Genetic Relationships

1. Abdel-Gadir, A.Y., R.L. Krahmer and M.D. McKimmy. 1993. Relationships between intra-ring variables in mature Douglas-fir trees from provenance plantations. Wood-and-Fiber-Science 25(2): 182-191.

Keywords: genetic tree improvement
wood quality
genetic relationships

Abstract: Relationships among a variety of densitometric characteristics of juvenile and mature wood from 360 trees growing in two plantations of Douglas fir (Pseudotsuga menziesii) in Oregon and Washington were examined. Variables included earlywood density (EWD) and width (EWW); latewood density (LWD), width (LWW), and proportion (LWP); average ring density (RD); and total ring width (RW). The RD components (EWD and LWD) had strong phenotypic and genetic correlations with their respective RW components (EWW and LWW). However, no phenotypic correlation existed between average RD and total RW, and genotypic correlation was weak. The relation between wood density and radial growth varied by plantation and genotype. It was shown that the potential exists for improving wood density in juvenile and mature wood by selection, with only a minor effect on radial growth. Selection during the juvenile period to improve mature wood quality would be feasible for RD, EWD, LWW, and LWP. Further, selection to improve juvenile RW would not result in reduced wood density during maturity.

OSU Link
Non-OSU Link

2. Adams, W.T., S.N. Aitken, D.G. Joyce, G.T. Howe and J. Vargas-Hernandez. 2001. Evaluating efficacy of early testing for stem growth in coastal Douglas-fir. Silvae-Genetica 50(3/4): 167-175.

Keywords: genetic tree improvement
nursery operations
growth
genetic relationships

Abstract: In a test to evaluate the ability to predict stem growth of families in the field from nursery performance (i.e., early testing), 67 open-pollinated families and 66 full-sib families of coastal Douglas-fir (Pseudotsuga menziesii var. menziesii) were sown in two nursery conditions, each replicated as separate experiments: two bareroot nursery trials established in successive years in the same nursery, and two container-sown greenhouse trials sown in different greenhouses in the same year. First year heights in the seedling trials were compared to mean stem volumes of the same open-pollinated families in eight 15-year-old field progeny tests and the same full-sib families in eleven 12-year-old tests. Family mean nursery-field correlations (rxy) were similar for all four seedling trials for both open-pollinated (OP) and full-sib (FS) families, and generally ranged between 0.30 and 0.40. Although low, it is shown that nursery-field correlations of this magnitude can be quite useful in tree improvement programmes. For example, based on the data in this study, it is estimated that a single stage of family selection for first year seedling height would be about 50% as effective in improving 15-year volume as direct selection for this trait in field tests. Early testing, however, is probably of more practical significance as a tool for culling families prior to out-planting field tests in two-stage selection

schemes. It is estimated that 25% of the OP families in this study could have been culled in an early test (first stage selection), with gain in 15-year volume after subsequent field testing and selection of the remaining families (second stage selection) being nearly the same as if all families had been field tested. Thus, early testing is an effective tool for reducing the size and cost of field progeny tests without sacrificing genetic gain.

OSU Link
Non-OSU Link

3. Adams, W.T., J. Zuo, J.Y. Shimizu, J.C. Tappeiner and J.H. Zuo. 1998. Impact of alternative regeneration methods on genetic diversity in coastal Douglas-fir. Forest Science 44:390-396.

Keywords: planting operations
genetic relationships

Abstract: Genetic markers (17 allozyme loci) were used to study the genetic implications of natural and artificial regeneration following 3 regeneration methods (group selection, shelterwood, and clearcut) in coastal Douglas fir (Pseudotsuga menziesii var. menziesii) forests in the Willamette Valley, Oregon, USA. In general, harvesting followed by either natural or artificial regeneration resulted in offspring populations which were very similar to those in the previous generation. The removal of the smallest trees to form shelterwoods resulted in the removal of rare, presumably deleterious, alleles. Fewer alleles per locus were observed among residual trees (2.76) and natural regeneration (2.75) than were found in uncut (control) stands (2.86). The shelterwood regime appeared quite compatible with gene conservation, and it was considered that it was best to leave parent trees of a range of sizes to act as gene conservation reserves, in order to maximize the number of alleles (regardless of current adaptive value) in naturally regenerated offspring. Seedling stocks used for artificial regeneration in clearcut, shelterwood, and group selection stands (7 total) had significantly greater levels of genetic diversity, on average, than natural regenerated seedlings.

OSU Link
Non-OSU Link

4. Aitken, S.N. and W.T. Adams. 1996. Genetics of fall and winter cold hardiness of coastal Douglas-fir in Oregon. Canadian-Journal-of-Forest-Research 26(10): 1828-1837.

Keywords: genetic tree improvement
tree/stand protection
tree/stand health
tree physiology
genetic relationships

Abstract: Genetic variation in autumn cold hardiness was studied in two western Oregon breeding populations of coastal Douglas fir (Pseudotsuga menziesii var. menziesii), one on the west slope of the Cascade Mountains and the other in the Coastal Range. On six sampling dates (September, October and November 1992 and January, September and October 1993), shoot cuttings from 40 open-pollinated families in each of two progeny test sites for each breeding zone were subject to artificial freezing at two test temperatures. Damage in each shoot was recorded as visible injury to needle, stem

and bud tissue separately. Considerable family variation was found for cold injury scores in all tissues in early to mid autumn, but differences were often smaller or nonsignificant in late autumn and midwinter. Individual heritability estimates for needle cold injury were low (<0.40) and generally decreased in late autumn and midwinter. Family rankings for autumn cold hardiness, however, are expected to be relatively consistent over sites and years, although needles appear to display more family-by-site interaction than stems or buds. Genetic correlations between tissues in cold injury varied considerably and were sometimes weak, indicating that the evaluation of a single tissue is probably not adequate for assessing overall cold hardiness of genotypes. Autumn and winter cold hardiness seem to be largely under separate genetic control since genetic correlations between hardiness at these two stages were weak. This study confirms earlier results in Washington breeding populations and shows that coastal Douglas fir families can be effectively ranked for autumn cold hardiness by conducting artificial freeze tests on cut shoots in mid-autumn (October) and scoring damage to stems and at least one other tissue.

OSU Link
Non-OSU Link

5. Aitken, S.N. and W.T. Adams. 1997. Spring cold hardiness under strong genetic control in Oregon populations of Pseudotsuga menziesii var. menziesii. Canadian-Journal-of-Forest-Research 27(11): 1773-1780.

Keywords: genetic tree improvement
tree/stand protection
tree/stand health
tree phenology
tree physiology
genetic relationships

Abstract: Genetic variation in spring cold hardiness of shoots prior to bud break was studied in two Oregon breeding populations of Pseudotsuga menziesii var. menziesii, one on the west slope of the Cascade Mountains and the other in the Coast Range. In March and April 1993, and April 1994, shoot cuttings from 40 open-pollinated families in each of two progeny test sites in each breeding zone were subjected to artificial freezing. Visible cold damage to needle, stem, and bud tissues was recorded. Date of bud burst (all sites), and injury resulting from a 1992 natural frost event (one site), were also recorded. Spring cold injury varied widely among families. Individual heritabilities for spring cold injury scores averaged 0.76 in the Coastal zone and 0.42 in the Cascade zone. Genetic correlations among tissues, sites, sampling dates, and years, and between April cold injury and date of bud burst were high, in most cases over 0.80. Correlations were also strong between natural frost damage in 1992 and artificial cold injury scores in 1993. Artificial freeze testing stem tissues of cut shoots sampled in April from a single test site should effectively rank families in this region for spring cold hardiness.

OSU Link
Non-OSU Link

6. Aitken, S.N., W.T. Adams, N. Schermann and L.H. Fuchigami. 1996. Family variation for fall cold hardiness in two Washington populations of coastal Douglas-fir (Pseudotsuga menziesii var. menziesii (Mirb.) Franco). Forest-Ecology-and-Management 80(1/3): 187-195.

Keywords: genetic tree improvement
tree/stand protection
tree/stand health
tree physiology
tree phenology
genetic relationships

Abstract: In order to assess the genetics of autumn (fall) cold hardiness in coastal Douglas fir (Pseudotsuga menziesii var. menziesii), shoot cuttings were collected in October from saplings (9-year-old trees) of open-pollinated families in two progeny tests in each of two breeding zones in Washington, one in the Coast range (80 families) and one on the west slope of the Cascade Mountains (89 families). Samples from over 5500 trees were subjected to artificial freezing and visually evaluated for needle, stem and bud tissue injury. The extent to which cold injury is genetically related to tree height and shoot phenology (timing of bud burst and bud set) was also evaluated. Significant family variation was found for all cold hardiness traits; however, individual heritability estimates were relatively low (ranging from 0.09 to 0.22). Significant family-by-test site interaction was detected for needle injury in the Cascade breeding zone, but not in the coastal zone. Genetic correlations (rA) among needle, stem and bud tissues for cold damage were weak (0.16<less or =>rA<less or =>0.58) indicating that genes controlling autumn cold hardening are somewhat different for different tissues. Timing of bud burst and bud set were only weakly correlated with cold injury (rA<less or =>0.49). Thus, bud phenology is a poor predictor of autumn cold hardiness in this species. There was no consistent relationship between tree height and cold injury in the coastal zone. In the Cascade zone, taller trees appeared to be more susceptible to cold injury, but the association was weak (mean rA=0.38, range 0.20-0.72).

OSU Link
Non-OSU Link

7. Anekonda, T.S., M.C. Lomas, W.T. Adams, K.L. Kavanagh and S.N. Aitken. 2002. Genetic variation in drought hardiness of coastal Douglas-fir seedlings from British Columbia. Canadian-Journal-of-Forest-Research 32(10): 1701-1716.

Keywords: genetic tree improvement
tree/stand protection
growth
tree/stand health
genetic relationships
tree physiology

Abstract: Genetic variation in drought hardiness traits and their genetic correlations with growth potential and recovery traits were investigated in 39 full-sib families of coastal Douglas-fir (Pseudotsuga menziesii var. menziesii) from southwestern British Columbia, Canada. Seedlings of these families were grown in raised nursery beds and subjected to three moisture regimes each in the second (well-watered or control, mild, and moderate drought) and third (control, severe drought, and recovery from second-year moderate drought) seasons. Traits assessed included drought hardiness (foliage damage, cavitation of xylem tracheids, xylem hydraulic conductivity, and height and diameter growth increment) in the drought treatments, growth potential (total height and diameter) in the control treatment, and height and diameter growth increments in the recovery treatment. Xylem cavitation in the growth ring produced in a particular year was nearly three times greater under the moderate drought and four times greater under the severe drought than in the control treatment. Xylem hydraulic conductivity of seedlings in the severe drought treatment was 40% lower than conductivity of seedlings under the control treatment. Mean foliage damage in seedlings subjected to severe drought (third season) was much greater (33%) than in seedlings subjected to mild or moderate drought (second season). Families differed significantly in most drought hardiness traits, with individual tree heritabilities averaging 0.19. Thus, much potential exists for identifying drought-hardy families at the seedling stage and using this information for deployment or breeding purposes. In addition, most hardiness traits were strongly intercorrelated (genetic correlations often exceeded |0.80|) indicating that these traits are controlled largely by the same set of genes and that selection for hardiness based on one trait will increase hardiness as reflected in the other traits as well. Genetic correlations were only moderate (0.49) between hardiness traits measured in different years, perhaps due to the large difference in severity of the drought applied in the two seasons. Although injury to seedlings, as reflected in foliage damage and xylem cavitation, was relatively low under the moderate drought of the second season, it did result in reduced growth increment the following (recovery) year. Growth potential under favourable moisture regimes was nearly uncorrelated with drought hardiness, suggesting that drought hardiness could be improved in this southwestern British Columbia breeding population without negatively impacting growth potential in favourable moisture conditions.

