INHERITANCE OF WOOD SPECIFIC GRAVITY AND ITS GENETIC
CORRELATION WITH GROWTH TRAITS IN YOUNG
PINUS BRUTIA PROGENIES

A THESIS SUBMITTED TO
THE GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
OF
MIDDLE EAST TECHNICAL UNIVERSITY

BY

KUBİLAY YILDIRIM

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR
THE DEGREE OF MASTER OF SCIENCE
IN
BIOTECHNOLOGY

FEBRUARY 2008

Approval of the Thesis:

INHERITANCE OF WOOD SPECIFIC GRAVITY AND ITS GENETIC CORRELATION WİTH GROWTH TRAITS IN YOUNG *PINUS BRUTIA* PROGENIES

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ABSTRACT

INHERITANCE OF WOOD SPECIFIC GRAVITY AND ITS GENETIC CORRELATION WİTH GROWTH TRAITS IN YOUNG *PINUS BRUTIA* PROGENIES

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January 2008, 73 pages

In long term, to discover the genes responsible for wood production, genetic control of wood specific gravity (WSG) in *Pinus brutia Ten.* (Turkish red pine) open pollinated Ceyhan progeny trial, which was established with the seeds collected from 168 clones originated from six clonal Turkish red pine seed orchards was studied. Wood samples were taken by destructive sampling during the rouging of this trial at the age of seven. Specifically; (1) to examine the magnitude of family differences and its components for wood specific gravity (WSG) and growth traits (height, diameter and stem volume); (2) to determine WSG inheritance and its genetic correlation with growth traits; and (3) to estimate breeding values of 168 families for the WSG and to predict genetic gain if selection is based on phenotypic, rouged and genotypic seed orchard by reselecting the best parents with respect to WSG.

Differences among the 168 families for mean WSG was large (ranged from 0.35 to 0.44), as indicated by high individual (0.42 ± 0.07) and family mean (0.55 ± 0.03) heritabilities. Family differences and high heritabilities were also observed for all growth traits. Genetic correlations between WSG and growth traits were statistically insignificant (near zero), while low and insignificant negative phenotypic correlations among the same traits were observed.

Realized genetic gain for single trait selection at age seven was insignificant (0.37 %) for WSG and 8.4 % for stem volume in phenotypic seed orchards. Average genetic gain in breeding zone after roguing, by leaving the best 20 clones in each seed orchard, reached 1.7 % for WSG and 16.1 % for stem volume. Genetic gain (relative to controls) at the age of seven obtained from the first generation genotypic seed orchards consisting the best 30 clones was estimated 5.2 % for WSG and 35 % for stem volume. Multi-trait selection was also proposed in this study for the same traits. Selection of best 10 families for the highest WSG and stem volume breeding values produce 5.6 % genetic gain for WSG and 27.7 % genetic gain for stem volume. For the future, the 168 families with known phenotypic and genotypic values regarding to WSG will be screened for the genes responsible for wood production.

Keywords: *Pinus brutia*, Wood Specific Gravity, Progeny Test, Heritabilities, Genetic and Phenotypic Correlations, Genetic Gain

ÖZ

GENÇ *PINUS BRUTIA* DÖL DENEMESİNDE ÖZGÜL AĞIRLIĞIN KALITIMI VE BÜYÜME KARAKTERLERİYLE OLAN İLİŞKİSİNİN BELİRLENMESİ

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Uzun vadede odun üretimden sorumlu genlerin belirlenmesi için, Ceyhan Orman Fidanlığında altı adet klonal tohum bahçesinden toplanan tohumlarla kurulan 168 üvey kardeş aileli Kızılçam döl denemesi kullanılarak, bu türdeki odun özgül ağılığının genetik kontrolü çalışılmıştır. Gerekli odun örnekleri denemenin yedinci yaştaki aralama esnasında kesilen ağaçlardan elde edilmiştir. Bu çalışmadaki ulaşılmak istenen ana amaçlar; (1) odun özgül ağırlığı ve büyüme karakterleri açısından test edilen aileler arasındaki farklılıklar ile bu farklılığa ait bileşenlerin araştırılması, (2) özgül ağırlığın kalıtımsal özelliği ile büyüme karakteri arasındaki genetik korelasyoların belirlenmesi, (3) fenotipik, ayıklanmış ve genotipik tohum bahçelerinin kurulmasıyla elde edilecek genetik kazancın hesaplanması için özgül ağırlık açısından 168 aileye ait ısla değerlerinin ortaya konması olarak belirlenmiştir.

Odun özgül ağırlığı açısından 168 aile birbirinden oldukça farklı değerler göstermiştir (0.35 ile 0.44 arasında). Elde edilen bu farklılık tahmin edilen aile (0.55$\pm$0,03) ve bireysel (0.42$\pm$ 0,07) kalıtım değerlerine de yansımış olup her iki degerde oldukça yüksek olarak bulunmuştur. Kalıtım derecelerinde ve aileler arasındaki farklılıklar aynı şekilde büyüme karakterlerinde de gözlenmiştir. Özgül ağırlık ile büyüme karakterleri arasındaki genetik korelasyonlar istatistiki olarak anlamasız bulumuştur. Aynı şekilde fenotipik korelasyonlarda da anlamsız ve negatif olarak bulunmuştur.

Yedinci yaştaki tek bir karaktere göre yapılan seleksiyonda kontrol materyaline göre fenotipik tohum bahçelerinden elde edilen genetik kazanç, gövde hacmi için % 8.4 olarak hesaplanırken, bu değer özgül ağırlık açısından oldukça düşük olup (%0.37) istatistiki olarak anlamsızdır. Her bir tohum bahçesinde 20 klon bırakılacak şekilde bir genetik ayıklama yapılması sonucunda tohum bahçelerinden elde edilecek genetik kazanç ise gövde hacmi için % 16.1 ve özgül ağırlık içinde %1.7 olarak tahmin edilmiştir. Islah değerlerine göre bir ve ikinci seri denemelerde en yüksek ıslah değerine sahip 30 klonla kurulacak genotipik tohum bahçelerinden elde edilecek genetik kazanç, gövde hacminde % 35, özgül ağırlıkta ise %5.2 olarak bulunmuştur. Özgül ağırlık ile büyüme karakterleri arasında genetik ve fenotipik bir ilişkini olmaması her iki karakter açısından da bir seleksiyon yapılabilmesine olanak sağlamıştır. Her iki karakter açısından en yüksek 10 ailenin seçilmesiyle elde edilen genetik kazanç gövde hacmi için % 27.7 iken özgül ağırlık için % 5.6 olarak hesaplanmıştır. Bundan sonraki çalışmada odun özgül ağırlığı bakımından fenotipik ve genotipik değerleri bilinen 168 aile, odun üretimden sorumlu genlerin tayini amacıyla kullanılacaktır.

Anahtar Kelimeler: *Pinus brutia*, Odun Özgül Ağırlığı, Döl Denemeleri, Kalıtım Derecesi, Genetik ve Fenotipik Korelasyonlar, Genetik Kazanç

To My Family

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σ^2_s: Set variation,

σ^2_b: Block variance in the set,

σ^2_f: Family variance,

σ^2_T: Total variance,

σ^2_a: Additive genetic variance ,

CV_{ga}: Coefficient of genetic variance,

CV_p: Coefficient of phenotypic variance

σ^2_{pi}: Phenotypic variance,

σ^2_{pfam}: Phenotypic variance of family means,

h^2_i: Individual heritability,

h^2_f: Family heritability,

S.E.: Standard error

$R_{g(x, y)}$: Genetic correlations

$R_{P(x ,y)}$: Phenotypic correlations

$COV_{PF(x, y)}$: Phenotypic covariance

$COV_{F(x, y)}$: Family covariance

Y_{ijkl}: Observed value of l [th] individual in the i [th] set j [th] block , k [th] family.

μ: Experimental mean,

S_i: Environmental effect of i [th] set, i=1, 2, 3, 4 ;

$B_{j(i)}$: Effect of j [th] block in the i [th] set , j=1, 2, … , bi ;

$F_{k(i)}$: Effect of k [th] family in the i th set, k=1, 2, …, fi ;

$FB_{jk(i)}$: Family - block interaction,

e_{ijkl} : Experimental error,

GCA: General combining ability,

WSG: Wood specific gravity,

HT7: Height at age of seven,

HT4: Height at age of four,

BV: Breeding value,

ABV: Absolute bree,ding value

FMİN: Minimum family mean,

FMAX: Maximum family mean,

Dia: Diameter at age of seven,

FTSBRD: Forest trees and seeds breeding research directorate

TSI: Turkish Standards Institution

CHAPTER 1

INTRODUCTION

1.1 Brief Characteristics Of The Forestry Sector In Turkey

According to current forest inventories and management plans, Turkey's forest area covers 21.2 million ha; that is, about 27.2 percent of Turkey's land area. The forest area is nearly evenly divided between conifers and broadleaves. Only about 50 % of the forest area contains productive forest. Of this, 8 million ha are classified as productive high forest and about 2.5 million ha as productive coppice forest (Anonymous, 2006). In comparison with other countries per capita total forest area in Turkey is not very high due to the increasing population. Despite the large area of forests, it accounts for only 0.32 ha per capita in Turkey, while the same indicator is 1.13 ha for the USA, 4.2 ha for Finland, 2 ha for Norway, 3.1 ha for Sweden, 0.92 for ha Greece 1.4 ha for all Europe and 0.6 ha for the world (FRA, 2000). The story becomes more dramatic when we compare per capita productive forests. For example in Turkey it is only 0.15 ha per capita, while it is 4.53 ha for Finland, 4.2 ha for Russia, 3.76 ha for Brazil, 0.26 ha for Europe and 0.64 ha for the world as a whole (Danchev *et al.*, 2005).

Although the total standing stock is estimated as 1.17 billion m^3 in Turkey, the average volume (56 m^3/ha) appears to be low because of the large degraded and under-stocked forest. In the productive high forest, stocking

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is 125 m^3/ha, just below the European average of about 130 m^3/ha, while stocking in productive coppice forests averages 33 m^3/ha. The estimated current annual growth for all Turkey's forests is 32.4 million m^3 (Anonymous, 2001a).

In Turkey, about 99.9 % of forest lands and resources are under the direct control of the agencies of the Ministry of Environment and Forestry. The round wood production made from state forestry meets about 73 % of the total round wood demand. Roughly, 7.5-8 million m³ of industrial round wood and 5.0 million m³ fuelwood are produced from the state forests by General Directorate of Forest (GDF) annually. Despite the small area of private forests, which are mostly poplar plantations (200,000 ha), its share in industrial round wood market is relatively high. Private sector fast-growing plantations and agro-forestry sites produce about 3.2 million m³ industrial round wood and 1.5 million m³ fuel-wood annually (Ramazan, 2005). In spite of these production amounts from state and private forest, wood production is not enough to compensate the rising demand for forest products. As it can be seen from Table 1.1, the annual apparent consumption of industrial wood is about 13-13.5 million m³ and fuel wood (illegal cutting) apparent consumption is about 6-6.5 million m³.

Beside this deficit in the fuel and industrial wood production, the supply of high quality round-wood is also far from meeting domestic demand in Turkey. Most of the produced round-wood is of low quality, as a result of decreasing areas of old growth and high quality forest. The share of first and second quality wood less than five percent; the remainder is third quality (Anonymous, 2001b). Therefore, there is a large gap between domestic demand and production of high quality and quantity logs. This deficit, which is predicted to reach 3.5 million m^3 in 2020, is met through illegal cuttings (mostly to meet fuel wood needs of forest village dwellers)

and with imports of round-wood for industry. Illegal cutting of fuel wood from the state forests is estimated as 5-6 million m^3 annually (Konukcu, 2001). Although amount of wood import changes significantly year to year, depending on the certain factors such as currency rates, domestic demand and prices, this amount varied from 1 million m³ to 2.1 million m³ in last decade (Table 1.1).

Table 1.1 Industrial wood production and consumption data of Turkey for the period of 1996-2004 (1000m^3)

X1000	1996	1997	1998	1999	2000	2001	2002	2003	2004
PRODUCTION	26 042	24 598	23 935	23 796	23 440	22 425	23 607	22 605	23 478
GDF	15 331	13 992	13 444	13 446	13 225	12 461	13 695	13 182	14 343
Illegal	6 312	6 110	5 915	5 725	5 475	5 213	4 950	4 650	4 350
Private sec	4 399	4 495	4 577	4 625	4 740	4 751	4 762	4 773	4 785
CONSUMPTION	26 948	25 641	25 146	25 389	25 911	23 521	24 900	24 050	25 106
Net Import	1170	1099	1 271	1 500	1 880	1 068	1 490	1 448	2 103

Source: Anonymous 2001(a) and 2006

To meet current and future demands without increasing pressures on old-growth and ecologically sensitive forest lands, timber productivity per unit area must be increased in Turkey. Current studies indicated that intensively managed plantations, employing the best genetically improved planting stock and best silvicultural practices, are believed to be the most effective strategies to meet wood demands, rather than managing more hectares of forest.

1.2 Potential Gains From Tree Improvement Programs

Productivity improvement from forest genetics has helped to provide a reliable, ecologically sustainable, and economically affordable supply of wood throughout the world in the last 50 years. Plantations of genetically improved forest trees were critical to maintain sustainable wood supplies in the last decades. According to ABARE (1999), although plantations accounting for only five percent of the total global forest cover, it has supplied about 35 % of global round-wood. In several countries industrial wood production from forest plantations has significantly substituted for wood supply from natural forest resources. Forest plantations in New Zealand met 99 percent of the country's needs for industrial round-wood in 1997; the corresponding figure for Chile was 84 %, for Brazil 62 % and 50 % for Zambia and Zimbabwe (FRA, 2000).

In the U.S., Southern Tree Improvement Program has completed 56 years of genetic improvement for loblolly pine (*Pinus taeda*) and slash pine (*Pinus elliotti*)*,* which are the most commonly planted species in the country, with about 11 million ha in plantations. The Southern Tree Improvement Program plants approximately 1.2 billion seedlings annually, 80% of which are loblolly pine seedlings and 20% are slash pine seedlings. Most importantly, all planting stocks are genetically improved seedlings from seed orchards (Li *et al,* 1999, White *et al,* 2003). Trees grown from seeds of first-generation seed orchards have produced 7-12% more volume per acre at harvest than trees grown from seed collected from stands. The second-generation seed orchards are now producing more than 50% of the total seed harvest in the region with estimated gains ranging from 13% to 21% in rotation volume over unimproved seedlots. When the second-generation seed orchards are rogued to the best, retaining 30% of the parents, gains of 26% to 35% in volume production at

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harvest are expected. Additional gains over the first-generation are estimated 14-23% for rogued seed orchards. Genetically improved stock has not only demonstrated outstanding growth, but has also lower infection from fusiform rust, typically 20%-25% below the unimproved seedlots. It is suggested that with additional improvements in value from quality traits (stem straightness and wood quality), the estimated genetic gains in value is expected to be much greater (McKeand *et al* 2003). Although only 15 % of the commercial forests are currently in plantations, in Southern US about 50 % of the South's timber supply cames from these pine plantations. These plantations also contribute about 15% to 20% of the world's industrial wood fiber supply, which is the largest share of any region in the world (FAO, 2002).

