

Substantial genome size variation in algae genus *Synura*

Dora Čertnerová¹, Martin Čertner^{1,2}, & Pavel Škaloud¹



INSTITUTE OF BOTANY CAS

1) Department of Botany, Faculty of Science, Charles University, Benátská 2, 128 01 Prague 2, Czech Republic

2) Institute of Botany, The Czech Academy of Sciences, Zámek 1, 252 43 Průhonice, Czech Republic

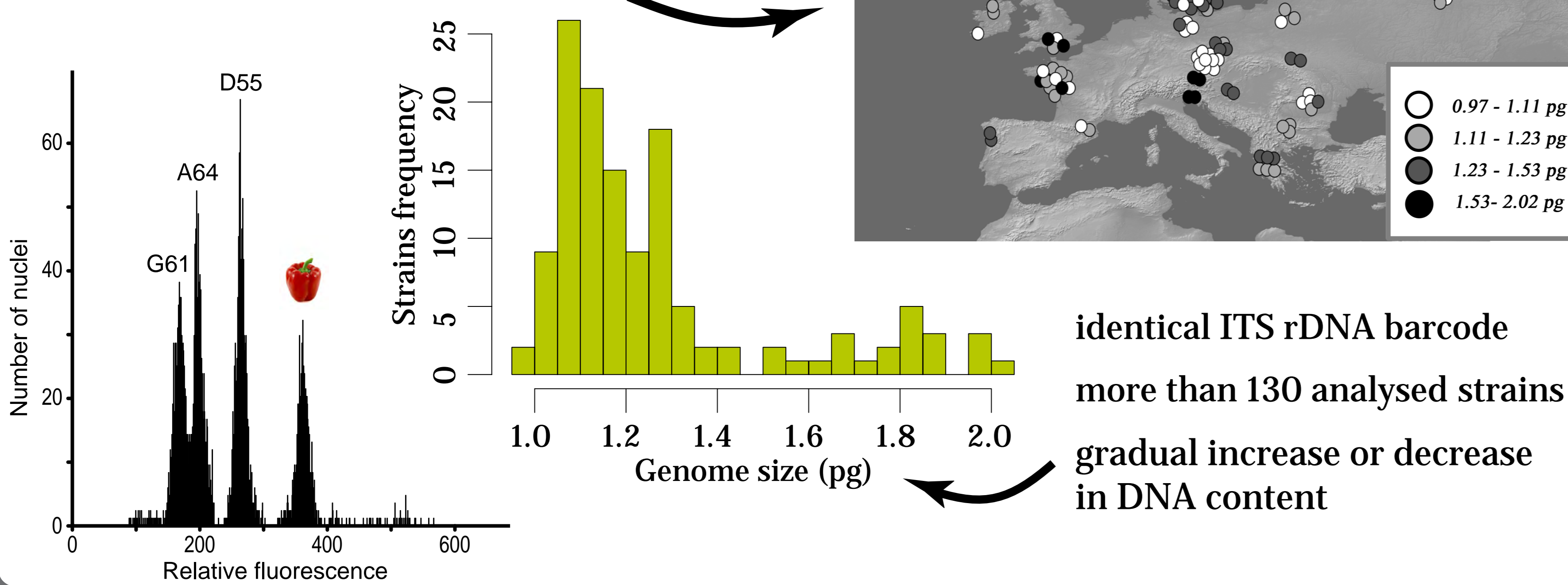


Pronounced intraspecific variation

Synura petersenii

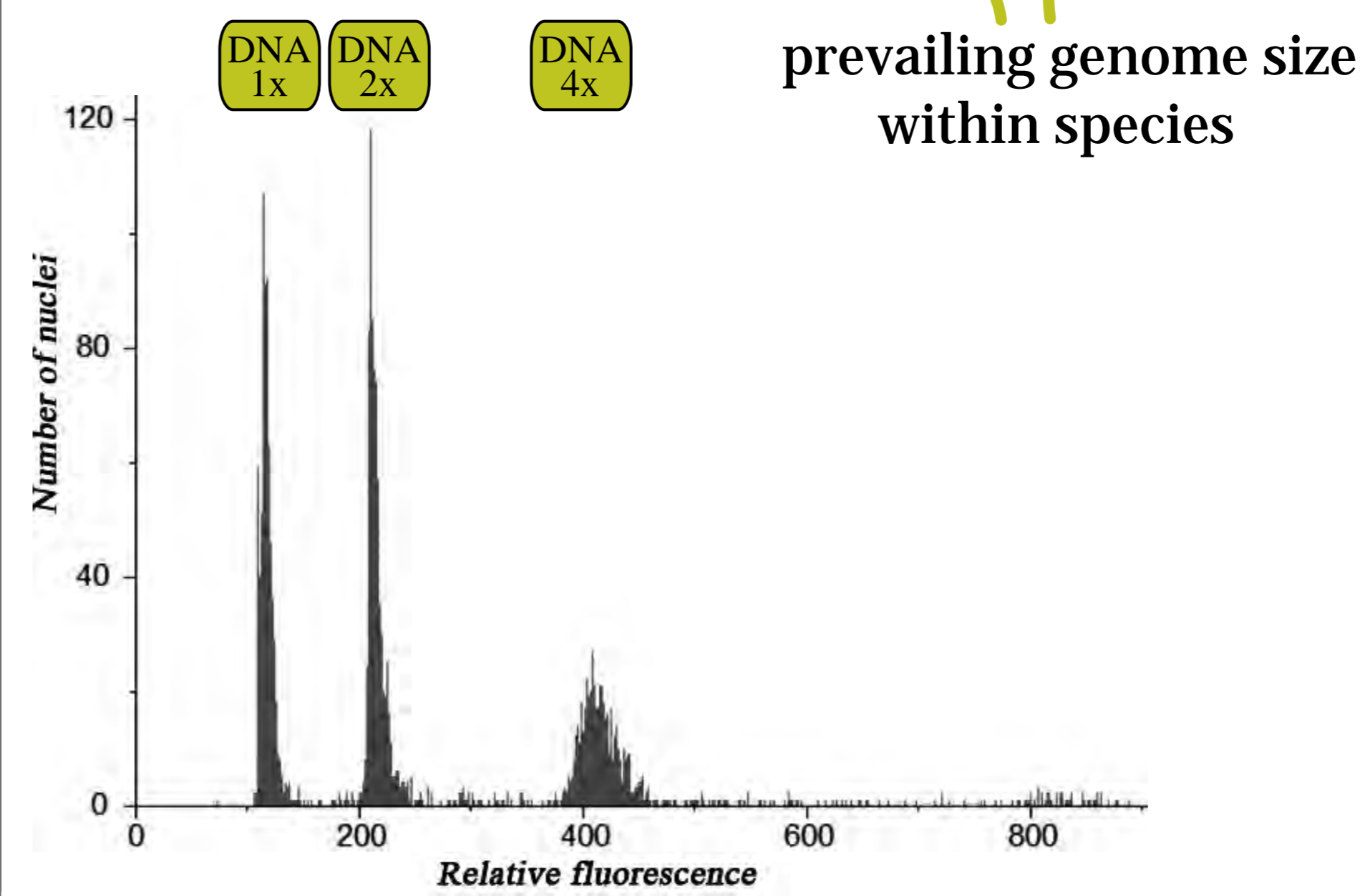
GS ranges 0.971 – 2.022 pg (0.949 – 1.978 Gbp), median = 1.170 pg

