

Consequences of Range Peripheries: Genetic and phenotypic variation in Sitka spruce

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Objectives:

Peripheral populations are usually smaller and inhabit less optimal environments than core populations. Gene flow can inhibit local adaptation at range peripheries by introducing maladapted alleles. Disjunct peripheral populations may be 1) severely maladapted due to small population size, low genetic diversity and inbreeding or 2) locally adapted due to selection and isolation. We examine gamete pools of pollen, a major determinant of gene flow in wind-pollinated conifers, and evaluate some fitness-related quantitative traits to understand the evolutionary dynamics and fitness of peripheral populations.

Figure 2: genetic diversity

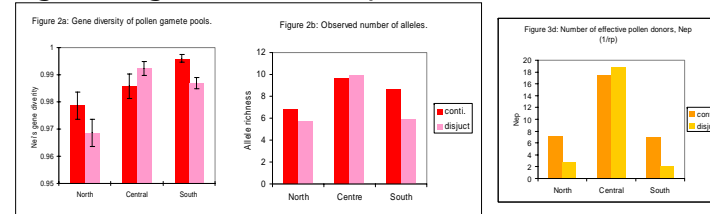


Figure 3: mating system

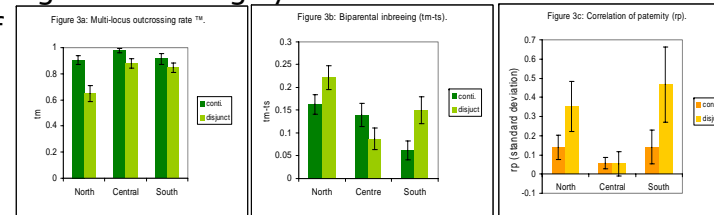
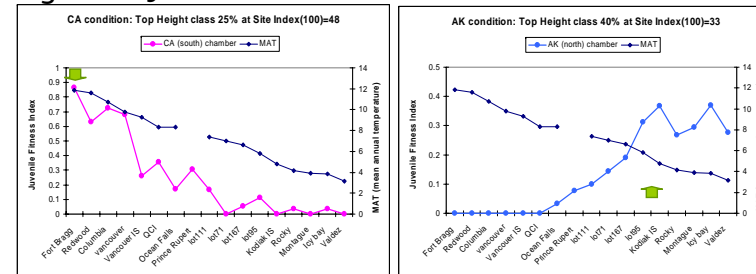


Figure 6: Juvenile Fitness Index



Results :

Genetic data:

- Allelic diversity and outcrossing rate both decreased toward the range periphery (Fig. 2b and 3b).
- Geographic trends in gene diversity and biparental inbreeding differed between continuous and disjunct populations (Fig. 2a and 3a).
- Correlation of paternity is high in disjunct peripheral populations but low in continuous and disjunct central populations, indicating a high number of effective pollen donor in continuous populations (Fig. 3c, 3d).
- The microsatellite-specific genetic distance measure R_{st} predicts geographic distance between populations more strongly than F_{st} (Fig. 4).

Quantitative data:

- Most quantitative traits show a clinal relationship with geographic distance from central populations (Fig. 5).
- Q_{st} is higher than F_{st} or R_{st} indicating traits are under differential selection among populations (Table 1).
- Disjunct peripheral populations had high fitness compared to nearest continuous populations despite higher inbreeding (Fig. 6)

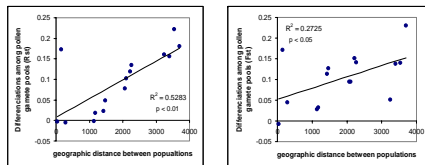


Figure 4: Relationship between geographic and genetic distance.

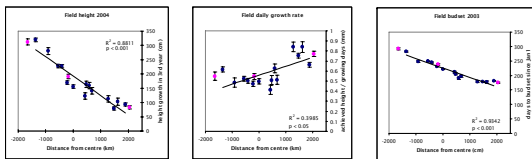


Figure 5: Trends in quantitative traits in field experiment

Materials and Methods

Variation in pollen gamete pools: Three pair of continuous and disjunct populations were selected from central (BC) and peripheral (north and south) populations (Fig.1). Five sets of microsatellite markers were used to determine pollen gamete haplotypes for DNA from diploid embryos and haploid megagametophytes. Nei's gene diversity, mating system parameters, and differentiation among populations were estimated using the programs Arlequin and MTLR.

Variation in Quantitative Traits: Two-year-old seedlings were transplanted in the UBC field and three growth chambers with different day/night temperatures and photoperiods mimicking southern(CA), central (BC) and northern (AK) climates. The chamber conditions were changed every two weeks April–December 2004. Bud phenology, height, biomass, daily growth rate were recorded. Data were analyzed using SAS GLM and VARCOMP procedures to estimate genetic clines, least squared means, heritabilities and Q_{st} for each trait. Juvenile Fitness Index is defined as the proportion of trees that fall into the top height class in each population. The top height class was defined by predicting survival rates for seedlings to 100 years of age using the Sitka spruce Stand Density Management Diagram (SDMD) with a starting density 2000/ha based on site index (100 years) = 33m (southeast AK conditions) and 48m (south OR conditions).

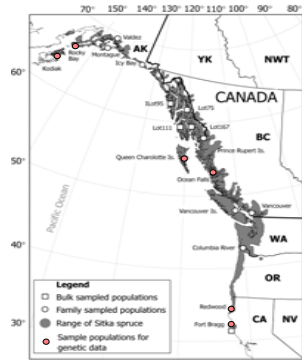


Figure 1: Sampled populations

Table 1: differentiations of genetic variations among populations

Quantitative Traits	Q_{st}
Height2003	0.51
Height2004	0.83
Growth rate	0.28
Biomass	n/a
Budget	0.90
Budburst	0.45
Pollen Haplotypes	F_{st} or R_{st}
F_{st}	0.11
R_{st}	0.09