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Genetic Variation in Early Growth Characteristics of Two Populations of Wild Service Tree (*Sorbus torminalis* (L.) Crantz) and Their Interrelationship

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Abstract

This study was performed in order to compare two wild service tree populations (*Sorbus torminalis* (L.) Crantz) for their early growth and to find useful vegetative characteristics to be used in indirect selection of fast and tall growing trees of the species in the field. We used phenotypic and genotypic correlation coefficients estimated on data from 30 three-year old seedlings of each 40 randomly selected adult trees. Assuming genetic differences between the trees sampled, path analysis was performed on genotypic and phenotypic levels.

Results showed that plus trees of one of the sites may be used for clonal seed orchard establishment. But the other site is suggested as a better site for breeding purposes with more effective *Sorbus* population. Collar diameter had the strongest positive direct effect and strongest correlation with plant height at the phenotypic level. In contrast, lateral branches showed very weak direct effect but relatively strong total indirect effect on plant height. Path analysis on the genotypic correlation coefficients detected negative indirect effect between the characters. Collar diameter could be regarded as a good

predictor of plant height because of its strong direct and indirect phenotypic and genotypic correlations. The use of recommended selection criteria is discussed.

Key words: Genotypic correlation, Half-Sib progenies, Path analysis, Vegetative characteristics.

Introduction

Sorbus torminalis (L.) Crantz is a tree species with high economical values (DEMESURE et al., 2000). Its natural distribution is rather large, from the north of Maghreb to the south of Denmark and from the east of Great Britain to the north of Iran (DEMESURE et al., 2000). Medicinal importance of the *Sorbus* species is also emphasized (TERMENTZI et al., 2006). The increasing concern on *Sorbus* species during last decades in European countries enables enlargement of genetic knowledge on them (BALIUCKAS et al., 2005). The species is scattered on the south edge of the Caspian Sea in forests of northern Iran along with beech (*Fagus orientalis* Lipsky.), Caucasian oak (*Quercus castaneifolia* C.A.M.), and hornbeam (*Carpinus betulus* L.). The best quality of wild service tree is found in northern and northeast aspects of the area on deep soil, where the species can grow as tall as 30 meter and exceed a diameter at breast height of 100 centimeter.

Genetic variation is the corner stone of all breeding strategies in forests reclamations, and is vastly considered in the literature. Genetic variability of various morphological and molecular aspects of the species is considered by numerous authors who have used various methods to characterize populations of the species (ANGELONE

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et al., 2007; BEDNORZ et al., 2004 and 2006b; BEDNORZ, 2006; BIEDENKOPF et al., 2007; CHESTER et al., 2007; HOEBEE et al., 2006; RASPE and KOHN, 2007). Based on our knowledge, there are not enough records on characterizing the inter-relationship between the characters of the species.

One of the primary objectives of a forest tree breeding program is to increase the speed of quality and quantity of wood growth. This ultimate goal can be achieved through indirect selection of superior trees. Fast growing trees can be found in genetically variable populations. Detecting the best genotype in such populations is breeding art which is performed through various methods. Plant height growth is regarded as the most appropriate character for assessing growth rate of the forest trees. This character is interrelated to several other vegetative characters such as collar diameter and number of lateral branches at seedling stage. Such interdependence of contributing traits often affects their direct relationship with plant height growth making correlation coefficient unreliable as selection indices. As more variables are included in the correlation studies, the inherent association becomes more complex; hence, the role of path coefficient analysis becomes important (CHATURVEDI and PANDEY, 2004). Understanding the nature of inter-relationship between the characters is the corner-stone of any breeding efforts. This knowledge would enable the breeder to know how the selection pressure exerted by the breeder on one trait would cause changes in other traits, furthermore, the direction and magnitude of such changes would be clarified (ALIYU, 2006). Path coefficient analysis is a statistic method which is used for partitioning the correlation coefficients into direct effect through a given causal

character and indirect effects through other variables. Both phenotypic and genotypic correlation coefficients are used for path analysis. The genotypic correlation coefficients are more reliable for examining the degree of relationship between character pairs (CHATURVEDI and PANDEY, 2004).

