GENETIC VARIATION IN GROWTH, BIOMASS AND STEM QUALITY TRAITS IN *PINUS BRUTIA* IN SOUTHERN TURKEY'

Fikret Isik[2], Kani Isik[3,4] and Steve J. Lees

INTRODUCTION

Turkish red pine *(Pinus brutia* Ten.) is naturally distributed mainly in the Mediterranean and Aegean region of Turkey, along with east Aegean Islands, Crete in Greece, Cyprus, Syria, and northern Iraq. In recent years the species has been introduced into several other countries where Mediterranean climate predominates, such as France, northern Africa, Israel, Australia, California, and Mexico (Selik 1958, Chritchfield and Little 1966, Arbez 1974, Panetsos 1981, Kara *et al.* 1997). The species can form closed stands from sea level up to 1200 meters above sea level, and exhibits a considerable phenotypic variation in bole straightness, branching, crown and growth traits in its natural habitats (Arbez 1974, Isik 1986). If these traits are genetically controlled, then, significant genetic gain could be realised using tree improvement techniques of selection and breeding.

New plant breeding concepts such as "ideotype" and "crop ideotypes" have been proposed in forestry to increase the yield per unit area (Cannell 1978, Kuuluvainen 1991, St. Clair 1994). Such ideotypes are expected to use resources more efficiently. For example, tall, narrower crowns (with less biomass allocation to branches and foliage and greater partitioning to stem) are desirable characteristics associated with a good crop ideotype for Douglas-fir, Scots pine and Norway spruce (St. Clair 1994, Korki and Tigerstedt 1985, Kuuluvainen *et al.* 1988, Kuuluvainen 1988). Such information is also needed for Turkish red pine as a basis for planning effective tree breeding programs.

The objectives of this particular study are (i) to estimate genetic parameters of the traits studied (ii) to investigate genetic differences between and within populations in biomass and stem quality traits, (iii) to examine biomass partitioning between different parts of tree, (iv) to derive linear models which can predict stem biomass indirectly through employing more easily measured traits.

Keywords: *Pinus brutia,* provenance test, heritability, genetic correlation, biomass traits

MATERIALS AND METHODS

For the experiment, six natural populations were sampled from two altitudinal transects extending from the Mediterranean coast through the Taurus Mountains in Antalya region of Turkey. Two populations from low **(S, D),** two from middle (B, M) and two from high altitudes (K and H) were sampled (Isik 1986). Each population was represented by 10 open pollinated families. Seedlings were raised in a nursery, and then transplanted to four test sites in the field. The field experimental design applied on the test sites was single-tree-plot, randomised complete block design with three interlocked replications (Libby and Cockerham 1980). Data for this study came from the Duzlercami site (altitude 350 m) The

---

A detailed version of the paper is to be published in *Forest Genetics* 6 (2):103-113.

[2] Southwest Anatolia Forest Research Institute (SAFRI), P.O.Box 264, Antalya, Turkey, Fax: +90-242-345-0442 e-mail: fikret-isik@rocketmail.com

'Professor, Akdeniz University, Faculty of Arts and Sciences, Dept. of Biology, 07058 Antalya, Turkey e-mail: kani@pascal.sci.akdeniz.edu.tr

[4] Author to whom all correspondence should be addressed.

[5] Forestry Commission, Northern Research Station, Roslin, Midlothian EH25 9SY, UK. Fax: 0131 445 5124 e-mail: s.j.lee@forestry.gov.uk

trial was thinned at age 13 and at age 17 by removing 600 trees each time. Assessments of the traits in this study were carried out on the thinned trees.

Certain growth (height, diameter over bark, diameter under bark), biomass (dead branch weight, live branch weight, fresh weight of stem wood, harvest index) and stem quality traits (bark thickness at ground level, bark thickness at 1.3 height level, taper, bole straightness, forking) were measured or estimated.

A linear model was used for the analysis of variance. The variance components were estimated using REML option (SAS/Stat, 1989). Regression models were derived to predict fresh stem weight based on more easily measured characters. Individual heritability was estimated according to Namkoong *et al.* 1966). In this study, σ^2_A is taken as three times of $\sigma^2_{f(p)}$ as a precautionary consideration, due to probability of close breeding and/or inbreeding within natural populations (Squillace 1974, Sorensen and White 1988). Family means heritability was estimated according to Shelbourne (1992).

