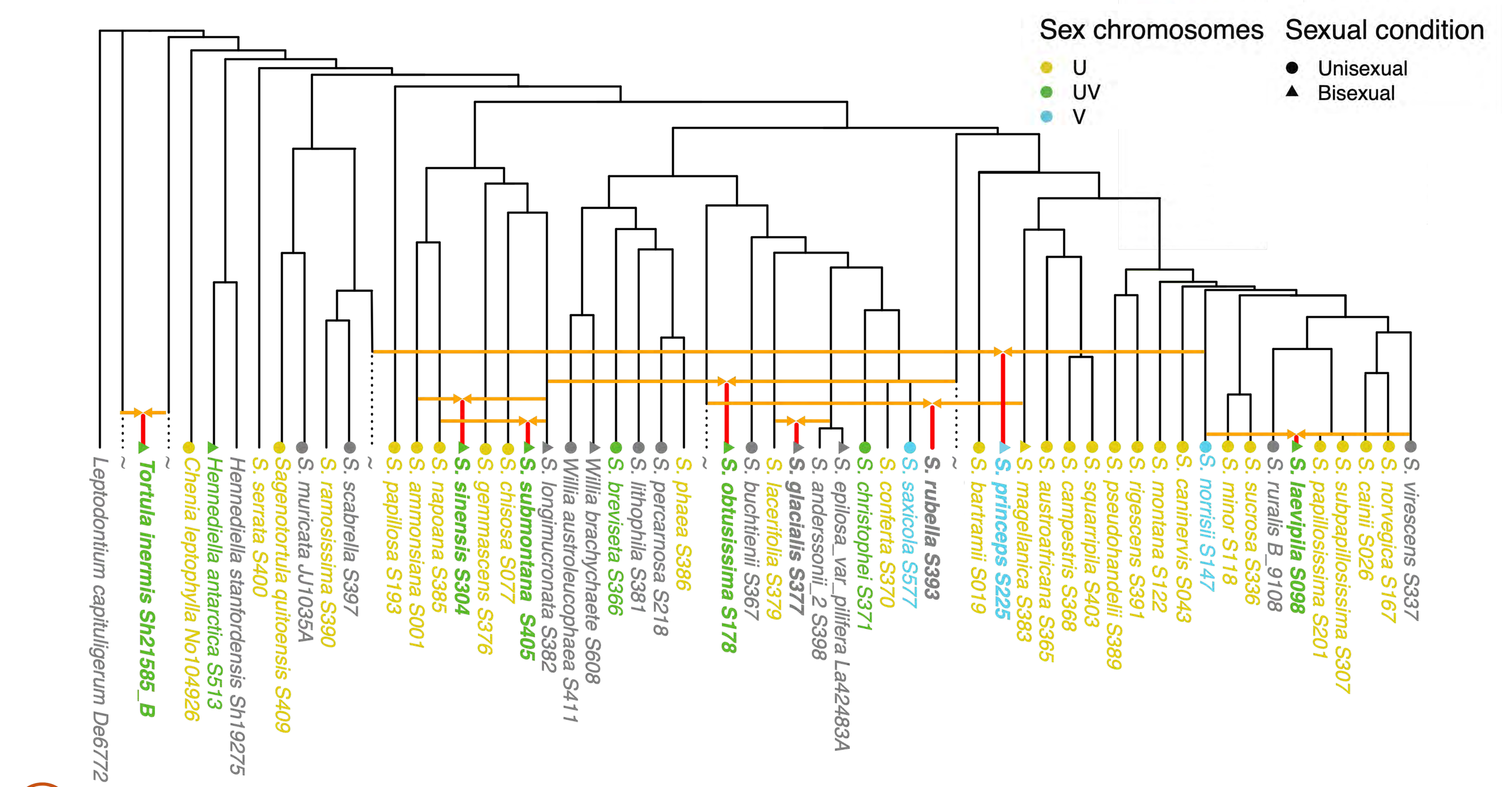

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S. laevipila

n = 12, 15, 26

(Patel *et al.*, 2021)

- A species complex
- Worldwide distribution, but primarily in the N. Hemisphere
- Bark epiphyte
- Bisexual; some populations reported to be unisexual

Ekwealor, JTB, S. Roy, J. Brinda, C. Anajemba, R. Dikow, J. Jauregui-Lazo, B. Mishler, M. Oliver, and C. Rothfels, et al. In prep.