Due to long rotation length of the trees, particularly wild service tree the analysis of seedling characters is an efficient approach to determine the relative contribution of different characters as the determinant of plant height growth rate.

The objectives of this study were as follow:

- Defining genetic variability within two local populations of *Sorbus torminalis* (L.) Crantz.
- Quantifying the phenotypic and genotypic correlation coefficients between plant height growth rate in the species and three other morphological characteristics.
- Partitioning the correlation coefficients between the dependent character and other related characters.
- Specifying the morphological traits of the species to be used for efficient future indirect selection.

Materials and Methods

Seed was collected from a total of 40 randomly selected individual trees of wild service tree (*Sorbus torminalis* (L.) Crantz) from two sites named Sangdeh (1600 to 1800 m a.s.l.) and Ashak (2100 to 2300 m a.s.l.) both located in Mazandaran forest in north of Iran (Figure 1). It is worth to mention that there are about 40000 hectares of forests in the area in which wild service tree presents with a remarkable differences of plant composition and stand ages from site to site. Soil is deep in

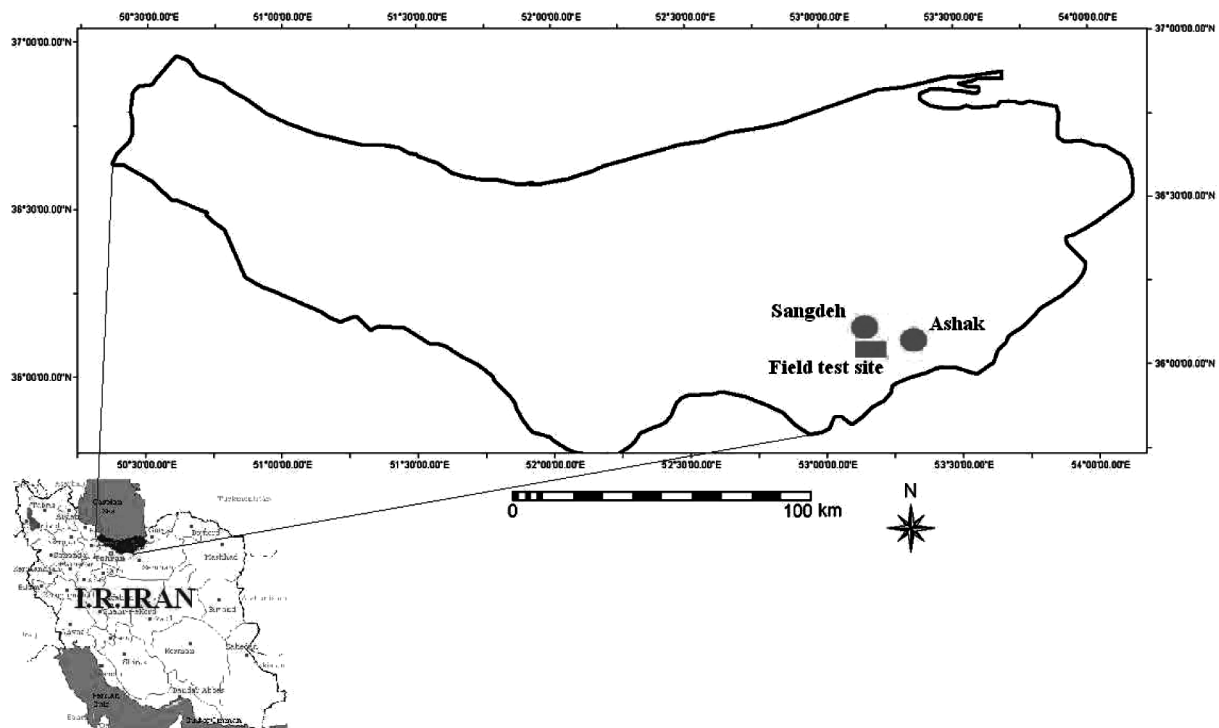


Figure 1. – Map of Mazandaran province, located in north of Iran, showing geographical origins of the two locations, Sangdeh and Ashak and the field test site.

