

## DISEASE RESISTANCE EVALUATION OF JACK PINE FOR WESTERN GALL RUST

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### INTRODUCTION

A program to develop genetically improved jack pine for Manitoba and Saskatchewan was initiated in 1967 by the Forestry Branch, Canada Department of Forestry and Rural Development, predecessor of Forestry Canada. Family tests consisting of replicated plantations of open-pollinated families were established in three areas in 1972, 1974, and 1976 to provide genetic quality information and breeding materials (Klein 1982). The test established in 1972 consisted of four plantations in eastern Manitoba. Each plantation had the same 209 open-pollinated families derived from wild parent trees selected in eastern Manitoba south of 51°15'N, six families from trees selected in Saskatchewan, and one bulked control lot from southeastern Manitoba (Fig. 1).

Western gall rust, caused by the rust fungus *Endocronartium harknessii* (J.P. Moore) Y. Hiratsuka, has been observed in this plantation since shortly after planting. This disease is widespread on hard pines in Canada and is especially important in intensively managed stands (Bella and Navratil 1988; Hiratsuka 1981; Hiratsuka and Powell 1976; Powell and Hiratsuka 1973). Because of its potential impact on jack pine plantations, resistance to western gall rust infection should be included as a selection criterion in this breeding program, as in any hard pine breeding program in Canada (Yanchuk et al. 1988). An initial step in incorporating rust resistance into jack pine breeding is to develop and evaluate techniques for assessing host response to infection. This paper reports on assessment of host response to natural infection in family test plantations, and to greenhouse inoculation of seedlings with field-collected spores.

### MATERIALS AND METHODS

#### Field Surveys

Assessment of response to infection under field conditions was done by recording occurrence of rust galls on all plot trees in four eastern Manitoba family test plantations at 17 years from planting (Fig. 1). Galls were counted on about 6400 trees in 216 family lots and 15 replications. Number of trees

