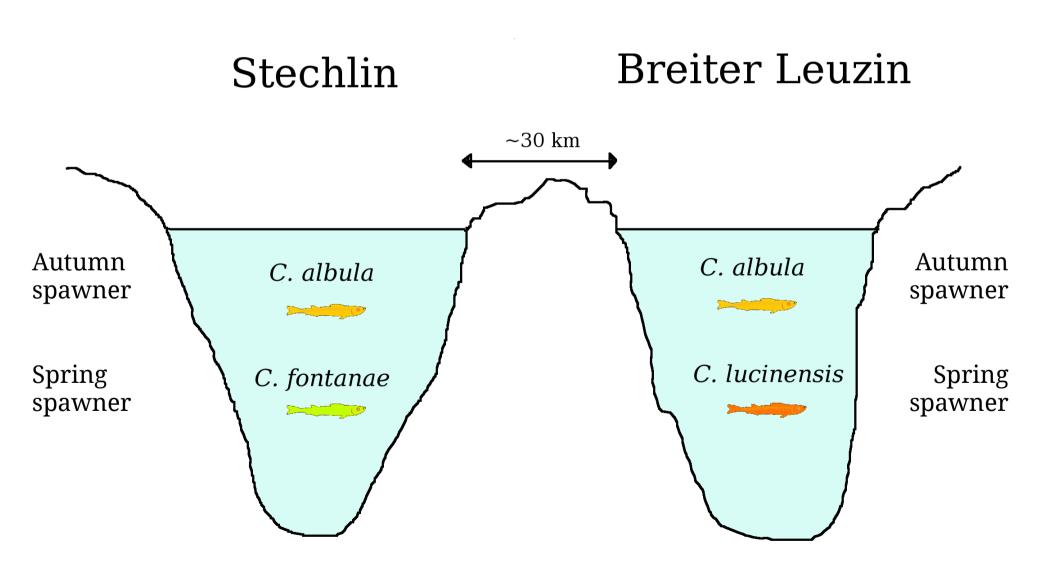
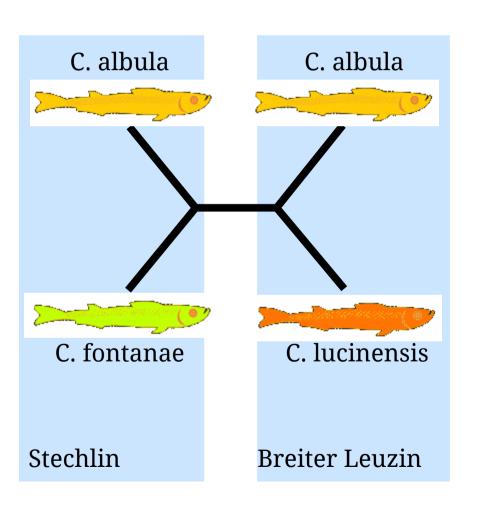
Sympatric speciation or secondary contact of Baltic ciscoes?

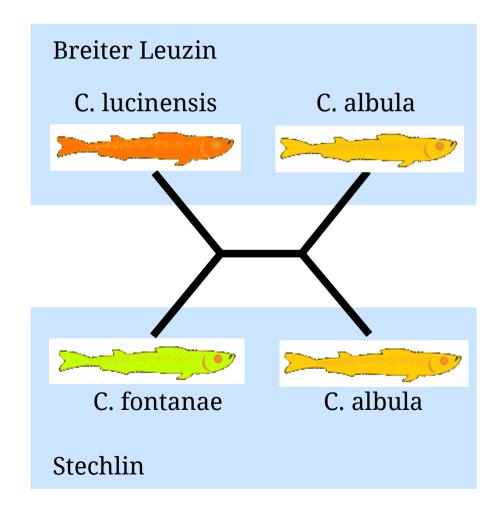
J. Ignacio Lucas Lledó Michael T. Monaghan Thomas Mehner

Coregonus albula complex (Salmonidae)



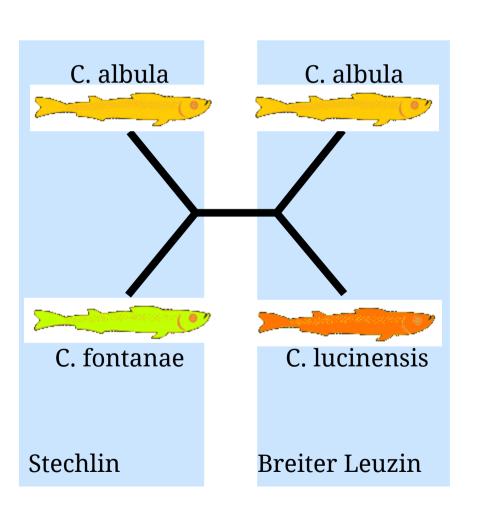
Parallel speciation or secondary contact?