Sangdeh, with a slope of 10 to 30%, north to northeast exposure. It is dominated by *Fagus orientalis* along with *Carpinus betulus*, *Acer velutinum*, *Acer cappadocicum*, *Fraxinus excelsior* subsp. *coriariifolia* and *Alnus subcordata*. Ashak site is a mountain forest, with a shallow soil and slope of 20 to 40% and south to southwest exposure. *Sorbus torminalis* is denser but smaller dimensions and *Fagus orientalis* is less present in this site. *Quercus castaneaefolia* C.A.M entered to this site mixed with *Carpinus betulus* L. The two sites are separated by a distance of about 10 km.

The mother trees were selected with a dbh (diameter at breast height) of 20 to 80 cm and an average interval of about 80 m to avoid sampling the same clone. The progeny test site was located at Orymalek in the same forest, where the bedrock is limestone and the soil is forest brown with sandy-loam texture. Average annual precipitation during the last 30 years was 821 mm. Amount of precipitation during spring and fall were 27.5 and 27.1 percent of total annual rain respectively. Average snowfall was reported as 26.4 percent of the precipitation. Average yearly temperature in the nursery was 9°C and average humidity was 79.6 percent.

Two hundred sound seeds of each selected mother tree were sown in plastic pots and raised to one-year-old seedlings. Thirty seedlings were used from each of the mother trees and planted in the forest site in a randomised complete block design with three replications. Ten seedlings from each mother tree were randomly allocated to each plot per replication with an interval between single plants of 50 centimetres. Collar diameter (cm), plant height (cm), number of branches (number) and branch angle (degree) of the seedlings were recorded when the seedlings were three years old.

Analysis of variance was carried out on the data with the GLM procedure of SAS software (SAS Institute Inc. 1989), for testing the statistical differences between the populations and mother trees nested in the populations, based on the recorded characteristics.

First a linear random model was used for a joint analysis of the two populations. The statistical model and its components were as follow:

$$Y_{ijkl} = \mu + \eta_k + \beta_j + \alpha_{i(k)} + \alpha_{i(k)}\beta_j + \rho_{lik} + \varepsilon_{ijkl}$$

In which

Y_{ijkl} = the phenotypic value of the i th progeny of the i th mother tree nested within the k th population in the j th block; μ = the grand mean; η_k = the effect of k th population; β_j = the effect of the j th block; $\alpha_{i(k)}$ = the effect of i th mother tree nested within the k th population; $\alpha_{i(k)}\beta_j$ = the interaction effect of the j th block and i th mother tree nested within the k th population; ρ_{lik} = within plot variation; ε_{ijkl} = the random error effect.

i = index of genotype = 1 to g , where $g = 20$; j = index of replication = 1 to r , where $r = 3$; k = index of population = 1 to o , where $o = 2$; l = index of progeny per plot = 1 to p , where $p = 10$.

Then an analysis of variance was performed on the data recorded on each population separately, to estimate the components of variance of the populations and narrow sense heritability of the characters.

The statistical model and its components were as follow:

$$Y_{ijl} = \mu + \beta_j + \alpha_i + \alpha_i\beta_j + \rho_{li} + \varepsilon_{ijl}$$

In which

Y_{ijl} = the phenotypic value of the i th progeny of the i th mother tree in the j th block; μ = the grand mean; β_j = the effect of the j th block; α_i = the effect of i th mother tree; $\alpha_i\beta_j$ = the interaction effect of the j th block and i th mother tree; ρ_{li} = within plot variation; ε_{ijl} = the random error effect. The indices are as before. Mother trees effect was nested in population effect. All of the models effects were considered random and normally distributed. Since a number of individual trees of several experimental units lost before data recording, the data were not balance and analyzed by GLM procedure of SAS (SAS Institute Inc., 1989) by which the expected mean squares (EMS) of unbalance data were estimated. The expected mean squares of the second analysis were used for partitioning the mean squares of the characteristics by equating the type III mean squares in the ANOVA table to their expectations and solving the equations. The standard error of an estimated component was computed as follows: (BECKER, 1985).

$$SE = \sqrt{\frac{2}{k^2} \sum_g \frac{MS_g^2}{f_g + 2}}$$

Where k is coefficient of variance component being estimated, MS_g = the g th mean square used to estimate the variance component and f_g = degree of freedom of the g th mean square.