Economical importance of tree improvements programs was very well summarized by Willan (1988).He stated that "… in the case of a fast-growing tropical pine, planted at a rate of 1000 ha a year, with a rotation of 16 years, 10% genetic improvement and 6% interest, the project could show a revenue of around $0.6 million when the youngest of the 16 annual 1000 ha blocks of improved commercial plantations is harvested."

Tree breeding activities, in addition to its primary purposes, also provide opportunities for conserving forest gene resources. Through the forest tree breeding studies within the last 50 years improved wood production on limited commercial lands reduced the logging pressures on natural forests, old-growth and ecologically sensitive forests, in southern U.S. Furthermore, establishment of seed orchards as an *ex-situ* program and the designation of gene conservation forests as an *in-situ* program, significantly contributed to the conservation and sustained use of forest resources (Li, 1999).

1.3 Tree Improvement Practices In Turkey

Tree breeding program in Turkey was initiated with determination of seed transfer and breeding zones for many tree species in 1960s. Fallowing this determination, 344 seed stands covering 46.327.5 ha for 27 different forest tree species were identified. From these seed stands 6920 plus trees were selected and transferred to 166 clonal seed orchards covering 1155 ha for 11 species. In addition to the clonal ones, 35 seedling seed orchards covering 184 ha were also established for 19 species that form seed in an early age (Anonymous, 2006). Although several seed production plans have been made up to now, a systematic-long term breeding plan was not available until preparation of ''National Tree Breeding and Seed Production Programme for Turkey'' (Koski and Antola, 1993). Within this framework, *Cedrus libani*, *Pinus sylvestiris, Fagus orientalis, Pinus nigra,* and *Pinus brutia* were determined as target species for intensive tree breeding studies due to their economical and biological importance. However, the highest priority was given to *Pinus brutia* (Turkish red pine) in National Tree Breeding Program (NTBP) because of its;

- Wide distribution and large of potential plantation area in Turkey,

- Fast growing and flowering ability at early ages,

- High genetic diversity and resistance to environmental stresses,

- High wood density and

- Valuable timber and timber products.

1.4. Economical And Biological Properties Of Turkish Red Pine

Because of large distribution area, planting program and the high economic importance of the species, Turkish red pine (*Pinus brutia Ten.*) is considered as the single forest tree species in Turkish forestry that deserves most attention for future selection, breeding and gene conservation activities. Turkish red pine is a member of Division Gymnospermae, Class Coniferae and Family Pinacea, Genus *Pinus.* Natural range of Turkish red pine in the world is restricted in the eastern Mediterranean region (Figure 1.1). Although its main distribution is in Turkey, it is possible to see this species in Greece, Cyprus, Syria, Lebanon, Jordan, northern Iraq, over the north coast of Black Sea in Crimea and the many Islands of Aegean and Mediterranean Sea (Alan, 2006).

Despite the wide distribution area in eastern Mediterranean region, Turkish red pine reaches its greatest distribution in southern Turkey, where it has become one of most valuable commercial and widely planted tree species. According to the latest forest surveys, Turkish red pine forest covers an area of 4.2 million ha. (2.7 million ha. productive and 1.5 million ha. degraded), which constitutes 51% of the coniferous and 20% of the total forests areas in Turkey (Anonymous, 2006). In accordance with its wide distribution, proportion of Turkish Red Pine within annual industrial wood production is 47%, which is the largest share of any tree species in Turkey (Konukcu, 2001).

In addition to its wide distribution area, the amount of potential plantation area is also very important to reduce cost of the tree breeding studies. For example; the cost of the genetically improved seed for 100 ha/year plantations was calculated as 212 US $, although this value was just 33.8

Figure 1.1 Distribution range of *Pinus brutia* (Critchfield and Little, 1996)

US $ for 10.000 ha/year plantations (Willan, 1988).The estimated potential plantation area for Turkish Red Pine, which is used widely in afforestation and reforestation programs, is estimated as 2.2 million ha in Turkey. According to the records of General Directorate of Forestry, in Turkey, 620.000 ha of forested land were planted with Turkish red pine at the end of 2006 with yearly average plantings being approximately 42.000 hectares. Areas planted with Turkish red pine accounted for 37% of the total planted area of the country.

For most forest trees, the generation time is long because of long rotation ages and a period of 10 to 20 years is required before abundant flowering occurs. Therefore, it takes years to do the necessary selection, breeding, and testing to obtain the desired improvements (Zobel and Talbert, 1984).

Fortunately, it is observed that vigorous open-grown Turkish red pine seedlings start bearing male and female flowers as early as at the age of 4-5 years. The first crops of viable seed commonly appear at age of 7 to 8 years and production is regular from 10 years in plantation and 15-20 years in natural stands. Some seeds are available every year but good seed crops are produced in two-year intervals (Gezer, 1986). The rotation age of natural Turkish red pine forests is 50 years for good sites and 60 years for medium and poor sites. However, the rotation age of Turkish red pine is expected to decrease from 60 to 25-35 years in good sites plantations, by applying tree breeding activities. (Usta, 1991)

In addition to its flowering ability at early ages, Turkish red pine is also accepted as fast growing species compared to other forest trees in Turkey. The maximum mean annual increment (yield class) is 50.5-75 m^3 per ha in natural stands. The amount can reach up to 100-120 m^3/year in Turkish red pine stands found in good sites. The current annual increment is estimated as 150 m^3 for future plantations, using seeds from suitable provenance and applying intensive soil cultivation (Erkan, 1996).

Genetic variability is the major driving forces in tree breeding programs since suitable management of this diversity may produce considerable gain in quality and quantity of wood produced by trees. Isoenzyme, molecular marker and morphological studies indicated that genetic diversity in Turkish red pine populations is generally high. An isozyme study revealed that genetic diversity in a Turkish red pine seed orchard was shown to be higher than two natural populations close to this seed orchard (Kaya, 2001). According to a molecular marker study investigating genetic consequences of forest management and tree breeding activities of Turkish red pine revealed high genetic diversity in Turkish red pine populations and successful transformation of this variation from seed

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stands to the seed orchards and plantations (İçgen *et al,* 2006) Genetic diversity analysis also demonstrated that highest proportion of genetic diversity was within populations (89%).This suggests that, considerable genetic gain could be realized for growth traits if selection is applied at the population, family and within family levels for a given breeding zone (Işık, 1993)

The maintenance of high levels of genetic diversity of coniferous trees in breeding and production populations is closely related with their viability, survival, and adaptability to different environments (Hamrick and Godt, 1989). It is known that Turkish red pine is a coastal and a drought resistant species that withstands more aridity and poor soils than most other timber species growing in Mediterranean climate. Although it requires mild winters, some of its provenances can grow successfully, out of its natural habitat, on sites of drier and cooler climate (Gezer and Aslan, 1980).

Wide-range utilization of a species wood in various wood-based industries is also very important for breeding studies. Different usage of the wood makes a major economic contribution to the social use of the people, who are employed in the forests and forest industries. Timber of Turkish red pine is used in a very wide range from fencing posts through telephone and transmission poles to pit wood, railway sleepers and sawlogs for box-making, general construction and joinery industries. Because of its high density wood and long, suitable wood fibre, Turkish red pine is especially preferred for pulp, paper and board manufacturing (Goksel and Özden, 1993). It is also subject to produce great amount (around 3 thousand tons/year) of turpentine each year. In addition to this, its bark is also suitable for adhesive production (Berkel, 1957).

1.5 Breeding And Genetic Improvement Studies Of Turkish Red Pine

Due to its biological and economical importance mentioned in section 1.4, Turkish red pine is the most important tree species in Turkey and has been given the highest priority for tree improvement program relative to other species. In Turkey, tree improvement studies have been accelerated after 1993 by preparation of "National Tree Breeding and Seed Production Programme for Turkey" (Koski and Antola, 1993). However, determination of seed transfer and breeding zones, selection of many seed stands, plus trees and establishment of clonal seed orchards had been accomplished before preparation of this program.

In Turkey, the first tree breeding activities for Turkish red pine were initiated by the determination of seed transfer zones of this species according to ecological similarities and length of the vegetation period (Urgenç, 1967). Then, due to its wide distribution in different ecological regions Turkish red pine tree breeding program has been partitioned into six main breeding zones, based on major climatic and geographical gradients and early genetic test results, i.e., Mediterranean, Aegean, Marmara, Amanos mountains, Western Anatolian and Black Sea regions. Each main zone was also divided into the sub-zones according to different elevation ranges (Figure 1). Each sub-zone was considered as a separate breeding unit (Atalay, 1998). Following the determination of breeding zones, 78 high quality natural stands (11,650 ha.) have been identified and managed for seed production and plantation establishment. According to proposed plan, it was determined to select 500 trees from each sub-zone with a total of 3500 trees for the species (Koski and Antola, 1993). However, up to now about 2450 phenotypically superior plus trees have been selected extensively from all breeding zones and have been grafted in 63 seed orchards, all of which are first-generation seed orchards and

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Breeding Zones			Elevation Range	Altitude
I	Mediterranean	1.1	Low	0-400
		1.2	Middle	401-800
		1.3	High	801-1200
II	Aegean	2.1	Low	0-400
		2.2	Middle	401-800
III	Marmara	3.1	Low	200-600
IV	Amanos Mountain	4.2	Middle	401-800
V	Western Anatolian	5.2	Middle	300-800
VI	Black Sea	6.1	Low	0-500
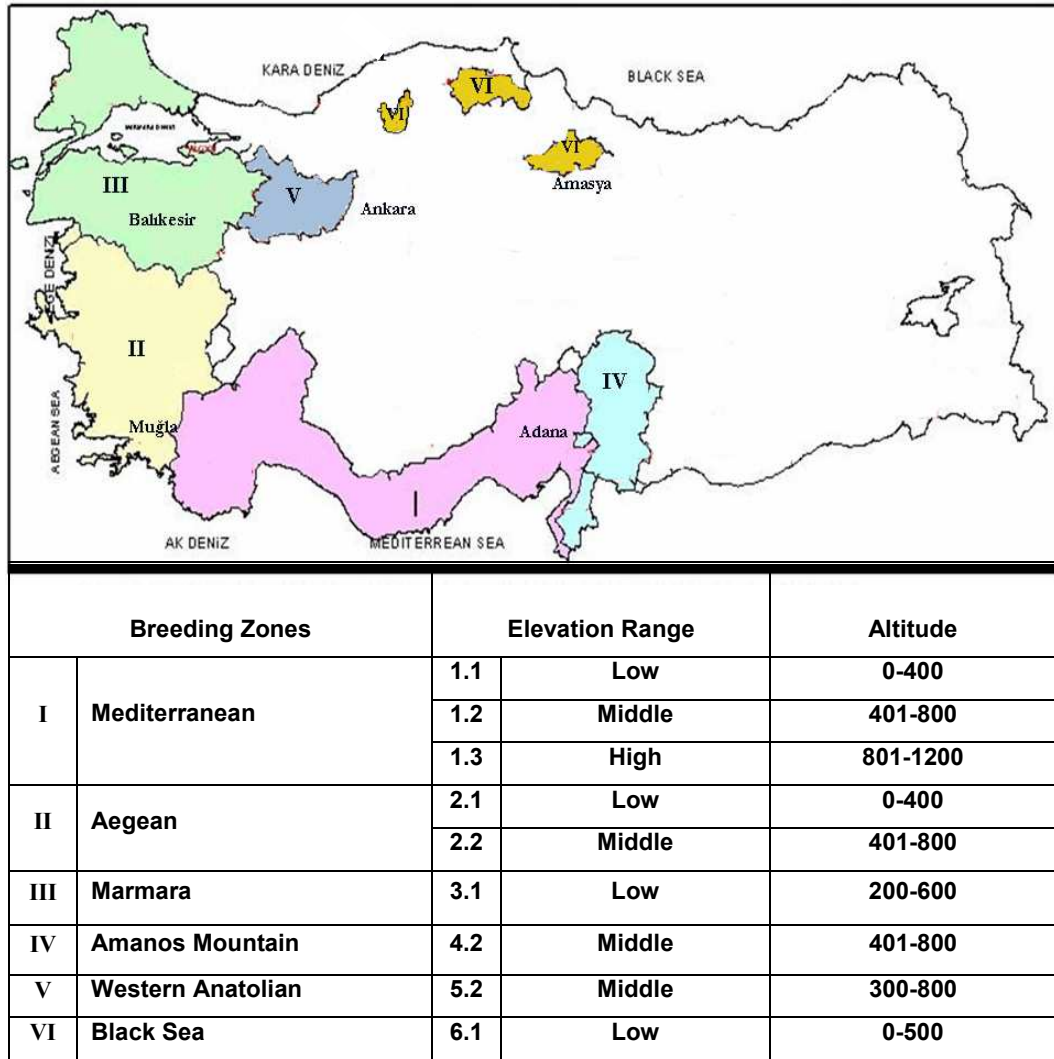
Figure 1.2 Distribution and location of breeding zones for *Pinus brutia*

they have not been subjected to genetic roguing yet (Anonymous, 2001b). Today, a large proportion of the seeds used for plantations are still collected from 78 seed stands located at different places within the natural range of the species. A considerable amount of seeds is also obtained from 58 seed orchards (Boydak *et al,* 2006). It is possible to state that seeds produced from seed stands and seed orchards are enough for

Turkish red pine reforestation activities in Turkey. Certainly seeds from those resources will expand the yield level of Turkish red pine forests but to get much more gain from breeding activities, heavy rouging of seed orchards based on their genetic quality is required. However, all the plus tree selections were primarily based on their phenotypes in natural forests. Thus, nothing certain can be said about this tree's genotype, because phenotypic appearance is influenced by its genetic potential as well as the quality of the environment in which the tree is growing.

The best way to tell if a parent tree has superior genetic quality is to compare the performance of its offspring against of the other parent trees. With appropriate checklots and family overlapping in progeny trials, calculation of parent's breeding values, estimating genetic gains over unimproved population, and establishing second generation seed orchards by combining the best clones from several seed orchards are all possible (Squillace, 1970). Therefore, progeny trials have been primary concern in the genetic improvement of Turkish red pine in the region. For these purposes, 25 (90 ha) progeny trials concerning clones of Turkish red pine seed orchards and plus trees were accomplished in five breeding zones (Anonymous, 2006).

Because of its high wood density, high resin content and long, wood fibre, Turkish red pine is especially preferred for pulp and paper manufacture. Therefore, production of fast growing trees with high quality wood for pulp industry was the main target in *"National Turkish red pine tree breeding program"*. To reach this objective especially wood specific gravity, which has a direct effect on quality and yield of wood, was selected as ideal trait to be improved by tree breeding studies.

1.6 Wood Specific Gravity (WSG)

Wood specific gravity is perhaps the oldest and most widely used criterion for evaluating quality of wood and its strength properties. Specific gravity itself is dimensionless and defined as the ratio of the dry weight of wood substance to the weight of an equal volume of distilled water at 4 ^{0}C. Wood density, on the other hand, is the ratio of the dry weight of wood to its volume and is normally expressed as kilograms per cubic meter (kg/m^3) (Brown *et al, 1949).* In fact wood density and wood specific gravity are different ways of expressing the amount of actual wood substance present in a unit volume of wood. WSG was primarily used in this study, but either specific gravity or density can be calculated by knowing the other. Using the metric system, wood density and specific gravity are easily converted. When wood density is expressed in kg/m^3, division by 1000 produces the equivalent specific gravity value. For example, 425 kg/m^3 equals a specific gravity of 0.425 (Belonger, 1998)

While commonly referred to as an individual trait, wood specific gravity is actually a composite of several wood properties such as chemical content of the wood, cell wall thickness, cell diameter and earlywood to latewood ratio, each of which has a strong inheritance (Kaya *et al, 2003*). Especially in conifers, cell wall material has a strong relationship with the WSG. This material is very dense and consists of 40-50 % cellulose, 20-35 % hemicellulose and 15-35 % lignin produced by the assimilation of photosynthate. Together, these tree major components determine the specific gravity of cell wall and wood tissue (Barnett and Jeronimidis, 2003).