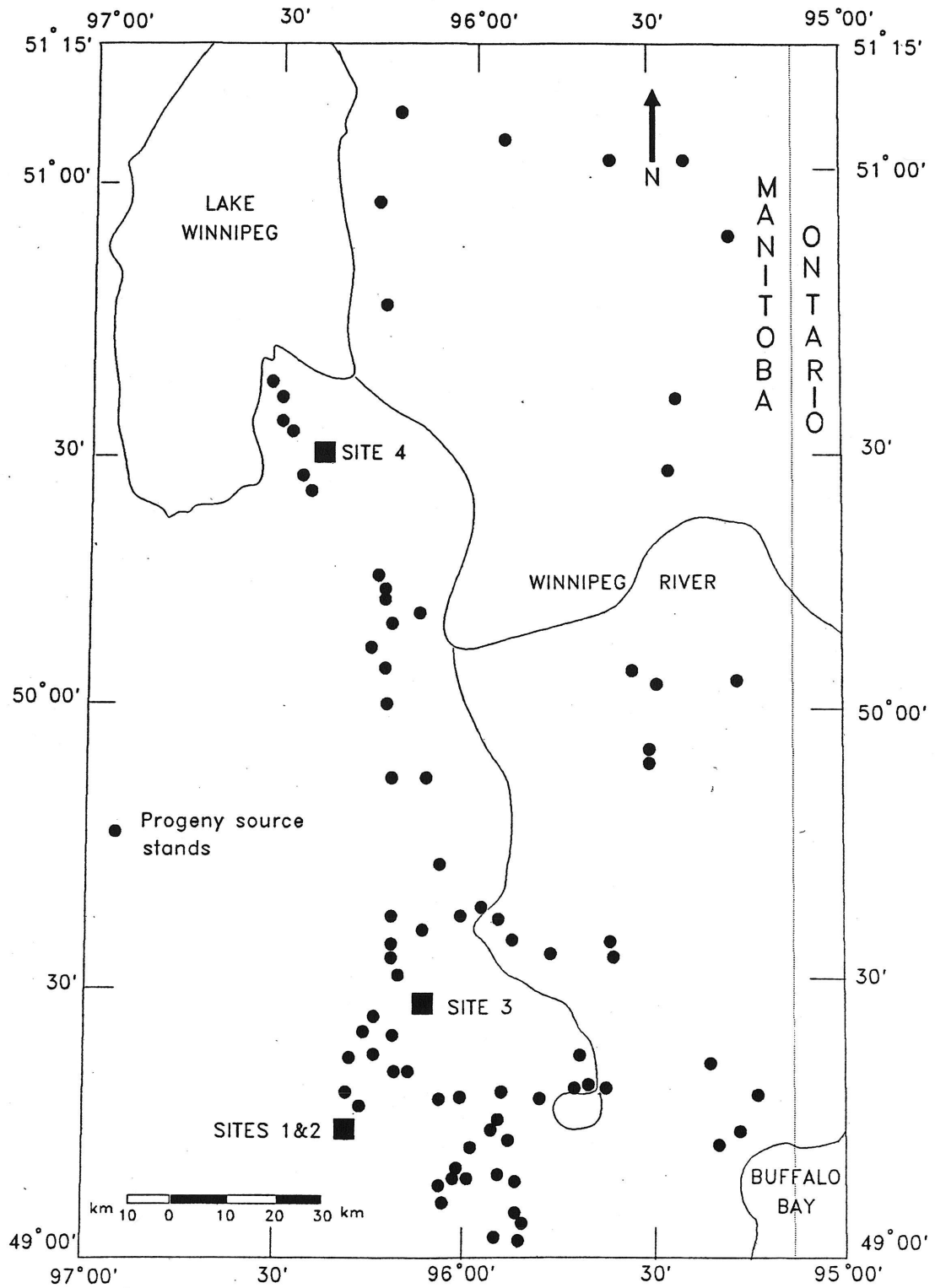


Figure 1. Location of planting sites and source stands in Manitoba, Canada.

per family ranged from 19 to 31. Only the proportion of trees in each family with at least one gall was used in this report.

### **Greenhouse Inoculation**

Seedlings used for the inoculation experiments were reared from seed produced by controlled matings between trees grown in the family test plantations. Forty open-pollinated families found to be genetically superior for growth and straightness were grouped into 20 pairs. More than one tree from each selected family was used in the mating to ensure adequate seed yield. Consequently, individuals from the same mating are related as first cousins rather than as full-sibs, and the seedlots are referred to as first-cousin families.

The main purpose of the matings was to produce stock for a seed orchard. Seed that was surplus to the requirements for the seed orchard was used for this study. This seed yielded from 6 to 129 seedlings per mating, with a total of 724 seedlings.

Seedlings of the 20 first-cousin families were reared in the Northern Forestry Centre greenhouse in Spencer-Lemaire "Five" Roottrainers, having a cavity volume of 55 cm<sup>3</sup>, for 7 weeks prior to inoculation. A mixture of spores collected at several locations in central Manitoba was used for inoculation. Seedlings were sprayed with distilled water using an atomizer, then dry spores were applied to elongating epicotyl tissue with a soft paintbrush. Trays of inoculated seedlings were then incubated under a polyethylene sheet for several days. One month after inoculation the seedlings were transplanted into 4-L pots and were kept in the greenhouse under growth-promoting conditions through the observation period.

Seedlings were scored for visible reaction to inoculation in January (7 months after inoculation) and in May 1989 (11 months after inoculation). The rating scale, ranging from 0 for no symptoms to 5 for a complete gall, is illustrated in Figures 2 and 3. Mean score was calculated for each first-cousin family.

## **RESULTS**

### **Field Survey**

Percentage of trees in a family with at least one gall ranged from 0 to 79, with a mean of 25%, a standard deviation among families of 14%, and the standard error of a family mean of 1%. When family infection rates were grouped into frequency classes with an interval of 10%, the largest number of families was in the 21-30% class, and the frequency distribution was skewed to the right (Fig. 4).

### **Greenhouse Inoculation**

Family mean scores in January ranged from 0.23 to 4.42, with a mean of 1.95, standard deviation among families of 1.08, and standard error of family mean of 0.24. Between the January and May assessments, some families changed in reaction scores within the 1.1-4.0 range, but there were no shifts from below 1.1 to above 4.0, indicating that satisfactory evaluation of resistance can be done 7 months after inoculation (Fig. 5).

