PARENT-PROGENY CORRELATION OF BUDBREAK IN WHITE SPRUCE AT PETAWAWA, ONTATIO

C. W. Yeatman[1] and C. S. Venkatesh[2]

INTRODUCTION

Spring frost injury frequently retards establishment and causes serious losses to white spruce (*Picea glauca* (Moench) Voss) planted in the open (Rowe, 1955; McLeon, 1964). Damage is avoided or greatly reduced in trees with late budbreak (flushing) which therefore is an important selection criterion in central and northeastern United States and Canada (Nienstaedt & King, 1969; Nienstaedt & Teich, 1972). This paper presents additional evidence of the high heritability of flushing time apparent from observations of five mature white spruce and their 'half- and full-sib progenies growing at the Petawawa Forest Experiment Station (P.F.E.S.) near Chalk River, Ontario.

[1] Canadian Forestry Service, Petawawa Forest Experiment Station, Chalk River, Ontario.

[2] C.I.D.A.-Colombo Plan visiting fellow from Forest Research Institute, Dehra Dun, India.

MATERIAL AND METHODS

Controlled pollinations were made in 1967 among five dominant white spruce trees (Station Nos. 2010, 2011, 2012, 2013, 2014) growing in a stand of natural origin at P.F.E.S. (fig. 1, table 1). Both open and control pollinated seed was sown in paper tubes in a greenhouse in March, 1971, and the seedlings transplanted into nursery beds in August of the same year.