We assumed the progenies of each mother tree as true half-sibs and additive genetic variance (σ_A^2) was estimated as $\sigma_A^2 = 4\sigma_f^2$ where σ_f^2 is the genetic variance among families within population (FALCONER and MACKAY, 1996). The effects of progeny nested in mother trees were included in the phenotypic variance. The formula used for the individual narrow sense heritability was as follows (SEBBENN et al., 2003):

$$h_n^2 = \frac{4\sigma_f^2}{\sigma_f^2 + \sigma_w^2 + \sigma_e^2}$$

In which σ_f^2 and σ_w^2 are among and within family variance components respectively and σ_e^2 is variance due to the random error. Expected genetic gain by individual selection was estimated by the following formula (BOGDAN et al., 2004).

$$\Delta G = i\sigma_p h_i^2$$

Where ΔG , i , σ_p , and h_i^2 , are expected genetic gain, selection intensity (10% of the studied plus trees), square root of phenotypic variance, and heritability, respectively.

Phenotypic variance was estimated as:

$$\sigma_p^2 = (\sigma_f^2 + \sigma_w^2 + \sigma_e^2)$$

Genetic advance was also estimated as: (KUMAR, 2007).

$$G = (\Delta G / \text{mean}) * 100$$

Approving the significant differences between the trees based on the studied characteristics, phenotypic and genotypic correlation coefficients between all pairs of the studied traits were determined by the following equations (SALEEM et al., 2006).

$$rg = \frac{Cov_{gij}}{(\sigma_{gi}^2 \sigma_{gj}^2)^{1/2}}, \quad rp = \frac{M_{ij}}{(M_{ii} M_{jj})^{1/2}}$$

Where rg and rp are genotypic and phenotypic correlation coefficient, Cov_{gij} , σ_{gi}^2 and σ_{gj}^2 are the estimates of covariance and variances, for traits i and j . M_{ij} is the mean product, M_{ii} and M_{jj} are mean squares for trait i and j , respectively.

Path coefficients were obtained by solving simultaneous equations. Indirect path coefficients were determined by multiplying appropriate correlation coefficients and path coefficient values. Statistical analyses were performed using SAS software (SAS Institute Inc. 1989). Path analysis was performed by a Qbasic program written by the second author based on the method presented by (DEWAY and LU, 1959; CHATURVEDI and PANDEY, 2004). Path analysis can be used to estimate direct and indirect contributions between the standardized predictor and criterion variables (SOKAL and ROHLF, 1995).

Results

A summary of the results of ANOVA for the studied characters is shown in *Table 1*. Analysis of variance revealed significant differences between the populations and trees within the populations based on the studied characters (*Table 1*). The same trends of differences were observed between the trees in the second analysis. *Table 2* summarizes mean values of the studied characters and corresponding standard errors. Variance components of the second analysis are presented in *Table 3*, along with their corresponding standard errors. Narrow sense heritability, genetic gain, and genetic advance estimated values are also presented in *Table 3*. Heritability values are generally larger for Ashak population, resulting in larger genetic gain and genetic advance values.

Regarding correlation coefficients, all of the phenotypic correlation coefficient values were positive and significant at 1%. Plant height showed positive significant phenotypic correlation with all of the studied characters, indicating that trees with larger collar diameter, more lateral branches and wider branch angle were taller. Generally, the genotypic correlation coefficient values were stronger than corresponding phenotypic correlation values (*Table 4*). The strongest positive phenotypic

Table 1. – Mean squares resulted of analysis of variance of the data recorded on four characteristics of 40 half-sib families randomly collected from two populations of wild service tree (*Sorbus torminalis*).