Microsatellite data

Parallel speciation



- 6 markers.
- >30 fish/population.
- Greater
 differentiation
 between allopatric
 taxa.

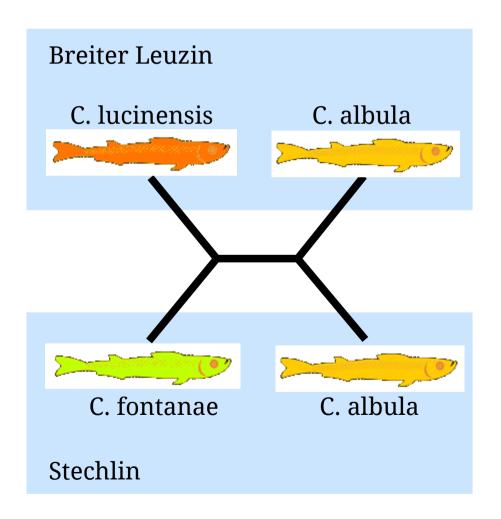
Schulz, M. et al. 2006. Journal of Fish Biology 68 (Suppl. A): 119-135

mtDNA data

Secondary contact

- 12 variable sites in ND-3 region.
- 12 haplotypes.
- ~20 fish/population.
- Greater differentiation between sympatric taxa.

Schulz, M. et al. 2006. Journal of Fish Biology 68 (Suppl. A): 119-135

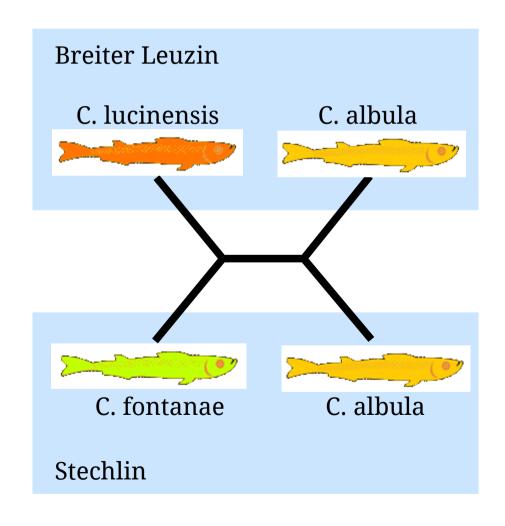


AFLP data

Secondary contact

- >1200 loci.
- >20 fish/population.
- Greater
 differentiation
 between sympatric
 taxa.

Mehner, T. et al. 2010. BMC Evolutionary Biology 10(85):1-14.

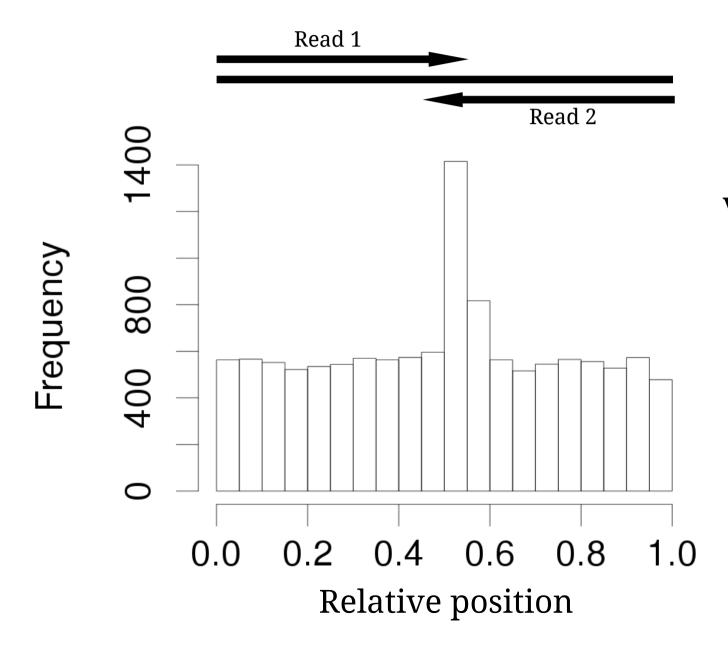


ddRAD-seq data

- Most studies:
 - SNPs.
 - 100 bp reads.
 - Illumina HiSeq.
 - >20 ind./population.
 - F_{ST}, Structure...