OSU Link
Non-OSU Link

8. Barclay, H.J. and Y.A. El-Kassaby. 1988. Selection for cone production in Douglas-fir adversely affects growth. *In* Proceedings: 10th North American Forest Biology Workshop: 'Physiology and genetics of reforestation', University of British Columbia, Vancouver, British Columbia, July 10-22, 1988. Eds. J. Worrall, J. Loo-Dinkins and D.P. Lester. pp. 149-151.

Keywords: genetic tree improvement
genetic relationships
growth
reproduction

Abstract: Cone production and radial growth increment were studied for 8 years in a Douglas fir (Pseudotsuga menziesii) seed orchard on Vancouver Island, British Columbia, in 365 trees representing 29 open-pollinated (half-sib) families. Genetic correlations for the two traits were compared for each of the 8 years. Six of the correlations were significantly negative, while the remaining two were significantly positive. The predominantly negative correlation between cone production and growth indicates that selection for one of these two characters will effectively select against the other. The practice of selecting for high cone-producing trees in seed orchards may also be expected to yield slower-growing trees.

Non-OSU Link

9. Birot, Y. and C. Christophe. 1983. Genetic structures and expected genetic gains from multitrait selection in wild populations of Douglas fir and Sitka spruce. I. Genetic variation between and within populations. Silvae-Genetica 32(5/6): 141-151.

Keywords: genetic tree improvement
genetic relationships

growth
tree phenology
tree morphology

Abstract: For Douglas fir, 371 open-pollinated progenies from 26 provenances ranging from N. to S. along the western foothills of the Cascade Mts., Washington, were tested. For Sitka spruce, 292 open-pollinated progenies from 21 provenances ranging from S. British Columbia to middle-Oregon were tested. Observations were made on growth, phenology and form from the nursery stage up to age 12. Classical patterns of geographic variation were observed for both species. Heritability and genetic correlations varied from one provenance to another, especially for Douglas fir, and also changed over time. Sitka spruce showed high additive effects, offering good prospects of future genetic gains. It was concluded that preliminary investigations on genetic parameters were necessary before setting up a breeding strategy.

OSU Link
Non-OSU Link

10. Copes, D.L. and R.A. Sniezko. 1991. The influence of floral bud phenology on the potential mating system of a wind pollinated Douglas-fir orchard. Canadian-Journal-of-Forest-Research 21(6): 813-820.

Keywords: genetic tree improvement
tree phenology
reproduction
genetic relationships

Abstract: Reproductive bud phenology was recorded from 1983 to 1989 in a Douglas fir (Pseudotsuga menziesii) clonal orchard near Monmouth, Oregon. Potential outcross efficiency was calculated for 20 clones from dates of male and female bud opening and pollination mechanism information. Potential outcross efficiency was limited to a maximum of 58% (1983) to 87% (1987). Cool weather before bud opening of the earliest clones delayed and compressed the breeding period and resulted in a greater percentage of trees having synchronous periods of pollen release and receptive seed strobili. Length of breeding season among years averaged 20 days and ranged from 16 to 27 days. Differences in phenology significantly affected the breeding system because the overall breeding period of the orchard clones exceeded the 8-day receptive period of individual clones by two or three times, and often prohibited or limited potential outcrossing between the earliest and latest clones. Outcrossing was greatest in clones with intermediate phenology and least in the earliest clones. The breeding system appears to be an almost continuous series of overlapping breeding subpopulations. Each year's breeding subpopulations were different from those of other years because of (1) large shifts in rank order of bud opening by 10 to 20% of the clones and (2) differences in the length of breeding season. Average temperature during March was linearly associated with time of floral bud opening. Geneticists may be able to use average temperature of the 4-week periods prior to opening of the earliest floral buds as a tool to identify seed crops formed during years with compressed breeding seasons. Such seed crops are potentially more diverse than seed crops produced during years with extended breeding seasons.

OSU Link
Non-OSU Link

11. Copes, D.L. 1999. Breeding graft-compatible Douglas-fir rootstocks (Pseudotsuga menziesii (MIRB.) FRANCO). Silvae-Genetica 48(3/4): 188-193.

Keywords: genetic tree improvement
tree grafting
tree/stand protection
growth
tree phenology
tree/stand health
genetic relationships

Abstract: A study encompassing 24 years was conducted to determine if a breeding programme could produce highly graft-compatible rootstocks for P. menziesii. A total of 27 trees of apparent high graft compatibility were selected and crossed to produce 226 control-pollinated families. Seedlings were grown, field planted and grafted with test scions. Graft unions from field tests were evaluated anatomically for internal symptoms of incompatibility. Average compatibility of progeny from the 226 crosses was 90.6%, compared with 65% in native populations. Breeding values were calculated for each parent by the best linear prediction (BLP) procedure. Average compatibility resulting from crossing among the top 10 parents was estimated by breeding values as 95.4%. Field-test results of progeny from 34 crosses among the 10 most compatible parents showed 96% compatibility. In addition to field-tests for graft compatibility, nursery tests of seedlings from 124 crosses were evaluated for second-year vegetative bud flush and seedling height. It was possible, while maintaining adequately high levels of graft compatibility, to breed both for resistance to spring frost damage and for increased seedling height.

OSU Link
Non-OSU Link

12. Edwards, D.G.W. and Y.A. El-Kassaby. 1995. Douglas-fir genotypic response to seed stratification. Seed-Science-and-Technology 23(3): 771-778.

Keywords: seed orchard management
reproduction
genetic relationships

Abstract: Douglas fir (Pseudotsuga menziesii) responses to stratification duration were studied using wind-pollinated seeds from 15 seed-orchard clones, collected from a low elevation Douglas fir seed orchard in Saanichton, British Columbia, Canada. Germinativeparameters (germination capacity, peak value, germination value, and germination rate and speed) were evaluated in response to four stratification periods (0, 3, 5, and 7 weeks). Significant differences among germinative parameters were observed indicating that the five-week stratification period represents the most appropriate treatment in minimizing variation caused by genetic differences. The results indicate that the International Seed Testing Association (ISTA) rules, which focus only on germination capacity, do not provide an adequate expression of seedlot dormancy, and since the rules are aimed at bulked seedlots, genetic differences, which can be large in heterogeneous forest tree seeds, are hidden. The results also demonstrate that extended stratification not only reduces the time in which seedlings become established, but also reduces seedling-emergence variation among parental lines.

OSU Link
Non-OSU Link

13. El Kassaby, Y.A. 1995. Evaluation of the tree-improvement delivery system: factors affecting genetic potential. Tree Physiology 15:545-550.

Keywords: genetic tree improvement
nursery operations
seed orchard management
genetic relationships
reproduction

Abstract: Possible causes of the genetic erosion that occurs during the fragmented phases of the tree-improvement delivery system (a term used for the domestication process in forest trees) are reviewed. The impacts of intentional and unintentional directional selection during phenotypic selection, seed production (with its associated reproductive-phenology asynchrony, fecundity differential and varying propensity to inbreeding), seed processing and storage, and seedling production are evaluated. Allozyme analysis data were used to compareheterozygosity of first-generation seed orchards of western red cedar (Thuja plicata), Sitka spruce (Picea sitchensis) and Douglas fir (Pseudotsuga menziesii) with that of their corresponding natural populations. In general, genetic diversity and heterozygosity parameters of seed orchards are higher or similar to those observed in their natural-population counterparts. However, parental contribution to the resultant seed orchard seed crops is consistently asymmetrical, and this is a major cause of genetic erosion. In most cases, less than 20% of an orchard's clones contribute 80% of the cone crop, thus reducing the effective population size. Because seed germination of coniferous tree species is under strong maternal genetic control, the combined effects of differences in reproductive output and germination, as well as of management practices (e.g., simulated long-term storage of seed showed that loss of viability during storage is genotype specific), cause unintentional directional selection during seedling production. This review confirms the need for genetic monitoring of each phase of the tree-improvement delivery system, so that practical solutions can be developed to alleviate genetic erosion.

OSU Link
Non-OSU Link

14. El Kassaby, Y.A. 2000. Representation of Douglas-fir and western hemlock families in seedling crops as affected by seed biology and nursery crop management practices. Forest Genetics 7(4): 305-315.

Keywords: genetic tree improvement
nursery operations
genetic relationships
tree/stand health
reproduction

Abstract: The impact of container-nursery management practices on the genetic representation of seedling crops of Douglas fir (Pseudotsuga menziesii) and western hemlock (Tsuga heterophylla) were evaluated. Two experiments, one for each species, were conducted inBritish Columbia, Canada, to determine the cumulative effects of seed-donor variation on germination parameters (percent and

speed) and their interaction with container-nursery practices of thinning and culling on the genetic representation of each seed-donor in the resultant seedling crops. The experimental work was conducted on seedlots that were represented with equal contribution of seeds from 15 seed orchard parents (families). In each experiment, a total of 25 920 seeds were sown in four different arrangements to compare the crop development under single-, two-, and three-seeds per cavity (seeds within cavity were selected randomly among the 15 families) and family blocks (seeds within block belonged to one family). This experimental design allowed determination of inter- and intra-family competition. Within each experiment, a total of 15 015 cavities were used and the identity of every seed within every cavity within each arrangement was maintained throughout the study. Families were compared based on: (1) changes in their rank order from seedling emergence (germination) to post-thinning and post-culling status, and (2) relative performance of each family from seed contribution to seedling production. Changes were observed in both assessments (i.e., rank and relative contribution). Path analysis was used to determine the percent contribution of each factor to seedling production. It was determined that seedling germination, germinant thinning, and seedling culling all affected seedling production, indicating the presence of several consecutive unintentional bottlenecks in the process. Family sowing with culling standards that recognize the growth differences among families in the nursery and single seed sowing after understanding the inter-/intra-family competition are recommended for seedling production to maintain seedling-crop family representation.

OSU Link

15. El Kassaby, Y.A. and A. Benowicz. 2000. Effects of commercial thinning on genetic, plant species and structural diversity in second growth Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) stands. Forest-Genetics 7(3): 193-203.

Keywords: thinning
commercial thinning
genetic relationships

Abstract: The impact of commercial thinning on biodiversity was studied in two Douglas-fir (Pseudotsuga menziesii) plantations, Weeks Lake (WL) and Fairservice Creek (FC) located on southern Vancouver Island, British Columbia, Canada. The age of the stands at thinning was 53 and 70 years for FC and WL, respectively. Other tree species were also present in both sites due to natural regeneration. Biodiversity was evaluated before and after commercial thinning with respect to tree species composition/abundance, tree species genetic diversity assessed by allozyme analysis and stand structural diversity represented by the diameter class (5-cm) distribution. In addition, understorey plant species diversity was monitored in WL and FC for 4 and 5 years following thinning, respectively. Tree species composition changed in both plantations in a similar fashion as the proportion of Douglas-fir increased at the expense of all other tree species. Stand structural diversity was simplified due to the decreased number of trees in small diameter classes. These results were expected since the commercial thinning was conducted to promote the growth of Douglas-fir. Genetic diversity parameters (average number of alleles per locus, percent polymorphic loci and expected heterozygosities) did not differ significantly before and after thinning; however, thinning resulted in a loss of 8 and 7 alleles across species for FC and WL, respectively. Most of the allelic loss occurred in the naturally regenerated species (93%). This allelic loss represents 7 and 6% of the total alleles present in FC and WL, respectively. Thus, only one allele was lost from the crop tree in the FC plantation. Understorey vegetation species richness decreased the year following commercial thinning and then consistently increased over time in both plantations. A total of 17 and 9 new species colonized FC and WL, respectively. One species was replaced in each plantation. In FC, diversity of the understorey plant community based on the Shannon diversity index (H) changed in an increasing linear trend that corresponded to the increase in species richness. On the other hand, H in WL remained stable. Species evenness (H/Hmax) did not change in WL and FC over the course of study except for seasonal fluctuations. Rare species diversity increased over time in both plantations.