RESULTS AND DISCUSSION

Comparison of Populations

There were significant differences between populations and families for height and diameters at age both 13 and 17 years ($p<0.02$ to $p<0.0001$). Mid-altitude population M (486m) was the best performing followed by lower-high elevation population K (932 m). The better growth performance of mid and upper mid altitude populations was explained by adaptive shoot growth patterns and 'liberal growth strategy' (Lanner 1976, Isik *et al.* 1987, Yildirim 1992).

Taper is a good indicator of how well a stem deviates from a cylinder. There were significant differences between populations and families for taper index at age 13 ($p<0.009$) and at age 17 ($p<0.0001$). M, K and B from mid elevations showed the most desirable taper, whilst S and D from lower elevations had more conical stems which are less desirable for sawlogs. There were significant differences among populations for forking behaviour at age 17. *P. brutia* seems to grow with only one dominant apical shoot when it is young, i.e. until about age 10 years. As the trees get older, the upper crown grows wider, and tends to develop more than one terminal shoot, especially in the populations from lower elevations. Populations S and D had higher forking frequency at age 17, than the remaining four populations which were very similar among themselves. The mean forking value of S and D was six or seven times greater than K and M. This implies an important stem defect for the lower altitude populations. Populations and families within populations differed significantly in bole straightness at age 17. The mid-altitude population K showed the straightest stems, followed by M and B. Lower altitude populations D and S had particularly poor bole straightness with scores that were about two points lower than those of K and M.

The forking and crooked-stem-form tendency of lower altitude populations was explained as an adaptation mechanism to compete with the dense maqui (woody) shrubs within the immediate surroundings of *P. brutia* at younger stages of their development (Isik *et al.* 1987). At lower altitudes, intense competition between trees at their younger stages and neighbouring maqui (woody) shrubs for light and moisture could have favoured trees with wider crowns. Selection of straight trees for harvest in lower altitudes, which have been easily accessible by man for millennia (Wissmann 1972, Runnels 1995), might have altered the genetic composition of lower altitude populations toward genotypes with higher frequency of forking. Similar case has also been observed on *Pinus massoniana* in China (C.J.A. Shelbourne pers. comm.).

Bark thickness at ground level differed among and within populations at age 17. Populations S and M had the thickest bark, while the four remaining populations with relatively thinner barks did not differ from each other. Bark thickness at breast height also showed similar trends as that at ground level. In general, trees with larger diameter also had relatively thick barks. Therefore, one must consider the relative bark basal area within the cross section of the stem. When populations were ranked for relative bark basal area at ground level at age 17, population D and S ranked first and second. Bark thickness at ground level decreased as the altitude of family origin increased ($r = -0.36$, $p<0.01$ at 13 years, $r = -0.29$, $p<0.05$ at 17 years). Relatively thicker barks in low-elevation populations might have an adaptive advantage to avoid frequent forest fires, especially ground fires, during the long dry summers in this part of Turkey.

Harvest Index (HI), which is the proportion of fresh stem weight to the total above ground biomass is of major importance among the biomass traits. Populations did not differ for HI at age 13, but by age 17 years, K, M and B had significantly better HI than S and D. On average, the proportion of biomass accumulated in the stem was 61 % at age 13, and 86 % at age 17. Harvest Index was highly correlated with height ($r_p=0.60$, $p<0.001$) and diameter at breast height ($r_p=0.81$, $p<0.001$) at age 17. Due to the practical difficulties in weighing oven-dry biomass, the relationships between fresh weights and dry weights were not investigated. However, it may be interesting to note that for a 16 year-old progeny trial of Scots pine, strong correlation was detected between stem fresh weight and air dry weight in family ranking (Welling and Tigersted 1984). Families from higher altitudes tend to allocate more biomass to stem than to the other parts of a tree ($r=0.48$, $p<0.001$). We attempted to derive some models to predict certain biomass traits using easily measurable growth traits such as height and diameter. The relationship between fresh stem weight and dbh^2 at age 13 years was significantly linear ($R2=0.96$).