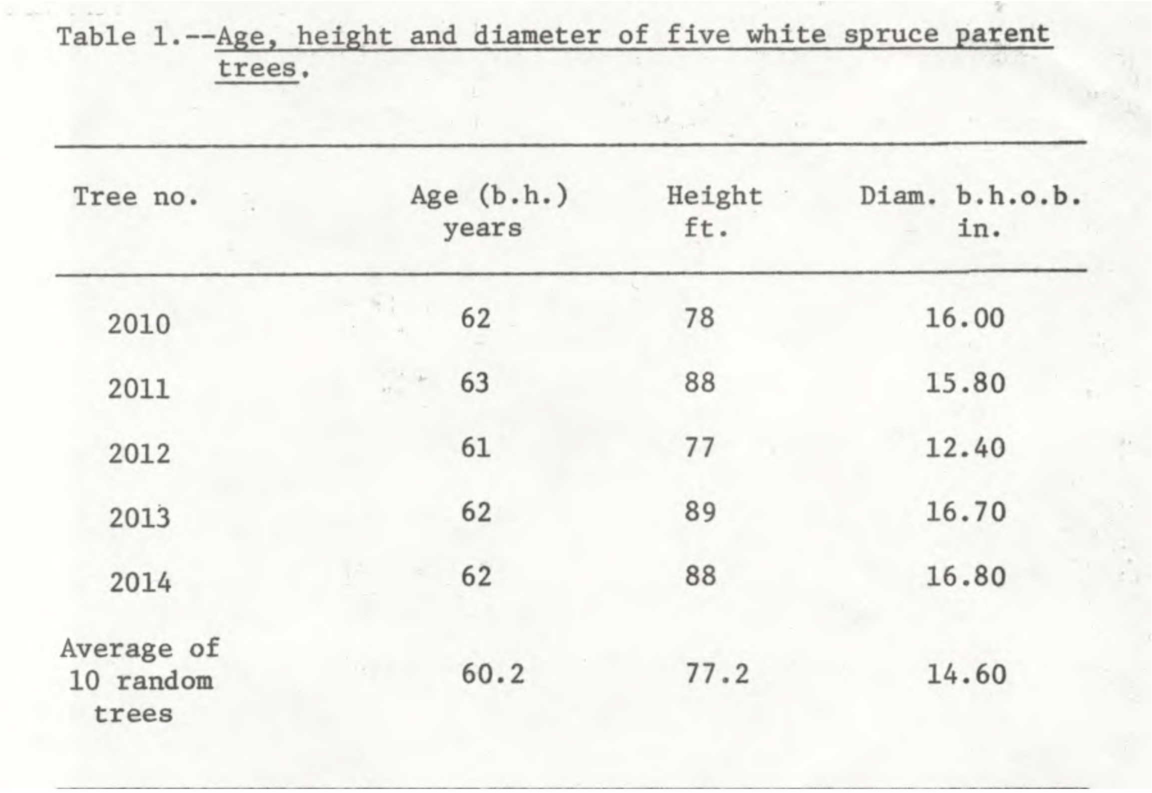

Table 1.--Age, height and diameter of five white spruce parent trees.

Tree no.	Age (b.h.) years	Height ft.	Diam. b.h.o.b. in.
2010	62	78	16.00
2011	63	88	15.80
2012	61	77	12.40
2013	62	89	16.70
2014	62	88	16.80
Average of 10 random trees	60.2	77.2	14.60

Families were arranged in 10-tree plots randomized within each of six replications. Observations on budbreak were made of both parents and progenies in spring, 1973. Figure 2 gives the temperature records near ground level in the nursery for the period when the seedlings were being scored for flushing. Figure 3 gives the temperature record from the standard meterological station at the time the parent trees were flushing. Necessarily different systems of scoring had to be used for the small-crowned seedlings to determine family means and for individual mature parents. For seedlings within progenies the following scale was used for scoring at 1- or 2-day intervals:

Score	Proportion of buds flushed
0	None
1	10%
2	50%
3	75%
4	All except apical bud
5	All living buds

Figure 1.--Control-pollination of 60-year-old white spruce at Petawawa Forest Experiment Station, 1967. Both large isolation tents and small bags were employed in a diallel crossing scheme.