If we assume that the density of cell wall is constant, the density of wood is mainly determined by the fibre properties such as, size of wood cells or

their lumens and by the thickness of cell wall. Hannrup *et al* (2001) found that proportion of latewood has been proved to be a good predictor of wood density. They emphasize that early lumen diameter and latewood proportions have the strongest correlation with WSG in mature wood. With multiple regression analysis, they could explain up to 73% of the variation in WSG. According to Zobel and Talbert (1984), latewood includes tracheids in which the common wall between two cells is exactly half or over half the radial width of lumen. In other words, the double wall thickness is equal to or greater than the half-with of the cell lumen. Since latewood cell walls are much thicker than those of earlywood it follows that the higher the latewood–earlywood ratio the higher will be the specific gravity of the wood. Owing to this difference between earlywood and latewood, the most important variation in WSG is observed within one growth ring. WSG also varies with species, provenance, site location and within each tree depending on the point in the tree at which it is measured (Belonger, 1998).

1.6.1 Effect Of Position In The Tree On The Variation Of WSG

There is considerable evidence to indicate that the wood in many tree species, particularly in coniferous trees, decreases in WSG with increasing distance above the ground. The presence of juvenile wood, which is produced by live crown and characterized by low WSG and low percentage of latewood, has been suggested as being one of the most important causes of this perpendicular variation in wood properties of conifers (Larson, 1969). Barnett and Jeronimidis (2003), concluded that the decrease in the specific gravity of the wood is due to the decrease in the percentage of latewood in any given increment, from the base of the trunk upward; since the density of pinewood, to a large extent, is a function of the amount of latewood present. The specific gravity of the wood in any given increment, thus would decrease progressively upward.

At any given height in a tree-trunk, the density of the wood also varies considerably along a radius. In coniferous trees, wood of rapid growth and with a relatively large percentage of juvenile wood and hence low in specific gravity is frequently formed near the pith. As the rate of growth decreases because of more crowded conditions developing in the stand, the specific gravity tends to increase because of increase in latewood to early wood ratio. In over mature trees, on the other hand, the wood density may again decrease toward the bark at a given level. In old coniferous trees, for the reason stated, the wood of highest density is commonly found in the intermediate zone, the lightest wood near the center of the tree, while the density of the wood in the outer zone ranges from low to high (Woodcock, 2002).

This large variation in WSG from base to top and pit to bark within a tree makes it difficult to be measured. Fortunately, investigators have found that breast height sampling is acceptable for estimating average tree, characterizing tree-to-tree variability, and studying the inheritance of wood density. Zobel and van Buijtenen (1989) reported an average correlation coefficient of 0.8 between breast height samples and whole-tree density for many conifers.

1.6.2 Importance Of WSG In Terms Of Tree Breeding Studies

From tree breeding perspective, the importance of specific gravity many times overshadows the importance of other wood properties, because of its strong effect on quality and yield, high heritability and large economic gain from selection. Among the different wood properties such as chemical characteristics (lignin and extractives content), module of elasticity, spiral grain and fibre characteristics, WSG has a direct effect on tracheid yield, paper strength and utility of solid wood products as well as the quality of

the final product (Drovak, 1997). In most tree breeding programs which have pulp and paper as the final products, specific gravity is the only wood characteristic desired to be improved. Because for paper properties, high WSG generally indicates lower tensile, burst, and fold strengths, greater bulk and higher tear strength (Smook, 1992).

1.6.3 Inheritance Of WSG

Strong inheritance of WSG in trees is very important for breeding activities, because it enables us to correlate its value in juvenile wood with its value in mature material for next generations. This correlation presents advantages in shortening the breeding programs and obtaining good gains from genetic manipulation. Inheritance of WSG for many tree species well summarized by Zobel (1961). He concluded in this review that ''narrow-sense heritabilities were found to be remarkably high for the specific gravity, with values reported as high as 0.6 or 0.7. These approached the values of broad-sense heritabilities, which were remarkably similar for several species, ranging from 0.50 to 0.85 for WSG''

Zobel and Rhodes (1957) studied progenies of several 12-year-old selfed trees, as well as open-pollinated progenies of *Pinus taeda.* In every instance, high specific gravities of the progenies were associated with high parental specific gravities. Brown and Klein (1961) found that when high specific gravity *Pinus taeda* parents were crossed, the 2-year-old progeny had a specific gravity of 0.39, while the progeny of high x low specific gravity parents averaged 0.35. They concluded that progeny groups did inherit specific gravity differences from the parent trees. In the same study the results obtained from 17 control-pollinated crosses made among 8 trees selected for high and low specific gravity was also reported. About 0.2 of the variability between parental combinations for WSG appeared to be genetically transmitted.

1.6.4 Gain In WSG From Tree Breeding

Studies have provided evidence that selection for specific gravity could result in large economic gains. Borralho *et al.* (1993) showed that profits in a chemical craft mill in Portugal could be increased by $475,000 per year if selection efforts in *Eucalyptus* included wood density, pulp yield and volume. Similarly, Lowe *et al* (1999) found that selection on wood density could increase profits in loblolly pine pulp mills by more than 3%. Blair *et al.* (1975) have published predictions of gain in pulp yield and tear strength in young loblolly pine through genetic increases in wood density. They found that yield increases from breeding for high wood density could be in the order of 10 to 15 % of the mean pulp yield, and tear strength could be increased by about 10 %.

1.7 Objectives

The trend in many tree breeding studies in recent decades has been towards enhanced growth and shorter rotations, thus increasing log production (Barbaour & Kellogg, 1990). However, intensive timber production may cause changes in the anatomical and technical properties of the wood, thus reducing the suitability of the wood for many products. In The Turkish National Tree Breeding Program, because of its suitable traits Turkish red pine was especially preferred for pulp and paper manufacture. Therefore, production of fast growing trees with high quality wood for pulp industry is the main target in National Turkish red pine Tree Breeding Program (Koski and Antola, 1993). To achieve this objective, wood specific gravity along with the stem volume was selected as ideal traits to be improved in this program. For this reason, six progeny trials were established in Fethiye, Antalya and Ceyhan for the Turkish red pine low-elevation (0-400) breeding zone of Mediterranean region in 1998 in order to test the seed orchards and selected plus trees according to their WSG

and growth performance. Ceyhan nursery, which was established with 168 half sib families, is the subject of this study. Because, it reached its thinning program earlier than the others, in 2005. Therefore, the wood samples to determine WSG were obtained by destructive sampling from trees which were removed during the thinning program of Ceyhan Forest Nursery. In long term, families in Turkish red pine breeding program will be screened and genotyped for the genes responsible for wood production and eventually those genetic studies incorporate to the breeding program. But first the following objectives should be achieved;

- Investigation of the magnitude of 168 family variation in wood specific gravity (WSG) and growth traits,
- Determination of wood specific gravity inheritance strength and its genetic correlation with growth traits such as height, diameter and stem volume,
- Estimation of parental breeding values of families for WSG and growth traits, and development of an approach for using these parameters for the predicting genetic gain being obtained from phenotypic, rouged and genotypic seed orchard by reselecting the best parents,
- Providing basic information to have effective tree breeding and guidance in the Turkish red pine Tree Breeding Program.

All these information obtained by completion of this project will be able to be used for development of plus trees (mother trees) with high breeding values that are the breeding materials for the low elevation Turkish red pine breeding zone. Also, the practiced selection programs will yield genotypes with high and quality (wood fiber characteristics, spring and summer wood ratios) wood products to be used for industrial plantations.

CHAPTER 2

MATERIAL AND METHODS

2.1 Establishment of Progeny Trials

Depending on the objectives of a tree improvement program, progeny tests with seed consist of either "one-parent" tests or "two-parent" tests. For the one-parent tests, open pollinated seeds are collected and the female parent is the only one specifically known. Although less refined than the two-parent tests, establishment of open pollinated tests can be started without any delay. Furthermore, considerable information can be obtained on the inheritance pattern by these tests and they are especially useful if early information is desired on how much improvement in a certain characteristic is obtainable (Mergen, 1969). Therefore, in "National Tree Breeding and Seed Production Programme For Turkey 1994-2003" open pollinated progeny trials was suggested. For this purpose, in low elevation zone (0- 400 m) of the Mediterranean Ecoregion, progeny trials concerning Turkish red pine seed orchards and plus trees, were established based on "one-parent tests" in Fethiye, Antalya and Ceyhan by the Forest Trees and Seeds Breeding Research Directorate (FTSBRD) in 1997. Entries which were to be tested in these progeny trials were divided into two series. Establishment of the first series progeny trials were accomplished with the cones collected from six clonal seed orchards. The second series's entries were the original plus trees in natural stands. The details for all of these trials were provided thoroughly in Öztürk *et al* (2004)

In the first series progeny trials the cones were collected from 168 low elevation clones in six clonal seed orchards. Due to the undesired pollination from different pollen sources, each cone was collected from the trees that found at the center of the seed orchards. Information about progeny trials was given in Tables 2.1 and 2.2, while origins of these orchards are described in Table A.1 (Appendix A).

Table 2.1 First serial progeny trials in low elevation breeding zone of Mediterrenian Region (Öztürk *et al,* 2004)

	First serial progeny trials (1997)		
	Fethiye 1A	**Antalya 1B**	**Ceyhan 1C**
Number of families	168	168	168
Number of checklots	6	6	6
Number of sets	4	4	4
Family number in a set	42	42	42
Sub-blocking type	B*	B*	R**
Number of blocks	15	25	7
Planting design	2 trees nc	Single tree plot	4 trees row plot

* Set in replication   ** Replication in set   nc : noncontiguous

Bulk seeds from six seed stands were collected and included as checklots to compare test sites and to calculate genetic gain. Basic information about checklots and their original seed orchards were presented in Table B.2 (Appendix B). Each clonal seed orchard was originated from a separate stand.The cone collection from seed orchards was accomplished

Table 2.2 Distribution of families and control group to sets tested in first series progeny trials in Ceyhan Forest Nursery (Öztürk *et al*, 2004)

Numbers of The Seed Orchards and Their Origin	Sets				Total
	1	2	3	4	
3 (Antakya -Uluçınar)	14	10			24
7 (Mersin-Anamur)	14	16			30
4 (Mersin-Silifke)	14	16	5		35
5 (Antalya-Alanya)			15	14	29
11(Antalya-Kumluca)			11	14	25
16 (Antalya-Kemer)			11	14	25
Total	42	42	42	42	168
Number of Checklots	6	6	6	6	24

in 1996 and the seeds were extracted in the same year. The seedlings were raised in Gökova Nursery in 1997 and progeny tests were established in three test sites (Ceyhan 1A, Antalya 1B and Fethiye 1C) in subsequent year by the FTSBRD.

The number of trees in each progeny group is important that it must be great enough to keep the sampling error down. When a large number of trees are used in each block, the land area to be used is increased and this increases the degree of heterogeneity in the environment. The amount of variability between the different progeny groups is mostly not uniform and this introduces another variable (Schmidt, 1993). These difficulties were partially overcome by sub-blocking of the test sites. In this technique,
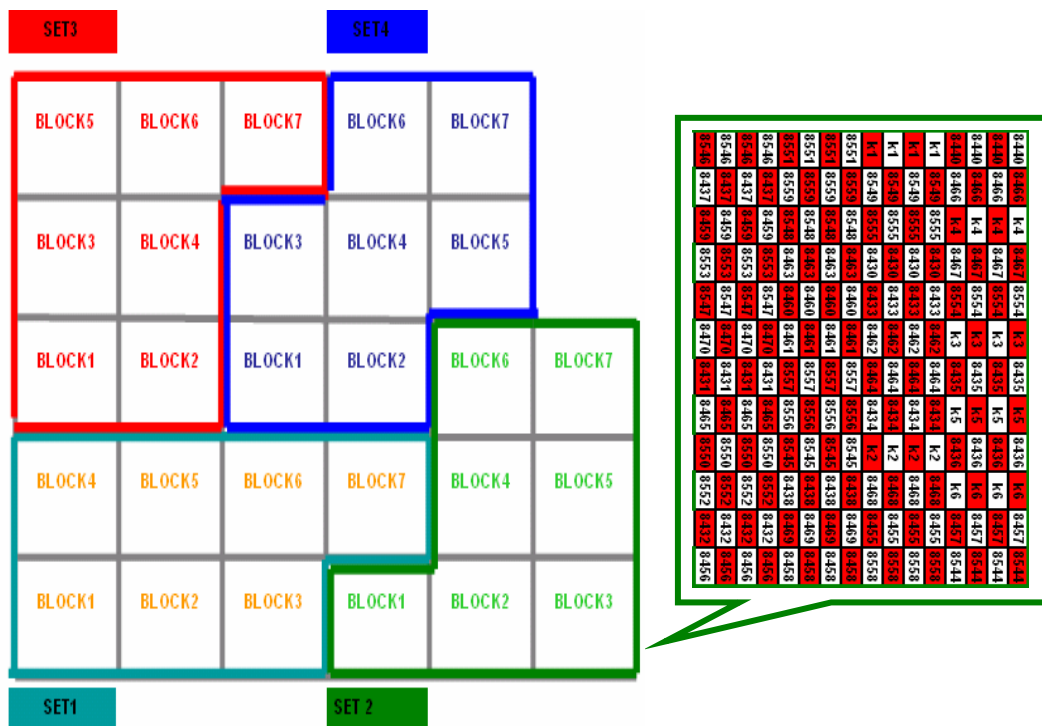
Figure 2.1: Schematic representation of Ceyhan progeny trial and numbered trees found in 2th set and 3th block Replication in sets design were used in trial and 4872 (168 family+6 checklots) X (28 trees) trees were included to the test site (Öztürk *et al*, 2004)

each set is divided into several sub blocks or replications. In the first series of progeny trials B type experimental design (four sets in different number of reps) was used in Fethiye 1A, Antalya 1B, while R type (reps in sets) was used in Ceyhan(1C) (Öztürk *et al*, 2004). In R type experimental design each set is established as a different trial and blocks are placed into these sets. As can be seen in Figure 2.1 each family, represented by 28 trees, distributed to the trial with four row plot and checklots (presented as k in the figure) were included to each block.

2.2. Collection of Wood Samples

In tree breeding studies progeny tests usually form a part of some larger forest and are usually thinned at some stage to maintain productivity and /or quality. The Ceyhan progeny trial was established an agricultural land and reached its thinning age in 2005 at the age of seven. Therefore, the wood samples to determine WSG were obtained by destructive sampling from this progeny. In Figure 2.1, removed trees during thinning of the trial were represented by red color for second set and third block. As mentioned earlier, WSG variation can be described in terms of geographic, tree-to-tree, within tree, and within annual ring components. Fortunately, investigators have found that breast height sampling is acceptable for estimating average tree wood density, characterizing tree-to-tree variability, and studying the inheritance of wood density (Wahlgren and Fassnacht, 1959). Therefore, after measuring the diameter and height of each tree, north sides of them were marked and 10 cm thick wood disks were taken from 1.30 m (breast height) above ground parts of stems of 2436 trees (168 families + 6 checklots x 14 trees) ,which were removed during the thinning program in the spring of 2005 by the FTSBRD.