OSU Link

16. El Kassaby, Y.A., K. Chaisurisri, D.G.W. Edwards and D.W. Taylor. 1993. Genetic control of germination parameters of Douglas-fir, Sitka spruce, western redcedar, and yellow-cedar and its impact on container nursery production. *In* Dormancy and barriers to germination. Proceedings of an international symposium of IUFRO Project Group P2.04-00 (Seed problems), Pacific Forestry Centre, Victoria, British Columbia, Canada. Ed. D.G.W. Edwards. pp. 37-42.

Keywords: genetic tree improvement
nursery operations
genetic relationships
reproduction

Abstract: The genetic control of germination parameters (germination capacity, peak value, and germination value) in Douglas-fir (Psuedotsuga menziesii (Mirb.) Franco), Sitka spruce (Picea sitchensis (Bong.) Carr.), western redcedar (Thuja plicata Donn), and yellow-cedar (Chamaecyparis nootkatensis (D.Don) Spach.) was studied using wind-pollinated seeds collected from several seed orchards. The extent of genetic control over rhese parameters was assessed through the determination of broad-sense heritabilities. The impact of genetic control of these parameters on the expected genetic diversity of container nursery seedling crops is evaluated.

OSU Link
Non-OSU Link

17. El Kassaby, Y.A. and C. Cook. 1994. Female reproductive energy and reproductive success in a Douglas-fir seed orchard and its impact on genetic diversity. Silvae-Genetica 43(4): 243-246.

Keywords: genetic tree improvement
genetic relationships
reproduction

Abstract: The relationship between reproductive energy and reproductive success and its impact on clonal female gamete contribution were studied in a clonal Pseudotsuga menziesii seed orchard. The effect of among- vs. within-clonal variation on seed-cone crop (energy) and filled-seed yield (success) was determined by partitioning their respective variance components. Clonal gametic representations were expressed using Griffin's [Australian Forest Research (1982) 12, 295-302] parental-balance curves and Crow and Kimura's [An introduction to population genetic theory (1970) New York, USA; Harper and Row Publishers] effective population number. Seed-cone and filled-seed yields produced similar parental-balance curves and female effective population numbers. Although similar parental-balance curves and female effective population numbers were produced, the actual clonal gametic representation differed when the contribution of any set of specific clones were

considered. It was concluded that parental-balance curves and female effective population numbers provide a static description of the genetic representation and do not illustrate the dynamics of clonal reproductive outputs.

OSU Link
Non-OSU Link

18. El Kassaby, Y.A. and R. Davidson. 1990. Impact of crop management practices on the seed crop genetic quality in a Douglas-fir seed orchard. Silvae-Genetica 39(5-6): 230-237.

Keywords: genetic tree improvement
seed orchard management
genetic relationships

Abstract: The impact of 2 crop management practices, supplemental-mass-pollination (SMP) and overhead cooling, on levels of pollen contamination and outcrossing was assessed in a 13-year-old seedling Douglas fir (Pseudotsuga menziesii) seed orchard with the aid of 6allozyme loci. A 2 x 2 factorial arrangement of SMP/no SMP and cooling/no cooling was applied to 4 genetically similar blocks of trees. The 4 treatment combinations used were spatially and temporally isolated by buffer blocks and 9-day reproductive bud phenology delay, respectively. The study led to the following conclusions: (1) no contamination was observed when cooling and/or SMP was used, (2) no inbreeding was observed when cooling and SMP were used concurrently and (3) SMP was effective in reducing consanguineous mating, but not to the level achieved by cooling and SMP combined. In addition, the results obtained from the control block (i.e. no cooling and no SMP) indicated that (1) isolation zones are effective in reducing contamination, and (2) randomization of trees within seed orchard blocks is associated with a high outcrossing rate.

OSU Link
Non-OSU Link

19. El Kassaby, Y.A. and Y.S. Park. 1993. Genetic variation and correlation in growth, biomass, and phenology of Douglas-fir diallel progeny at different spacings. Silvae-Genetica 42(6): 289-297.

Keywords: genetic tree improvement
nursery operations
genetic relationships
growth
carbon allocation
tree phenology

Abstract: Parents of coastal Douglas fir (Pseudotsuga menziesii) selected from natural stands on sites ranging from 0 to 450 m altitude on Vancouver Island and in southeastern British Columbia were crossed and the resulting 104 full-sib families evaluated for 3 years after germination. The full-sib families were produced by a disconnected diallel mating scheme, consisting of 7 sets of 6-parent partial diallels, grown under 2 spacing treatments in a nursery. The objectives of the study were to determine the extent of genetic control of growth traits, biomass distribution and allocation strategies, and vegetative phenology. Spacing had a significant effect on 6 of the 11 traits studied. Significant GCA

variance was found for all traits except 1-year height. Individual tree narrow-sense heritability varied from 0.06 to 0.69 for root dry weight and vegetative phenology, respectively. Spacing x family interaction variance was significant for only 2 traits. Two harvest indices, based on total and above-ground dry weights, were used to assess dry matter allocation strategy and to explore potential usefulness in tree breeding. Both indices had similar heritability estimates and their genetic correlation was high (0.91), indicating that use of an index based on above ground dry weight is a good surrogate for that based on total dry weight. Genetic correlations among growth and biomass traits were generally high, while those correlations with the harvest indices were variable.

OSU Link
Non-OSU Link

20. El Kassaby, Y.A., J. Parkinson and W.J.B. Devitt. 1986. The effect of crown segment on the mating system in a Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) seed orchard. Silvae-Genetica 35(4): 149-155.

Keywords: genetic tree improvement
seed orchard management
genetic relationships
reproduction

Abstract: The mating system in a mixed clonal/seedling Douglas fir seed orchard was studied by analysing 6 polymorphic allozyme loci. Trees were subjected to cooling treatment to retard bud development and compact the pollination period. The outcrossing rates of upper and lower crown levels and northern and southern crown aspects were estimated and compared for clonal and seedling material separately using single and multilocus methods. Single locus estimates of outcrossing rate ranged from 0.645 to 0.999 and were significantly heterogeneous. No significant differences between the multilocus estimates were observed between crown levels or aspects for either the clonal or seedling material. For all comparisons, the unweighted or weighted single locus means were lower than those obtained by themultilocus method, indicating the presence of other types of consanguineous mating in addition to selfing. In general, higher outcrossing rates were observed in the clonal trees than in those derived from seedlings. The implications of these results for seed orchard management are discussed.

OSU Link
Non-OSU Link

21. El Kassaby, Y.A. and K. Ritland. 1986. The relation of outcrossing and contamination to reproductive phenology and supplemental mass pollination in a Douglas-fir seed orchard. Silvae-Genetica 35(5/6): 240-244.

Keywords: genetic tree improvement
seed orchard management
tree phenology
genetic relationships
economics
reproduction

Abstract: A study was made using allozyme markers of outcrossing and contamination rates in relation to reproductive phenology and supplemental mass pollination in a Douglas fir seed orchard in British Columbia, Canada. Supplemental mass pollination was applied only to the intermediate reproductive phenology class, which showed a high outcrossing rate and no contamination. Both early and late reproductive phenology classes showed significant contamination, but the outcrossing rate for the former was significantly higher than for the latter. These results show that interpretation of seed crop genetic quality based on outcrossing alone could be misleading. The rate and source of contamination, reproductive phenology and crop size should also be considered. The practicability and economics of supplemental mass pollination in avoiding both selfing and contamination are discussed. It was concluded that waterspray cooling and/or supplemental mass pollination of early and late reproductive phenology classes in moderate or good cone-crop years would be an effective management practice. The option of aborting small cone crops in mature orchards is also discussed.

OSU Link
Non-OSU Link

22. El Kassaby, Y.A. and A.J. Thomson. 1996. Parental rank changes associated with seed biology and nursery practices in Douglas-fir. Forest Science 42:228-235.

Keywords: genetic tree improvement
nursery operations
reproduction
genetic relationships
tree/stand health

Abstract: The impact of container-nursery management practices on the genetic composition of seedling crops was evaluated in an experimental study in a seed orchard in British Columbia. The study was designed to determine the cumulative effects of: (1) differences in parental reproductive output in bulk seedlots; (2) parental variation in germination parameters (percentage and speed); and (3) the interaction of these parameters with container-nursery practices of thinning and culling, and their effect on the genetic representation of parents in the resultant seedling crops. Results from the experimental study were compared with predictions of a stochastic simulation designed to estimate the consequences of differential parental seed contribution, and seed germination percentage and germination speed on indicators of crop performance. The experimental study was conducted on a Douglas-fir (Pseudotsuga menziesii) bulk seedlot that was representative of the differential seed contributions from 19 seed orchard parents. The nursery study included a total of 42 000 seeds. Seeds were sown at three seeds per cavity. Within the 14 000 cavities used, the identity of every seed was maintained throughout the study. Comparisons of parents were made based on: (1) changes in their rank order from sowing to postthinning and postculling status; and (2) relative performance from seed contribution to seedling production. Changes were observed in both assessments. Path analysis was used to determine the percentage contribution of each factor to seedling production. It was determined that germination, thinning, and culling contributed 66, 20, and 14%, respectively, to seedling production, indicating the presence of three consecutive bottlenecks in the process. Single seed or individual family sowing in the nursery was recommended for seedling production to maintain genetic diversity.

OSU Link
Non-OSU Link

23. Fashler, A.M.K. and Y.A. El-Kassaby. 1987. The effect of water spray cooling treatment on reproductive phenology in a Douglas-fir seed orchard. Silvae-Genetica 36(5-6): 245-249.

Keywords: genetic tree improvement
seed orchard management
tree/stand protection
genetic relationships
reproduction
tree/stand health

Abstract: The effectiveness of reproductive bud cooling on genetic efficiency in a Douglas fir seed orchard in British Columbia, Canada, was tested by comparing the reproductive bud phenology in 3 cooled and 3 uncooled years. The cooling system was found to affect 2 major elements affecting seed orchard genetic efficiency, namely pollen contamination levels and panmictic equilibrium, as well as insect infestation, frost damage, seed yield and management effectiveness. Based on these results, a permanent irrigation/cooling system isrecommended for Douglas fir seed orchards.

OSU Link
Non-OSU Link

24. Jermstad, K.D., D.L. Bassoni, N.C. Wheeler, T.S. Anekonda, S.N. Aitken, W.T. Adams and D.B. Neale. 2001b. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. II. Spring and fall cold-hardiness. Theoretical-and-Applied-Genetics 102(8): 1152-1158.

Keywords: genetic tree improvement
tree/stand protection
genetic relationships
tree physiology
tree phenology

Abstract: Quantitative trait loci (QTLs) affecting fall and spring cold hardiness (cold resistance) were identified in a three-generation outbred pedigree of coastal Douglas-fir (Pseudotsuga meniziesii var. menziesii [Pseudotsuga menziesii]) in a field experiment conducted in Washington and Oregon, USA, during 1996-97. Eleven QTLs controlling fall cold hardiness were detected on four linkage groups, and 15 QTLs controlling spring cold hardiness were detected on four linkage groups. Only one linkage group contained QTLs for both spring and fall cold hardiness, and these QTLs tended to map in close proximity to one another. Several QTLs were associated with hardiness in all three shoot tissues assayed in the spring, supporting previous reports that there is synchronization of plant tissues during de-acclimatization. For fall cold hardiness, co-location of QTLs was not observed for the different tissues assayed, which was consistent with previous reports of less synchronization of hardening in the fall. In several cases, QTLs for spring or fall cold hardiness mapped to the same location as QTLs controlling spring bud flush. QTL estimations, relative magnitudes of heritabilities, and genetic correlations based on clonal data in this single full-sib family, supports conclusions about the genetic control and relationships among cold hardiness traits observed in population samples of Douglas-fir in previous studies.

OSU Link
Non-OSU Link

25. Johnson, G.R. 1997. Site-to-site genetic correlations and their implications on breeding zone size and optimum number of progeny test sites for coastal Douglas-fir. Silvae-Genetica 46(5): 280-285.