overlapping distribution of different GS strains



Polyploidization

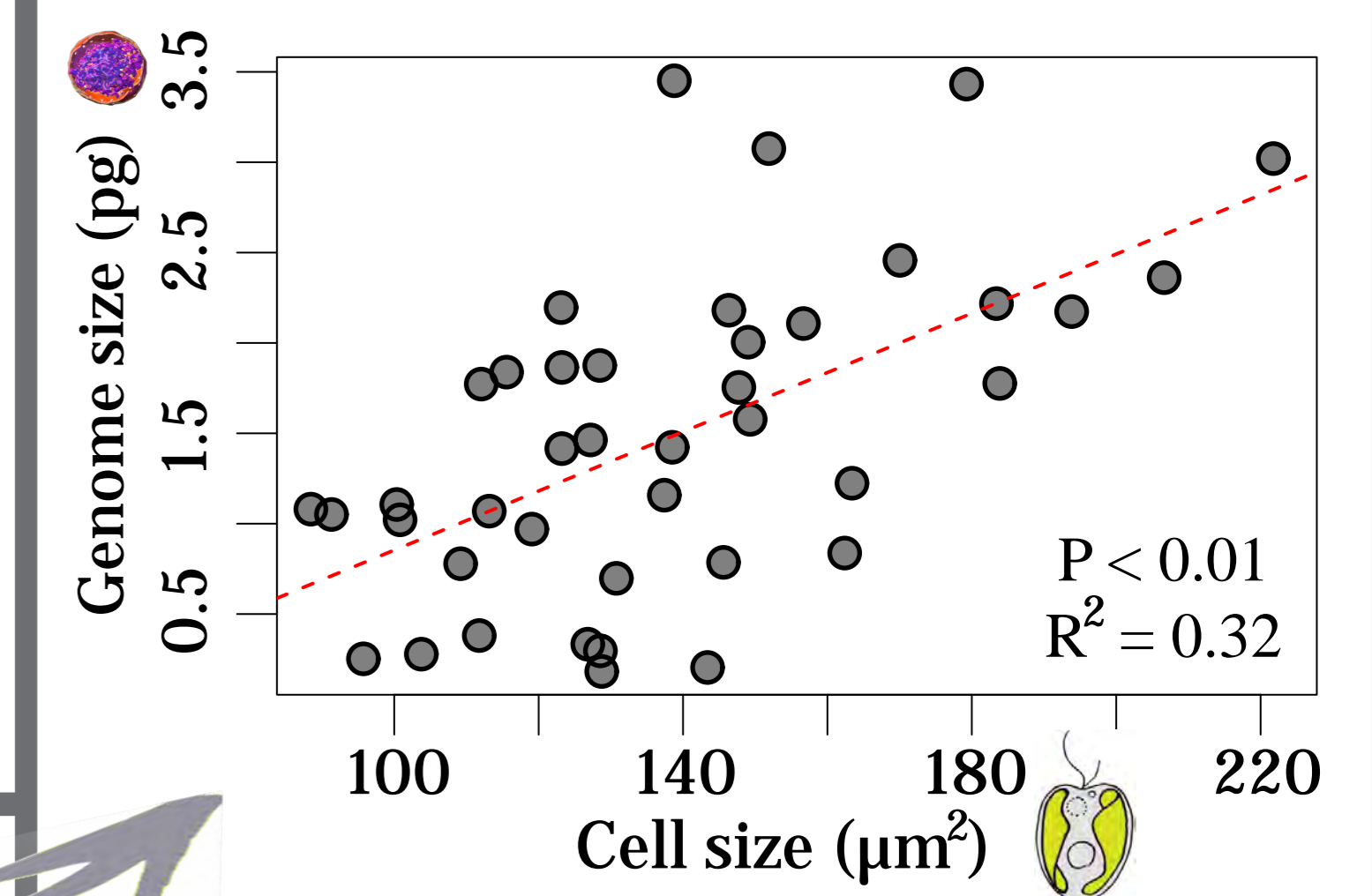
	DNA 1x	DNA 2x	DNA 3x	DNA 4x ?
• <i>S. glabra</i>	1.02 pg	1.96 pg		3.80 pg
• <i>S. heteropora</i>	0.79 pg	1.45 pg		3.00 pg
• <i>S. macropora</i>	1.48 pg	3.53 pg		
• <i>S. curtispina</i>	0.79 pg		2.20 pg	



Have a question?
Ask this girl!