Distribution of Variation and Heritabilities

The proportions of variation due to both populations and families were less than 10% each, for all the traits studied, with the only exception of bole straightness. Variances within families were in general over 85% of the total variance. Among-population-variance components generally increased with age, while among family variance components decreased substantially. The distribution of variation in bole straightness was clearly different, showing higher percentage attributed to the genetic differences among populations, i.e. 24.2% and 39.5% of the total variation at ages 13 and 17 years respectively. Hence, it will be quite effective to improve bole straightness by selecting the best populations alone.

Individual heritabilities for height (0.12, 0.11) were moderate and remained constant from age 13 to 17 years. These heritability values were consistent with that presented by Panetsos (1981) on 7 year-old plants (i.e. 0.17). Heritabilities for diameter over bark (0.21) and diameter under bark (0.16) were moderate at age 13. But, since the family variance decreased with age, heritability estimates for diameter at age 17 were correspondingly reduced (0.06 and 0.09). Heritability for forking was low, but for bole straightness (0.21) and taper (0.25) were moderate at age 13 years. Family means heritabilities for all the traits were higher than individual heritabilities, and they usually showed parallel changes. There was no significant relationship between coefficients of additive genetic variation (CV_g) and heritabilities. Cornelius (1994) also reported that higher CV_g might not be reflected in higher heritabilities. Excluding forking, which was assessed on a present/absent basis, Fresh Stem Weight was genetically and phenotypically the most variable trait studied. Additive genetic variation and heritabilities decreased with age for the characters in *Pinus brutia*. This age trend in Turkish red pine is similar to the most of the reported heritabilities for conifers in the literature (Birot and Christophe 1983, Dean *et al.* 1986, Hodge and White 1992). The change in genetic parameters may be an outcome of sampling effect with different sets of trees used for estimating parameters at different ages. Furthermore, such changes in genetic parameters are also expected because of different genes involvement at different developmental stages of the traits studied (Namkoong *et al.* 1988).

In conclusion, populations from the mid and lower-high altitude origins among the six populations of Turkish red pine from Antalya Region performed best in height and diameter growth at the Duzlercami test site. These populations also showed desirable bole straightness, and allocated a higher proportion of biomass to the stem rather than to the branches. Thus, major emphasis should be given mainly to mid altitude populations for further family selection and improvement in Antalya Region. Cautions are needed to apply these results to wider areas. Genetic variation in growth, quality and biomass traits between populations and between families within populations in *Pinus brutia* is quite high. Growth, stem quality and stem biomass traits are under moderate additive genetic control. The results suggest that considerable improvement could be realised by combined selection if selection is applied at population, family and within-family levels.

LITERATURE CITED

Arbez, M. 1974. Distribution, ecology and variation of *Pinus brutia* in Turkey. Forest Genetic Resources Information 3, FAO Rome: 21-23.

Birot, Y. and C. Cristophe. 1983. Genetic structures and expected gains from multi-trait selection in wild populations of Douglas-fir and Sitka Spruce: I. Genetic variation between and within populations. *Silvae Genetica* 32: 141-151.

Cannell, M. G. R. 1978. Improving per hectare forest productivity. *In:* proceeding of 5th North American Forest Biology workshop. *Edited* by C. A. Hollis and A. E. Squillace. 13-15 March 1978, Gainsville, Fla.: 120-148.

Cornelius, J. 1994. Heritabilities and additive genetic coefficients of variation in forest trees. *Canadian Journal of Forest Research* 24: 372-379.

Critchfield, W. B. and E. L. Little, Jr. 1966. Geographic distribution of the pines of the world. USDA Forest Service, Miscellaneous Publications 991, 91 pp.

Dean, C .A., P. P.Cotterill, and R. L Eisemann. 1986. Genetic parameters and gains expected from selection in *Pinus carribaea var hondurensis* in Northern Queensland, Australia. *Silvae Genetica* 35 (5-6): 229-236.

Hodge G. R. and T. L White. 1992. Genetic parameter estimates for growth traits at different ages in slash pine and some implications for breeding. *Silvae Genetica* 41 (4-5): 252-262.