Keywords: genetic tree improvement
genetic relationships

Abstract: Type B genetic correlations were used to examine the relationship among geographic differences between sites and their site-to-site genetic (Type B) correlations. Examination of six local breeding zones in Oregon indicated that breeding zones were, for the most part, not too large because few environmental variables were correlated with Type B genetic correlations. The data also were used to examine expected gains from using combinations of sites in selection indices. Even though additional sites always increased the expected genetic gain, the marginal increase was only minimal if 3 or 4 sites were already in the index. The trend was consistent over all 6 breeding zones.

OSU Link
Non-OSU Link

26. Johnson, G.R. 2002. Genetic variation in tolerance of Douglas fir to Swiss needle cast as assessed by symptom expression. Silvae-Genetica 51(2/3): 80-86.

Keywords: genetic tree improvement
tree/stand protection
tree/stand health
growth
genetic relationships

Abstract: The incidence of Swiss needle cast (caused by Phaeocryptopus gaeumannii) on Douglas fir (Pseudotsuga menziesii) has increased significantly in recent years on the Oregon coast. Genetic variation in symptoms of disease infection, as measured by foliage traits, was assessed in two series of progeny trials to determine whether these "crown health" indicators were under genetic control and correlated with tolerance (tolerance being continued growth in the presence of high disease pressure). Foliage traits generally had lowerheritabilities than growth traits and were usually correlated with diameter growth. Foliage traits of crown density and colour appeared to be reasonable indicators of disease tolerance. In the absence of basal area data, assessing crown density and colour can help screen for families that show tolerance to the disease.

OSU Link
Non-OSU Link

27. Johnson, G.R., R.A. Sniezko and N.L. Mandel. 1997. Age trends in Douglas-fir genetic parameters and implications for optimum selection age. Silvae-Genetica 46(6): 349-358.

Keywords: genetic tree improvement
growth

genetic relationships

Abstract: Trends in genetic variation in Douglas fir (Pseudotsuga menziesii) were examined over 51 progeny test sites throughout western Oregon. Narrow sense heritabilities for height and diameter showed an increasing trend to age 25, the oldest age examined. Before age 10, height heritabilities were relatively unstable. Type B site-site genetic correlations increased slowly with age for height and remained relatively stable for diameter. Age-age correlations were used to develop an equation to predict age-age correlations by using the log of the age ratios (LAR). Optimum selection age was calculated for a 60-year rotation by using two measures of efficiency: gain per year and discounted gain. The optimum selection age for height tended to be 2 to 3 years earlier than for diameter. Gain per year was maximized at age 10 for height and age 13 for diameter.

OSU Link
Non-OSU Link

28. Johnson, R. 1998. Breeding design considerations for coastal Douglas-fir. Pacific-Northwest-Research-Station, USDA-Forest-Service General-Technical-Report PNW-GTR-411. iii + 34 p.

Keywords: genetic tree improvement
seed orchard management
genetic relationships

Abstract: The basic principles of designing forest tree breeding programmes are reviewed for Douglas fir (Pseudotsuga menziesii) in the Pacific Northwest (USA). Breeding populations are discussed given current and future breeding zone sizes and seed orchard designs. Seed orchard composition is discussed for potential genetic gain and maintaining genetic diversity in the forest. Mating and field testing designs are described and compared. Recommendations of the Breeding Zone Evaluation and Restructuring Cooperatives Working Group of the Northwest Tree Improvement Cooperative are presented.

OSU Link
Non-OSU Link

29. Kaya, Z. 1992. The effects of test environments on estimation of genetic parameters for seedling traits in 2-year-old Douglas-fir. Scandinavian-Journal-of-Forest-Research 7(3): 287-296.

Keywords: genetic tree improvement
nursery operations
genetic relationships
growth
tree phenology

Abstract: The effects of test environments (dry versus wet) on the estimation of genetic parameters in seedling traits were studied in 160 open-pollinated families of Douglas fir (Pseudotsuga menziesii) from southwestern Oregon. Seedlings from four populations were grown in two test nursery environments between which a water potential difference of -9 bars was created over two growing seasons, by withholding water for 4 and 8 wk, respectively. Estimated genetic variances in most growth and phenology traits were considerably higher for seedlings grown in the wet environment than for

those in the dry. Estimated genetic correlations between the same traits measured in different test environments indicated that most seedling traits studied for two growing seasons were genetically stable in both environments, suggesting that genotype environment interaction in these traits are weak. However, it is emphasized that the effect of test environment on estimation of genetic parameters in seedling traits, especially in adaptive seedling traits, should be evaluated very carefully when early evaluation of genetic entries is practised in Douglas-fir, since these traits (budburst timing, lammas growth and free growth) appear to be plastic in character.

OSU Link
Non-OSU Link

30. Kaya, Z. 1993. Genetic variation in shoot growth components and their correlations in Pseudotsuga menziesii var. menziesii seedlings. Scandinavian-Journal-of-Forest-Research 8(1): 1-7.

Keywords: genetic tree improvement
genetic relationships
growth

Abstract: Stem-unit measurements could be useful for early selection if these dimensions were highly heritable and strongly correlated with traits of commercial interest, such as height growth. Height increments and the number and length of stem segments were measured in the first and second growth period in predetermined and free growth of Douglas-fir (Pseudotsuga menziesii var. menziesii) seedlings from 40 families in each of 2 populations from southwestern Oregon, USA. Populations, or families in populations, exhibited genetic variation in all traits except number of stem units in predetermined growth. Heritabilities for stem-unit measurements were higher than those for height increment in the first growing season, but not in the second. Correlations among measurements of stem units and height increments were only moderate (generally <0.70). It is concluded that stem units are not likely to be better measurements of height in early selection of Douglas-fir than are measurements of either predetermined or free growth.

OSU Link
Non-OSU Link

31. Kaya, Z., R.K. Campbell and W.T. Adams. 1989. Correlated responses of height increment and components of increment in 2-year-old Douglas fir. Canadian-Journal-of-Forest-Research 19(9): 1124-1130.

Keywords: genetic tree improvement
tree phenology
growth
genetic relationships

Abstract: The consequences for growth and phenology of early selection for height or its growth components were evaluated in 160 open-pollinated families of Douglas fir (Pseudotsuga menziesii) from SW Oregon. Seedlings from 2 inland and 2 coastal populations (40 families each) were grown for 2 growing seasons in a 'moist' and 'dry' nursery environment. Predicted response to selection suggests that risk of low juvenile-mature correlation and maladaptation with early selection would be less in the

inland than in the coastal region. Early bud set in the 1st yr was genetically correlated with larger overwintering buds in seedlings from both inland and coastal regions. These larger buds yielded a large increment of predetermined growth in the 2nd yr, followed by little or no free growth and early bud set. Seedlings with late bud set in the 1st yr had the converse pattern. Inland seedlings set buds much earlier on av. than coastal seedlings, hence seedlings from the 2 regions had different growth patterns. Risks that can attend early selection for ht. generally would be decreased in both regions by selecting for predetermined growth, but several qualifications are discussed.

OSU Link
Non-OSU Link

32. Kimball, B.A., G.R. Johnson, D.L. Nolte and D.L. Griffin. 1999. An examination of the genetic control of Douglas-fir vascular tissue phytochemicals: implications for black bear foraging. Forest-Ecology-and-Management 123(2/3): 245-251.

Keywords: genetic tree improvement
tree/stand protection
growth
tree physiology
genetic relationships

Abstract: Silvicultural practices can influence black bear (Ursus americanus) foraging preferences for Douglas fir (Pseudotsuga menziesii) cambial-zone vascular tissues, but little is known about the role of genetics. To study the impact of genetic selection, vascular tissue samples were collected from Douglas fir trees in 6 half-sib families from 5 different sites in north central Oregon. Four replications of 3-tree non-contiguous plots were sampled at each site to examine inter-and intra-site variation. Tree growth was measured as tree diameter at breast height, and the absolute concentrations of 26 different terpenoids were determined by gas chromatography/flame ionization detection from ethyl acetate extracts. The simple carbohydrates fructose, glucose, and sucrose, and the phenolic glycoside coniferin were quantified using anion-exchange chromatography with pulsed amperometric detection. Cluster analysis was used to reduce the number of variables used in analyses of variance. Results for the families studied here indicate that tree growth and some terpenoids were under some level of genetic control. Furthermore, allocation of constitutive terpenoids in vascular tissues was not at the expense of tree growth. The sugars present in vascular tissue were affected by environment (site) and genetics (family) and their interaction.

OSU Link
Non-OSU Link

33. King, J.N., F.C. Yeh and J.C.H. Heaman. 1988. Selection of growth and yield traits in controlled crosses of coastal Douglas-fir. Silvae-Genetica 37(3-4): 158-164.

Keywords: genetic tree improvement
growth
genetic relationships

Abstract: Analysis of variance of several yield traits including height, height increment, diameter and volume in a full-sib progeny test of Douglas fir (Pseudotsuga menziesii) on 2 sites in British Columbia revealed significant amounts of additive genetic variance but small and non-significant amounts of dominance genetic variance. Individual tree heritabilities were between 0.08 and 0.16 for growth traits and family heritabilities were between 0.55 and 0.73. Acceptable gains were predicted with progeny test re-selection (10% volume gain per unit selection intensity). Age 6 height was an effective selection trait, and correlated well with age 12 volume, giving 70% relative efficiency for family selection. Age 12 height measurement and height increment between 10 and 12 did not express significant genetic differences on the individual site analyses due in part to uncontrolled within-plot variation. Diameter showed higher heritabilities and was less sensitive to inadequacies in experimental design than the later height measurements. Index selection for stem volume also demonstrated that diameter was the most effective growth trait to predict the breeding value of parents for individual tree stem volumes.

OSU Link
Non-OSU Link

34. Koshy, M.P. and D.T. Lester. 1994. Genetic variation of wood shrinkage in a progeny test of coastal Douglas-fir. Canadian-Journal-of-Forest-Research 24(8): 1734-1740.

Keywords: genetic tree improvement
wood quality
genetic relationships

Abstract: Directional (longitudinal, tangential and radial) and volumetric wood shrinkage were analysed in 413 trees belonging to 48 full-sib families (4 paternal and 12 maternal parents) from an 18-year-old coastal Douglas fir (Pseudotsuga menziesii var. menziesii) progeny test in British Columbia. Six samples per ring position (ring positions 1-5 from pith along stem radii), with two rings in each ring position, were examined in a bolt taken at breast height from the tree. Genetic effects were minimal for shrinkage, except for longitudinal shrinkage at ring positions 1 and 2. High variability was expressed among trees within plots and among samples with trees. The lack of statistically significant family variance eliminates the possibility of improving the shrinkage traits by genetic means, except for longitudinal shrinkage in the first few rings. However, the high amount of variability expressed between trees within plots and between samples within trees warrants special attention for achieving uniformity of wood. Much of this variability can be reduced by silvicultural methods.

OSU Link
Non-OSU Link

35. Koshy, M.P. and D.T. Lester. 1997. Wood shrinkage and tree growth in coastal Douglas-fir: implications of selection. Canadian-Journal-of-Forest-Research 27(1): 135-138.

Keywords: genetic tree improvement
wood quality
growth
genetic relationships

Abstract: Phenotypic and genetic correlations of height and diameter at breast height with wood shrinkage were studied in an 18-year-old Douglas fir (Pseudotsuga menziesii) progeny trial in British Columbia. Correlations between growth traits and shrinkage were minimal except for longitudinal shrinkage at rings close to the pith. In early ring positions, there was a negative correlation between height and longitudinal shrinkage, such that selection for increased height is expected to reduce longitudinal shrinkage at ring positions closer to the pith. The results support current efforts to increase wood production through genetic improvement in growth rate by showing that current programmes of selection for rapid early height growth will not result in significant increase in wood shrinkage.