Despite the high correlation between breast height samples and whole-tree density, in some species, WSG variation with height along the stem was observed (Zobel and Talbert 1984). Because of this, to represent whole tree 10 cm disks at three different heights were also obtained from 0, 1.30 and 4 m ground parts of stems of 192 trees (48 families) located in fourth set and second block. All disks were numbered and placed in bags to transfer Ito the FTSRBD laboratory in Ankara. WSG measurements were done according to TSI 2472th procedure. Therefore, first barks of the discs were completely removed from disks and the samples were cut from south and north part of the disks at 2x2x3 cm in dimensions. Samples were air dried up at room temperature for two months.

2.3 Determination Of Specific Gravity And Volume

Each 2x2x3 cm wood sample was numbered and soaked in water bath filled with distilled water and kept in bath for up to two days until the constant weight was obtained. To determine specific gravity, disks were weighed (green-weight) and volumes of samples were determined by the water displacement method. Then, they were oven-dried at 102± 3°C for 48 hours until the constant dry-weight was obtained. At the end, samples were weighed again to obtain oven dry-weight of wood at 0 % moisture content. Wood specific gravity values were calculated by dividing weight of oven dried samples to the volume according to Turkish Standards Institution's (TSI) 2472th procedure. Stem volume calculations were done according Usta (1991).

$$\text{Wood Specific Gravity} = \frac{\text{weight of given volume of wood}}{\text{weight of an equal volume of water}} \qquad (2.1)$$

$$\text{Volume} = 0.125247 + \text{diameter}^{1.676818} + \text{height}^{0.845096} \qquad (2.2)$$

2.4 Statistical Analyses

All the statistical analyses of progeny trial were done via Statistical Analysis Software (SAS) package program (SAS Inst., 2004). Before analyses, all the extraordinary values, which occur due to the mistakes in measurements and damaged individuals found in progeny trial, were removed from the data. 99% confidence interval was used to remove this type of values. Analysis of variance (ANOVA) for all growth traits and WSG was carried out by using a Proc Mixed procedure of SAS to state if there is a significant differences between families and seed orchards. Estimation of covariance and variance components for each trait was performed according to the following statistical model;

$$Y_{ijkl} = \mu + S_i + B_{j(i)} + F_{k(i)} + FB_{jk(i)} + e_{ijkl} \qquad (2.3)$$

where,

Y_{ijkl} : Observed value of lth individual in the ith set, j^{th} block, k^{th} family.

μ: Experimental mean;

S_i: Environmental effect of ith set, i=1, 2, 3, 4 ;

$B_{j(i)}$: Effect of jth block in the i th set, j=1, 2, … , bi ;

$F_{k(i)}$: Effect of k th family in the i th set, k=1, 2, …, fi ;

$FB_{jk(i)}$: Family - block interaction;

e_{ijkl} : Experimental error.

As it was mentioned before, in the Ceyhan progeny trial replication in set (R type) test design was used. In trial, each set was established as a different progeny trial and blocks were placed into these sets. Öztürk *et al* (2004) stressed that in this type of test designs, families found in blocks can encounter with different micro-environmental conditions, which cause large environmental variations between sets. Therefore, effect of set was also taken into account in statistical analysis.

2.4.1. Estimation of heritabilities

a) Individual (h^2_i) heritability and its standard error were calculated according to the formulas (Lynch ve Walsh, 1998) written below, assuming that the trees of a given family are related as half-siblings wherein the family variance component estimates one-quarter of the additive genetic variance (Becker 1992).

$$h_i^2 = \frac{\sigma_a^2}{\sigma_{pi}^2} \qquad (2.4)$$

, where

$$\sigma^2_{pi} = \sigma^2_f + \sigma^2_{fb} + \sigma^2_e$$: Phenotypic variance;

σ^2_f : Family variance ;

σ^2_{fb} : Family-Block interaction ;

σ^2_e : Error variance;

σ^2_a : Additive genetic variance ($4\sigma^2_f$)

b) Standard Error of Individual Heritability estimation was carried out according to Delta model, which include all the components found in individual heritability (Lynch and Walsh 1998).

(2.5)

$$S.E(h^2_i) = \sqrt{\left(\frac{S.E(\sigma^2_a)}{S.E(\sigma^2_p)}\right)^2 + \left(\frac{S.E(\sigma^2_a)}{S.E(\sigma^2_f)} + \frac{S.E(\sigma^2_a)}{S.E(\sigma^2_p)} - \frac{2Cov.(S.E(\sigma^2_a)*S.E(\sigma^2_p))}{S.E(\sigma^2_a)*S.E(\sigma^2_p)}\right)}$$

where;

$S.E(h^2_i)$: Standard error of individual heritability

$S.E(\sigma^2_a)$: Standard error of additive genetic variance

$S.E(\sigma^2_p)$: Standard error of individual phenotypic variance

c) Family (h^2_f) heritability and its standard error were calculated by using the fallowing equations (Lynch and Walsh 1998).

$$h^2_f = \frac{\sigma^2_f}{\sigma^2_{pfam}}$$ (2.6)

where;

$$\sigma^2_{pfam} = \sigma^2_f + \sigma^2_{fb} \cdot \frac{c_1}{c_2} + \frac{\sigma^2_e}{c_1} \qquad (2.7)$$

σ^2_{pfam} **:** Family means phenotypic variance;

σ^2_f **:** Family Variance;

σ^2_{fb} **:** Family - Block Interaction;

σ^2_e **:** Error Variance

c_1 and c_2 are the family and block-family interaction variation coefficients, respectively. These values were found in the TYPEIII expected sum of squares means calculated by SAS Proc GLM and presented in ANOVA tables (Table B.1-Appendix B).

d) Standard Error of Family Heritability estimation was carried out according to Delta model (Lynch and Walsh 1998).

$$(2.8)$$

$$S.E(h^2_f) = \sqrt{\left(\frac{S.E(\sigma^2_f)}{S.E(\sigma^2_p)}\right)^2 + \left(\frac{S.E(\sigma^2_f)}{S.E(\sigma^2_f)} + \frac{S.E(\sigma^2_f)}{S.E(\sigma^2_p)} - \frac{2Cov.(S.E(\sigma^2_f)*S.E(\sigma^2_p))}{S.E(\sigma^2_f)*S.E(\sigma^2_p)}\right)}$$

$S.E(h^2_f)$: Standard error of family heritability

$S.E(\sigma^2_f)$: Standard error of family variance

$S.E(\sigma^2_p)$: Standard error of family phenotypic variance

2.4.2 Estimation Of Breeding Value (BV) And Genetic Gain

To bring the results of genetic trials into an application, it's often useful to express the results in terms of response to selection, or gain from selection. In this sense, the calculation of breeding values (BV) is attractive because it allows breeders flexibility to choose parents among high BV for a combination of traits and avoid the use of a theoretically based i values (i.e., selection intensity tables), which may not reflect the exact distribution of the data. Another important attribute of estimation BV is that expected gain can be calculated by simply averaging the BV's for selected population (Yanchuk and Kiss, 1993) The prediction of parental breeding values for a single trait can be calculated from;

$$BV = 2 . \text{GCA effect} . h^2_f \qquad\qquad (2.9)$$

where, general combining ability (GCA) effect(%) is the family mean deviation expressed as a percentage of grand mean and h^2_f is the heritability based on family means. Breeding value for each family was calculated via the best linear unbiased predictors (BLUPs) by using Proc Mixed procedure with restricted maximum likelihood (REML) option in SAS (SAS Inst.,2004).

As genetic gains from selection or breeding program are determined by a comparison with unimproved materials, combined checklots were treated and taken as the baseline in the prediction of breeding values of families found in trial. However, the average of estimated breeding value, calculated by the BLUP, is equal to zero. Therefore, it is not possible to compare tested material with the checklots. To overcome this problem, absolute breeding values (ABV) were calculated by adding general mean of the traits to the breeding values and genetic gains were calculated according to the fallowing formulas;

a) Genetic gain from phenotypic seed orchard (ΔG_{pso}): This value also indicates the genetic gain of the breeding zone.

$$\Delta G_{pso} = \frac{(BV_f - BV_c)}{ABV_c} \cdot 100 \qquad (2.10)$$

BV_f: Average breeding value of 168 tested family in progeny trial

BV_c: Average breeding value of checklots

ABV_c: Average absolute breeding value of checklots

b) Genetic gain from rogued phenotypic seed orchard (ΔG_{rso}): In order to increase genetic gain in breeding studies seed orchards subject to genetic rouguing by leaving certain number of clone in the orchards. Genetic gain from rouged seed orchards were calculated with this formula.

$$\Delta G_{rso} = \frac{(BV_{rf} - BV_c)}{ABV_c} \cdot 100 \qquad (2.11)$$

BV_{rf}: Breeding value of the highest 20 clone that are left in seed orchard and the other parameters are the same as described in equation 2.10

c) Genetic gain from genetic seed orchards: Establishment of a genetic seed orchard with the certain number of clones having the highest breeding values is the best way of maximizing the genetic gain in breeding programs. Genetic gain obtained from these orchards is calculated via the fallowing formula;

$$\Delta G_{gno} = \frac{(BV_b - BV_c)}{ABV_c} \cdot 100 \qquad (2.12)$$

BV_b : Average breeding value of the first highest 30 family and the other parameters are the same as described in equation 2.10

2.4.3 Genetic And Phenotypic Correlations

Analysis of covariance between traits and the calculation of covariance components were used in determining the genetic and phenotypic correlations. Variance components were estimated by using PROC VARCOMP REML option of SAS. Genetic correlations ($R_{g(x, y)}$) and phenotypic correlation ($R_{P(x, y)}$) between traits x and y was estimated as follows (Falconer and Mackay, 1996):

$$\textbf{Genetic Corr.} \left[\textbf{R}_{\textbf{g(x,y)}} \right] = \frac{Cov\, f(x, y)}{\sqrt{\sigma^2_{f\,x} \cdot \sigma^2_{fy}}} \qquad (2.13)$$

$Cov_{f(x, y)}$: family covariance between traits x and y calculated as

$$[(\sigma^2_{F(x+y)} - \sigma^2_{F(x)} - \sigma^2_{Fy})]$$

where,

$\sigma^2_{F(x+y)}$, $\sigma^2_{F(x)}$, $\sigma^2_{F(y)}$ are the family variance for traits **x+y**, **x**, and **y**, respectively;

$$\textbf{Phenotypic Cor.} \left[\textbf{R}_{\textbf{p(x,y)}} \right] = \frac{Cov\, pf(x, y)}{\sqrt{\sigma^2_{pfX} \cdot \sigma^2_{pfY}}} \qquad (2.14)$$

$COV_{pf(x,y)}$: phenotypic covariance between traits **x** and **y** and calculated by the similar formula;

$$[(\sigma^2_{PF(x+y)} - \sigma^2_{PF(x)} - \sigma^2_{PF(y)})]$$

where;

$\sigma^2_{PF(x+y)}$, $\sigma^2_{PF(x)}$, $\sigma^2_{PF(y)}$ are the phenotypic variances for traits **x+y, x,** and **y**, respectively, based on family means.

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Standard errors of estimated genetic correlation ($SE_{Rg(x, y)}$) estimates were computed using methods of Falconer and Mackay (1996) as

$$SE_{Rg(x,y)} = \frac{\dfrac{1 - R_g^2}{\sqrt{2}}}{\sqrt{\dfrac{SE_{h_{i(x)}^2} SE_{h_{i(y)}^2}}{h_{i(x)}^2 h_{i(y)}^2}}} \qquad (2.15)$$

, where

S.E.h $^2_{i(x)}$ and **SEh** $^2_{i(y)}$ are the standard errors of individual heritability estimates for traits **x** and **y**;

h $^2_{i(y)}$ and **h** $^2_{i(x)}$ are the individual heritability estimates of traits **x** and **y**.

CHAPTER 3

3. RESULTS and DISCUSSION:

3.1 Genetic Parameters:

ANOVA results indicated that (Appendix B) all evaluated growth traits (Height (HT), Diameter (diam) and volume), and WSG at the age of seven varied significantly at the family level test site (p<0.001). Contribution of set and block to the inter-tree variation in growth traits appeared to be very high. But a moderate block x family interaction, exist in all growth traits, accounting for 3.6% to 7.68% of the total variance encountered in studied 168 families. Such an interaction effect, however, was not found in wood density. The family by block interaction, similar to the set variation (2.0%), was small and non-significant for density (2.8%) (Appendix B)

As shown in Table 3.1 both wood density and growth traits show a large tree to tree variation. Average WSG of the trees, for instance, ranges from 0.35 to 0.62. Compared to growth traits, however, WSG characteristics show smaller inter-tree variation in 168 families. Coefficient of variation for wood density is %6.8, while it ranges from %13.1 to %42.4 for growth traits. Although WSG exhibits a low variation, a greater part of the total variation in this trait was due to family (Table 3.2). Source of variance among families was significant and accounted for 10% of the total variance for this trait. Significant family differences for WSG were also

Table 3.1: Means, their standard deviations (SD), ranges and coefficients of variation (CV%) of selected growth and wood characteristics for 168 families.

	Mean	Sd	Mean FMİN.	Mean FMAX.	CV %
WSG	0.438	0.03	0.35	0.62	6.7
Diam.(cm)	11.95	2.39	5.78	19	20
Stem Vol.(dm^3)	43.3	18.4	8.8	113	42.4
HT7 (cm)	685.2	104.5	322	1014	15.2
HT4 (cm)	268.6	51.5	129	431	13.1

reported in other species such as Pinus nigra (Kaya, 2003). Ponderosa pine (Koch and Fıns, 2000), Douglas-fir (Vargas and Adams, 1994), and loblolly pine (Jayawickkrama *et al.,* 1997). Variance among families was also significant at p<0.001 for all growth traits. The family variance components were estimated as 6%, 5.8%, 7.7% and 8.3 of the total variance for stem volume, diameter, height growth at the age of 4 and 7, respectively.

3.2 Heritabilities

The heritability estimates (Table 3.2) for WSG indicated that WSG is under strong genetic control, with an individual heritability of 0.42 (±0.07) and family heritability of 0.58 (±0.05). Several studies were carried out in different tree species and they mostly concluded that wood specific gravity was under subject to strong genetic control. Therefore, our heritability estimates of WSG for Turkish red pine are comparable to those reported

for other conifers. Zobel and Talbert (1984) reported that family tree heritabilities found to be high for juvenile wood density in pines, ranging from 0.5 to 0.9. Zobel and Jett, (1995) summarized findings from more than fifteen studies involving the individual heritabilities of density, ranging from 0.4 to 0.70 for juvenile wood; only one showed an individual-tree narrow sense heritability estimate less than 0.35. The results of this study are also consistent with those Rockwood and Goggard, (1980) who estimated individual and family heritabilities for eight year old Ocala Sand Pine wood as 0.39 and 0.49 respectively. Yanchuk and Kiss, (1993) estimated an h^2_i =0.44 and h^2_f=0.67 value for Picea glauca. Similar individual heritability values were obtained by, Nicholls *et al* (1980) for P.radiata and by Talbert (1982) for P. taeda. From all these comparisons, it is possible to conclude that for WSG individual tree heritability of Turkish red pine at the age of seven corresponds well with other species, on which tree breeding studies have been applied.