Isik, K. 1986. Altitudinal variation in *Pinus brutia* Ten.: Seed and seedling characteristics. *Silvae Genetica* 35 (2-3): 58-66.

Isik, K., M. Topak, and A. C. Keskin. 1987. Genetic variation among and within six *Pinus rutia* stands in southern Turkey: Six year results at five common garden plantations. Forest Trees and Seeds Improvement Institute publication no: 3, Ankara, 139 pp.

Kara, N., L. Korol, K. Isik, and G. Schiller. 1997. Genetic diversity in *Pinus brutia* Ten.: Altitudinal variation. *Silvae Genetica* 46 (2-3): 155-161.

Korki, L. and P.M.A.Tigerstedt. 1985. Definition and exploitation of forest tree ideotypes in Finland. *In:* M. G. R. Cannell and J. E. Jackson (Eds.), Attributes of Trees As Crop Plants, 102-109. Inst. of Terrestrial Ecology, UK.

Kuuluvainen, T., M. Kanninen, and J.P. Salmi. 1988. Tree architecture in young Scots pine: properties, spatial distribution and relationships of components of tree architecture. *Silvae Fennica* 22 (2):147 161.

Kuuluvainen, T. 1991. Effect of crown and canopy architecture on radiation interception and productivity in coniferous tree. D.Sci. Thesis, University of Joensuu, 346 pp.

Kuuluvainen, T. 1988. Crown architecture and stem wood production in Norway spruce *(Picea abies (L.)* Karst.). *Tree Physiology* 4: 337-346.

Lanner, R. M., 1976. Patterns of shoot development in *Pinus* and their relationship to growth potential. *In:* M. G. R. Cannell and F. T. Last (eds.), Tree physiology and Yield Improvement. Academic Press, London: 223-243.

Libby, W.J. and C.C. Cockerham. 1980. Random non-contiguous plots in interlocking field layouts. *Silvae Genetica* 29 (5-6): 183-190.

Namkoong, G., E.B.Synder, and R.W. Stonecypher. 1966. Heritability and gain concepts for evaluating breeding systems such as seedling seed orchards. *Silvae Genetica* 15 (3): 61-100.

Namkoong, G., H. C. Kang, and J. S. Brouard. 1988. Tree Breeding: Principles and Strategies. Springer-Verlag, New York, 180 pp.

Panetsos, P. K. 1981. Monograph of *Pinus halepensis* (Mill) and *Pinus brutia* Ten. *Annales Forestales* 9 (2): 39-77. Zagreb.

Runnels, C. N. 1995. Enviromental degradation in ancient Greece. *Scientific American,* March 1995: 96-99.

SAS/STAT User's Guide, Version 6, Fourth Ed., Volume 2, Cary, NC: SAS Institute Inc., 1989, 846 pp.

Selik, M. 1958. Botanical investigation on *Pinus brutia* especially in comparison with *P. halepensis. Istanbul University Faculty of Forestry Journal* 8a: 161-198.

Shelbourne, C.J.A. 1992. Genetic gain from different kinds of breeding population and seed or plant production population. Paper presented at the IUFRO symposium "Intensive Forestry:The Role of Eucalyptus" held in Durban South Africa, in September 1991:49-65.

Sorensen F. C., and T.L. White. 1988. Effect of natural inbreeding on variance structure in tests of wind pollination Douglas-Fir progenies. *Forest Science* 34 (1):102-118.

Squillace, A. E. 1974. Average genetic correlations among offsprings from open-pollinated forest trees. *Silvae Genetica* 23:149-156.

St.Clair, J.B. 1994. 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: 1226-1235.

Welling, P. and P. M. A. Tigersted. 1984. Harvest index in a progeny test of Scots pine with reference to the model of selection. *Silva Fennica* 18 (1): 21-32.

Wissmann, v. H. 1972. The role of nature and man in changing the face of the dry belt of Asia. In: William L. Thomas JR (ed.), Man's Role in Changing the Face of the Earth. Univ. of Chicago Press: 278-303.

Yildirim, T. 1992. Genetic variation in shoot growth patterns in *Pinus brutia* Ten. A master's thesis. Middle East Technical University, Graduate School of Natural and Applied Sciences. Ankara, Turkey, 53 pp.