



Heterozygote Deficiency in Adult Whitebark Pine Is Related to Level of Disease Infection



Andrew Bower and Sally Aitken, Centre for Forest Gene Conservation
University of British Columbia – Dept. of Forest Sciences

BACKGROUND AND INTRODUCTION

Whitebark pine's clumpy growth structure results in higher inbreeding rates than most conifers ($F_m = 0.82$; Bower unpublished data) and levels of inbreeding in British Columbia increase from north-to-south and from east-to-west (Krakowski *et al.* 2003), opposite to trends for blister rust infection. Conifers typically show a decrease in fixation index (F_{is}) with tree age, presumably due to selection against more homozygous, inbred individuals (see Table 1). We investigated whether this pattern occurs in whitebark pine, and whether infection by the introduced disease white pine blister rust (caused by the fungus *Cronartium ribicola*) affects changes in inbreeding with age. We hypothesized that if blister rust infection is selecting against less-fit, more homozygous, inbred individuals, the difference in F_{is} between the seedling and mature cohorts should be greater in stands with higher rust infection (see Figure 2a).

Hypothesis tested:

H_0 : No relationship between fixation index and level of blister rust infection at all age cohorts

H_a : Higher levels of blister rust will result in larger differences in F_{is} between seedling and mature cohorts

Figure 2: Predicted (a) and observed (b) trends in F_{is} with age for three blister rust infection classes

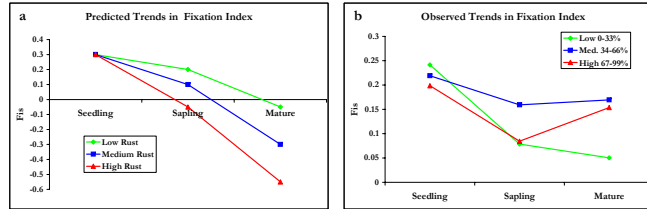


Table 1: Examples of the relationship of F_{is} with age in conifers

Species	F_{is} (seed)	F_{is} (sap)	F_{is} (age)	Reference
<i>P. sitchensis</i>	0.143	0.266 (11)	-0.123 (40)	(Shaw <i>et al.</i> 1992)
<i>P. flexilis</i>	0.12	0.005 (3)	-0.005 (3)	(Mason <i>et al.</i> 1987)
<i>P. radiata</i>	0.081	0.038 (3.4)	-0.119 (17.25)	(Preece and Strauss 1996)
<i>P. taeda</i>	0.126	-0.101 (5)	-0.095	(Morgan <i>et al.</i> 1993)
<i>P. canadensis</i>	0.142	-0.12 (5)	-0.079	(Pillou <i>et al.</i> 1992)
<i>P. albica</i>	-0.06	-0.025	-0.025	(Pillou <i>et al.</i> 1992)
<i>P. flexilis</i>	-0.04	-0.045	-0.045	(Pillou <i>et al.</i> 1992)
<i>P. contorta</i>	0.012	-0.22	-0.22	(Pillou and Kozubski 1994)
<i>P. ponderosa</i>	0.171	-0.022	-0.022	(Gunn and Millon 1984)
<i>P. resinosa</i>	0.011	-0.105 (10.34)	-0.105 (10.34)	(B. Kavanagh <i>et al.</i> 1997)
<i>Pseudotsuga racemata</i>	0.050	-0.027 (2.25)	-0.027 (2.25)	(Shaw and Allard 1982)
<i>Pinus strobus</i>	0.050	-0.043 (3.46)	-0.043 (3.46)	(Shaw 1997)
<i>Abies balsamea</i>	0.014	-0.100 (3.85)	-0.100 (3.85)	(Shaw 1997)
<i>Sequoiadendron giganteum</i>	0.043	-0.021	-0.021	(Finn and Libby 1982)



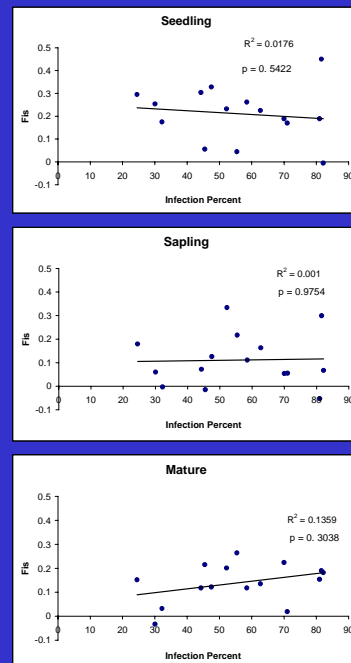
MATERIAL AND METHODS

Isozymes were used to determine the fixation index (F_{is}) ($F_{is} = 1 - H_o/H_e$) for three age cohorts on 15 sites throughout British Columbia and the northern U.S. Rockies (see Figure 2). Buds were sampled from 30 2-year-old seedlings growing in a common garden study in Vancouver for the seedling cohort, and 30 each for the sapling (<30-years-old) and mature cohorts in the field. A blister rust assessment was also done on each site to determine the level of infection. Eight isozyme loci with a total of ten loci were resolved for each sample.

Figure 1: Range of whitebark pine and sampling locations

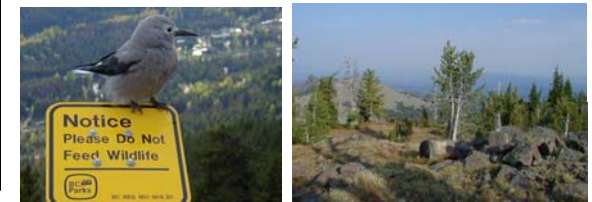
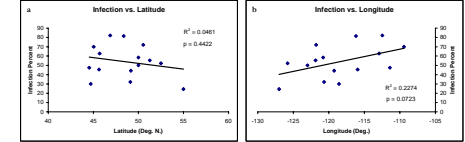


Figure 3: Relationship between F_{is} and blister rust infection level for three age cohorts.



RESULTS

Figure 4: Relationship of infection percent with latitude (a) and longitude (b)



CONCLUSIONS

- Whitebark pine shows significant levels of inbreeding at all ages (although growth does not seem to show inbreeding depression at the seedling stage - data not presented).
- When the level of blister rust infection is low, F_{is} decreases with age.
- When the level of blister rust infection is high however, F_{is} increases from the sapling to mature cohort.
- The high heterozygote deficiency in the mature cohort in stands with high levels of blister rust infection may indicate that whitebark pine harbors recessive alleles for disease resistance.
- Deficiency of heterozygotes and lack of evidence of inbreeding depression in growth may indicate that chronic inbreeding has purged some deleterious alleles that would result in lower fitness for more homozygous individuals.

ACKNOWLEDGEMENTS

The authors would like to thank the many people who helped in the field and the lab to make this project successful, and the numerous people who provided seed. Funding was provided by the Forest Investment Account. A special thanks to Dorothy Watson for lab and field assistance, editing, and moral support.