Although Zobel and Talbert (1984) emphasize that growth traits such as height and diameter are under a lesser degree of genetic control than WSG and are strongly influenced by environment, in this study height at the age of seven and four showed much higher individual heritability values than WSG. h^2_i for height, diameter and stem volume at age seven were estimated as 0.55($\pm$0.09), 0.40($\pm$0.08) and 0.40($\pm$0.08) respectively. However, individual heritability values of growth traits were reported to be found between 0.15-0.25 for other pines (Shelbourne *et al*, 1997). According to Öztürk *et al* (2004), who investigated fourth year results of whole Turkish red pine progeny trials found in low elevation zone of Mediterranean region, the individual heritability result of Ceyhan progeny trial for height was found to be the highest (0.52$\pm$0.08) among the other trials located in Fethiye and Antalya. This situation was explained by the higher homogeneity and lower degree of environmental variation of the

Table 3.2 Estimated variance components, their proportion in the total variance and some genetic parameters for WSG and growth traits

Parameters	WSG			Stem Volume			Diameter			Height 7			Height 4		
	Mean	± SD	%	Mean	± SD	%	Mean	± SD	%	Mean	± SD	%	Mean	± SD	%
σ^2_s	0.00043	0.00051	1.6 ns	0.473	0.4532	21.3**	1.205	1.162	19.3**	2605	248.7	21**	403.3	156.3	13.6**
σ^2_b	0.00055	0.00026	2.0**	0.533	0.1588	24**	1.398	0.419	22.4**	2807	839.3	21.7**	639.9	182.1	21.6**
σ^2_f	0.00274	0.00054	10.1**	0.132	0.0261	6.0**	0.361	0.075	5.8**	964.6	170.0	7.49**	245.6	122.0	8.33**
σ^2_{fb}	0.00076	0.00084	2.8 ns	0.095	0.0389	4.3*	0.304	0.118	4.9*	444.7	219.5	3.45**	225.6	134.5	7.65**
σ^2_e	0.02722	0.00106	83.5	0.987	0.0461	44.4	2.969	0.139	47.6	5666	264.6	46.2*	1436	245.4	48.6
σ^2_t	0.03170			2.220			6.237			12487.3			3072		
σ^2_a	0.01096	0.00217	40.3	0.529	0.1047	23.8	1.446	0.300	23.2	3858	680.0	30	984	160.0	33.3
σ^2_{pi}	0.02624	0.00089		1.215	0.0417		3.635	0.124		7075	250.3		1908	172.5	
σ^2_{pfam}	0.00474	0.00053		0.227	0.0257		0.651	0.073		1499	168.0		403	188.3	
CV_{ga}	4.53			11.30			10.05			9.05			12.4		
h^2_i ± S.E	0.42± 0.07			0.40± 0.08			0.40 +0.08			0.55+0.09			0.52+0.08		
h^2_f ± S.E	0.58± 0.05			0.58+0.05			0.56+0.05			0.64+0.04			0.61+0.05		

σ^2_s: Set variation, σ^2_b: Block variance in the set, σ^2_f: Family variance, σ^2_t: Total variance, σ^2_a: Additive genetic variance (4 σ^2_f), CV_{ga}: Coefficient of genetic variance, σ^2_{pi}: Phenotypic variance, σ^2_{pfam}: Phenotypic variance of family means, h^2_i:Individual heritability, h^2_f: Family heritability, **S.E** : Standard error. *:significant at p<0.05, **:significant at p<0.01, ns: non-significant.

Ceyhan progeny trial than the others. Thus, Ceyhan progeny trial was selected as the most suitable trial to make individual selection within family However, individual heritability for height for overall sites was estimated as 0.15 ($\pm$0.02), which present a low genetic control on this trait. These results enable us to make o conclusion that investigation of one progeny trial is not enough to make accurate estimations about heritabilities and genetic controls of WSG and growth traits. On the other hand, Felconer and Mackay (1996) proposed that if individual heritability for a trait is found to be low or moderate, family heritabilities should be used for genetic selections. Because the effects of environmental factors within the test are averaged out for the family mean, it reaches much higher values than the individual heritability. Family heritability for WSG was calculated as 0.55 ($\pm$00.3), while the same value ranged from 0.53 to 0.64 for growth traits. Therefore, family selection seems to be the most effective way to obtain the highest genetic gain for WSG and growth traits in short terms as it was suggested in the *National Tree Breeding Program* (Koski and Antola, 1993)*.

3.3 Mean WSG And Growth Traits With Respect To Age

The analysis of WSG results indicated that Turkish red pine has quite superior wood with 0.438 SG, ranging from 0.350 to 0.620, at age of seven. Despite this satisfactory value in WSG, it should be underlined that all measurements were taken at very young ages and it is known that in most cases trees younger than 10 years produce essentially all juvenile wood, which is characterized by low wood density, short thin-walled tracheids, and low latewood-earlywood ratio (Zobel and Talbert 1984). In addition, it is reported that density or WSG rises rapidly until age's 10 to15 and tends to remain constant or increase slightly after the transition from juvenile to mature wood in most conifer species (Zobel and Van Buijtenen,

1989). Therefore, we can conclude that our results only pertain to wood which could be classified as exhibiting ''juvenile'' characteristics and in the long run WSG or density will attain much higher values than 0,438. Goksel and Ozden (1993) confirmed this estimation with the results of WSG values at different age of Turkish red pine. In their study, WSG values exhibited an increase from 0.413 at the age of 12 to 0.492 at age of 36. Similar results were also reported by Talbert *et al* (1982) in loblolly pine. Mean juvenile wood specific gravity values increased from 0.353 to 0.402 during the 13 year period (from age 7 to 20).

In addition to the juvenile wood, fertilization, soil type and intensive silvicultural practices increase the growth rate, thus reducing the wood specific gravity of the wood because of low latewood to earlywood ratio (Barnett and Jeronimidis, 2003). Ceyhan nursery was established on an agricultural land, therefore trees that grown on this trial showed much faster growth than the other progeny trials established in Fethiye and Antalya (Öztürk *et al* 2004). While the average annual increment in height in first four year was 67cm, the annual increment reached at 139 cm in last three years. Thus, the mean of height at the age of seven (685.2 $\pm$ 104.5) reached two fold taller values than the same trait at age of four (268 $\pm$ 51.5). Similar increments were also observed in diameter and stem volume, which were 11.95$\pm$ 2.39 cm and 43.3$\pm$18.4 dm^3, respectively.

In most tree species, it is a known fact that fast growth rate decreases the specific gravity of the wood. Although very slight negative correlation between WSG and growth traits was observed in this study, WSG results obtained from an agricultural area can be expected to be lower than the same values obtained from plantations and stands, in which competition for resources (light, water, nutrient) slows the growth, thus increasing the WSG. Zobel and Talbert (1984) confirmed this expectation by stating that

'' WSG of the trees grown in trials are nearly always 0.20 to 0.40gcm^{-3} less than that of trees of the same age grown in natural stands and plantations under similar environmental conditions''.

Despite its juvenile wood and fast growth rate, in terms of WSG, Turkish red pine wood exhibited a higher wood quaity than lots of species, on which tree breeding studies have been applied in USA (Table C.1-Appendix C). As it can be understood by investigation of Table 3.3, the mean WSG value of this study was also correspond well with other studies carried out Turkish red pine and other species grown in Turkey. All these comparisons have indicated that by intensive tree selection based on the highest WSG values, Turkish red pine breeding program could produce quite superior trees with high density wood for pulp and paper industry.

Table 3.3 Mean WSG values of some species grown in Turkey

Tree Species	WSG	Source
Abies nordmanniana	0.41	Bozkurt and Erdin (2000)
Cedrus libani	0.43	Bozkurt and Erdin (2000)
Juniperus foetidissima	0.47	Bozkurt and Erdin (2000)
Picea orientalis	0.43	Bozkurt and Erdin (2000)
Pinus sylvestris	0.49	Bozkurt and Erdin (2000)
Pinus pinea	0.47	Erten and Sözen (1997)
Pinus halepensis	0.47	Erten and Sözen (1997)
Pinus brutia	0.44	Öktem (1996)
Pinus brutia	0.47	Öktem and Sözen (1996)
Pinus brutia	**0.43**	In this study

In the current study breeding for high density wood has generally been emphasized. However, when defining breeding objectives and selection criteria, it is always important to keep the end product in mind. It is difficult to predict the future requirements of the paper and pulp industry with respect to wood properties, since developments are continuously being made in technology for forming, pressing and coating paper (Stener and Hedenberg, 2003). Culling families with extreme WSG values as well as low ones in the tree breeding process would be a simple, feasible way to improve Turkish red pine wood and thus increase wood production efficiency. Therefore, families with the highest and lowest WSG breeding values were indicated in Table D.1 (Appendix D), which gives flexibility to breeders to choose desired trees with low and high density wood at any time. In addition to WSG stem volume breeding values were represented in Table D.2 (Appendix D)

3.4. WSG Variations At Different Height Level Of Tree Height

In the current study, perpendicular change in WSG along the stem was also investigated. For this reason, samples from each tree at different heights (0, 1.30 and 4 meter) were taken by sampled trees located in 2nd block of 4th set,. From this analysis, it was found that average wood specific gravity decreases abruptly above the base and then remains relatively uniform in the upper part of the stem. The average WSG values were 0.473, 0.437, and 0.430 from base to top respectively. The density differences between breast height and top samples were not significant at $p < 0.01$ level. Similar results were also indicated by many other studies.

The presence of juvenile wood has been suggested as being one of the greatest causes of this perpendicular variation in wood. According to Zobel and Talbert (1984), the actual age of the tree is not of importance, but the

number of rings from tree center or pith determines whether juvenile wood will be formed or not. The number of rings from the tree center during which juvenile wood is formed varies from about 20 in *P ponderosa* to 10 in *P taeda,* 7 in *P eliottii* and 5 or 6 in *P caribaea*. In the current study the basal samples were consisted of 7 rings, while the breast height samples included 5 and top samples (4 meter) had 3 rings. The decreases in density with increasing distance above the ground, presented a transition from juvenile to mature wood at the age of seven. Larson (1969) explained this perpendicular change and juvenile to mature transition by the presence of live crown. He stated that the crown of a tree through its metabolic activities invokes dramatic changes during the wood formation process. As a consequence of perhaps nothing more than transport distance, those forces are most evident in the properties of the wood produced within the tree crown itself. Zobel and van Buijtenen (1989) emphasized that the influence of the live crown is what gives validity to the notion of top or crown wood and helps explain the consistency of its properties with those of juvenile wood in the lower bole. It also helps define the conical shape of the juvenile core of mature conifers; a broad base narrowing with increasing height to include the entire crown Average radial density therefore, decreases from the base of the tree to the crown, and at any point along the bole of the tree will have a similar density profile from pith to bark given the age of the cambium.

3.5 Genetic And Phenotypic Correlations Between WSG And Growth Traits

The relationship between growth rate and wood density is of critical importance for tree breeders and forest managers. Zhang and Jiang (1998) stressed that the relationship between these two traits directly influences genetic gain, economic return of breeding program, and the

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quality of wood from intensively managed plantations. The subject is highly important because if two traits are related to each other, changing in one trait may cause an inadvertent change in second. For example, if one selects for high wood specific gravity, and if it is negatively correlated with growth rate, one would unintentionally select for slow growth as well. Or, as is normally practiced, selection for superior growth will, on average, not adversely affect dry weight yield at harvest. Although, many researches have undertaken on this relationship over decades, many controversial results have been reported (Louzada and Fonseca 2002). In this context, the relationships between WSG and growth traits were examined by genetic and phenotypic correlations, and the results were provided in Table 3.4.

Although a slightly negative genetic correlation between WSG and height at age four was observed (r_g = -0,21), this correlation was estimated to be not significant at the age of seven (r_g = -0.03). Estimated genetic correlations between WSG and diameter as well as stem volume (r_g=0.01) were also insignificant (near zero). Although estimated low and the negative phenotypic correlations between growth traits and WSG suggest that a negative relationship between stem growth and WSG may be developing, all these correlations were found to be non-significant. Phenotypic correlations are generally expected to be lower than genetic correlations because they contain non-genetic effects (White and Hodge 1989). The genetic correlations between growth traits were positive and quite high, as were phenotypic correlations. Thus, selection of families with high diameter growth would cause an indirect and positive selection on height and stem volume increment.

Table 3.4 Estimated genetic (top diagonal) and phenotypic correlations (below diagonal) between wood specific gravity (WSG) and growth traits as well as between growth traits Standard errors of genetic correlations are in brackets.

	Dia.	HT7	HT4	Stem Vol.	WSG
Dia.		0.69 (0.02)	0.81 (0.01)	0.96 (0.003)	0.00 (0.04)
HT7	0.76		0.85 (0.01)	0.86 (0.01)	-0.03 (0.05)
HT4	0.77	0.80		0.86 (0.01)	-0.21 (0.04)
Stem Vol.	0.97	0.85	0.80		0.01 (0.04)
WSG	-0.15 ns	-0.11 ns	-0.17 ns	-0.13 ns	

ns: non-significant

Although many controversial results have been reported, the results of genotypic and phenotypic correlations of this study corresponded well with Zobel and van Buijtenen (1989) and Zobel and Jett (1995), who summarized hundreds of papers, covering several studies of the effect of growth rate on wood density. For example, at the genetic level Zobel and Jett rewieved 38 references and found that there is a number of reports of a weak genetic correlation between growth rate and wood density in several genera such as *Picea spp*. and *Abies spp*., but especially for the hard pines it shows a little or no meaningful genetic correlation between these traits. As well as Megraw (1985) summarized for *P taeda:* ''An inherent relationship between growth rate and specific gravity does not exist. Fast growth rate does not imply lower specific gravity.''

At a phenotypic level, Zobel and van Buijtenen (1989) have also listed 59 references about the relationship between growth rate and wood density in hard pines (e.g. *P taeda,* P *radiata,* P *elliattii,* P *sylvestris,* P *cantarta).* Of these studies, 35 showed no relationship between growth rate and wood density, 9 showed only a weak correlation and 11 showed a significant negative correlation in wood density. Only four studies showed a higher density for the fastest growing trees.

Abdel-Gadir *et al* (1993) stated"… most hard pines show a lack of correlation between growth rate and wood density". The same conclusion was expressed by Zobel and Jett (1995): "… weak or moderately positive genetic correlations have been found in loblolly pine, slash pine, maritime pine and poplar hybrids. However, most of the conifers with dense wood, especially the hard pines, show little or no meaningful relationship between growth rate and specific gravity."

It is extremely fortunate that WSG, which is the most desired characteristic, is not related closely to growth rate, thus enabling gains to be achieved by breeding for each independently without loss of quantity production. From the genetic and phenotypic correlations, it appears that, genetic dependency does not exists between WSG and growth traits in Turkish red pine, at least at the age of seven.