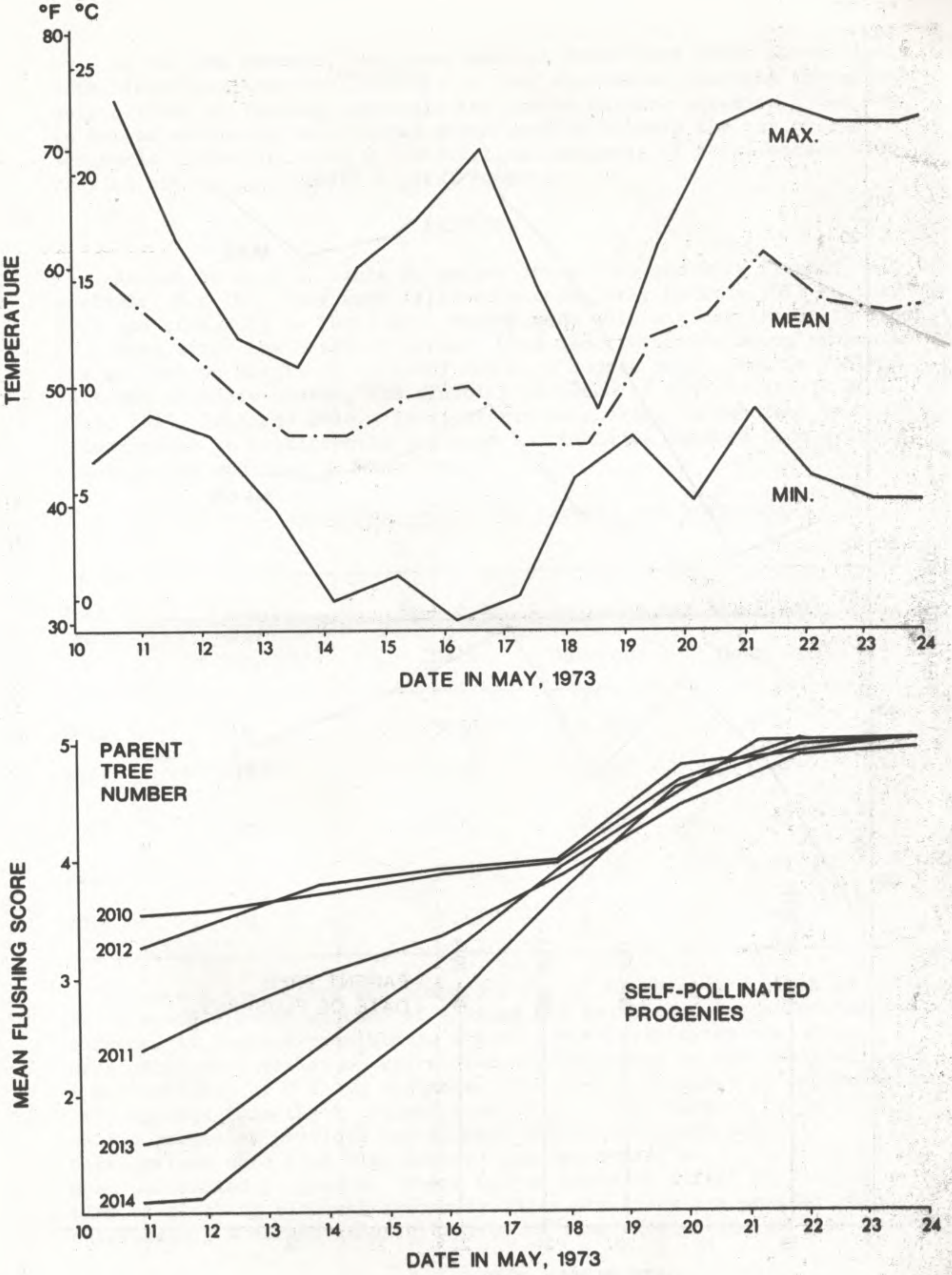

Figure 2.--Record of temperature near ground level in the nursery during bud break of white spruce seedlings. The lower graph indicates mean of flushing scores for the self-pollinated progenies of the five numbered parents.