Sex chromosomes
- U
- UV
- V

Sexual condition
- Unisexual
- Bisexual

S. laevipila

n = 12, 15, 26

(Patel *et al.*, 2021)

Leptodontium capituligerum De6772
Tortula inermis Sh21585_B
Chenia leptophylla No104926
Hennediella antarctica S513
Hennediella stanfordensis Sh19275
S. serrata S400
Sagenotortula quitoensis S409
S. muricata JJ1035A
S. ramosissima S390
S. scabrella S397
S. papillosa S193
S. ammonsiana S001
S. napoana S385
S. sinensis S304
S. gemmascens S376
S. chisosa S077
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Willia brachychaete S608
S. breviseta S366
S. lithophila S381
S. percarnosa S218
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S. obtusissima S178
S. buchtienii S367
S. glacialis S377
S. lacerifolia S379
S. epilosa_var_pilifera La42483A
S. anderssonii_2 S398
S. christophei S371
S. conferta S370
S. saxicola S577
S. rubella S393
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S. obtusissima

n = ?

- Southwest US and Mexican-Andean disjunction
- Bisexual; some populations are reported to be unisexual

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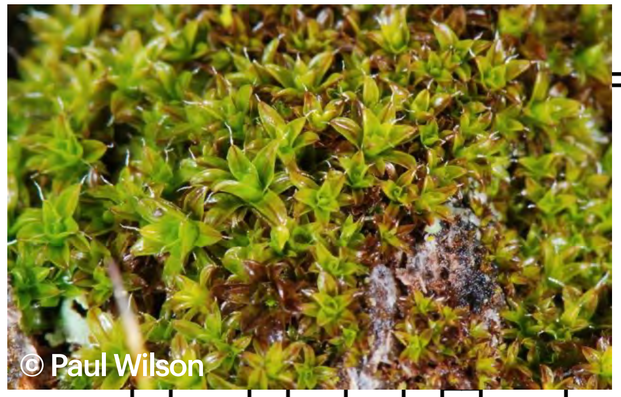

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Sexual condition
Unisexual
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S. obtusissima

n = ?

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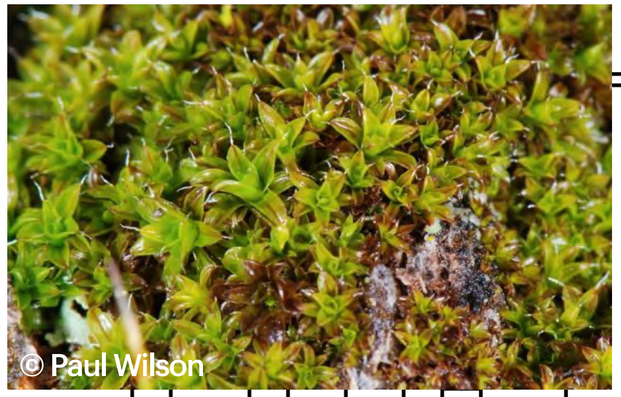

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Sexual condition
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S. princeps

n = 12, 24, 26, 28, 36

(Patel *et al.*, 2021)

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- Worldwide distribution, primarily in N. Hemisphere
- Bisexual

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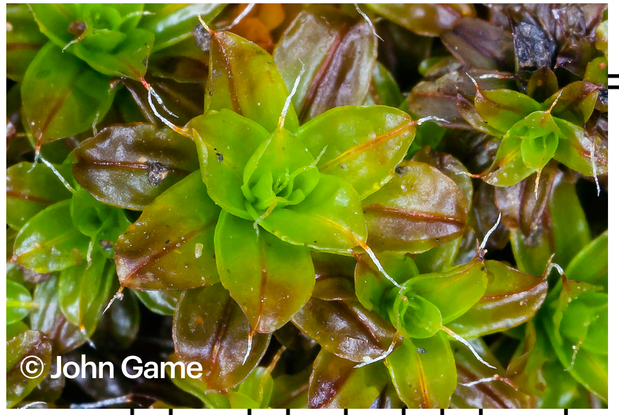

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S. princeps

n = 12, 24, 26, 28, 36

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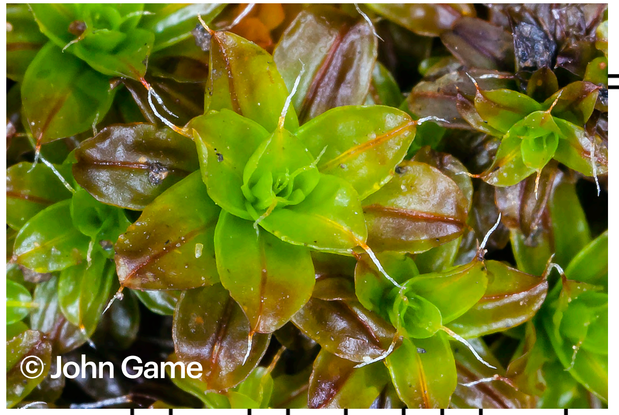

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S. minor S118
S. sucrosa S336
S. ruralis B_9108
S. laevipila S098
S. papillosissima S201
S. subpapillosissima S307
S. cainii S026
S. norvegica S167
S. virescens S337

Ekwealor, JTB, S. Roy, J. Brinda, C. Anajemba, R. Dikow, J. Jauregui-Lazo, B. Mishler, M. Oliver, and C. Rothfels, et al. In prep.