Lack of this genetic dependency enabled breeders to apply multi-trait selection in Turkish red pine breeding program for both growth traits and WSG. Figure 3.1 exhibited this simultaneous independent culling of the families with the highest WSG and stem volume. In the graph, all 168 families were distributed based on their breeding values. Numbered points in the graph represent the families with WSG over 0.45 and stem volume over 45 dm^3
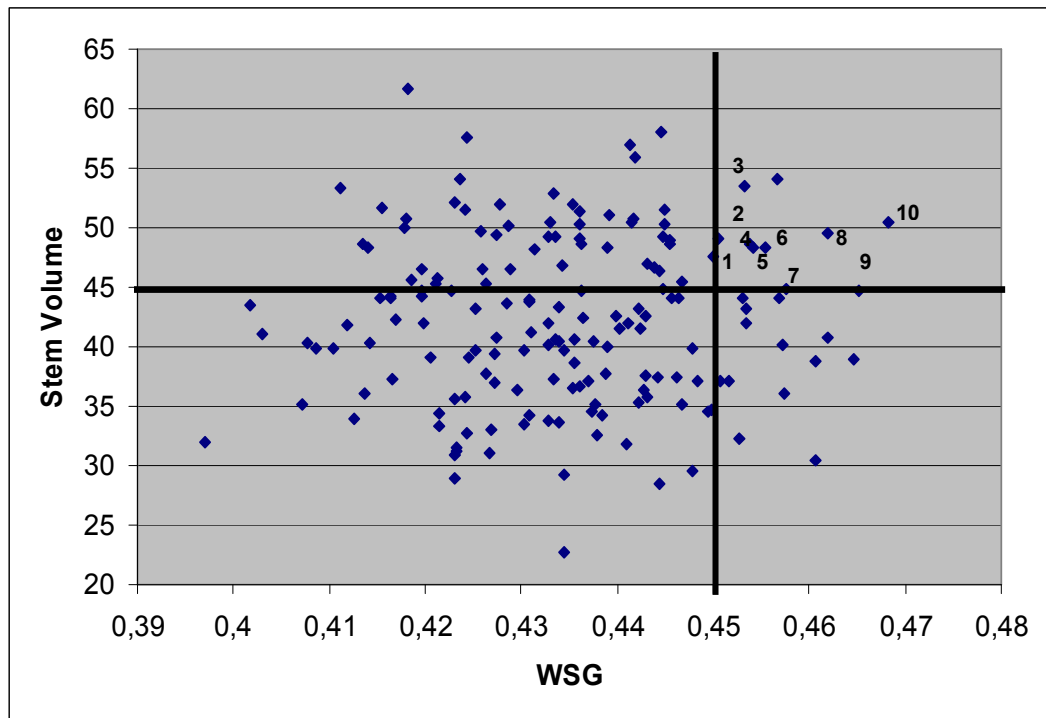
Figure 3.1 Relationship between predicted breeding values for WSG and stem volume for 168 open pollinated *P. brutia* families found in Ceyhan progeny. Numbered points are individuals (listed in Table3.5) that meet minimum requirements for WSG and stem volume

Table 3.5 presented these ten families with their absolute breeding values (ABV) and their originals with respect to original seed orchards. As can be understood from the table, average stem volume and WSG values of this ten families were estimated as 49.42 dm^3 and 0.456 respectively. If the seeds collected from these families used for plantations, the estimated genetic gain found to be reach satisfactory values.It is possible to obtain a 5.6 %, genetic gain for WSG and 27.7 % genetic gain for stem volume simultaneously.

Table 3.5. Selected families for both WSG and stem volume, their seed orchard origins, absolute breeding values and genetic gains obtained by multi-trait selection.

Number	Seed Orchards	Family Codes	ABV (Volume)	ABV (Density)
1	4 (Mersin-Silifke)	8468	44.70	0.450
2	4 (Mersin-Silifke)	8460	50.45	0.451
3	5(Antalya-Alanya)	8481	49.53	0.453
4	5(Antalya-Alanya)	8482	48.27	0.454
5	5(Antalya-Alanya)	8477	48.33	0.454
6	4 (Mersin-Silifke)	8463	48.68	0.455
7	4 (Mersin-Silifke)	8453	47.59	0.457
8	11(Antalya-Kumluca)	8633	49.06	0.462
9	4 (Mersin-Silifke)	8474	53.53	0.465
10	4 (Mersin-Silifke)	8464	54.03	0.468
Average			49.42	0.456
Gen. Gain %			27.7	5.6

3.6 Estimated Breeding Values And Genetic Gain

The existence of strong inheritance pattern and no meaningful relationship between growth and WSG in the current study, made it possible to obtain satisfactory genetic gain predictions from phenotypic and genotypic seed orchards of Turkish red pine. As genetic gains from selection or breeding program are determined by a comparison with unimproved materials, combined checklots were treated and taken as the baseline in the prediction of breeding values. Although most growth assessments have been based on height, gains have been increased when volume growth has actually been determined (Zobel and Talbert 1984). Therefore, for genetic gain estimations instead of whole growth traits, just stem volume trait along with WSG was taken into consideration. On the other hand, measurement of a sample of trees for specific gravity enables volume production per hectare to be converted to weight production per hectare.

The genotypic coefficients of variation (CV_g) are of great value for evaluating how traits will respond to selection. In the present study, the CV_g values (Table 3.2) of the growth traits were high, varying from 9 to 11.3, while the same value for WSG was quite low (4.53). These results indicated that genetic variation in WSG among families much lower than the growth traits. Thus, selection for wood density may well be based on phenotypic selection, while there is more to gain by progeny testing for stem volume increment. This result was confirmed by the estimation of genetic gain from breeding values.

Table 3.6 Average breeding values of the seed orchards and genetic gains from phenotypic, rouged and genotypic seed orchard.

Number of Seed Orchard	WSG			Stem Volume		
	Mean ABV	Genetic Gain From Phenotypic SeedOrc. (%)	Genetic Gain After Rouging (%)	Mean ABV	Genetic Gain From Phenotypic Seed Orc. (%)	Genetic Gain After Rouging (%)
3 (Antakya Uluçınar)	0.432	0.0	0.7	39.64	2.5	7.1
4(Mersin-Silifke)	0.438	1.3	4.0	46.39	20.0	32.5
5(Antalya-Alanya)	0.434	0.4	2.2	45.35	17.3	26.2
7(Mersin-Anamur)	0.435	0.6	2.1	41.20	6.5	16.1
11(Antalya Kumluca)	0.437	1.1	2.2	40.88	5.7	10.3
16(Antalya Kemer)	0.428	-1.0	-0.9	38.63	0.0	4.5
General Mean	0.434	0.37	1.70	42.34	8.6	16.1
Checklots Mean	0.432			38.67		
Genetic Gain From Genotypic Seed Orchard (%)	5.2			35		

The mean of absolute breeding values of open pollinated families (Table3.6.), which were tested in the Ceyhan progeny trial, was 0.37 % bigger than mean value of the checklots for WSG. However, this difference was found to be insignificant, indicating the usage of seeds collected from all those seed orchards will not provide a genetic gain with respect to WSG. Among the seed orchard, except for the one coded as 16, other seed orchards' breeding values were above the mean breeding values of the checklots. However, only the 4th (Mersin-Silifke) seed orchard's genetic gain found to be significant high. The highest WSG mean (0.438) and genetic gain (1.3) were observed in this seed orchard. The lowest performance in terms of WSG was observed in Antalya-Kemer seed orchard. After genetic rouging by keeping best 20 clones in each seed orchard, the estimated genetic gain was reached satisfactory values in WSG. In the seed orchards numbered as 3, 4, 5, 7 and 11 estimated genetic gain (Figure 3.2), after genetic rouging, reached to 0.7 %, 4 %, 2.2 %, 2.1 % and 2.2 %, respectively. Even though, the average genetic gain in WSG from rouged seed orchard was estimated as 1.7%, which means 1.4% of additional genetic gain could be obtained by genetic rouging. Nevertheless, Antalya-Kemer seed orchard breeding values stayed under the mean breeding values of the checklots.

On the other hand, the mean of stem volume breeding values shows that considerable genetic gain could be obtained by means of using seeds produced from phenotypic seed orchards. The average genetic gain from these seed orchards were estimated as 8.6% for this trait. As stated earlier, except for Antalya-Kemer seed orchard, which has the lowest breeding value for WSG, all the other seed orchards' breeding values were above the mean breeding value of the checklots. In addition to the lowest mean WSG breeding values, Antalya-Kemer seed orchard also has the lowest mean breeding values of height at the age of four and seven,

diameter and stem volume traits. In this context, it can be proposed that seeds produced from this seed orchard for plantations should be avoided for plantations. The estimated genetic gain for stem volume from rouged seed orchards, keeping the best 20 clones, was quite high and satisfactory that 7.5% additional gain could be obtained by genetic rouging. As such in WSG trait, after this rouging the highest breeding values were observed in Mersin-Silifke seed orchard. Its estimated genetic gain was raised from 20% to 32.5% after genetic rouging.
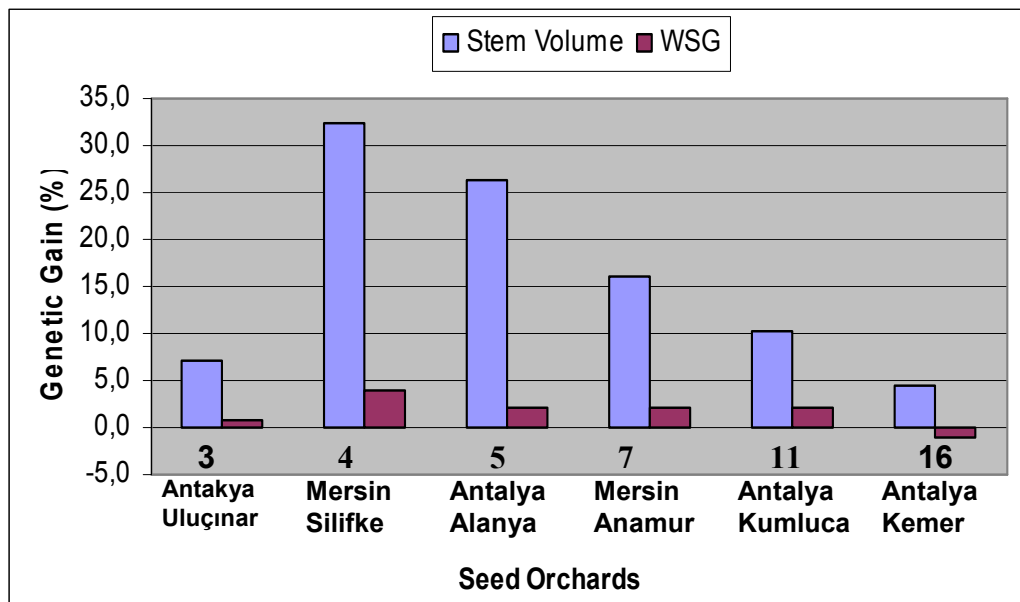
Figure 3.2 Genetic gain in WSG and Stem Volume that will be obtained in seed orchards after genetic rouging

In breeding studies, the highest genetic gains are obtained when only the very best definite numbers of parents from each seed orchard are brought together in new seed orchards (1.5 generation orchards). In this context, when 1.5 generation seed orchard is established with the best 30 open pollinated families depending on the WSG and stem volume traits, estimated genetic gain was calculated as 5.2% and 35% respectively (Figure 3.3)
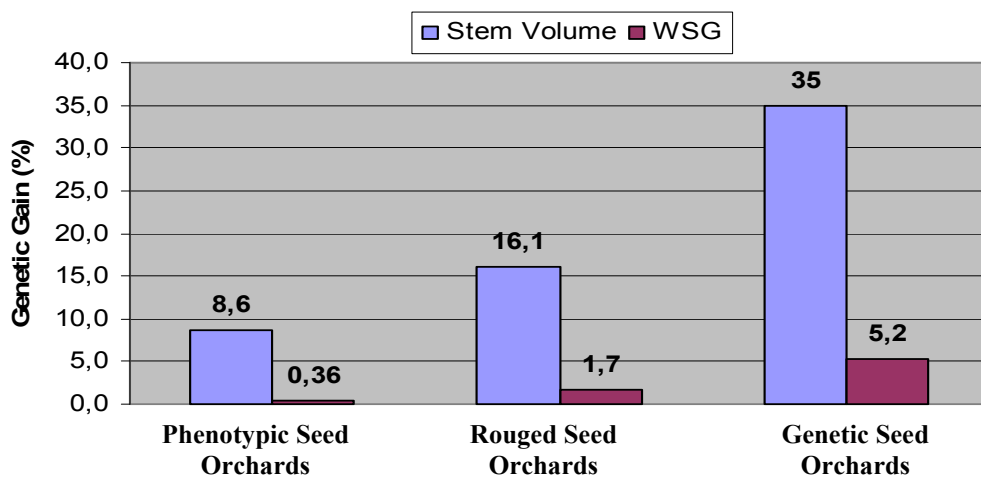
Figure 3.3 Estimated genetic gains in WSG and Stem volume for phenotypic, rogued and genotypic seed orchards.

Although, there are many reports in the literature of gains in volume growth of 50% or more, but it is preferred to cite 10 to 20 percent as a readily acceptable expectation. However there is limited number of reports for genetic gain from WSG in the literature, because WSG has not justified as a selection criterion for many breeding programs. The results of estimated genetic gain for WSG in this study correspond well with Stener

and Hedenberg (2003) and Hunnrup *et al* (1998). In the former study, genetic gain for WSG estimated approximately as 4% for the selection of best 20 families in *Betula pendula*, while the same value was 2.7 % for *Pinus sylvestris* in the latter one. Yanchuk and Kiss (1993) reported a 0.1% genetic gain in Interior Spruce for WSG by selecting best 10 families. Hollowell and-Porterfield (1986) suggested 8-15% volume gain at rotation age *for Pinus taeda* with a single cycle of selection and rouging of 30-55% individuals in the seed orchard. Additional gains of 1% for specific gravity and 5% for stem quality found were also reported. According to Nicles's (1970) tabular summary of growth gains in a number of coniferous species at ages between 6 and 15 years, volume gains varied from 10% for phenotypic selection with wind pollination to over 20% for selection on the basis of progeny test. Eldridge (1982) found that seed from an unrouged, phenotypically selected seed orchard of *Pinus radiata* in Australia produced an average of about 15% greater volume increment per hectare at ages 10-12 than standard commercial seed source. In the less variable Pinus elliottii, genetic gain in overall volume production at 20 years was estimated from a survey of seed orchards. Genetic gains were estimated as 7 % for unrouged orchards and 13.2 % after rouging (University of Florida 1988).

CHAPTER 4

CONCLUSION

- Although the results of this study are based on only one trial, introducing WSG as a selection trait in Turkish red pine breeding program may be justified from these results. Analysis of the WSG data and comparison with the other species revealed that, selection of the best genotypes in terms of WSG could produce quite superior trees with high wood density and high quality wood for plantations.

- Individual and family heritability estimates exhibited a strong genetic control of WSG and growth traits in Turkish red pine, which means a great potential to improve these traits in the future generation through genetic selection. Family selection was suggested to have an effective way to obtain genetic gain in short terms in this study.