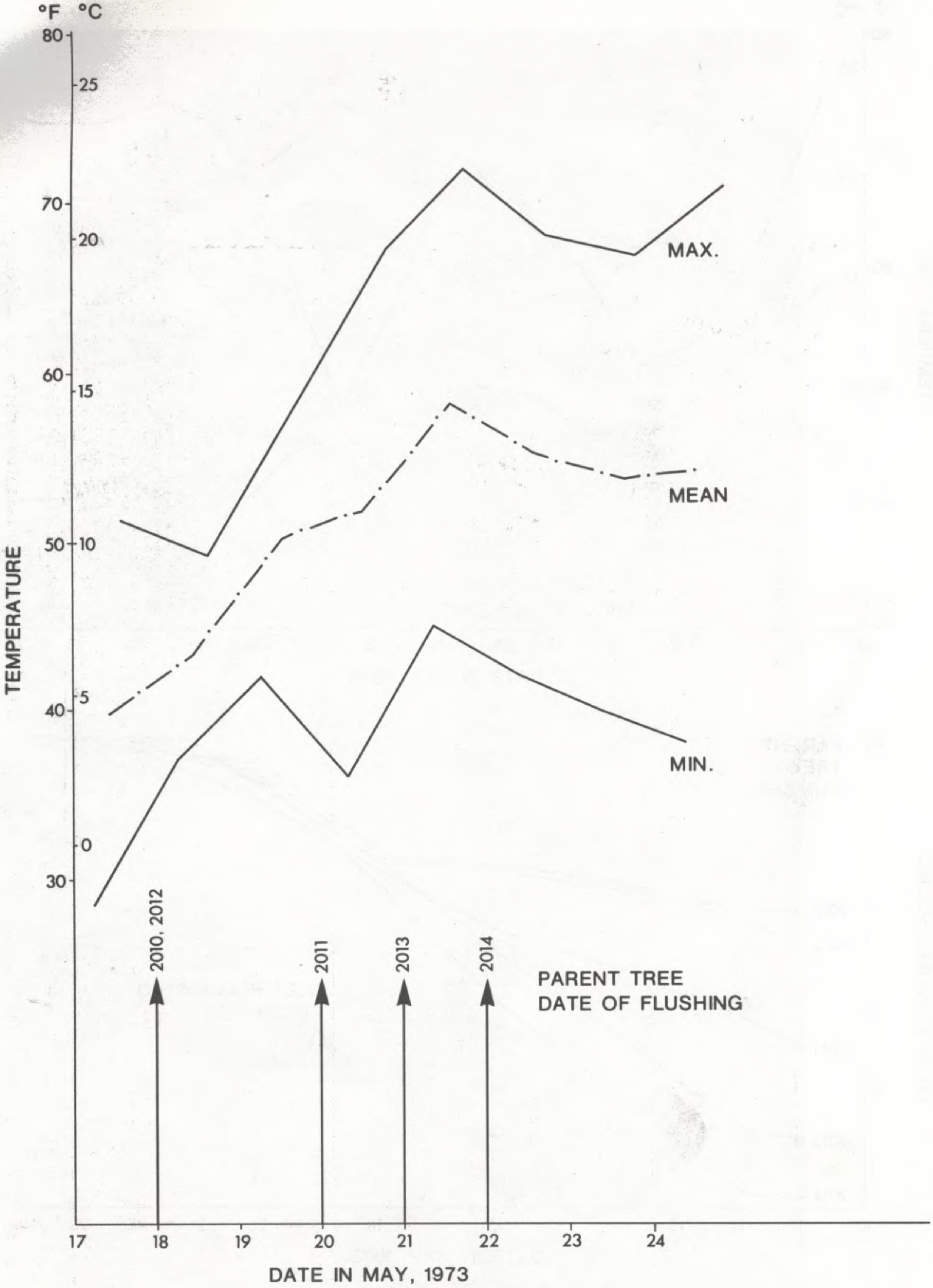

Figure 3.--Temperature record from the standard meteorological station at the time the parent trees were flushing. Vertical arrows indicate the day of flushing of the five numbered parents.

As for the parents, the trees were at first kept under surveillance with binoculars from the ground. As they approached flushing time, they were climbed at two-day intervals and scored on each occasion. The day in May on which all buds showed green needles beneath the cap of bud scales is listed in Table 2. Statistical analysis of total scores was carried out using a PDP/8L digital computer.

RESULTS

As can be seen in Table 2, parent trees 2010 and 2012 flushed earliest, May 18. They were followed successively by tree 2011 on the 20th and tree 2013 on the 21st. Parent tree 2014 was the latest to flush, four days after the earliest trees. Good discrimination among progenies was evident on May 11 (F = 11.90) and mean scores are listed in Table 2. In terms of these scores, the flushing sequence of the parents is 2010, 2012, 2011, 2013 and 2014. Particularly noteworthy is the fact that this linear order is consistently the same for families derived from selfing, out-crossing and open pollination.

Table 2.--Flushing values for parents and progenies.

Tree No.	Parent day in May, 1973	Mean progeny score on day 11 of May, 1973		
		Self	Outcross	Open poll.
2010	18	3.53	2.90	2.94
2011	20	2.40	2.13	1.88
2012	18	3.29	2.46	2.49
2013	21	1.60	1.72	1.84
2014	22	1.10	1.55	1.74

Progeny mean score and midparent day of flushing are given in Table 3. Since different systems of scoring had to be used for progenies and parents, it was not possible to estimate heritability by the straightforward method of regression of off-spring on midparent values. A heritability of 0.91 is estimated from the coefficient of determination (r) derived from the correlation analysis. From Table 4 it is clear selfed progenies provided the highest correlation with parents. Correlations were also high between progeny types, selfs, outcrosses and open pollinated progenies. There was no apparent effect of --citing on time of flushing although typically these progenies are smaller than outcrosses. A strong genetic control of time of flushing is thus indicated.

Table 3.--Mid-parent scores.