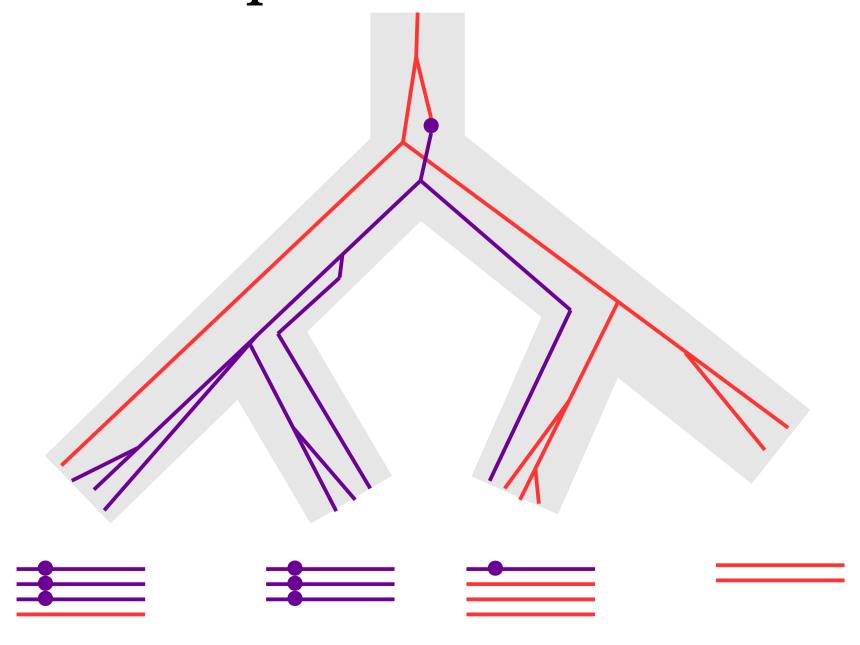
- This study:
 - Haplotypes.
 - 2*300 bp reads.
 - Illumina MiSeq.
 - 6 ind./population.
 - Coalescence.

ddRAD-seq data



Distribution of variable sites along assembled reads (500-588 bp). The excess of variable sites in the middle must be due to sequencing errors. Those sites are removed from the analysis.

"Multispecies" coalescence



"Multispecies" coalescence

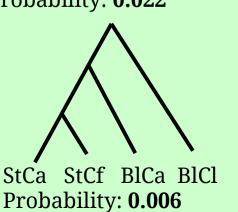
- *BEAST.
- 106 genes with 2 or 3 informative sites.
- jModelTest to determine best gene-specific molecular model.
- 200,000,000 generations.

Results

Parallel speciationOverall prob.: **0.912**

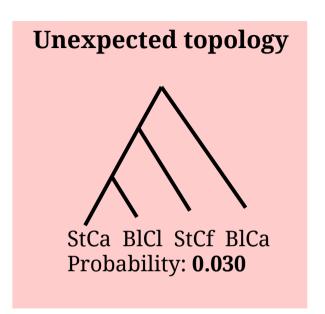






Secondary contact





StCa: Lake Stechlin, *Coregonus albula* (autumn spawner).

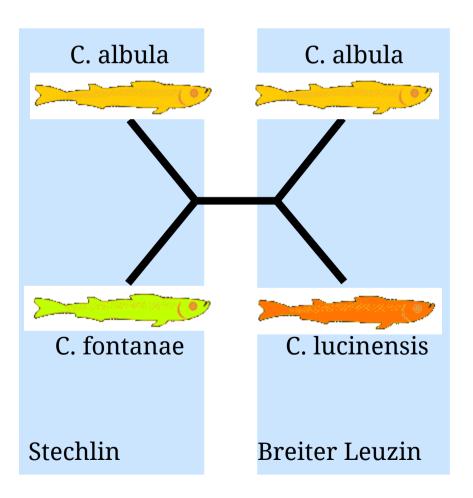
StCf: Lake Stechlin, *Coregonus fontanae* (spring spawner).

BlCa: Lake Breiter Leuzin, C. albula (autumn spawner).

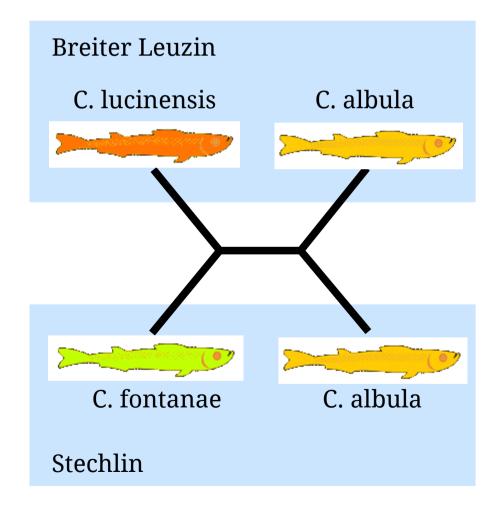
BlCl: Lake Breiter Leuzin, *C. lucinensis* (spring spawner).

Results

Parallel speciation **0.912**



Secondary contact **0.058**



Next steps

- Include more genes.
- Fit a model with migration.
- Revise the MCMC (priors, convergence...).
- Explain incongruence among data types.

https://github.com/IgnasiLucas

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Thomas Mehner (IGB, Berlin)



Forschen für die Zukunft unserer Gewässer