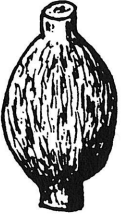





5		<p><b>Complete gall, often with smooth surface</b></p>
4		<p><b>Partial gall, often with rough bark and necrotic canker</b></p>
3		<p><b>Some swelling with rough bark and open necrotic canker</b></p>
2		<p><b>Definite canker but no swelling</b></p>
1		<p><b>Visible discoloration or definite indication of infection such as acute bending of stem</b></p>
0		<p><b>No symptom</b></p>

Figure 2. Evaluation criteria for jack pine seedlings for western gall rust.

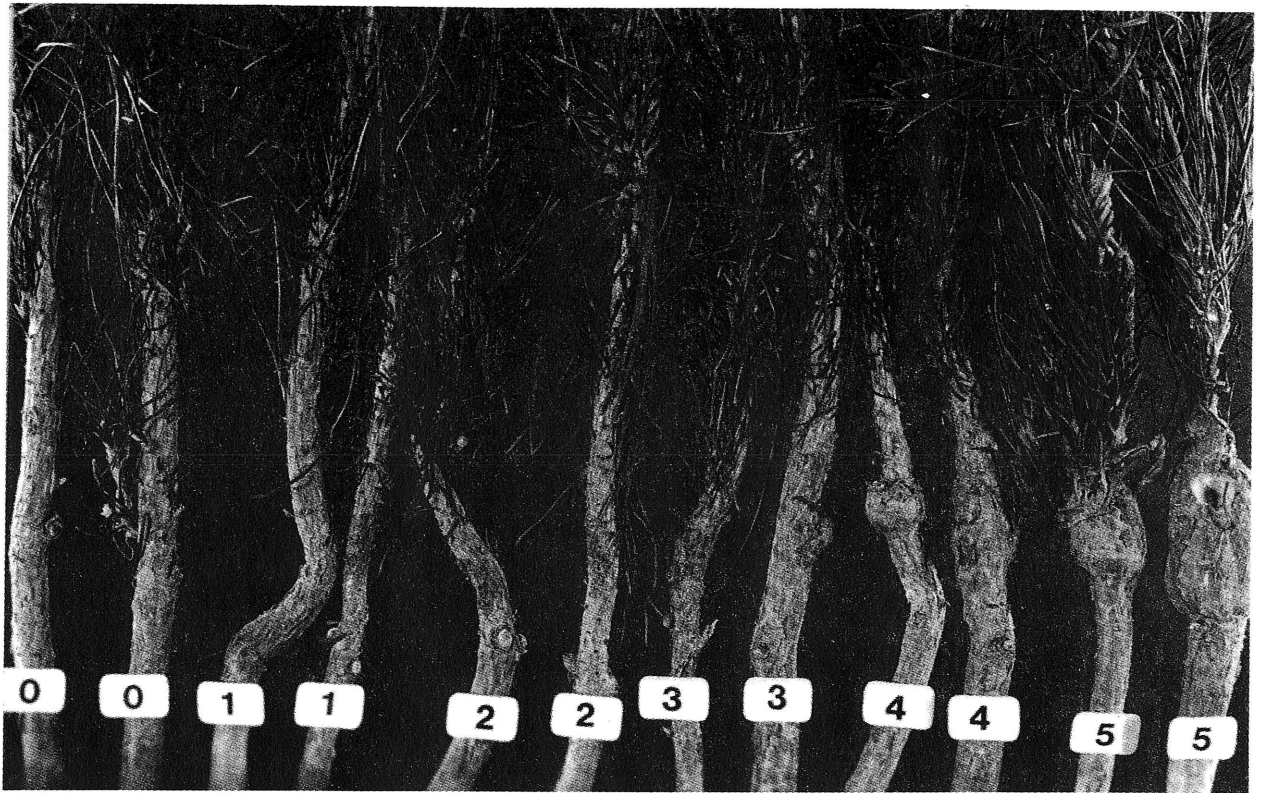


Figure 3. Jack pine seedlings after 7 months of inoculation, with evaluation numbers.