Station tree crosses and selfs	Mid-parent day	Progeny mean score
2010 x 2010	18.00	3.53
2010 x 2011	19.00	3.03
2010 x 2012	18.00	3.39
2010 x 2013	19.50	2.43
2011 x 2011	20.00	2.42
2011 x 2012	19.00	2.62
2011 x 2013	20.50	2.11
2011 x 2014	21.00	1.22
2012 x 2012	18.00	3.29
2012 x 2013	19.50	20.6
2012 x 2014	20.00	1.79
2013 x 2013	21.00	1.60
2013 x 2014	21.50	1.10
2014 x 2014	22.00	1.10

$r^2 = 0.91$

Table 4.--Coefficients of determination (r^2) among parents and progenies in time of budbreak. Parental day versus progeny score on day 11.

	Self	Outcross	Open pollin.
Parent	.98	.91	.82
Self		.95	.83
Outcross			.90

CONCLUSION

The date of budbreak in white spruce is known to vary as widely as 21 days among trees in a stand (Nienstaedt & Teich, 1972). The five parent trees used in the present experiment at Petawawa belonged to the same stand and broke bud within a few days of each other. Parents and progenies were highly correlated in the time of budbreak and flushing, giving high heritability values indicating thereby a strong genetic control of this character. The difference between the first and the last flushing parent tree was of the order of only 4 days, yet the progenies of all trees bred true to their respective parents even within this narrow range of difference. Therefore, selection for late flushing is of value even over a small differential and will lead to perceptible improvement in the offspring in frost resistance and concomitant growth rate.

LITERATURE CITED

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DISCUSSION

Morgenstern - I have a question for Jerry Klein. I would like to know if the number of families selected from a stand was just one or several. A second question is whether you have thought about the genotype-environment interaction as a problem in selection?

Klein - In our case three trees were selected in each stand examined. Some times where we hadn't found any stands and there is a small grove, one tree was selected in it. In phenotypic selection in seedling seed orchards where there is genotype-environment interaction, you have no way of detecting or correcting for this effect. The fact that the geographic origins of trees being compared are similar suggests that at least the geographic components of the genotype will not contribute very much to the interaction.

Morgenstern - No, I disagree. You have distances of up to 170 miles.

Klein - Trees being compared are always from within one source area, that is within one of the eleven source areas that I have. There is no comparison between trees whose source is separated by 130 miles. Maybe I should go back to the diagram. This is the biggest source area--that's about 50 miles across the northern part and a much smaller spread, with regard to latitude. There is no phenotypic comparison between these trees (pointing to different source areas on diagram) and they are going to pollinate each other in the final orchard, but their comparison is entirely within those areas.

Kriebel - I have two questions, Jerry: 1. how did you separate those contiguous areas? On what basis did you delineate them; 2. since you have only one tree per family per plot, what do you do about mortality, and how does this affect your results?

Klein - Well, I just plotted all tree locations on the map and then I drew boundaries to get twenty families within each area.

Kriebel - There are no particular characteristics that differ between these areas?

Klein - No, there is no difference. Climate or soil--it is just to put them in compact grouping. Where there is mortality, then we just don't get a comparison. And we lose that family in that plot.

Kriebel - Then if I understood correctly, a particular family wouldn't be very evenly distributed in your final seed orchard. It might be missing from part of the orchard.

Klein - No, this is individual selection in the plot. The trees are selected on their own merit. I don't plan to take information from performance of sibs in the seed orchard or in the family-test plantations. If there were true random breeding in the source plantations, then among the trees on a seed orchard plot, there would be three times as much variation due to genetic variation within families, as that due to genetic variation among families. There probably is not true random breeding in the source areas, nonetheless, I am assuming that there is a substantial amount of genetic variation within families. And we are trying to put that to work in this seedling seed orchard.

Kriebel - You might lose some good families just by mortality?

Klein - Within one plot, yes. But other seedlings of those families would survive in other blocks,

Long - It is conceivable that after thinning you can have at least one member of every family in the orchard plantation.