OSU Link
Non-OSU Link

36. Li, P. and W.T. Adams. 1993. Genetic control of bud phenology in pole-size trees and seedlings of coastal Douglas-fir. Canadian-Journal-of-Forest-Research 23(6): 1043-1051.

Keywords: genetic tree improvement
genetic relationships
tree phenology
growth

Abstract: The extent to which bud phenology is genetically controlled and related to growth traits was examined in seedlings and pole-size trees of coastal Douglas-fir (Pseudotsuga menziesii var. menziesii). Data on bud burst, bud set, and stem growth were collected from pole-size trees of 60 open-pollinated families growing in four plantations in Oregon, and from seedlings of 45 of these same families growing in a bare-root trial in Washington, and greenhouse and transplant trials in Washington and Oregon. In both age-classes, bud burst was under moderate to strong genetic control (hsuperscript 2<more or =>0.44) and family breeding values were stable across test environments, indicating that this trait could be readily altered in breeding programmes. Bud set was inherited strongly in pole-size trees (hsuperscript2=0.81) but weakly in seedlings (hsuperscript 2<less or =>0.30). Both bud burst and bud set were positively correlated with growth in seedlings and pole-size trees. Thus, selection for greater growth at either age-class is expected to delay bud burst and bud set. An evaluation was made of the accuracy of two alternatives for assessing bud burst phenology in pole-size trees compared with the traditional method. It was shown that bud-burst date on lateral branches can be used to rank accurately both individuals and families for bud-burst date on less accessible leader shoots. In addition, it was found that families can be ranked for mean bud-burst date by the proportion of trees per family that have flushed on a given scoring day. This method is only effective, however, when between 25 and 75% of all trees in the test have flushed at the time of scoring.

OSU Link
Non-OSU Link

37. Li, P. and W.T. Adams. 1994. Genetic variation in cambial phenology of coastal Douglas-fir. Canadian-Journal-of-Forest-Research 24(9): 1864-1870.

Keywords: genetic tree improvement
genetic relationships
tree phenology

growth

Abstract: The objectives of this study were to (i) determine the extent of genetic variation and genetic control of cambial phenology in coastal Douglas fir (Pseudotsuga menziesii var. menziesii), (ii) assess the degree to which cambial phenology is genetically related to bud-burst timing, (iii) examine genetic relationships between cambial phenology and growth traits, and (iv) evaluate the potential for indirectly altering cambial phenology in breeding programmes when selection is for stem volume. Dates of diameter-growth initiation and cessation, and duration of diameter growth (i.e., cambial phenology traits), as well as diameter increment for the 1987 growing season (15-yr-old), were estimated from cumulative diameter growth curves of individual trees of 60 open-pollinated families growing in one plantation in Oregon. Data on stem height and diameter at breast height (d.b.h.), and date of bud burst in 1987 were also collected. Dates of diameter-growth initiation and cessation differed significantly among families, but had lower estimated individual heritabilities (<less or =>0.23) than date of bud burst (0.87). Weak genetic correlations between date of bud burst and dates of diameter-growth initiation and cessation (range -0.09 to 0.26) indicate that timing of diameter growth cannot be reliably predicted from observations of the more easily measured bud burst. Cambial phenology traits were weakly correlated with 1987 diameter increment and moderately correlated with 15-year d.b.h. and volume. Selection of parents in this study for stem volume at age 15 and subsequent crosses among them, would be expected to lead to earlier initiation of diameter growth in the offspring, and possibly later cessation as well. The practical implications of these indirect responses in terms of increased risk of frost damage are unclear, since projected changes are small (i.e., a few days).

OSU Link
Non-OSU Link

38. Magnussen, S. and F.C. Sorensen. 1991. Outliers in forest genetics trials: an example of analysis with truncated data. Scandinavian-Journal-of-Forest-Research 6(3): 335-352.

Keywords: genetic tree improvement
genetic relationships

Abstract: Previously published data for distribution of height in a Douglas fir (Pseudotsuga menziesii) progeny trial in the Oregon Cascades with open (wind) pollinated (OP) and control pollinated (CP) progenies showed an excess of short trees, especially in OP (inbred) progeny, compared with a normally distributed population. Short trees had a disproportionate influence on variance components and heritability estimates. Data truncation of potential outliers was carried out with varying intensity in order to investigate its influence on genetic parameter estimates. Truncation was done by either fixed threshold values or by a proportional elimination of trees from below. Truncated data was analysed either directly or subsequent to a maximum likelihood (ML) recovery of the estimated means and variances of the expected completed samples. ML estimates became increasingly stable as truncation proceeded into the main body of data. Prior to data truncation, the estimated additive variance and heritability estimates of the CP population were significantly greater than corresponding estimates for the OP population. However, ML estimates obtained after a proportional elimination of about 12% of the trees in each plot supported the contention that there was no important difference in additive genetic variance or heritability between OP and CP populations.

OSU Link
Non-OSU Link

39. Magnussen, S. and A.D. Yanchuk. 1994. Time trends of predicted breeding values in selected crosses of coastal Douglas-fir in British Columbia: a methodological study. Forest-Science 40(4): 663-685.

Keywords: genetic tree improvement
genetic relationships
growth

Abstract: Analytical techniques for estimating time trends and projections of breeding values from sparse data, unbalanced mating designs and irregular assessments periods are presented and discussed. Time trends (ages 4 to 23 yr) in genetic parameters of tree heights in 14 full-sib and 4 half-sib Douglas fir (Pseudotsuga menziesii) crosses among six male trees from Coastal British Columbia and six female trees from Washington and Oregon planted on four test sites on Vancouver Island were examined, and tentative projections of genetic gains were made. Annual height estimates were derived by fitting splines to height measures at ages 4, 7, 12, 18 and 23 yr. Genetic variances were derived from direct computations of covariances among all possible half-sib combinations; a method deemed superior to the conventional factorial analysis. Irregular fluctuations in genetic parameter estimates vanished after minor adjustments (<1.5%) of variance-covariance matrices with negative eigenvalues. Sites effects were highly significant, but site-to-site correlations for pair-cross means were all nonsignificant. Additive genetic control of height growth was weak to moderate (hsuperscript 2=0.1), but generally increasing with age. The best genetic discrimination was observed on the more productive sites. A stable ranking of full-sib family means was reached at age 7 yr on one site versus age 18 for the other sites. Trends in breeding values were described with a mixed linear autoregressive time series model from which 10-yr projections were made. Projections took into consideration both the error structure surrounding the breeding values and the errors of the parameter estimates in the time series model. Selection of the best parent out of six for breeding and deployment on a single site type would generate an expected gain of about 2-5% in height growth between ages 4 and 23 yr.

OSU Link
Non-OSU Link

40. Malavasi, U.C. and D.A. Perry. 1993. Genetic variation in competitive ability of some shade-tolerant and shade-intolerant Pacific Coast (USA) conifers. Forest-Ecology-and-Management 56(1-4): 69-81.

Keywords: planting operations
genetic relationships
growth

Abstract: Variability in growth response to stocking density and neighbour composition was compared in Oregon among half-sibling families of four tree species representing two pairs of shade-tolerant (ST) and shade-intolerant (SI) species, each pair from the same life zone. The hypothesis was that the wider regeneration niche of ST species, which can become established both in disturbed areas and within closed forests, would produce greater genetic variability among families than occurs in SI species, which establish primarily in disturbed areas. Families of western hemlock (Tsuga heterophylla - ST), coastal Douglas fir (Pseudotsuga menziesii - SI) and Pacific silver fir (Abies amabilis - ST) varied in their responses to stocking density, but those of noble fir (A. procera - SI) did not. As hypothesized, the ST species were significantly more variable than SI ones, a result consistent with electrophoretic studies of ST and SI plants and supportive of the hypothesis that at least a portion of genetic variability contained within populations represents adaptation to variable environments.

OSU Link
Non-OSU Link

41. O'-Neill, G.A., W.T. Adams and S.N. Aitken. 2001. Quantitative genetics of spring and fall cold hardiness in seedlings from two Oregon populations of coastal Douglas-fir. Forest-Ecology-and-Management 149(1/3): 305-318.

Keywords: genetic tree improvement
tree/stand protection
tree/stand health
genetic relationships

Abstract: Genetics of autumn and spring cold hardiness were investigated in two western Oregon (USA) breeding populations (Coast and Cascade mountains) of Douglas-fir (Pseudotsuga menziesii var. menziesii). Seedlings from 40 open-pollinated families from each population were grown in raised nursery beds and subjected to two soil moisture regimes (well-watered and mild drought) to evaluate the influence of summer drought on ranking of families for cold hardiness. Artificial freeze testing (AFT) of detached shoots, followed by visual scoring of injury, was used to evaluate needle, stem and bud cold hardiness on three dates in the autumn (September, October and November) after the second growing season, and once in the following spring (March). The Cascade population suffered significantly less cold injury than the Coast population in autumn AFT. However, in spring AFT the Cascade population was less cold hardy, although population differences were seldom significant. Families within both breeding zones varied significantly in cold hardiness, with mean estimates of individual heritabilities greater in spring (hi2=0.57) than autumn (hi2=0.37), greater in the Coast (hi2=0.52) than in the Cascade (hi2=0.42) population, and greater in the wet (hi2=0.54) than in the dry moisture regime (hi2=0.40) (autumn means based on October tests). A single test date seems adequate to assess autumn cold hardiness, because estimated genetic correlations for cold injury between autumn test dates were strong (rA=0.80). Genetic correlations between spring and autumn cold injury, however, were moderately negative (rB=-0.66 and -0.21, Coast and Cascade, respectively), indicating that cold hardiness needs to be managed as two traits (i.e. autumn and spring cold hardiness). Selection for cold hardiness based on a single shoot tissue is expected to increase cold hardiness in the other tissues as well, because genetic correlations between tissues in cold injury were moderately-to-strongly positive in both autumn (rB=0.67) and spring (rB=0.84). Seedlings grown under summer drought incurred significantly less cold injury in the autumn than those that were well-watered; nevertheless, strong genetic correlations in autumn cold injury between moisture regimes (rB=0.91) indicate that summer moisture conditions had little influence on family rankings for autumn cold hardiness. Correlations of injury resulting from a natural frost event in November of the first year with injury from AFT in the autumn of the second year (rA=0.72 and 0.78 for needle and bud injury, respectively) confirmed that AFT reliably predicts cold hardiness to natural frost events.

OSU Link
Non-OSU Link

42. O'-Neill, G.A., S.N. Aitken and W.T. Adams. 2000. Genetic selection for cold hardiness in coastal Douglas-fir seedlings and saplings. Canadian-Journal-of-Forest-Research 30(11): 1799-1807.

Keywords: genetic tree improvement
tree/stand protection

genetic relationships
tree phenology

Abstract: Genetic control of cold hardiness in two-year-old seedlings in a nursery in Oregon, USA, was compared with that in 7-year-old field saplings, for 40 open-pollinated families in each of two low-altitude breeding populations (Coast and Cascade) of coastal Douglas fir (Pseudotsuga menziesii var. menziesii) from western Oregon. The field trials were also in the Coast and Cascade breeding zones of Oregon (7 and 6 sites, respectively). In addition, the efficacy of bud phenology traits as predictors of cold hardiness at the two stages was explored. Autumn and spring cold hardiness were assessed using artificial freeze testing. Similar genetic control of cold hardiness in seedlings and saplings is suggested by strong type-B genetic correlations (rB) between the two ages for autumn and spring cold injury traits (rB<more or =>0.78) and by similar trends in individual tree heritability estimates (hi2), e.g., hi2 was greater in spring (mean 0.73) than in autumn (mean 0.36) and greater in the Coast population (0.69) than in the Cascade population (0.40) at both ages. Strong responses to direct selection are expected for spring cold hardiness at both ages and for autumn cold hardiness in seedlings, even under mild selection intensities. Similar heritabilities in seedlings and saplings, and strong genetic correlations between ages for cold-hardiness traits, ensure that selection at one age will produce similar gains at the other age. Type-A genetic correlations (rA) between autumn and spring cold hardiness were near zero in the Cascade population (0.08 and -0.14 at ages 2 and 7, respectively) but were moderate and negative in the Coast population (-0.54 and -0.36, respectively). Bud-burst timing appears to be a suitable surrogate to artificial freeze testing for assessing spring cold hardiness in both seedlings and saplings, as is bud set timing for assessing fall cold hardiness in seedlings, but bud set timing is a poor predictor of fall cold hardiness in saplings.