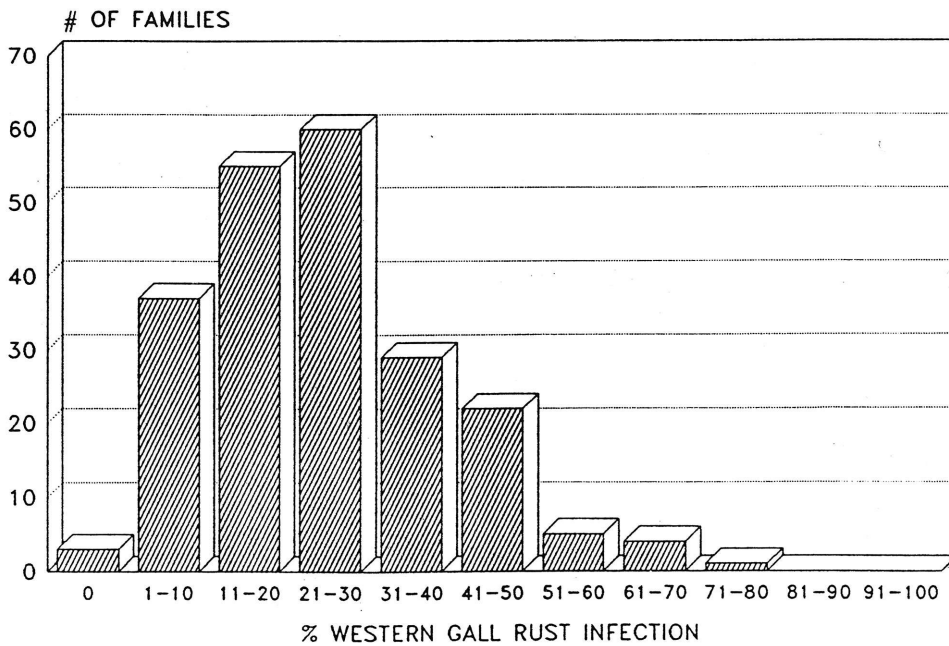
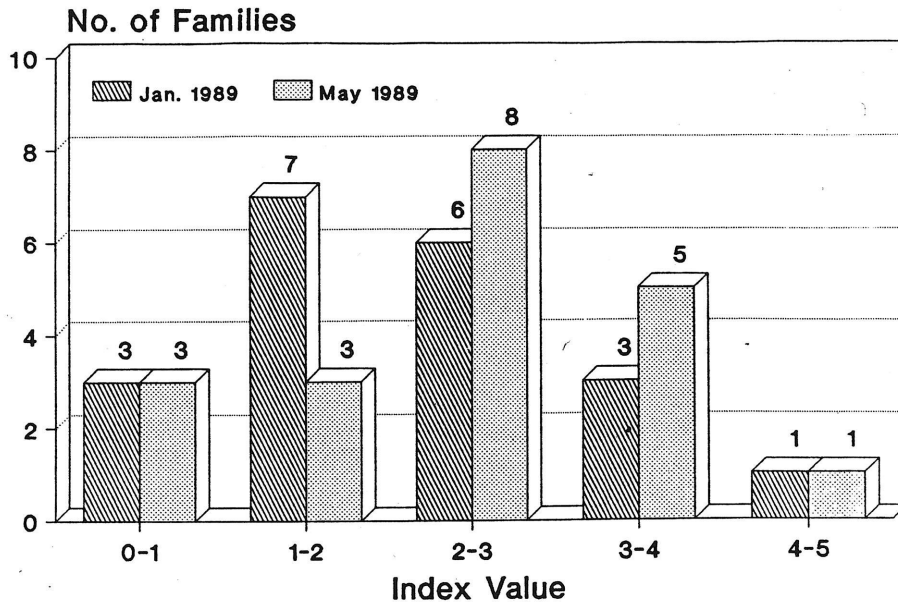


Figure 4. Incidence of western gall rust for the 216 families of 17-year-old jack pine.



**Figure 5. Shift of infection index values between evaluations after 7 months (January 1989) and 11 months (May 1989).**

### CONCLUSION

Field survey results from the family test plantations and results of greenhouse inoculation of first-cousin families show a wide range of family means, indicating the possibility of substantial genetic variation and the apparent effectiveness of assessment procedures used in these trials.

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