GS - cell size correlation

genome size positively relates to cell size



log Genome size

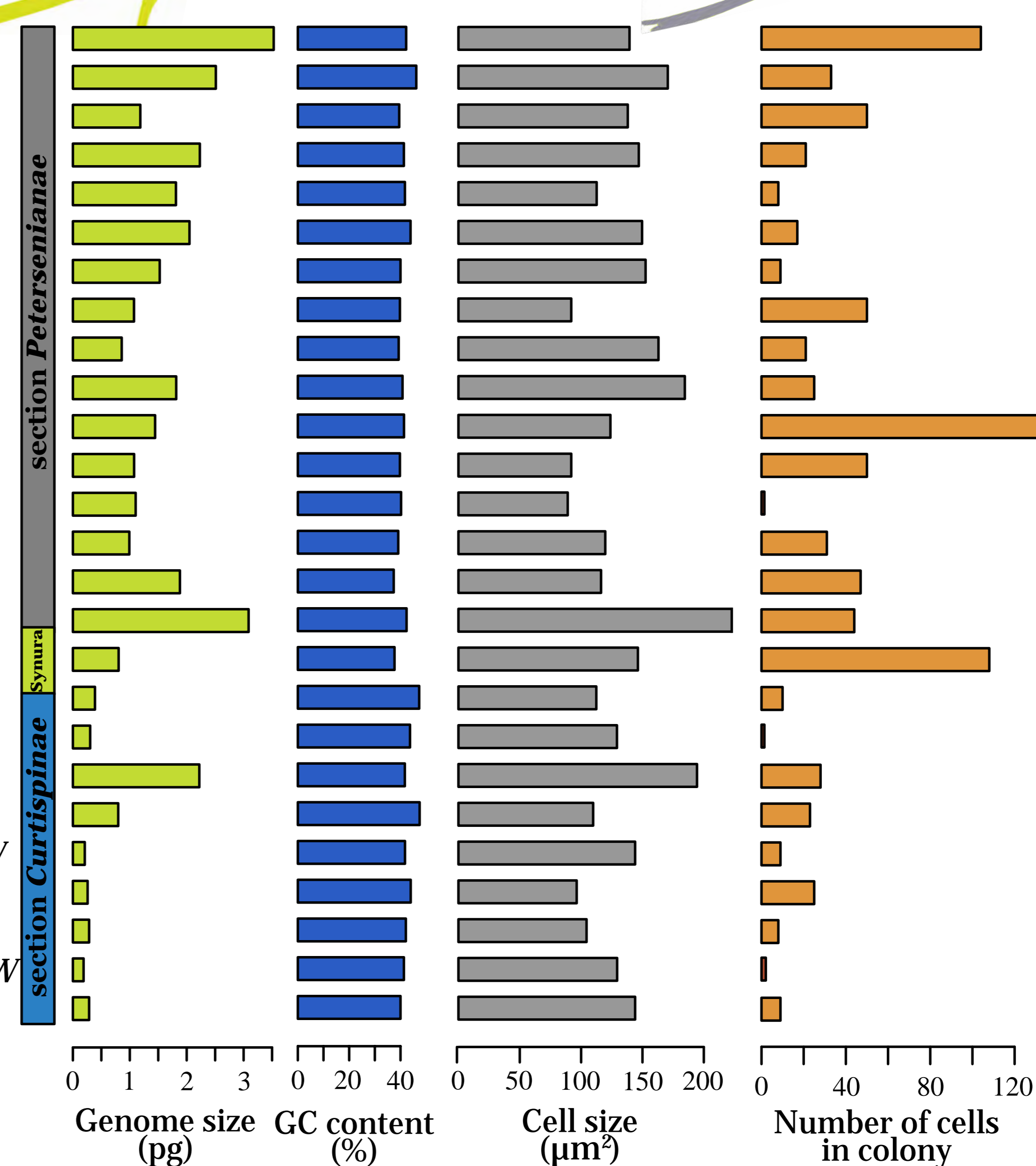
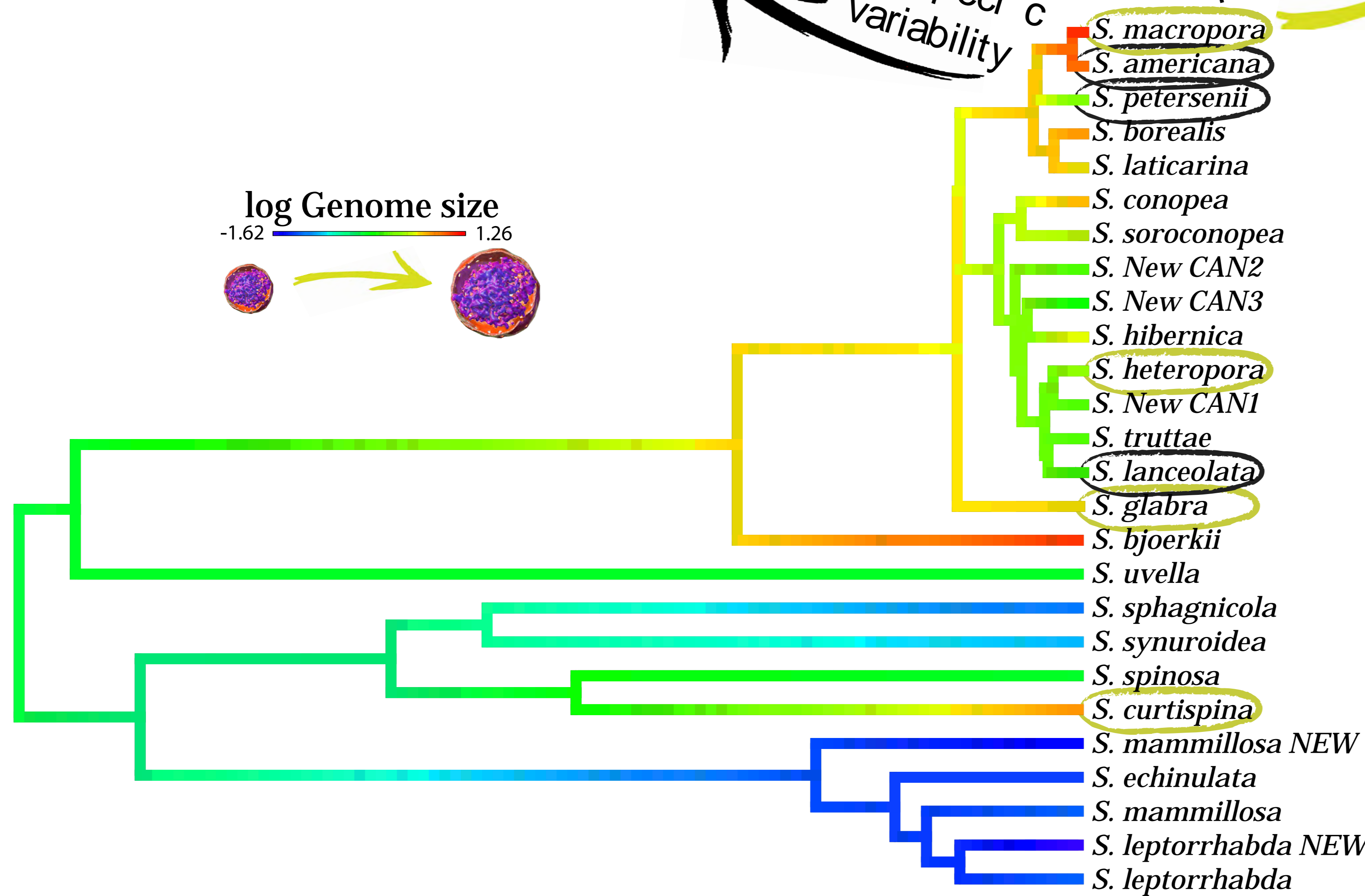
-1.62 1.26