OSU Link
Non-OSU Link

43. Riitters, K.H. and D.A. Perry. 1987. Early genetic evaluation of open-pollinated Douglas-fir families. Forest-Science 33(2): 577-582.

Keywords: genetic tree improvement
genetic relationships
growth
tree phenology

Abstract: A summary is given of experiments to determine the correlation of seed wt. and growth and phenology of seedlings of 14 families in a cold frame with ht. of saplings from earlier seed crops of the same families in 5 plantations at 9, 12 and 15 yr old. With some exceptions, correlations of seedling variables with field ht. were poor. Highest correlations with 15-yr ht. were for budset at 117 days, ht. and branching index of seedlings. Seedling growth and phenology values were generally poorly correlated with seed wt. Seedling/sapling correlations, however, were related to seedling/seed wt. correlations. Seedling/sapling correlations improved between 9 and 15 yr old.

OSU Link
Non-OSU Link

44. Schermann, N., W.T. Adams, S.N. Aitken and J.C. Bastien. 1997. Genetic parameters of stem form traits in a 9-year-old coastal Douglas-fir progeny test in Washington. Silvae-Genetica 46(2/3): 166-170.

Keywords: genetic tree improvement
growth
wood quality
genetic relationships
tree phenology

Abstract: The genetic control of stem form traits was investigated in a 9-year-old progeny test comparing 80 open-pollinated families of Pseudotsuga menziesii, located in a fertile Pacific coast site in Washington, USA. In addition to stem form traits (internode sinuosity, and number of forks and ramicorns per tree), stem volume (height and DBH), bud phenology (earliness of budburst and budset), and occurrence of second flushing on the leader shoot (9th growing season) were measured. Trees with at least one fork or ramicorn were frequent (26% and 46%, respectively), as were trees with second flushing (26%). Most of the trees exhibited sinuosity of limited magnitude. Due to strong differences among family means and at least modest family heritabilities (0.35 to 0.66), all traits were found to be amenable to genetic improvement. The estimated genetic correlation (rA) between numbers of forks and ramicorns was relatively strong (0.54), and both forking defects traits exhibited similar genetic associations with other traits. Forking defects were strongly and positively associated with frequency of second flushing, a trait which in turn is positively and moderately correlated with both DBH (0.32) and earliness of budburst (0.39). These results are consistent with previous findings. Breeding consequences for simultaneous improvement of both stem volume and form are discussed.

OSU Link
Non-OSU Link

45. Schowalter, T.D. 1988. Tree breeding and insects: effect of insects on the genetic diversity of Douglas-fir. Northwest-Environmental-Journal 4(2): 346-347.

Keywords: seed orchard management
nursery operations
tree/stand protection
tree/stand health
reproduction
genetic relationships

Abstract: Two studies on the effects of insects on Douglas fir [Pseudotsuga menziesii] seed and seedling production in Oregon are summarized. In the first study, seed losses due to Douglas fir cone gall midge [Cecidomyiidae] and Douglas fir seed chalcid [Megastigmusspermotrophus] were studied. It is suggested that resistance to these pests may be a heritable trait and that tree position within a stand can modify genetically-controlled susceptibility to insect attack. The second study indicated that genetically-controlled susceptibility of seedlings to attack by lygus bug [Lygus sp.] could be modified by their proximity to alternative food plants.

OSU Link
Non-OSU Link

46. Schowalter, T.D. and M.I. Harverty. 1989. Influence of host genotype on Douglas-fir seed losses to Contarinia oregonensis (Diptera: Cecidomyiidae)
and Megastigmus spermotrophus (Hymenoptera: Torymidae) in Western Oregon. Environmental-Entomology 18(1): 94-97.

Keywords: genetic tree improvement
seed orchard management
tree/stand protection
genetic relationships
tree/stand health

Abstract: Seed losses due to the cecidomyiid Contarinia oregonensis and the chalcid Megastigmus spermotrophus were measured in a Douglas-fir (Pseudotsuga menziesii) clonal seed orchard and in a Douglas-fir progeny plantation in western Oregon. Seed losses due to both insects differed significantly among clones and among the progeny of selected parental crosses. Seed loss differed more than 3 times between least-infested and most-infested clones or progeny. Seed losses in the progeny plantation indicated that resistance to these 2 insects is a heritable trait, with greater resistance showing a tendency to dominate over lesser resistance. Insect responses to host genotype may be modified by factors associated with the position of the tree within the stand. Implications of these results for tree improvementprogrammes and seed orchard management are discussed.

OSU Link
Non-OSU Link

47. Schowalter, T.D., M.I. Haverty, S.A. Dombrosky and J. Sexton. 1986. Response of Douglas-fir cone gall midge and Douglas-fir seed chalcid to host plant genotype. In Proceedings of the 2nd Conference of the Cone and Seed Insects Working Party, Station deZoologie Forestiere, Olivet, France, September 3-5, 1986. Ed. A. Roques. pp. 217-223.

Keywords: genetic tree improvement
seed orchard management
tree/stand protection
genetic relationships
tree/stand health

Abstract: Seed losses due to 2 species of insects were measured from cones of 51 parental crosses (or families, distinct combinations of 6X11 parents) in a 12-year-old progeny plantation of Douglas fir (Pseudotsuga menziesii) in western Oregon. In 1983 and 1984, seed losses due to Contarinia oregonensis were significantly different among host families. During 1984, 4 of 5 families with the highest midge damage (x=79%) shared a common parent and 4 of 5 families with the lowest midge damage (43%) shared a common parent. This indicates that resistance or susceptibility to the cecidomyiid is probably heritable. Losses due to Megastigmus spermotrophus were measured only in 1984 and were also significantly different among host families. Insect responses to host genotype appeared to be influenced by the position of the tree within the plantation, by the size of the cone crop and, in the case of M. spermotrophus, by prior activity of C. oregonensis.

48. Sorenson, F.C. and R.K. Campbell. 1993. Seed weight-seedling size correlation in coastal Douglas-fir: genetic and environmental components. Canadian-Journal-of-Forest-Research 23(2): 275-285.

Keywords: genetic tree improvement
growth
genetic relationships

Abstract: The effect of seed weight of coastal Douglas fir (Pseudotsuga menziesii var. menziesii) on nursery seedling height was analysed in two experiments. In the first experiment, 16 seeds per family from 111 families were individually weighed and sown in the autumn. In the second experiment, another group of 16 seeds were individually weighed and stratified and sown in the spring. Four-tree non-contiguous family plots were randomly assigned to two densities in two replications in each experiment. Date of emergence and duration and rate of shoot elongation were determined over 2 years of growth. Seedlings in the first experiment were unintentionally exposed to damaging frost after emergence. Some seedlings in the second experiment suffered Lygus bud damage to the terminal shoot. Developmental associations between seed weight, a maternally inherited trait, and seedling height and its components were examined using sets of path analyses with and without adjustments for planned and accidental treatment effects. Results suggested both 'environmental' and 'genetic' contributions of seed weight to seedling height. The weight (environmental) component, alone, decreased with time. The genetic component, which was indicated by lack of direct effect of seed weight on seedling height in the path analyses and by changing female:malevariance ratios over time, was quite stable across treatment effects. Because of the genetic relation, seed weight adjustment is not recommended as a procedure for increasing precision in early selection of coastal Douglas fir families.

OSU Link
Non-OSU Link

49. St-Clair, J.B. 1994a. Genetic variation in tree structure and its relation to size in Douglas-fir. I. Biomass partitioning, foliage efficiency, stem form, and wood density. Canadian-Journal-of-Forest-Research 24(6): 1226-1235.

Keywords: genetic tree improvement
genetic relationships
carbon allocation
wood quality
growth

Abstract: Genetic variation and covariation among traits of tree size (volume, basal area, diameter at breast height and height) and structure were assessed in 1991 in an 18-year-old Douglas fir (Pseudotsuga menziesii var. menziesii) genetic test in the Coast Range of Oregon. Considerable genetic variation was found in size, biomass partitioning and wood density, and genetic gains may be expected from selection and breeding of desirable genotypes. Estimates of heritability for partitioning traits, including harvest index (the proportion of fixed carbon converted to stemwood), were particularly high. Foliage efficiency (stem increment per unit leaf area) was correlated with harvest index and may represent an alternative measure of partitioning to the stem. Estimates of foliage efficiency where leaf area was estimated based on stem diameter or sapwood area were unrelated to foliage efficiency where leaf area was measured directly. Strong negative genetic correlations were found between harvest index and stem size, and between wood density and stem size. Large trees were more tapered than small trees. It is concluded that simultaneous genetic gain in stem size and either harvest index or wood density would be difficult to achieve.

OSU Link
Non-OSU Link

50. St-Clair, J.B. 1994b. Genetic variation in tree structure and its relation to size in Douglas-fir. II. Crown form, branch characters, and foliage characters. Canadian-Journal-of-Forest-Research 24(6): 1236-1247.

Keywords: genetic tree improvement
carbon allocation
tree morphology
wood quality
genetic relationships

Abstract: Genetic variation and covariation among traits of tree size (volume, basal area, diameter at breast height and height) and structure were assessed in 1991 in an 18-year-old Douglas fir (Pseudotsuga menziesii var. menziesii) genetic test in the Coast Range of Oregon. Considerable genetic variation was found for relative crown width, stem increment per crown projection area, leaf area and branch weight relative to crown size, branch diameter and length adjusted for stem size, branch stoutness, cross-sectional area of branches per crown length and needle size. Little genetic variation was found for branch numbers per whorl, branch angle and specific leaf area. At both the phenotypic and genetic level, large trees growing in relatively small spaces had tall, narrow crowns, high leaf areas per crown projection area or branch length, greater partitioning to leaves versus branches, and stouter branches. Thus, large, efficient trees were those that invested more in the photosynthetic machinery of leaf area and the branch biomass necessary to support that leaf area, but distributed that leaf area over a greater vertical distance. Unfortunately, these traits were also associated with increased branchiness, and selection for these traits would be accompanied by reductions in harvest index and wood quality.

OSU Link
Non-OSU Link

51. St-Clair, J.B. and W.T. Adams. 1991a. Effects of seed weight and rate of emergence on early growth of open-pollinated Douglas-fir families. Forest-Science 37(4): 987-997.

Keywords: genetic tree improvement
nursery operations
reproduction
genetic relationships
growth

Abstract: Open-pollinated seeds were collected from 39 Douglas fir
(Pseudotsuga menziesii var. menziesii) families in second-growth stands in the Coast Range of west-central Oregon (150-500 m altitude) in autumn 1985. Seed weight, time of emergence, and three measures of seedling size were recorded for each family in order to assess family variation in seed weight and emergence, and the influence of these seed traits on early growth. Seeds were dewinged, cleaned and stored at 0 degrees C. In April 1986, seeds and germinantswere sown at a depth of 8 mm to

test whether using germinants minimized seed effects on early growth. To evaluate the effect of competition on the relationships of seed weight and rate of emergence to seedling size, individuals of families were planted in mixed-family blocks at close spacing (4x4 cm), in single (pure) family blocks at close spacing (4x4 cm) and in mixed family blocks at a wide, noncompetitive spacing (16x16 cm). Families differed significantly in seed weight, total emergence percentage and rate of emergence. However, correlations of seed weight to rate of emergence, and seed weight and rate of emergence to seedling size, were not strong. Using germinants was ineffective in diminishing seed effects. Interfamily competition had a minor influence on enhancing the effect of seed traits on seedling growth.