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S. rubella (unknown sexual condition and unknown chromosomes)

Future Research

Next Steps

Future Research

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- Check and validate assembly pipeline for accuracy with allopolyploids of known ancestry
- Investigate more potential polyploids
- Chromosome and sexual condition correlation analyses in phylogenetic network framework

Future Research

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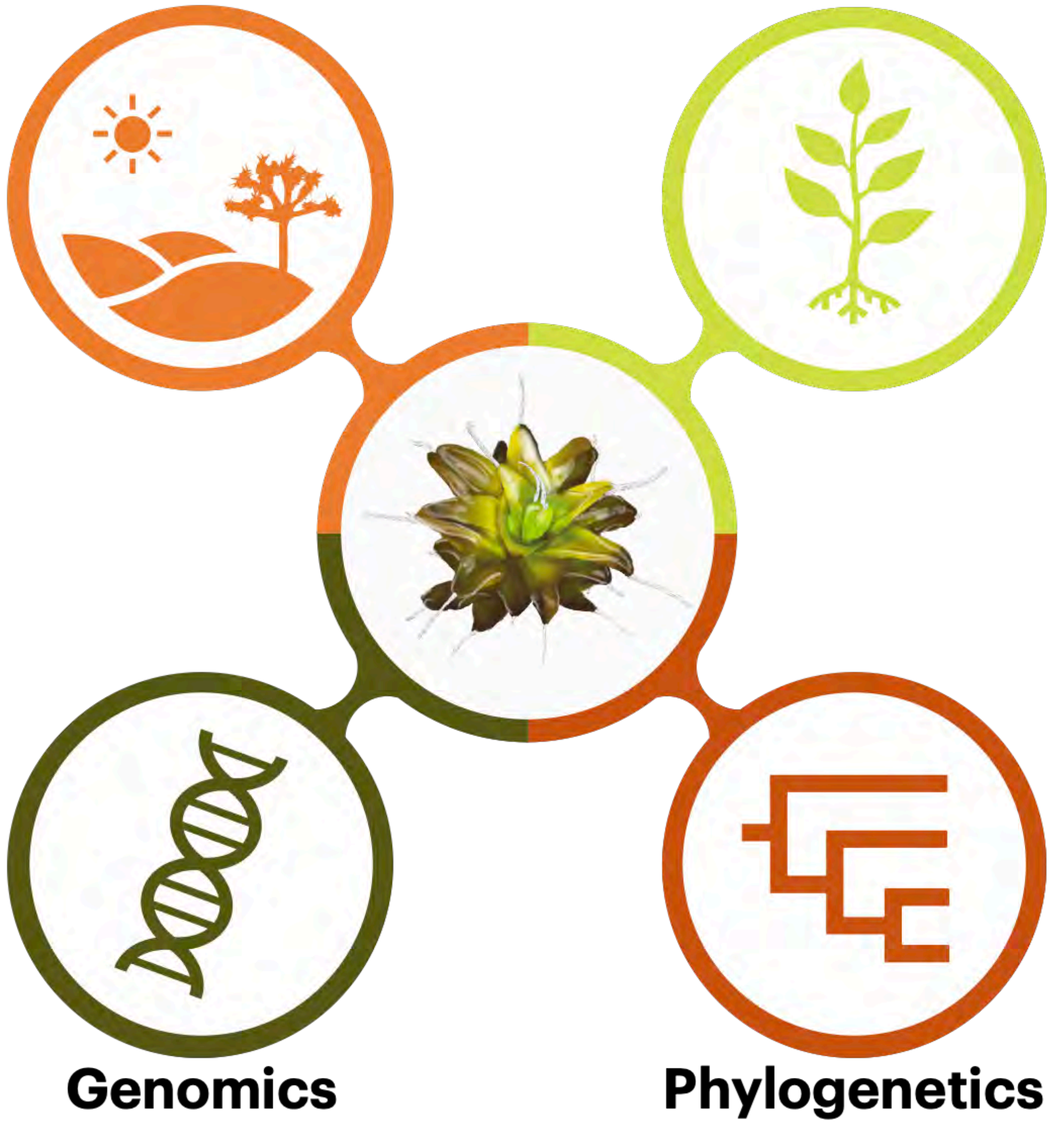

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