- Because selection based the WSG of juvenile wood is an indirect selection of WSG at the mature ages, strong genetic correlation between juvenile WSG and mature ages require maximizing the genetic gain per time. Analysis of WSG values at different height of tree trunk indicate a transition from juvenile to mature wood at the age of seven in Turkish red pine. Therefore, subsequent studies on WSG in following years are too important to get information about age-age and juvenile-mature correlations. These types of information are essential to make precise estimations about early selection age and ranking the families effectively.

- Genetic and phenotypic correlations between WSG and growth traits indicated that specific gravity was essentially independent of growth rate. Therefore, WSG could be included in Turkish red pine breeding program without affecting negatively volume improvement. This lack of genetic dependency allowed to apply multi-trait selection that is, culling best 10 families based on their higher WSG and stem volume values. From this selection, genetic gains were estimated as 27.7% and 5.6% for stem volume and WSG, respectively.

- Single trait selections for both growth and WSG also provided satisfactory values. To achieve the highest genetic gain, establishment of genotypic seed orchard with the best 30 families was suggested. In this case genetic gain compared the checklots could reach at 5.2% for WSG and 35 % for stem volume. However, this seven year's evaluation in an only one progeny test is not enough to select best genotypes used in genotypic seed orchard establishment. Therefore, until genotypic seed orchards are available for seed production, the most suitable seed sources are rouged seed orchards. However, to rouge the phenotypic seed orchards, investigation and evaluation of the other progeny trials, located in Antalya and Fethiye, should be evaluated as soon as possible.

- To have maximum economic value with the improvement of WSG and growth, a multi-trait selection index should be developed by giving appropriate weight to each trait according to its relative economical importance and genetic parameters. Such index selection will provide the flexibility to breeders during culling of families in later ages in the future.

- The results of this present study should be interpreted with caution owing to the lack of the knowledge about basic parameters, parameters such as age-age genetic correlation and correlations of heritabilities at different ages. Furthermore, the results are based on only one trial. The results may reflect the specific conditions at the Ceyhan test site in the restricted period examined. Thus, further investigations on the other progeny trials located in Fethiye and Antalya are needed before any definitive conclusions can be reached about the value of introducing wood density as a supplementary trait in the long-term *National* Turkish red pine *breeding program*

- Due to the complex nature of WSG, studying the genetic control of earlywood and latewood proportion will contribute greatly to better understanding of the genetics of WSG, which will be essential for efficient incorporation of this wood quality characteristic in Turkish red pine tree breeding program. Fibre characteristics and their relationship with the WSG are also very important for an efficient breeding program. Therefore all those traits should be also investigated.

- Since 168 families in Turkish red pine breeding program have been evaluated for their phenotypes and genotypes regarding WSG and growth traits, in the next step, these families along additional materials from other breeding zones will be screened and genotyped for the genes responsible for wood production and growth. Then those, with promising potential will be incorporated in to Turkish red pine breeding program.

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APPENDİX A

ORIGINE OF THE FAMILIES AND THE CHECKLOTS

Table A.1 Information about the origins of the clones in the seed orchards (Öztürk *et al*, 2004)

Origin of the seed orchards	Seed Orchard No					
	3	4	5	7	11	16
Province	K.maraş	Mersin	Antalya	Mersin	Antalya	Antalya
District	Antakya	Silifke	Alanya	Anamur	Kumluca	Antalya
Sub-district	Uluçınar	Akdere	Kargı	Gökçesu	Kumluca	Kemer
Provenance no.	21	32	37	25	39	45
Age	76	57	83	97	80	63
Altitude (m)	385	100	350	400	250	320
Latitude (m)	36° 21'K	36° 13'K	36° 36'K	36° 11'K	36° 26'K	36° 35'K
Longitude (m)	30° 57'D	33° 42'D	31° 57'D	32° 45'D	30° 15'D	30° 28'D
Mean temp.(C^o)	19.7	18.8	18.1	19.3	18.4	18.4
Annual precip.(mm)	740.7	611.6	1000.3	970.2	933.3	1043

Table A.2: Information about origin of check lots

Checklot Id	1	2	3	4	5	6
Seed Orchard No	32	11	31	37	25	349
Province	Mersin	Antalya	Mersin	Antalya	Mersin	Amasya
District	Silifke	Serik	Mersin	Alanya	Anamur	Bafra
Sub-district	Akdere	Pınargözü	Fındıkpınarı	Kargı	Gökçesu	Alaçam
Breeding zone	1.1	1.2	1.3	1.1	1.1	6.1
Altitude (m)	100	500	825	350	500	100
Latitude(m)	36°13'25	36° 16'00'	36°56'40'	36° 36'36'	36° 11'10'	41° 38'36'
Longitude(m)	33°42'55	30° 59'40'	34° 26'20'	31° 57'55'	30° 15'D	30° 26'10'

APPENDIX B

ANALYSIS OF VARİANCE TABLE FOR WSG AND GROWTH TRAITS

Table B.1 ANOVA table for wood specific gravity (WSG),volume (VOL), diameter (DIAM) and height traits at the age of seven (H 7) and for height at age four (H 4) in Ceyhan progeny trial

	Source	DF	MS	Error DF	F Value	Prob F
W S G	Set	3	0.123	18.685	1.91	0.1653
	Block x Set	24	0.065**	1079	2.71	<.0001
	Family	173	0.053**	1115.8	2.25	<.0001
	Block x Fam	1082	0.024	1079	0.99	0.5671
V O L	Set	3	43.5**	18.14	8.51	0.0002
	Block x Set	24	34.6**	1079	30.19	<.0001
	Family	173	2.7**	1101	2.4	<.0001
	Block x Fam	1082	1.16*	1079	1.15	0.0142
D I A M	Set	3	118.4**	18.12	8.4	0.0002
	Block x Set	24	93.03**	1079	26.65	<.0001
	Family	173	8.02**	1095.	2.29	<.0001
	Block x Fam	1082	3.53*	1079	1.16	0.0083
H 7	Set	3	209771**	18.13	7.93	<.0001
	Block x Set	24	175796**	1079	27.49	<.0001
	Family	173	17070**	1096.	2.66	<.0001
	Block x Fam	1082	6552.6*	1079	1.14	0.013
H 4	Set	3	751595.4**	250531	184.2	<.0001
	Block x Set	24	1080988**	45041.1	33.12	<.0001
	Family	173	845255.8**	4885.87	3.59	<.0001
	Block x Fam	1082	2036085**	1881.78	1.38	<.0001

**Significant at p<0.01 * Significant at p<0.05

APPENDIX C

COMPARISION OF WSG VALUES IN TURKISH RED PINE WITH OTHER SPECIES

Table C.1 Maximum, minimum and average wood specific gravity values of *Pinus brutia* and some tree species grown in USA

Species	Avarage	Low	High
Cedar			
Alaska (*Chamaecyparis nootkatensis***)**	0.42	0.34	0.50
Incense (*Calocedrus decurrens*)	0,35	0,28	0,42
Port Orford (*Chamaecyparis lawsoniana*)	0,39	0,31	0,47
Western redcedar (Thuja plicata)	0,31	0,25	0,37
Coast Douglas fir (*Pseudotsuga menziesii*)	0,45	0,36	0,54
Fir			
Grand (*Abies grandis*)	0.35	0.28	0.42
Noble (Abies procera)	0.37	0.30	0.44
Pasific silver (Abies amabilis)	0.40	0.32	0.48
White (Abies concolor)	0.37	0.30	0.44
Hemlock.western (Tsuga heterophylla)	0.42	0.34	0.50
Lacrh.Western (*Larix laricina*)	0.48	0.38	0.58
Pine			
Lodgepole (Pinus contorta)	0.38	0.30	0.46
Ponderosa (Pinus ponderosa).	0.38	0.30	0.46
Sugar (Pinus lambertiana)	0.34	0.27	0.41
Western white (Pinus monticola)	0.35	0.28	0.42
Slash (Pinus elliottii)	0.61	0.53	0.71
Loblolly (Pinus taeda)	0.54	0.42	0.66
Redwood			
Old growth	0.38	0.30	0.46
Young growth	0.34	0.27	0.41
Turkish red pine (*Pinus Brutia*)	**0.43**	**0.35**	**0.62**

Source: USFS (1987)

APPENDIX D

BREEDING VALUES OF WSG AND STEM VOLUME FOR FAMILIES TESTED IN CEYHAN TRIAL

Table D.1 Breeding (BV) and absolute breeding values (ABV_BV), seed orchards, means and general combining abilities (GCA) of WSG trait in 168 family found in Ceyhan progeny trial

No	Family Code	Seed Orchard No	Mean	GCA	BV	ABS_BV
1	8460	4	0.4674	0.017	0.034	0.4683
2	8468	4	0.4698	0.0154	0.0308	0.4651
3	8469	4	0.4645	0.0152	0.0303	0.4646
4	8481	5	0.4564	0.0138	0.0276	0.4619
5	8549	7	0.4635	0.0138	0.0276	0.4619
7	8428	3	0.4607	0.0132	0.0263	0.4607
6	8783	16	0.4542	0.0132	0.0264	0.4607
8	8637	11	0.4504	0.0117	0.0233	0.4576
9	8535	7	0.4592	0.0116	0.0232	0.4575
10	8639	11	0.4496	0.0115	0.0229	0.4572
11	8448	4	0.4574	0.0113	0.0225	0.4569
12	8464	4	0.4581	0.0112	0.0223	0.4566
13	8482	5	0.4505	0.0105	0.021	0.4554
14	8477	5	0.4472	0.0099	0.0198	0.4541
15	8463	4	0.4547	0.0097	0.0195	0.4538
16	8640	11	0.4472	0.0096	0.0192	0.4535
17	8543	7	0.4566	0.0096	0.0191	0.4534
18	8474	4	0.4486	0.0095	0.0189	0.4532
19	8487	5	0.4484	0.0093	0.0187	0.453
20	8473	4	0.449	0.0092	0.0184	0.4527
21	8484	5	0.4471	0.0087	0.0173	0.4516

Table D.1 Continued

No	Family Code	Seed Orchard No	Mean	GCA	BV	ABS_BV
22	8655	11	0.447	0.0082	0.0164	0.4507
23	8633	11	0.448	0.0081	0.0162	0.4505
24	8453	4	0.4521	0.0079	0.0157	0.45
25	8647	11	0.4461	0.0078	0.0155	0.4498
26	8424	3	0.4526	0.0076	0.0151	0.4494
27	8461	4	0.4489	0.007	0.014	0.4483
28	8534	7	0.4509	0.0068	0.0136	0.4479
29	8416	3	0.4509	0.0068	0.0135	0.4478
30	8436	3	0.4481	0.0062	0.0124	0.4468
31	8451	4	0.4504	0.0062	0.0123	0.4467
32	8531	7	0.4489	0.006	0.0121	0.4464
33	8636	11	0.4413	0.0059	0.0119	0.4462
34	8556	7	0.4469	0.0057	0.0113	0.4456
35	8498	5	0.4413	0.0056	0.0111	0.4454
36	8632	11	0.4439	0.0056	0.0111	0.4454
38	8450	4	0.4478	0.0053	0.0107	0.445
37	8455	4	0.4459	0.0053	0.0107	0.445
39	8631	11	0.4396	0.0052	0.0105	0.4448
40	8646	11	0.4411	0.0052	0.0104	0.4447
41	8475	4	0.4402	0.0051	0.0102	0.4445
43	8467	4	0.4457	0.005	0.01	0.4444
42	8532	7	0.4468	0.005	0.0101	0.4444
44	8422	3	0.4467	0.005	0.01	0.4443
45	8769	16	0.4422	0.0047	0.0094	0.4438
46	8495	5	0.4397	0.0044	0.0089	0.4432
47	8784	16	0.4388	0.0044	0.0088	0.4431
48	8503	5	0.4386	0.0044	0.0087	0.443
49	8478	5	0.4382	0.0043	0.0086	0.4429
50	8558	7	0.4462	0.0042	0.0084	0.4427
51	8504	5	0.4387	0.0041	0.0082	0.4425
52	8546	7	0.4439	0.0039	0.0079	0.4422
53	8548	7	0.4448	0.0039	0.0078	0.4422
54	8442	4	0.445	0.0037	0.0075	0.4418
55	8501	5	0.438	0.0036	0.0072	0.4416
56	8472	4	0.4379	0.0036	0.0071	0.4415
57	8547	7	0.4433	0.0035	0.007	0.4413
58	8440	3	0.4431	0.0035	0.0069	0.4412
59	8775	16	0.4379	0.0033	0.0066	0.4409
60	8642	11	0.4357	0.003	0.0059	0.4402

Table D.1 Continued

No	Family Code	Seed Orchard No	Mean	GCA	BV	ABS_BV
61	8458	4	0.4418	0.0028	0.0056	0.4399
62	8465	4	0.4413	0.0024	0.0048	0.4391
63	8541	7	0.4422	0.0024	0.0047	0.439
64	8485	5	0.4344	0.0023	0.0046	0.4389
65	8466	4	0.4408	0.0023	0.0045	0.4388
66	8432	3	0.4416	0.0021	0.0041	0.4384
67	8771	16	0.436	0.0018	0.0035	0.4379
68	8650	11	0.4349	0.0017	0.0035	0.4378
69	8479	5	0.4342	0.0017	0.0033	0.4376
70	8489	5	0.4333	0.0015	0.0029	0.4373
71	8488	5	0.4329	0.0013	0.0027	0.437
72	8652	11	0.4326	0.0011	0.0021	0.4364
74	8437	3	0.4387	0.0009	0.0019	0.4362
73	8500	5	0.433	0.0009	0.0019	0.4362
75	8443	4	0.4397	0.0009	0.0018	0.4361
76	8654	11	0.432	0.0009	0.0018	0.4361
78	8456	4	0.4386	0.0008	0.0017	0.436
77	8559	7	0.4386	0.0008	0.0017	0.436
79	8506	5	0.432	0.0006	0.0013	0.4356
80	8551	7	0.4381	0.0006	0.0012	0.4355
81	8776	16	0.4312	0.0006	0.0011	0.4354
82	8426	3	0.439	0.0005	0.001	0.4353
83	8417	3	0.4384	0.0001	0.0002	0.4345
85	8536	7	0.4381	0.0001	0.0001	0.4345
84	8788	16	0.4304	0.0001	0.0002	0.4345
86	8557	7	0.4372	0	0	0.4343
87	8433	3	0.4369	-0.0001	-0.0003	0.434
88	8648	11	0.4313	-0.0002	-0.0003	0.434
89	8765	16	0.4289	-0.0002	-0.0005	0.4339
91	8435	3	0.4365	-0.0004	-0.0008	0.4335
90	8471	4	0.4303	-0.0004	-0.0008	0.4335
92	8429	3	0.437	-0.0005	-0.001	0.4334
93	8787	16	0.4297	-0.0005	-0.001	0.4333
94	8649	11	0.43	-0.0006	-0.0013	0.433
95	8554	7	0.4361	-0.0007	-0.0014	0.4329
96	8641	11	0.4285	-0.0007	-0.0014	0.4329
97	8420	3	0.4369	-0.0008	-0.0015	0.4328
98	8553	7	0.4366	-0.0007	-0.0015	0.4328