Source of variation	DF	Collar diameter	Plant height	Lateral branches	Branch angle
Joint analysis of the two populations, trees nested in populations					
Population	1	301.96**	29455.91**	1991.32**	762.79*
Replication	2	41.20**	2240.82**	49.86*	5152.51**
Tree (Population)	38	20.59**	1079.92**	33.64*	381.39*
Rep*Tree (Population)	78	11.45**	432.28**	20.87**	245.46**
Within plot variation	9	3.59	469.63	21.52	274.16
Error	665	5.14	269.79	13.87	148.08
Mean squares of Ashak population					
Replication	2	61.42**	2772.97**	13.12ns	1955.71**
Tree	19	32.52**	1463.01**	24.25**	343.55**
Rep*Tree	38	10.52**	435.66**	8.35ns	251.78**
Within plot variation	160	3.57	332.65	6.54	138.90
Error	279	4.83	233.93	6.82	156.43
Mean squares of Sangdeh population					
Replication	2	8.87*	138.59ns	97.86**	3412.60**
Tree	19	7.97*	672.46**	42.02*	418.68*
Rep*Tree	38	11.47**	404.964ns	31.21**	249.94**
Within plot variation	177	1.84	282.72	30.13	174.53
Error	209	5.44	299.29	19.06	144.50

**, * = Significant at 1% and 5% level of probabilities respectively, ns = Non-significant.

correlation was found between plant height and collar diameter ($r = 0.70$) while the strongest genotypic correlation was found between plant height and lateral branches ($r = 0.84$). Branch angle showed the weakest phenotypic correlation coefficient with collar diameter and lateral branches ($r = 0.15$).

Path analysis based on the phenotypic correlation coefficients revealed that at phenotypic level collar diameter had the strongest positive direct effect (0.66) and strongest correlation (0.70) with plant height (Table 5). Total indirect effects of collar diameter on plant height are not noticeable (0.044). In contrast, number of lateral branches showed very weak direct effect on plant height at phenotypic level (0.055).

Partitioning the genotypic correlation coefficients revealed one negative indirect effect (Table 6). Collar diameter showed a negative indirect effect on plant height through branch angle (-0.083), but a positive indirect effect through lateral branches (0.197), and a positive direct effect (0.051) which resulted in a positive genotypic correlation of 0.16. Lateral branches showed a strong genotypic direct effect on plant height (0.651).

Positive total indirect effect of this character (0.186) increased the total genotypic correlation with plant height to 0.84. Strong correlation of branch angle with plant height (0.69) was mainly caused by a strong positive direct effect (0.452) and indirect effect (0.245) through lateral branches.

Discussion

Substantial differences of the vegetative characteristics were observed within the studied mother trees and the populations. Differences between the trees based on the studied characters recorded on their progenies would imply enough variability to be used in the correlation coefficient studies. For instance, mean values of the three-year old progenies on collar diameter varied from 6.55 to 12.54 cm (91.45% difference). The mean values of the seedlings on plant height also varied from 25.79 to 65.63 cm, a difference of 154.5% which is remarkable. Lateral branches means ranged from 2.66 for the tree number 4 of Ashak to 11.19 for the tree number 30 of Sangdeh site (320.7% difference). These differences sug-

Table 2. – General means with standard errors of four growth characteristics recorded on 40 half-sib families at early growth stage of *Sorbus torminalis*. Means number 1–20 belong to the progenies of the mother trees sampled from Ashak site and the means number 21–40 belong to the progenies of the mother trees sampled from Sangdeh site.