Klein - There are twenty-four blocks and 20 families from each source area, so it is possible that we could end up in different plots with different families representing for the sources.

Teich - I think it would only take a little more work if you took family-height averages and used this to help you make a decision in your thinning. If you came across two trees, one a little smaller than its neighbor but it came from an extremely good family, then it should be selected.

Klein - I still have that option. I could use family information. Genetic improvement is only one of the objectives of the seed orchard. Another one was to see what would happen when we analyze situations where you have a broad population and there is no possible way of getting information from relatives. And see what sort of things happen when you select on the basis of individual performance. There are two or three years to decide how I'm going to do this before the first thinning comes due.

Morgenstern - Some form of plus-tree selection?

Klein - That is an interesting subject. There is an analogy with phenotypic selection in the wild. And I am particularly interested in the different circumstances here. There you are selecting on the mature trees, which is an advantage; and you have a chance for selection intensity higher than 1 in 20. Here you have the disadvantage of the younger age and you have the advantages of a standardized history of the trees, which you don't have in the wild stand. I am not prepared to concede that phenotypic selection will not be more effective under these circumstances, with standardized history of the trees, and the closer spacing so that there is less site variation than in wild selection.

Venkatesh - I would like to have you explain what you mean by accumulating temperatures or degree days.

Nienstaedt - Probably the main factor that controls flushing is temperature, accumulated temperatures. If you determine the degree day requirement, you can demonstrate very clearly that certain clones of white spruce require much fewer degree days in order to reach flushing. In other words, an early flushing clone will require maybe 385 to 390 degree days, 40° plus. A late flushing clone may require 630 degree days--in that neighborhood. Now this changes from year to year depending on the earliness of the season. Apparently, photoperiod modifies the degree day requirements so that in a late season the degree day requirements are less; for example, a late flushing clone would require maybe 516 instead of 630 degree days. But the sequence of events when you look at a population of clones will always be the same; the early will be early whether it is an early year or a late year.

Khalil - Would you explain how you would set up your test and score the clones?

Morgenstern - You mean how a clonal test is set up? It is in a randomized plot design in a clonal test and the difference between the clone is consistent from year to year and you look at any one day and the difference in the score is highly significant statistically. In other words, what you can do is you say here is my array of clones and you can score them with a system using six classes. You come out with an average score per plot. So you can analyze it as a single random study and demonstrate that this is the clonal material in this case that has progenies in randomized plots. He gets an average score for the plot and uses that.

Yeatman - In this case the estimate of variability is the coefficient of determination which is the square of the correlation between the parents and progenies. In spite of the difference in flushing of only four days between parents, the correlations without cross- and self-pollinated progenies are 95% or better. The square of the parent-progeny correlation of the open-pollinated progenies is 82%.

Zsuffa - I have a question for Jerry Klein. Evidently you are establishing jack pine seedling seed orchards in Alberta. I heard comments earlier that the jack pine cone collection damaged the trees. How do you plan to overcome this difficulty?

Klein - I have heard of that, too, but I don't know what I am going to d o about it. Other people are more familiar with this problem, but I think Kit Yeatman suggests harvesting the trees and planting other trees instead. When the trees are young and the cones open it may be possible to make physical arrangements to collect the seed from the plant or ground.

Yeatman - I agree that the cones from young trees can be collected from the ground rather easily but as trees get beyond easy reach the difficulties of avoiding damage from cone harvesting increase. I will discuss later on this afternoon why I propose to cut the trees down and carry on with another generation of seed production trees.

Nienstaedt - I don't question the data at all and I am pleased to see my own data backed up. I would like to point out though that if you would base a breeding program on the selection differential of four days, whether you have heritability of .3 or 1.0, you really aren't going to gain a thing. You are going to have to work with a much greater selection of plants in order to have a meaningful selection differential. In my material we have a spread of 21 days to work with--the possibility is there. You are going to have to make a much bigger selection to get the potential to work with.