FACTORS AFFECTING SEED ORCHARD CROP RATINGS

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Abstract. Many factors influence the genetic value of seeds produced in conifer seed orchards. Orchard design factors such as number of genotypes, coancestry among parents, clonal (family) size and spatial arrangement coupled with reproductive phenology and output traits and pollen contamination must be considered when preparing estimates of crop worth. Management practices such as supplemental mass pollination, bloom delay, and selective flower induction as well as selective cone harvesting can be used to adjust the genetic contributions of individual genotypes and to mitigate problems arising from non-orchard pollen. The general genetic value of the population (orchard or seed crop) can be summarized by estimating the average genetic breeding value weighted by the gametic contributions and by the effective population size. Changes in these estimators can be used as indices of the efficacy of management practices and orchard design.

Evaluation of conifer seed orchards on the basis of genetic value is essential for determining the degree of success that has been attained in a breeding program and the performance to be expected from the reforested lands. Seed orchard performance is often rated by the level of annual cone production and the orchards' genetic values are usually listed as average breeding values calculated from progeny test data. Actual genetic value or realized genetic gain potential can be vastly different than progeny test averages and are influenced by factors that are both internal and external to the seed orchard.

An orchard's genetic base is established when trees are chosen and arranged in the orchard. Clonal and seedling orchards have different genetic properties, potentials, and problems.

Clonal and full-sib seedling orchards' breeding values are similar to the clonal value or the mid-point of both full-sib family parent breeding values, respectively. On the other hand, half-sib or wind-pollinated families breeding values represent only 50% of the parents' breeding values.

As indicated earlier, the basic genetic properties of any orchard are defined

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by the genetic values of the included parent trees. Tested orchards can be rated from progeny test data in terms of maximum potential given the degree of additive genetic variance among the selections. Test conditions must be representative of operational conditions encountered in the reforestation program. That is, the reliability of the progeny test data to predict future forest potentials lies in the rigor and scope of the testing program. Yield trials are recommended to verify projections based on progeny tests. Orchard seed that is destined for environments excluded from the testing program may perform in unexpected ways. Untested orchards can only be judged from the selection criteria and purely phenotypic information.

Advancing generations of most breeding programs will provide increased information about the genetic value of the trees. Progeny selected from tested, genetically superior families will have parental and grandparental performance documentation. However, information about the genetic composition of any given wind-pollinated seed crop is still incomplete. Gamete contributions to the seed crop are the only reliable estimator of the genetic composition of the seeds and are a necessary ingredient in the calculation of the orchard's genetic value and the seeds' potential (Askew 1989, El-Kassaby and Askew 1991).

Estimating the genetic worth of advanced generation orchards is dependent on the breeding and selection strategy. Advanced orchards established from forward, backward, or forward and backward selections are analogous to tested and untested orchards (i.e. forward selections require further testing).

EXTERNAL FACTORS

Ideally, orchards should be isolated from all trees of the same species to protect the integrity of the pollen cloud. This is rarely the case and isolation or dilution zones are used to minimize the problem of non-orchard pollen contamination (Squillace 1967). However, high levels of non-orchard pollen are often found in the seeds despite the use of dilution zones (Squillace and Long 1981, Friedman and Adams 1985, El-Kassaby and Ritland 1986a, Wheeler and Jech 1986). Contaminating pollen will confound the estimates of genetic value and may eliminate the gain obtained by the breeding program. Stands of trees proximate to the orchard may produce great amounts of pollen and may dominate the pollen cloud. In orchards where reproductive phenology is not synchronized between pollen shedding and flower receptivity (El-Kassaby and Reynolds 1990) or in young orchards, the contamination problem may be overwhelming.

Orchards that are part of a multi-orchard complex may receive contaminating pollen from adjacent orchards of high breeding value. However serious adaptation problems may occur if the orchards represent distinct breeding populations (Friedman and Adams 1985, Wheeler and Jech 1986).

MANAGEMENT PRACTICES

Bloom Delay

Manipulation of reproductive phenology development of seed orchard trees by overhead cooling has proven to be effective in reducing pollen contamination in Douglas-fir seed orchards (El-Kassaby and Ritland 1986a, El-Kassaby and Davidson 1990). Cooling from water spray and evaporation causes floral bud burst to be delayed for as long as two weeks after local pollen release, hence avoiding pollen introgression from outside sources (Silen and Keane 1969, Fashler and Devitt 1980, Fashler and El-Kassaby 1987) . Reproductive bud development progresses at a faster pace after the cessation of the cooling treatment and the length of the pollination season is substantially shortened, thus improving panmixis (El-Kassaby et al 1984, Fashler and El-Kassaby 1987). The effectiveness of this method on other coniferous trees has not yet been determined.

Supplemental Mass Pollination

Supplemental mass pollination (SMP) used to enhance the genetic value of orchard seeds by emphasizing specific parents is designed to impact the genetic value of the seed in a positive manner. Effective use of SMP implies the orchard manager has a working knowledge of the reproductive phenology of the orchard.

