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Running for the PYRN Award

Siberian treeline dynamics in a warming climate

– results from larch *population genetics* and *vegetation modelling* –

Motivation

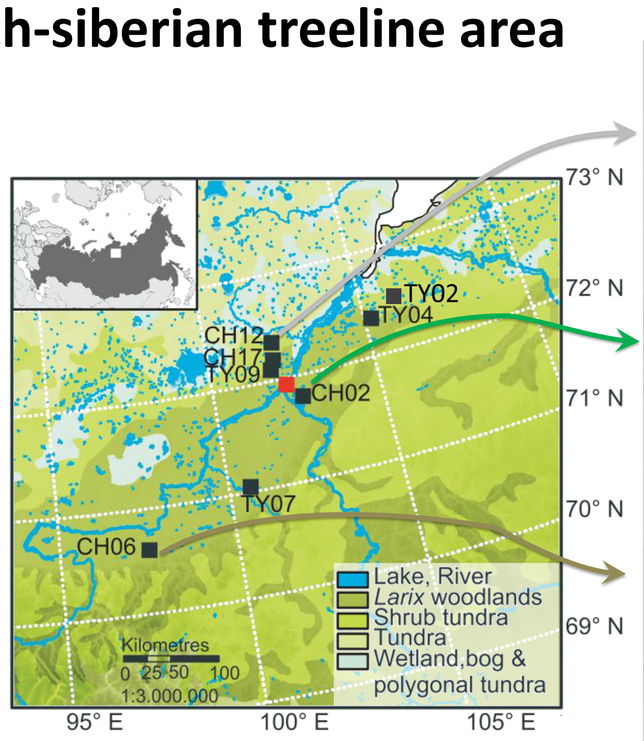
- to **realistically forecast the migration of tree species** in dynamic vegetation models, it is crucial to incorporate reliable estimates of seed dispersal distances
- we can **overcome this hard-to-track process** with the help of **modern molecular techniques** and **population genetics**

Our leading hypothesis

Parameterizing seed dispersal processes within our complex **individual-based model** LAVESI with spatiotemporal stand information inferred from **genetic structure** can **reveal treeline dynamics in past and future climates.**

Population genetics of north-siberian treeline area

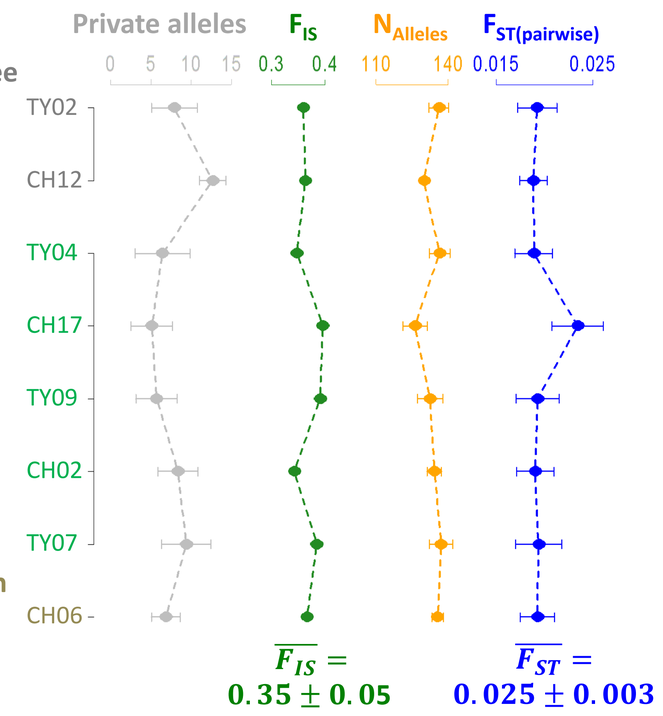
- we used **12 highly polymorphic nuclear micro-satellites** to infer the **genetic structure of 8 stands**
- in total **637 individuals** of 3 **different size/age classes**:
  - seedlings $_{\text{Height<0.4 m}}$
  - saplings $_{\text{2 <H>0.4 m}}$
  - trees $_{\text{H>2 m}}$



Single-tree → tundra

Forest → tundra

Northern → taiga



Pairwise genetic distances

	TY02	CH12	TY04	CH17	TY09	CH02	TY07	CH06
TY02								
CH12	0.017							
TY04	0.017	0.019						
CH17	0.023	0.024	0.023					
TY09	0.019	0.016	0.018	0.023				
CH02	0.020	0.017	0.018	0.021	0.018			
TY07	0.018	0.018	0.018	0.024	0.019	0.020		
CH06	0.017	0.019	0.017	0.025	0.019	0.018	0.017	

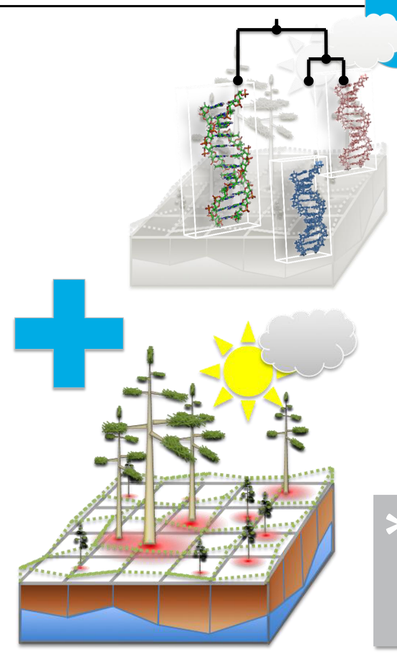
- **intermediate** treeline **stands** are **more distinct** than those at the margins

Conclusions

- **clonal growth** prevails **in very harsh environments**
- low genetic differentiation (small F_{ST}) suggests **high genetic exchange between stands**
- ***but* high inbreeding** coefficients (F_{IS}) point towards pronounced local reproduction

The individual-based model LAVESI

- we developed an **individual-based spatially explicit simulation model** for *Larix* populations at treeline (LAVESI)[1]
- **simulation experiments support the models' reliability**
- **individual seed dispersal allows to incorporate genetic information**



Work in progress

- *estimate gene flow between treeline stands*
- *parameterize seed (and pollen) dispersal in our individual-based model by parentage analysis on 100x100 m sample plots*

* *For more details about the model, see the other poster C.03 – Kruse et al. Time-lagged response … IBM*

References:

1 – Stefan Kruse, Mareike Wieczorek, Florian Jeltsch, Ulrike Herzschuh: **Treeline dynamics in Siberia under changing climates as inferred from an individual-based model for *Larix*.** In resubmission (June 2016), *Ecological Modelling*

Map – see references in: Klemm, J., Herzschuh, U., & Pestryakova, L. A. (2015). Vegetation, climate and lake changes over the last 7000 years at the boreal treeline in north-central Siberia. *Quaternary Science Reviews*

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