Tree numbers	Collar diameter (mm)	Plant height (cm)	Lateral branches (Number)	Branch angle (Degree)
1	11.80 ±2.48	60.75 ±21.02	6.35 ±2.51	70.00 ±11.19
2	12.54 ±2.99	54.66 ±14.77	6.79 ±2.87	74.73 ±7.69
3	9.44 ±2.45	47.87 ±20.18	3.93 ±1.65	70.22 ±14.45
4	6.55 ±1.73	25.79 ±13.96	2.66 ±1.49	57.75 ±15.91
5	10.20 ±3.47	39.57 ±18.13	4.15 ±2.11	69.38 ±15.67
6	9.40 ±1.97	38.45 ±14.86	3.08 ±1.31	72.59 ±8.08
7	9.71 ±2.15	38.09 ±14.95	3.25 ±1.23	63.57 ±20.47
8	8.87 ±2.50	34.20 ±15.72	5.13 ±4.37	71.12 ±11.04
9	7.69 ±2.03	28.64 ±9.91	4.50 ±2.95	68.60 ±8.68
10	11.51 ±2.60	36.95 ±15.69	5.72 ±2.61	75.40 ±7.40
11	10.02 ±3.11	42.27 ±12.37	6.11 ±2.97	70.76 ±14.96
12	9.73 ±2.20	45.75 ±14.95	4.05 ±2.03	68.23 ±16.42
13	10.00 ±2.51	46.39 ±9.19	4.89 ±2.99	70.08 ±14.17
14	11.82 ±1.94	59.15 ±13.97	5.09 ±2.09	67.06 ±17.13
15	11.36 ±2.25	54.89 ±17.24	5.29 ±2.57	71.43 ±13.97
16	8.35 ±2.28	38.53 ±13.04	4.71 ±1.81	67.51 ±13.54
17	9.12 ±2.33	30.88 ±22.73	5.48 ±2.84	58.37 ±13.66
18	9.30 ±1.78	43.74 ±13.45	5.73 ±3.60	67.16 ±12.37
19	10.48 ±2.92	52.16 ±17.25	7.25 ±3.17	71.56 ±11.79
20	8.51 ±2.02	35.46 ±16.21	5.46 ±2.50	65.73 ±11.68
21	9.63 ±2.53	42.08 ±11.07	6.16 ±2.36	59.69 ±14.73
22	11.04 ±2.43	55.77 ±13.15	8.25 ±4.22	73.46 ±16.31
23	11.59 ±3.42	53.21 ±20.78	9.21 ±3.64	62.40 ±9.21
24	11.45 ±2.24	59.52 ±18.55	8.12 ±3.13	59.35 ±15.25
25	11.36 ±2.78	65.63 ±22.99	7.83 ±3.66	64.22 ±15.34
26	11.07 ±1.84	53.10 ±14.23	7.47 ±4.27	64.00 ±14.23
27	11.67 ±2.27	53.89 ±15.66	9.30 ±3.36	63.60 ±11.90
28	11.50 ±2.94	54.35 ±22.72	9.35 ±4.12	67.00 ±7.72
29	11.03 ±3.05	46.09 ±17.46	7.59 ±3.78	71.78 ±15.91
30	11.50 ±2.30	57.92 ±16.77	11.19 ±3.66	73.18 ±7.44
31	11.05 ±1.64	58.28 ±11.76	9.52 ±4.99	67.10 ±8.33
32	11.54 ±2.61	56.58 ±17.44	8.72 ±3.85	69.50 ±17.67
33	9.82 ±2.06	61.34 ±19.26	4.88 ±2.90	66.62 ±14.45
34	10.61 ±2.24	48.86 ±12.48	8.31 ±3.66	62.21 ±11.26
35	11.05 ±2.30	61.18 ±16.30	8.13 ±3.32	64.77 ±13.83
36	11.10 ±2.51	54.47 ±17.20	9.00 ±3.25	67.92 ±10.90
37	11.04 ±2.00	48.86 ±15.63	9.63 ±2.71	64.40 ±13.70
38	12.04 ±3.00	60.21 ±19.96	8.38 ±3.18	70.90 ±11.72
39	11.55 ±2.28	61.64 ±16.00	9.39 ±3.43	66.80 ±14.45
40	11.88 ±2.44	63.21 ±15.15	8.34 ±3.71	73.09 ±11.19
Ashak	10.01 ±2.76	44.27 ±19.00	5.14 ±2.84	68.49 ±13.83
Sangdeh	11.21 ±2.45	56.45 ±18.04	8.48 ±4.67	66.99 ±13.62
CV%	20.24	30.26	32.10	18.32

Table 3. – Variance components, narrow sense heritability, genetic gain, and genetic advance estimated based on expected mean squares (EMS) and adjusted coefficients resulted from analysis of variance of the data recorded on four characteristics of 40 half-sib families sampled from the two populations of *Sorbus torminalis*.