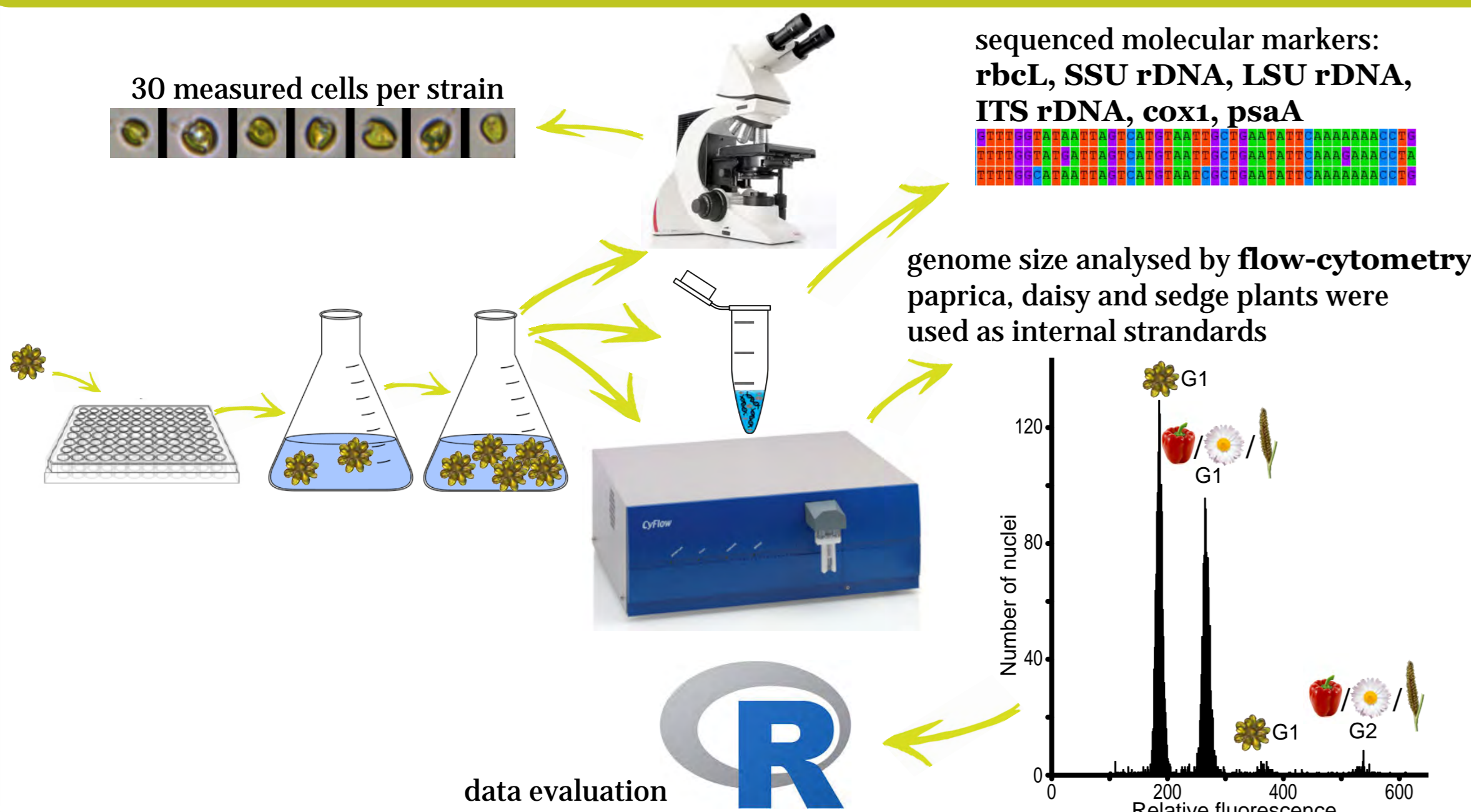
Intraspecific variability

Polyploidization

Cell size



Methods



The genome size within *Synura* genus is highly flexible, ranging from 0.19 pg to 3.53 pg (0.18 Gbp - 3.45 Gbp). The *Petersenianae* section tends to have bigger genomes when compared to the section *Curtispinae*.

Some lineages exhibit great intraspecific variability despite their identical ITS rDNA barcode, probably indicating cryptic diversity. In other lineages, multiple ploidy levels likely occur.