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 microsatellites to infer the genetic structure of 8 stands
- in total 637 individuals of 3 different size/age classes:
  - seedlings: Height<0.4 m
  - saplings: 2 < H ≤ 0.4 m
  - trees: H > 2 m
- intermediate treeline stands are more distinct than those at the margins

Conclusions

- clonal growth prevails in very harsh environments
- low genetic differentiation (small FST) suggests high genetic exchange between stands
- but high inbreeding coefficients (FIS) 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)
- 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