Effects	Collar diameter	Plant height	Lateral branches	Branch angle
Variance components of Ashak population				
Replication	0.54	24.53	005	17.82
	±0.45	±20.39	±0.10	±14.37
Tree	1.39	64.78	1.00	5.96
	±0.65	±28.95	±0.48	±7.56
Rep*Tree	1.03	36.53	0.28	17.27
	±0.43	±18.00	±0.35	±10.47
Within plot	-0.04	3.08	-0.01	-0.55
	±0.02	±1.31	±0.02	±0.63
Error	4.83	233.93	6.82	156.43
Heritability	0.90	0.86	0.51	0.15
Genetic Gain	0.22	1.49	0.14	0.19
Genetic Advance	2.23	3.37	2.78	0.27
Variance components of Sangdeh population				
Replication	0.02	-2.00	0.53	1.37
	±0.02	±1.07	±0.54	±2.33
Tree	-0.16	13.06	0.54	8.30
	±0.17	±11.00	±0.71	±6.80
Rep*Tree	0.84	14.74	1.70	14.71
	±0.36	±13.27	±1.01	±8.04
Within plot	-0.08	-0.38	0.26	0.70
	±0.01	±0.90	±0.09	±0.54
Error	5.44	299.29	19.06	144.50
Heritability	0.0	0.17	0.11	0.22
Genetic Gain	0.0	0.30	0.05	0.27
Genetic Advance	0.0	0.52	0.57	0.40

Table 4. – Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between all pair combinations of the characteristics, recorded on 40 half-sib families of wild service tree (*Sorbus torminalis*).

Traits	Collar diameter	Plant height	Lateral branches	Branch angle
Collar diameter	-	0.16**	0.30**	-0.18**
Plant height	0.70**	-	0.84**	0.69**
Lateral branches	0.49**	0.40**	-	0.38**
Branch angle	0.15**	0.22**	0.15**	-

**, * = Significant at 1% and 5% level of probabilities respectively.

gest a high range of variation and excellent possibilities of selection. A large number of branches per tree give rise to a denser crown which has a higher capacity for snow and water retention. Such an increase in precipitation retention may significantly contribute to preventing

avalanche initiation, soil erosion and flooding downstream (BLADA and POPESCU, 2007). Although apomictic reproduction system is said to be quite usual in *Sorbus* species (SPERENS, 1997) and they have the ability to resprout from stump or roots (BALIUCKAS et al., 2005), both cause the populations of the species to be less variable, but representative sampling and long distance between the selected mother trees assured enough genetic variation to be sampled in this study.

Based on the observed between and within population genetic variation, selection of faster growing genotypes for reforestation and operational tree improvement will be effective. A faster growing provenance would colonize the area much faster than a slow growing one (BLADA and POPESCU, 2007). The faster colonization of the steeper slopes of the Ashak site by the superior genotypes would be more efficient for site stabilization. Although mean values of collar diameter, plant height and lateral branches are larger for Sangdeh *Sorbus* population than those of Ashak population (Table 2), but genetic variation is more heritable in Ashak population for the characters than that of Sangdeh population (Table 3). This reflects superiority of selection for the traits from Ashak *Sorbus* population over Sangdeh population.

The greatest genetic advance was observed for plant height followed by lateral branches, both in Ashak population. Genetic gain and genetic advance values are positive for all of the studied characters in Ashak population. Several reasons may be counted for this difference between the two populations. Differences in climate aspects would lead to different natural selection intensity as well as differences in pollination pattern and hybridization extent. Genetic architecture of the two populations imply that if seed is collected for seedling production to be used for faster colonization in forest reclamation, Sangdeh would be a better site for seed collection. Plus trees of this site may be used for clonal seed orchard establishment. But for breeding purposes particularly for selection programs, Ashak is suggested as a better site with more effective *Sorbus* population. Morphologic characteristics were found considerably variable on other woody plant populations (ALDASORO et al., 1998; BLADA and POPESCU, 2007). Several other authors seek variation in fruit characteristics of *Sorbus* species as constant characters and important biological features which decide of generative propagation abilities (MACALLISTER, 2005; BEDNORZ et al., 2006a; BEDNORZ, 2007). Constant characters may be a good discriminating factors (BEDNORZ, 2007), mainly used for systematic purposes and may not be useful to be used for within populations and species genetic variation investigations. This study aimed to use genetic variation to investigate inter-relationship between vegetative characteristics. Although these characters are not of phylogenetic value but their strong inter-relationship may be used in breeding purposes particularly for indirect selection (FALCONER and MACKAY, 1996).