OSU Link
Non-OSU Link

52. St-Clair, J.B. and W.T. Adams. 1991b. Relative family performance and variance structure of open-pollinated Douglas-fir seedlings grown in three competitive environments. Theoretical-and-Applied-Genetics 81(4): 541-550.

Keywords: genetic tree improvement
nursery operations
genetic relationships
growth

Abstract: Open-pollinated Douglas fir (Pseudotsuga menziesii) var. menziesii families were tested in 3 contrasting competitive environments to test the hypothesis that relative performance as measured by total seedling dry weight is dependent upon distance or genotype ofneighbours. The 3 environments included (1) a mixture of individuals from all families sown at close spacing, (2) single (pure) family blocks sown at close spacing, and (3) individuals from all families sown at a wide, non-competitive spacing. Despite occasional large changes in rank between competitive environments and only moderate correlations of family means between competitive environments, the family x competitive environment interaction was non-significant. Furthermore, families did not differ significantly in competitive ability or density tolerance. The competitive environment in which seedlings were grown, however, had a large effect on estimates of variance components, which in turn led to large differences in estimates of heritability and genetic gain. Evaluation of families in mixture resulted in the largest estimates of heritability, while evaluation in pure family blocks resulted in the lowest. Analysis of correlated response to selection indicated that testing and selection in mixture resulted in the largest estimated gain, even if progeny of selected individuals are subsequently grown in a pure or non-competitive environment.

OSU Link
Non-OSU Link

53. St-Clair, J.B. and W.T. Adams. 1993. Family composition of Douglas-fir nursery stock as influenced by seed characters, mortality, and culling practices. New-Forests 7(4): 319-329.

Keywords: genetic tree improvement
reproduction
growth
genetic relationships

Abstract: Changes in family composition during nursery production were evaluated by following individual seeds and seedlings of 36 wind-pollinated Douglas fir (Pseudotsuga menziesii var. menziesii) families sown in mixture in two operational nurseries in westernWashington and Oregon. Families differed significantly in emergence (measured after 5 wk) and in percentage of seedlings culled for being too small (at end of second growing season: <4 mm stem diameter or <20 cm stem height). Filled seed germination rates (tested in the laboratory) were not related to emergence rates. Differences overall were small enough that family composition was largely unaffected. Observed changes in family composition did not markedly reduce genetic diversity and did not affect the genetic gain that may be expected from an improved population. The plantable nursery stock was, for the most part, representative of the composition of families originally sown.

OSU Link
Non-OSU Link

54. Stoehr, M.U., B.L. Orvar, T.M. Vo, J.R. Gawley, J.E. Webber and C.H. Newton. 1998. Application of a chloroplast DNA marker in seed orchard management evaluations of Douglas-fir. Canadian-Journal-of-Forest-Research 28(2): 187-195.

Keywords: genetic tree improvement
genetic relationships
reproduction

Abstract: Pollen contamination, supplemental mass pollination efficacies, and natural selfing were evaluated in a Douglas fir (Pseudotsuga menziesii) clonal-row seed orchard near Victoria, British Columbia, using a genetic marker on the paternally inherited chloroplast (cp) genome. A primer pair for the polymerase chain reaction amplification of a variable region on the cpDNA in Douglas fir was developed. The amplified DNA product was highly variable in size, yielding 13 different haplotype bands from 20 orchard genotypes growing in theclonal-row seed orchard. Observed band sizes ranged from 859 to 1110 base pairs (bp). To estimate variation levels in the orchard background pollen pool, 96 assayed genotypes from surrounding stands gave rise to 36 different haplotypes, ranging from 367 to 1119 bp in size, resulting in a gene diversity estimate of 0.91. Most orchard clones' haplotypes were also present in the background. After adjusting for the presence of orchard-type haplotypes in the background, contamination was found to be 40%. Natural selfing in six individual clones ranged from 0 to 19% with an average of 6%. Supplemental mass pollination efficacy was estimated to be 55%, ranging from 39 to 73%, depending on the maternal clone and flowering phenology. This DNA marker proved to be very useful in assessing seed orchard mating dynamics and orchard management efficacies for Douglas fir.

OSU Link
Non-OSU Link

55. Stoehr, M.U., J.E. Webber and R.A. Painter. 1994. Pollen contamination effects on progeny from an off-site Douglas-fir seed orchard. Canadian-Journal-of-Forest-Research 24(10): 2113-2117.

Keywords: genetic tree improvement
seed orchard management
growth

genetic relationships
reproduction

Abstract: The effects of background pollen contamination were evaluated for first-year height growth pattern of seedlings originating from a Douglas fir (Pseudotsuga menziesii) coastal-interior transition zone seed orchard located on southern Vancouver Island, British Columbia. Pollen collected from five stands surrounding the orchard (background pollen) and pollen from five half-sib families of the seed orchard were applied to six individual trees in the orchard. The resulting 60 seed lots were raised outdoors in a coastal-climate nursery with five seed lots collected from wild stands of the transition zone. Heights were measured at 10-day intervals during the growing season. Final heights, maximum height growth rate and growth cessation were subjected to analysis of variance. Growth rate and cessation were derived from data fitted to the logistic growth curve using nonlinear regression analysis. Seedlings sired by the background pollen had significantly greater final heights and growth rates. There were no differences in orchard seedlings in growth cessation probably because all seedlings were exposed to a blackout treatment to force bud set in mid-August. The average final height of wild-stand seedlings from the transition zone was 15% and 21% lower than that of pure orchard seedlings and seedlings sired by the background pollen lots, respectively. Standard deviations for measured traits were similar between orchard seedlings sired by background pollen and orchard pollen. If pollen contamination is not prevented, the faster growing seedlings sired by the background pollen may be preferentially selected during culling in the nursery and outplanted on sites to which they are maladapted.

OSU Link
Non-OSU Link

56. Stonecypher, R.W., R.F. Piesch, G.G. Helland, J.G. Chapman and H.J. Reno. 1996. Results from genetic tests of selected parents of Douglas-fir (Pseudotsuga menziesii [Mirb.] Franco) in an applied tree improvement program. Forest-Science-Monograph (32): 35.

Keywords: genetic tree improvement
planting operations
growth
tree phenology
genetic relationships

Abstract: Results from genetic tests, and genotype x environment interaction studies in six low-elevation breeding zones of Weyerhaeuser Company's Western Washington and Oregon Douglas fir (Pseudotsuga menziesii) tree improvement programme are summarized. Phenotypic selection in natural stands resulted in a 5% improvement in juvenile height over nonselect seed lots. Comparisons with nonselect sources, of offspring from parents in the top 50% performers in tests, indicated a 10% increase for the same trait. Seed produced in a 50% rogued seed orchard is thus expected to provide improved planting stock with a gain of 10% in juvenile height growth. Several select parents are producing offspring that are consistently performing in excess of 10% over nonselects. Estimates of breeding zone, breeding zone by location, and family by location interaction effects are small relative to family and planting location effects. Tests of families established on environmentally diverse sites indicate a striking lack of large family by planting location interaction. In tests showing statistically significant interactions, such interactions are caused by a relatively small number of families.
Earlier budbreak and a higher spring frost susceptibility of Oregon sources established

on Washington sites were observed. It is concluded that allocation and utilization of select families within Weyerhaeuser's Oregon and Washington ownership should not be constrained by the currently defined breeding zone boundaries, but based on parental performance and stability for growth and adaptive traits in general. It is suggested that the necessity for maintaining separate breeding zones, within Washington and Oregon, in subsequent cycles of recurrent selection is questionable. Average individual tree heritability, from 65 6-parent disconnected diallels, is 0.13 for age 6 and age 8 height. Dominance genetic variance is estimated to be one-half that of additive genetic variance for the same traits.

OSU Link
Non-OSU Link

57. Temel, F. and W.T. Adams. 2000. Persistence and age-age genetic correlations of stem defects in coastal Douglas-fir (Pseudotsuga menziesii var. menziesii (Mirb.) Franco). Forest-Genetics 7(2): 145-153.

Keywords: genetic tree improvement
genetic relationships
growth
wood quality

Abstract: Persistence of stem defects, including bole sinuosity, large branch size and the occurrence of steep-angled branches (i. e., forks and ramicorns), and the efficiency of early selection against these traits, were investigated in 90 open-pollinated families of Douglas fir (Pseudotsuga menziesii var. menziesii) from coastal Oregon, USA. Trees originally measured for these traits at age 12 were remeasured at age 24 in three progeny test plantations. The majority of trees scored as having ramicorn branches at age 12 (62%) still had them at age 24, but most forks (53%) had become ramicorns by the second measurement. Thus, there seems little need to score forks and ramicorns separately; simply counting the number of whorls with steep-angled branches seems sufficient for selection purposes. Branch size scores were relatively consistent between the two ages, but not scores for bole sinuosity. Because of low estimated individual and family heritability estimates (<less or =>0.13 and <less or =>0.41, respectively), predicted genetic responses in diameter at breast height (DBH) and individual stem-defect traits were only modest for this population. Nevertheless, with the exception of sinuosity, genetic correlations between comparable stem-defect traits at the two ages were strong (rA<more or => 0.82), and predicted responses in traits at age 24, from selection at age 12, were nearly as great as responses expected if selection was delayed until age 24. Branch size and occurrence of steep-angled branches were unfavourably (positively) correlated with DBH (estimated rA= 0.56 and 0.41, respectively). Thus, it is important to include these stem defect traits as selection criteria in Douglas fir breeding programmes, if stem volume growth is to be improved without sacrificing wood quality.

OSU Link

58. Vargas-Hernandez, J. and W.T. Adams. 1991. Genetic variation of wood density components in young coastal Douglas-fir: implications for tree breeding. Canadian-Journal-of-Forest-Research 21(12): 1801-1807.

Keywords: genetic tree improvement

genetic relationships
wood quality
growth

Abstract: A study was made of the genetic control of wood density components (earlywood density, latewood density, and latewood percentage) and their relationships with overall density in coastal Douglas fir (Pseudotsuga menziesii var. menziesii) to assess the usefulness of this information in breeding for wood density. The genetic relationships of wood density with intra-ring density variation and bole volume growth were also investigated. Increment cores were taken at breast height from 15-yr-old trees of 60 open-pollinated families growing in the Coyote Creek progeny test plantation near Eugene, Oregon, during summer 1988. Averages across each core for overall wood density, its components and intra-ring density variation were determined by using X-ray densitometry. Bole volume at age 15 yr for the same trees was derived from tree height and diameter at breast height measurements taken at the end of the 1987 growing season. Although wood density components varied significantly among families and were under moderate genetic control (individual-tree heritability (hisuperscript 2) >0.24), none had a higher heritability than overall density (hisuperscript 2 = 0.59). Density components had strong genetic correlations with overall density (r <more or => 0.74), but were also strongly related among themselves (0.57 <less or => r <less or =>0.92). Thus, density components have limited value in improving the efficiency of selection for overall density. Overall density was positively correlated with intra-ring density variation (r = 0.72) and negatively correlated with bole volume (r = -0.52). However, comparison of several selection indices incorporating wood density and one or more growth traits showed that it is possible to obtain substantial gains in bole volume without loss in (or even with a modest increase in) wood density. By restricting the response in wood density, the change in intra-ring density variation can also be limited.

OSU Link
Non-OSU Link

59. Vargas-Hernandez, J. and W.T. Adams. 1992. Age-age correlations and early selection for wood density in young coastal Douglas-fir. Forest-Science 38(2): 467-478.

