CLONAL-ROW AND RANDOM SEED ORCHARD DESIGNS: COMPARISON OF MATING PATTERN AND SEED YIELD

Yousry A. El-Kassaby

Director, Applied Forest Research, Pacific Forest Products Limited, Saanich Forestry Centre, Saanichton, B.C., V8M 1K1, Canada and Professor, Department of Forest Sciences, Faculty of Forestry, The University of British Columbia, Vancouver, B.C. V6T 1Z4, Canada

Abstract: Research on first generation seed orchards' genetics revealed that most if not all were efficient in seed production, however, they often did not fulfil the assumptions required for attaining maximum genetic efficiency (El-Kassaby 1989). The replacement of first-generation seed orchards by second- and/or advanced generations is expected to be associated with appreciable increase in the genetic worth of seed crops. This replacement requires consideration of alternative seed orchard designs that allow for maximizing the genetic worth of future seed crops as well as ease of management. Clonal-row seed orchard design has been advocated by Greenwood (1983) as an alternative that should be given serious consideration. Evaluation of this seed orchard design was only restricted to seed yield (Bramlett and Bridgwater 1987). Genetic evaluation of this type of seed orchard design is imperative due to the non-random of placement of clonal ramets in the orchard grid.

This paper evaluates and compares the mating pattern (selfing rate and level of correlated matings) and seed yield between clonal-row and the traditional random design in a western hemlock (Tsuga heterophylla (Raf.) Sarg.) seed orchard. A western hemlock (Hw) seed orchard was selected for this study for the following reasons: 1) the species has: a- wide reproductive phenology differences among its clones (i.e., the chance of selfing and correlated mating increase), b- unique pollination biology that is characterized by the presence of true pollen competition (i.e., increased chance of success of unrelated pollen) and long receptivity period (Colangeli and Owens 1989, 1990), 2) tree height is kept at a maximum of 3m, thus facilitating pollen management, 3) all Hw orchards rely on supplemental-mass-pollination (SMP) as a standard pollen management practice, and 4) pollen contamination is extremely low, thus seed yield and mating pattern results do not suffer from confounding factors.

This study included: 1) reproductive phenology survey to determine the extent of the pollination season, 2) controlled selfing trial to determine clonal propensity to selfing, 3) comparison of seed yield, and 4) determination of selfing and correlated selfing rate using allozyme markers.

The results are summarized as follows:

1) Reproductive phenology : reproductive phenology survey of the entire orchard (i.e., 100% sampling) indicated that the pollination season is typical to that of other conifers studied (El-Kassaby 1992). It is characterized by the presence of early, medium, and late reproductively active clones and covered a period of 22 days. This extended pollination season is expected to produce a continuum of temporally isolated sub-breeding populations over time, thus increasing the chance of inbreeding and restricting the number of available

mates at any specific time. This could be further accentuated by the short duration of maximum pollen receptivity and shedding (Colangeli and Owens 1988).

2) Selling trial: a total of 25 clones were self-pollinated and produced an overall selfing rate, as determined by the percent of filled seed, of 3.4% (SD= 6.16%). However, it should be emphasized that few clones showed higher propensity for selfing with percent of filled seed ranging from 8 to 29% . Controlled selling, as an exploratory procedure for this seed orchard design, is recommended for identifying clones with high selfing rate. These clones should be targeted for SMP application.

3) Seed yield: seed yield from a random sample of 45 seed-cones from each of 66 (clonal-row) and 56 (random) trees was determined. The number of filled seeds per cone was determined (# of filled seeds/# of seed-cones sampled). Seed-cone size within both orchard designs showed large differences, thus seed-cone size was included in the analysis as a covariate. Seed yield analysis produced no significant difference between the two seed orchard designs. Thus, seed orchard design has no effect on seed yield.

4) mating pattern: mating pattern was determined from a sample of approximately 750 seeds representing 20 clones per orchard design. Outcrossing rate estimates were 0.899 and 0.970 for the clonal-row and random seed orchards, respectively. These estimates are significant from complete outcrossing (i.e., $t = 1.0$) and are significantly different between the clonal-row and random seed orchard, indicating that selfing is higher in the former than the latter. As expected, estimates of correlated mating substantially varied between the two seed orchard designs with 35 and 8% for the clonal-row and random seed orchards, respectively. Results from the mating pattern have demonstrated the presence of genetic quality differences of seed produced from the two seed orchard designs.

The present study demonstrated that both orchard designs produced similar seed yield, however, the genetic quality of the produced seed differed. If clonal-row seed orchard design will be considered for second- and/or advanced generation seed orchard, then effective pollen management such as SMP is required to reduce the selfing rate as well as correlated matings.

References:

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