Table D.1 Continued

No	Family Code	Seed Orchard No	Mean	GCA	BV	ABS_BV
99	8444	4	0.4351	-0.0015	-0.0031	0.4313
101	8786	16	0.4276	-0.0017	-0.0034	0.431
103	8445	4	0.4348	-0.0017	-0.0035	0.4309
102	8780	16	0.4276	-0.0017	-0.0034	0.4309
104	8634	11	0.4274	-0.0018	-0.0036	0.4308
106	8653	11	0.4273	-0.002	-0.0041	0.4303
105	8772	16	0.4253	-0.002	-0.004	0.4303
107	8555	7	0.4331	-0.0024	-0.0048	0.4295
108	8533	7	0.4335	-0.0028	-0.0055	0.4288
109	8480	5	0.4252	-0.0028	-0.0056	0.4287
110	8502	5	0.4262	-0.0029	-0.0058	0.4285
111	8496	5	0.4251	-0.0033	-0.0067	0.4277
112	8476	5	0.4242	-0.0034	-0.0069	0.4274
113	8552	7	0.4313	-0.0035	-0.0069	0.4274
115	8645	11	0.4252	-0.0035	-0.0071	0.4273
114	8773	16	0.424	-0.0035	-0.007	0.4273
116	8423	3	0.4318	-0.0037	-0.0075	0.4268
117	8434	3	0.4297	-0.0038	-0.0077	0.4266
118	8491	5	0.4225	-0.004	-0.0079	0.4264
119	8499	5	0.4244	-0.004	-0.008	0.4263
120	8550	7	0.4301	-0.0042	-0.0083	0.426
121	8431	3	0.4295	-0.0043	-0.0085	0.4258
123	8635	11	0.4211	-0.0046	-0.0092	0.4252
122	8777	16	0.4215	-0.0046	-0.0091	0.4252
124	8540	7	0.4297	-0.0049	-0.0098	0.4245
125	8492	5	0.4216	-0.005	-0.0099	0.4244
126	8789	16	0.4222	-0.005	-0.0099	0.4244
127	8781	16	0.4221	-0.0051	-0.0101	0.4242
128	8470	4	0.4284	-0.0051	-0.0103	0.4241
129	8447	4	0.4286	-0.0053	-0.0107	0.4236
130	8427	3	0.4288	-0.0055	-0.011	0.4233
131	8644	11	0.417	-0.0055	-0.011	0.4233
132	8542	7	0.4286	-0.0056	-0.0112	0.4231
133	8774	16	0.4186	-0.0056	-0.0112	0.4231
134	8462	4	0.4269	-0.0057	-0.0113	0.423
135	8539	7	0.4285	-0.0057	-0.0114	0.423
136	8779	16	0.4212	-0.0057	-0.0115	0.4228
137	8530	7	0.4269	-0.0064	-0.0128	0.4215
138	8449	4	0.4267	-0.0065	-0.013	0.4214

Table D.1 Continued

No	Family Code	Seed Orchard No	Mean	GCA	BV	ABS_BV
139	8770	16	0.4185	-0.0066	-0.0131	0.4212
140	8545	7	0.4242	-0.0067	-0.0133	0.421
141	8778	16	0.4182	-0.0069	-0.0137	0.4206
142	8537	7	0.4259	-0.0072	-0.0144	0.4199
143	8418	3	0.4251	-0.0073	-0.0146	0.4197
144	8425	3	0.4225	-0.0074	-0.0147	0.4196
145	8538	7	0.4253	-0.0074	-0.0148	0.4196
146	8438	3	0.4232	-0.0079	-0.0158	0.4185
147	8497	5	0.4174	-0.0081	-0.0161	0.4182
148	8421	3	0.4243	-0.0082	-0.0163	0.418
149	8452	4	0.4241	-0.0083	-0.0165	0.4178
150	8766	16	0.4131	-0.0087	-0.0175	0.4169
151	8446	4	0.4225	-0.0089	-0.0178	0.4165
152	8494	5	0.4144	-0.009	-0.018	0.4164
153	8638	11	0.4096	-0.009	-0.0181	0.4163
154	8457	4	0.421	-0.0095	-0.0189	0.4154
155	8441	4	0.422	-0.0095	-0.019	0.4153
156	8768	16	0.4116	-0.01	-0.02	0.4143
157	8544	7	0.4194	-0.0101	-0.0202	0.4141
158	8651	11	0.4119	-0.0103	-0.0207	0.4136
159	8454	4	0.4186	-0.0104	-0.0208	0.4135
160	8785	16	0.4109	-0.0108	-0.0217	0.4126
161	8643	11	0.4058	-0.0112	-0.0224	0.4119
162	8505	5	0.4075	-0.0116	-0.0231	0.4112
163	8419	3	0.4151	-0.0119	-0.0239	0.4105
164	8767	16	0.4042	-0.0129	-0.0257	0.4086
165	8430	3	0.4096	-0.0133	-0.0265	0.4078
166	8782	16	0.4073	-0.0136	-0.0272	0.4072
167	8459	4	0.4093	-0.0156	-0.0313	0.4031
168	8483	5	0.3984	-0.0163	-0.0326	0.4017
169	8493	5	0.3969	-0.0187	-0.0373	0.397

Table D.2 Breeding (BV) and absolute breeding values (ABV_BV), seed orchards, means and general combining abilities (GCA) of stem volume trait in 168 family found in Ceyhan progeny trial

No	FAM	Seed Orchar No	Stem Volume	GCA	BV	ABS_BV
1	8497	5	57.72	9.76	19.52	61.74
2	8475	4	57.38	7.93	15.86	58.08
3	8492	5	58.17	7.64	15.29	57.51
4	8547	7	53.55	7.35	14.71	56.93
5	8442	4	67.55	6.81	13.62	55.84
6	8447	4	64.79	5.94	11.89	54.11
7	8464	4	51.77	5.91	11.81	54.03
8	8474	4	55.75	5.66	11.31	53.53
9	8505	5	52.76	5.55	11.11	53.33
10	8787	16	54.08	5.35	10.69	52.91
11	8539	7	62.86	4.93	9.87	52.09
12	8496	5	49.98	4.89	9.78	52.00
13	8426	3	62.77	4.88	9.76	51.98
14	8457	4	48.76	4.72	9.44	51.66
15	8455	4	49.72	4.67	9.35	51.57
16	8470	4	48.66	4.66	9.33	51.55
17	8443	4	62.22	4.55	9.10	51.32
18	8465	4	48.25	4.41	8.83	51.05
19	8421	3	61.77	4.28	8.55	50.77
20	8501	5	49.27	4.23	8.46	50.68
21	8460	4	46.19	4.12	8.23	50.45
22	8649	11	49.61	4.11	8.22	50.44
23	8472	4	51.75	4.09	8.19	50.41
24	8450	4	61.44	4.07	8.15	50.37
25	8559	7	47.64	4.05	8.10	50.32
26	8480	5	40.45	3.97	7.95	50.17
27	8452	4	61.06	3.85	7.70	49.92
28	8431	3	47.81	3.77	7.54	49.76
29	8481	5	39.49	3.66	7.31	49.53
30	8476	5	39.58	3.62	7.24	49.46
31	8471	4	45.64	3.55	7.09	49.31
32	8641	11	36.75	3.54	7.08	49.30
33	8631	11	38.49	3.54	7.07	49.29
34	8456	4	46.42	3.47	6.94	49.16
35	8633	11	40.38	3.42	6.84	49.06
36	8632	11	39.73	3.33	6.67	48.89
37	8463	4	46.41	3.23	6.46	48.68
38	8498	5	48.00	3.21	6.42	48.64
39	8500	5	48.71	3.20	6.41	48.63

Table D.2 Continued

No	FAM	Seed Orchar No	Stem Volume	GCA	BV	ABS_BV
40	8454	4	59.98	3.18	6.36	48.58
41	8544	7	46.38	3.09	6.17	48.39
42	8477	5	37.45	3.06	6.11	48.33
43	8482	5	34.60	3.02	6.05	48.27
44	8485	5	39.04	3.02	6.04	48.26
45	8444	4	59.98	3.00	6.00	48.22
46	8453	4	59.47	2.69	5.37	47.59
47	8495	5	48.98	2.36	4.71	46.93
48	8557	7	45.76	2.27	4.54	46.76
49	8769	16	38.77	2.19	4.38	46.60
50	8550	7	44.51	2.17	4.35	46.57
51	8538	7	57.78	2.16	4.31	46.53
52	8533	7	58.20	2.14	4.28	46.50
53	8467	4	44.39	2.10	4.20	46.42
54	8770	16	36.01	1.78	3.56	45.78
55	8438	3	43.66	1.71	3.43	45.65
56	8451	4	58.06	1.63	3.25	45.47
57	8545	7	42.77	1.53	3.05	45.27
58	8499	5	43.99	1.52	3.04	45.26
59	8637	11	33.94	1.33	2.67	44.89
60	8646	11	45.52	1.32	2.65	44.87
61	8779	16	42.86	1.26	2.51	44.73
62	8468	4	43.64	1.24	2.48	44.70
63	8425	3	56.93	1.22	2.43	44.65
64	8437	3	42.57	1.20	2.41	44.63
65	8638	11	33.37	0.99	1.99	44.21
66	8418	3	56.56	0.98	1.97	44.19
67	8448	4	56.23	0.96	1.92	44.14
68	8441	4	56.23	0.96	1.92	44.14
69	8531	7	56.43	0.95	1.91	44.13
70	8494	5	45.47	0.92	1.84	44.06
71	8556	7	42.20	0.92	1.84	44.06
72	8487	5	35.49	0.91	1.82	44.04
73	8445	4	56.13	0.89	1.77	43.99
74	8780	16	45.94	0.77	1.53	43.75
75	8502	5	42.61	0.69	1.38	43.60
76	8483	5	33.46	0.64	1.27	43.49
77	8433	3	41.81	0.55	1.11	43.33
78	8546	7	41.72	0.50	0.99	43.21
79	8543	7	55.94	0.46	0.91	43.13
80	8777	16	31.49	0.45	0.91	43.13
81	8503	5	43.19	0.15	0.30	42.52
82	8458	4	39.81	0.15	0.30	42.52
83	8652	11	45.01	0.12	0.23	42.45
84	8766	16	32.76	0.05	0.11	42.33

Table D.2 Continued

No	FAM	Seed Orchar No	Stem Volume	GCA	BV	ABS_BV
85	8537	7	54.48	-0.09	-0.19	42.03
86	8640	11	32.20	-0.10	-0.19	42.03
87	8554	7	40.80	-0.12	-0.23	41.99
88	8440	3	40.62	-0.16	-0.32	41.90
89	8643	11	32.71	-0.19	-0.39	41.83
90	8504	5	44.63	-0.33	-0.66	41.56
91	8642	11	30.43	-0.36	-0.72	41.50
92	8786	16	43.86	-0.48	-0.96	41.26
93	8459	4	38.97	-0.55	-1.09	41.13
94	8549	7	40.08	-0.71	-1.41	40.81
95	8552	7	39.70	-0.72	-1.43	40.79
96	8506	5	42.28	-0.79	-1.57	40.65
97	8435	3	39.50	-0.83	-1.66	40.56
98	8479	5	32.99	-0.87	-1.73	40.49
99	8648	11	39.17	-0.89	-1.77	40.45
100	8768	16	32.01	-0.95	-1.90	40.32
101	8430	3	40.76	-0.99	-1.98	40.24
102	8639	11	30.17	-1.04	-2.08	40.14
103	8420	3	53.06	-1.06	-2.13	40.09
104	8541	7	52.77	-1.12	-2.24	39.98
105	8767	16	33.43	-1.15	-2.31	39.91
106	8419	3	52.68	-1.18	-2.36	39.86
107	8534	7	52.63	-1.20	-2.41	39.81
108	8772	16	32.45	-1.24	-2.49	39.73
109	8635	11	32.04	-1.29	-2.57	39.65
110	8417	3	52.47	-1.30	-2.59	39.63
111	8773	16	30.73	-1.42	-2.84	39.38
112	8540	7	52.04	-1.53	-3.07	39.15
113	8778	16	29.77	-1.56	-3.12	39.10
114	8469	4	38.95	-1.61	-3.22	39.00
115	8783	16	39.91	-1.74	-3.48	38.74
116	8551	7	36.67	-1.78	-3.56	38.66
117	8466	4	36.08	-2.21	-4.42	37.80
118	8491	5	29.75	-2.25	-4.50	37.72
119	8478	5	26.81	-2.35	-4.71	37.51
120	8636	11	29.26	-2.38	-4.76	37.46
121	8422	3	50.26	-2.42	-4.84	37.38
122	8446	4	50.80	-2.44	-4.88	37.34
123	8429	3	50.35	-2.47	-4.93	37.29
124	8484	5	29.21	-2.53	-5.07	37.15
125	8488	5	28.45	-2.55	-5.10	37.12
126	8461	4	35.88	-2.55	-5.11	37.11
127	8655	11	38.19	-2.56	-5.12	37.10
128	8645	11	37.09	-2.62	-5.24	36.98
129	8654	11	42.50	-2.81	-5.62	36.60

Table D.2 Continued

No	FAM	Seed Orchar No	Stem Volume	GCA	BV	ABS_BV
130	8776	16	28.05	-2.82	-5.65	36.57
131	8555	7	36.05	-2.93	-5.87	36.35
132	8558	7	37.38	-2.94	-5.87	36.35
133	8535	7	49.59	-3.09	-6.17	36.05
134	8651	11	38.28	-3.11	-6.21	36.01
135	8784	16	38.12	-3.20	-6.39	35.83
136	8781	16	35.31	-3.27	-6.53	35.69
137	8542	7	49.15	-3.32	-6.65	35.57
138	8548	7	31.79	-3.44	-6.88	35.34
139	8782	16	35.75	-3.54	-7.07	35.15
140	8650	11	36.65	-3.56	-7.12	35.10
141	8436	3	32.92	-3.57	-7.14	35.08
142	8647	11	33.01	-3.72	-7.45	34.77
143	8424	3	47.26	-3.84	-7.67	34.55
144	8489	5	23.61	-3.84	-7.69	34.53
145	8530	7	48.00	-3.88	-7.76	34.46
146	8634	11	27.19	-3.96	-7.92	34.30
147	8432	3	33.72	-4.02	-8.04	34.18
148	8785	16	37.17	-4.17	-8.33	33.89
149	8553	7	33.80	-4.23	-8.46	33.76
150	8765	16	24.76	-4.32	-8.65	33.57
151	8653	11	34.51	-4.40	-8.80	33.42
152	8449	4	46.93	-4.42	-8.83	33.39
153	8423	3	46.97	-4.60	-9.20	33.02
154	8789	16	34.83	-4.72	-9.44	32.78
155	8771	16	22.66	-4.82	-9.64	32.58
156	8473	4	32.33	-4.96	-9.91	32.31
157	8493	5	33.92	-5.09	-10.19	32.03
158	8775	16	24.20	-5.19	-10.38	31.84
159	8427	3	45.56	-5.32	-10.64	31.58
160	8644	11	20.59	-5.51	-11.02	31.20
161	8434	3	32.10	-5.59	-11.18	31.04
162	8774	16	21.41	-5.67	-11.35	30.87
163	8428	3	44.89	-5.85	-11.69	30.53
164	8416	3	44.10	-6.30	-12.61	29.61
165	8788	16	30.98	-6.48	-12.95	29.27
166	8462	4	29.87	-6.66	-13.32	28.90
167	8532	7	43.13	-6.90	-13.81	28.41
168	8536	7	37.30	-9.77	-19.53	22.69