Keywords: genetic tree improvement
genetic relationships
wood quality

Abstract: Age-age correlations and age-associated changes in the genetic control of wood density and its components (earlywood density, latewood density, and latewood proportion) were investigated in 15-yr-old trees of 60 open-pollinated families of coastal Douglas-fir (Pseudotsuga menziesii var. menziesii) in Oregon. The possibility of using wood density components as secondary traits to increase the efficiency of early selection for overall wood density was also explored. Heritability estimates for overall density and its components increased with age, mainly because of a decrease in the error variance as the number of rings in the core sample increased. Overall density and its components at age 15 yr had strong genetic correlations with their respective traits at all younger ages analysed. Moreover, with few exceptions, age-age genetic correlations were greater than phenotypic correlations. Early selection to improve overall density at age 15 yr was quite efficient (relative efficiency >79%), even when selection was based on core density at the youngest age (7 yr). Using wood density components as secondary traits produced a slight increase in the efficiency of early selection only at the youngest ages, presumably because age-age correlations for overall core density were already strong, limiting the potential for additional improvement.

OSU Link
Non-OSU Link

60. Vargas-Hernandez, J. and W.T. Adams. 1994. Genetic relationships between wood density components and cambial growth rhythm in young coastal Douglas-fir. Canadian-Journal-of-Forest-Research 24(9): 1871-1876.

Keywords: genetic tree improvement
genetic relationships
wood quality
tree phenology
growth

Abstract: Genetic relationships of wood density, and its components, with cambial growth rhythm traits were examined in a 15-year-old progeny test of coastal Douglas fir (Pseudotsuga menziesii var. menziesii) in Oregon, in an attempt to better understand the genetic control of wood formation, and to assess the potential effect of selecting for increased wood density on adaptation of trees. Timing of diameter growth during the 1987 growing season was determined in an earlier study, and wood formation traits were estimated by X-ray densitometry of increment core samples. Wood formation traits were under weak genetic control (hisuperscript 2<0.20). Duration of earlywood and latewood formation were mostly determined by the timing of latewood transition. Overall core density was negatively correlated with the dates of cambial growth initiation (rA=-0.41) and latewood transition (rA=-0.62), and positively correlated with the date of cambial growth cessation (rA=0.40). As a result of these relationships, higher wood density was associated with a longer duration of cambial growth (rA=0.67) and a slower rate of wood formation (rA=-0.37). All density components showed similar relationships with cambial phenology and wood formation traits. Selection for increased wood density is expected to cause only a slight extension of the cambial growth period, but it would also cause an earlier transition to latewood formation, negatively affecting growth rate.

OSU Link
Non-OSU Link

61. Vargas-Hernandez, J., W.T. Adams and R.L. Krahmer. 1994. Family variation in age trends of wood density traits in young coastal Douglas-fir. Wood-and-Fiber-Science 26(2): 229-236.

Keywords: genetic tree improvement
genetic relationships
wood quality

Abstract: Changes in ring density and its components with increasing distance from the pith (i.e. age trends) were examined in 15-yr-old trees from 60 open-pollinated families of coastal Douglas fir [Pseudotsuga menziesii] grown in the Coyote Creek progeny test plantation near Eugene, Oregon. Earlywood, latewood, and overall densities of each annual ring, obtained by X-ray densitometry of increment cores, were weighted by the area of the ring occupied by each trait, relative to the total stem cross-sectional area at breast height for the trait. Age trends in weighted values differed among traits but, with the exception of earlywood density, family variation was not detected. Weighted earlywood density (WED) steadily increased from pith to bark in some trees, while in other trees a plateau occurred at age 11 or later. Significant family differences were found in the proportion of trees reaching a plateau in WED by age 12. This proportion was under moderate genetic control (family hsuperscript 2=0.30) and was not genetically correlated with overall core density or stem growth at age 15. Although there are reasons to hypothesize that the plateau in WED is an indication of transition from juvenile to mature wood formation, this hypothesis needs to be verified in older trees.

OSU Link
Non-OSU Link

62. Vargas-Hernandez, J.J., W.T. Adams and D.G. Joyce. 2003. Quantitative genetic structure of stem form and branching traits in Douglas-fir seedlings and implications for early selection. Silvae-Genetica 52(1): 36-44.

Keywords: genetic tree improvement
nursery operations
growth
genetic relationships
wood quality

Abstract: Open-pollinated (OP) and full-sib (FS) families of coastal Douglas fir (Pseudotsuga menziesii var. menziesii) were grown in two replicated nursery regimes to evaluate the magnitude and repeatability of genetic parameter estimates for stem form (stem sinuosity, forking) and branching (number, length and angle of branches) traits in 2-year-old seedlings, and the relationships of these traits with stem growth. With data from older trees of the OP families growing in the field (ages 12 and 24), genetic control of similar traits was compared at the different ages, and nursery-field correlations (rxy) were estimated. With the exception of forking, estimates of family heritability (h2f) were moderate to strong for stem form and branching traits in seedlings (0.32<less or =>h2f<less or =>0.94; mean=0.73), and similar to growth traits (0.45<less or =>h2f<less or =>0.90; mean=0.75). Family performance and estimates of genetic parameters were relatively stable across nursery regimes and family type. Genetic relationships among traits in seedlings were similar to those observed in older field-grown trees, indicating that these traits are controlled by similar sets of genes in the two age classes. Nursery-field correlations between comparable traits were consistent across nursery regimes, but rxy was strong enough to be useful for early testing purposes (i.e. | rxy | <more or =>0.30), only for number of whorls with steep-angled branches (WSAB), branch length, and branch angle in older trees. Predicted gains from early selection for these or correlated traits were at least 40-50% of those expected from selection at older ages. Because of unfavourable genetic correlations, selection for stem growth potential alone at the seedling stage is expected to produce unfavourable impacts on WSAB and stem sinuosity in older trees. To avoid such negative effects on wood quality, both stem form and branching traits should be included as selection criteria in Douglas fir breeding programmes.

OSU Link
Non-OSU Link

63. Woods, J.H., D. Kolotelo and A.D. Yanchuk. 1995. Early selection of coastal Douglas-fir in a farm-field test environment. Silvae-Genetica 44(4): 178-186.

Keywords: genetic tree improvement
planting operations
site preparation
mechanical preparation
release treatments
chemical release
manual release
genetic relationships
wood quality
growth

Abstract: Farm-field tests are progeny tests established using intensive site preparation, close spacing and nearly complete weed control. Early growth and wood density of coastal Douglas-fir (Pseudotsuga menziesii) in a farm-field environment for up to 7 years from seed were compared with stem volume and wood density from 11 field sites at age 13 (20-25 of commercial rotation). The farm-field test material comprised 70 full-sib families from six 6-tree half-diallels (some reciprocals and missing crosses) without selfs. Parent trees were from natural stand selections in the coastal area of British Columbia, Canada, and the farm-field test was conducted on southern Vancouver Island. Family heritabilities were high for almost all traits in both the farm-field and field sites. Breeding-value correlations of farm-field heights with field stem volume at age 13 increased from a low of 0.5 for farm-field age 1 and levelled off at about 0.7 by farm-field age 3. Farm-field diameter with field volume age 13 breeding-value correlations were initially lower than those for height, but increased to 0.82 by age 7. Wood density breeding value correlations between field pilodyn assessments at age 13 and farm-field stem sections at age 6 were 0.83. Maximum family-selection efficiency per year (including a 5-year breeding delay), relative to direct selection on field volume 13, reached 162% using index selection on farm-field height and diameter at age 3. Within-family selection efficiencies per year were highest at age 1 and declined quickly thereafter. All selection in the farm-field test had a higher efficiency per unit time than selection in field tests. It is concluded that correctly established farm-field tests will provide greater per year gains in stem yield and wood density traits than field sites.

OSU Link
Non-OSU Link

64. Woods, J.H., T. Wang and S.N. Aitken. 2002. Effects of inbreeding on coastal Douglas fir: nursery performance. Silvae-Genetica 51(4): 163-170.

Keywords: genetic tree improvement
growth
tree/stand health
reproduction
genetic relationships

Abstract: In advanced generation seed orchards, low levels of inbreeding may be inevitable as relatedness among individuals in breeding populations increases with each generation. Unlike selfing, low level inbreeding can produce relatively large number of viable seeds. Following previous study on the effects of inbreeding on coastal Douglas fir (Pseudotsuga menziesii var. menziesii) filled seed production, the present study investigated inbreeding on nursery performance over various cross-types, including outcrosses (inbreeding coefficient F=0), crosses between half-sibs (F = 0.125), between full-sibs

(F = 0.25), between parents and offspring (F = 0.25), and selfing (F = 0.5). Significant differences were found among cross-types for germination, seedling mortality, seedling diameter and height, and nursery cull rate. Inbreeding also increased among-family genetic variability. Cumulative losses of seedlings at the nursery stage were 18, 33, 31, 36 and 43%, respectively for the above types of crosses. This result indicates that seeds with low levels of inbreeding may produce relatively large numbers of seedlings that meet nursery culling standards and could be used for reforestation, resulting in negative impacts on the genetic gain realized in field plantations.

OSU Link
Non-OSU Link

65. Yanchuk, A.D. 1996. General and specific combining ability from disconnected partial diallels of coastal Douglas-fir. Silvae-Genetica 45(1): 37-45.

Keywords: genetic tree improvement
growth
genetic relationships

Abstract: GCA and SCA were examined in 36, 6-parent disconnected partial diallels across 4 experimental series in coastal Douglas-fir (Pseudotsuga menziesii var. menziesii) in British Columbia, to examine the ratios of the 2 genetic variances, the distribution of GCA and SCA effects, and estimates of genetic gain from GCA and SCA for 3 growth traits. Height at age 7 and height and volume at age 12 were measured on approximately 150 trees per full-sib family in each diallel, across 11 different test sites within each series. The average percentage ratio of SCA variance to GCA variance was 36% across all series and the 3 growth traits, with a range of 19 to 65%. GCA and SCA variances did not appreciably change for height growth from age 7 to age 12. Diallel set effects were generally negligible. From theoretical considerations assumed for the diallel model, clear separations of additive and dominance effects (vis-a-vis the assumptions of selecting on GCA and SCA variances) are likely not possible: the effects are subject to degrees of dominance, epistasis and linkage in the population. However, these genetic details did not manifest themselves in any noticeable pattern or correlation among GCA and SCA effects. While these results confirm current strategies in Douglas-fir breeding to select primarily on GCA, there are opportunities to utilize SCA variance in the production population. Controlled matings for elite production populations are now common in coastal Douglas-fir improvement programmes, and controlled crossing with specified parents could (i) elevate gains by as much as 3.0% in 12-year volume (assuming competition effects have not biased volume estimates), and (ii) access additional sets of parents that would otherwise be disregarded. Gains for height growth from utilizing SCA are lower, which reflect either (i) lower SCA variances associated with height, or (ii) competition has biased upward volume SCA variance by age 12 (relative to height).

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66. Yeh, F.C. and J.C. Heaman. 1987. Estimating genetic parameters of height growth in seven-year old coastal Douglas-fir from disconnected diallels. Forest-Science 33(4): 946-957.

Keywords: genetic tree improvement
genetic relationships

growth

Abstract: A disconnected diallele mating scheme was carried out on 10 sets each of 6 parents. Seedlings were raised at Cowichan Lake Research Station and planted out after 1 yr at 11 plantations in British Columbia where coastal Douglas fir would be a good choice for reforestation. Data on ht. and survival were collected after 7 yr and analysed to partition total phenotypic variation in ht. into portions of additive genetic effect (GCA), dominance genetic effect (SCA), interaction of plantations with additive and dominance genetic effects, residual effect and random error. The GCA of the parents within the sets was highly significant and its variance was the most important source of genetic variation. The GCA by plantation interaction was large and its variance was approx. 42% of the GCA variance. Effects due to SCA of parent trees and SCA by plantation interaction were also significant, but their variances were small in comparison with the GCA variance. The heritability estimate for 7-yr ht. was 0.13. Results are discussed in relation to gains to be expected from the improvement of this species.

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