Timing of flowering and degree of flower production are necessary ingredients for formulating a SMP plan. Application of SMP pollen must be in coordination with the flower receptivity of the target trees and will only improve the genetic value if the supplemented pollen genetic value is significantly higher than the ambient pollen cloud value at the time of application (Askew 1991).

The number of pollen sources to be included in the SMP mix will affect the genetic value of the pollen and the seed produced. Pollen mixes can be constituted to skew the pollen distribution in the toward the highest genetic value parents or they can be constituted by mixing together pollens that are poorly represented in the ambient cloud at the time of orchard receptivity due to asynchrony or poor production. Mixing of the lesser representatives may increase the genetic value of the seed and will increase the effective population size of the seed crop and push the crop closer towards uniform mating probabilities.

Effectiveness of SMP also depends on the viability of the pollen which may decline with age (Webber 1987). Viability tests should be used to allow for modification of the mix ratios and application rates. Viability estimates are also important for calculating the expected average genetic value. The number of applications will also affect the SMP success rate but the economics of SMP must be considered (Askew 1991). Orchards with widely varying phenologies will require more visits to reach the same end as a fairly uniform orchard. SMP success rate should be determined so the genetic value of treated seed crops should reflect the expected improvement.

Insects

Insect predation on large portions of the seed crop has been reported (Belcher and DeBarr 1975). Seed and cone losses may be particularly serious if the predation is not proportional to cone production of the individual clones or families (Askew, et al 1985). SMP work, spatial arrangement, and other management practices to regulate the gamete contribution proportions may be severely impacted if insect predation is non-random or skewed toward a few clones.

Harvesting

Harvesting systems can enhance or dilute the potential genetic gain inherent in the seed crop. Bulk harvests where all cones from all clones are pooled will produce an average valued seed lot. Gamete contributions of individual clones can be calculated from estimates of seed and pollen parent gamete contributions.

Segregating the seed crop by harvesting individual clones and not bulking the seeds allows for calculation of the genetic potential for single mother tree crops in which 1 parent contributes exactly 50% of the gametes. This minimizes the error rate in calculation of the gain (El-Kassaby and Thomson 1990). Matching of seed parents to specific site conditions based on progeny test information can enhance the level of realized gain.

SMP that targets specific clones rather than orchard wide enhancement lends more support to clonal harvests. Genetic gain calculations based on known seed and pollen parents has minimal error.

Contaminating Pollen

The degree of genetic loss inflicted by non-orchard pollen domination of the seed crop is, of course, determined by the genetic value of the contaminating pollen. Orchards located near stands with good phenotypes may cause less genetic loss than those near poor quality, high graded stands. In either case, some form of testing program is warranted to determine the degree of contamination that can be expected. Pollen trapping by sampling the ambient cloud on adhesive covered glass slides can give a fair index of the gross quantity of non-orchard pollen that is entering the orchard (Griffin 1980, Wheeler and Jech 1986). This system cannot establish the genotypes of the pollen or its genetic origin. Isozyme analysis of seeds collected from the surrounding stands can be used to determine the genotypes of the contaminating trees and refine the contamination figures (Smith and Adams 1983, El-Kassaby and Ritland 1986 a&b).

Orchards that are parts of orchard complexes pose another situation. In these cases, the contaminating pollen may originate from other orchards and be of equal or lesser quality to the desired pollen. Monitoring all orchards in the complex will provide some data about the degree of inter-orchard mating which can be used in the calculation of the gain potential (Friedman and Adams 1985).

Effective Population Size

Monitoring and evaluation of the sources and quantities of pollen relate to a common statistical estimate: effective population size. Small orchards with few potential parents will produce seed lots with narrow genetic bases. Risk factors for widespread use are fairly high relative to larger orchards. However, large orchards with a few parents that dominate the seed crop or the pollen cloud due to fecundity or phenology may reduce the effective population size to that of a small orchard. Contaminating pollen will tend to increase the effective population size by adding more parents to the pool even though the genetic qualities may be suspect. Reproductive phenology studies and genetic gain calculations should include consideration of the effective population size problem and management strategies should be adopted to provide adequate numbers of parent in the gamete pool. These include introduction of pollen (i.e. SMP) from parents that are not in the orchard.

Coancestry

Advanced generation orchards produced from populations generated by controlled mating designs will eventually develop some degree of relatedness among the selections. The degree of relatedness will be determined by the size of the mating design, the selection intensity and the level of avoidance employed during the selection process (Askew and Burrows 1983). Significant levels of coancestry may result in several inbreeding problems in the seed crops (Askew and Burrows 1990, Woods and Heaman 1989). Reduced seed sets have been documented in related matings and inbreeding depression in height growth or disease resistance may be a problem in some cases. Efforts to subline populations to avoid coancestry may be successful in the short term but eventually the full coancestry problem will be realized as generations continue to advance.

CONCLUSION

Relative values of seed crops are determined by many factors. Some factors are within our control and can be manipulated to attain predetermined goals. Other factors are functions of nature and require monitoring to accommodate their impacts. Estimation of orchard seed values and effects of management practices must utilize all information that is reasonably obtainable if the true value of a breeding program is to be determined.

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