Regarding the variance components it is worth mentioning that sometimes a higher degree of relatedness is assumed between the progenies of a single tree in an open-pollinated population. SÆBØ and JOHNSEN (2000) assumed that the family variance estimated one third of

Table 5. – Phenotypic correlations, direct and indirect path coefficients between dependent character, plant height, and independent characters, collar diameter, number of branches and branch angle, recorded on 40 half-sib families of wild service tree (*Sorbus torminalis*). Underlined numbers in the right part of the table are direct effects of independent characters on plant height. Above and below diagonal numbers are indirect effects of the characters on the rows through characters on the columns on plant height.

Independent characters	Phenotypic correlation with plant height	Total indirect effects	Direct and indirect effects of independent characters on plant height		
			Collar diameter	Lateral branches	Branch angle
Collar diameter	0.70	0.044	<u>0.660</u>	0.027	0.017
Lateral branches	0.40	0.342	0.325	<u>0.055</u>	0.017
Branch angle	0.22	0.107	0.098	0.008	<u>0.114</u>
Residual = 0.48					

Table 6. – Genotypic correlations, direct and indirect path coefficients between dependent character, plant height, and independent characters, collar diameter, number of branches and branch angle, recorded on 40 half-sib families of wild service tree (*Sorbus torminalis*). Underlined numbers in the right part of the table are direct effects of independent characters on plant height. Above and below diagonal numbers are indirect effects of the characters on the rows through characters on the columns on plant height.

Independent characters	Genotypic correlation with plant height	Total indirect effects	Direct and indirect effects of independent characters on plant height		
			Collar diameter	Lateral branches	Branch angle
Collar diameter	0.16	0.114	<u>0.051</u>	0.197	-0.083
Lateral branches	0.84	0.186	0.015	<u>0.651</u>	0.170
Branch angle	0.69	0.236	0.009	0.245	<u>0.452</u>
Residual = 0.136					

the additive variance. There are some possibilities of pollination within small groups of related trees giving room for a certain degree of full-sibs ending to over-estimation of the narrow sense heritability. In this case, as BALIUCKAS et al. (2005) argued, the estimates must be regarded as upper limits heritability. Negative values of variance components were observed in the partitioning of mean squares to variance components which were treated as zero estimates. The estimated variance components should theoretically be nonnegative. These negative estimates may arise for a variety of reasons. Large variability of the data and outliers could be involved in such result.

The phenotypic and genotypic trait-trait correlations were either significant ($p < 0.05$) or highly significant ($p < 0.01$) in almost all the cases recorded (*Table 4*). Knowledge of complex relationship between vegetative characters of wild service tree would be essential to effectively select superior mother plants for developing seed orchard of the species by which fast growing seedlings could be produced. Significant phenotypic correlations indicated that early and indirect selection is possible in other woody plant species (BLADA and POPES-

CU, 2007). The path coefficient analysis is simply a standardized partial regression coefficient which divides the correlation coefficient into the measures of direct and indirect contribution of independent variables on dependent variable (Plant height in this study). Phenotypic and genotypic correlation coefficients are mainly used for indirect selection in plant breeding programs. The nature of these correlations may enhance or retard the selection programs. A positive correlation indicates that the selection for improving one character would result in concomitant improvement of one or more other related characters. In our study, in general, the genotypic correlation coefficient values were stronger than corresponding phenotypic values. The genotypic correlation is an estimated value whereas; phenotypic correlation is a derived value from the genotype and environmental interaction. The genotypic correlation is, therefore, a more reliable estimate for examining the degree of relationship between character pairs (CHATURVEDI and PANDEY, 2004).

Strong positive phenotypic correlation (0.70) and direct effect of collar diameter with plant height (0.66) suggest that plant collar diameter is the best predictor

of plant height in wild service tree at phenotypic level. Total indirect effects of lateral branches contain the majority of its phenotypic correlation with plant height (0.342). The important point on this character is its indirect effects through collar diameter (0.325). In other words, lateral branches affect plant height mainly indirectly through collar diameter. A relatively high residual effect indicated that more correlated characters with plant height could be studied. Strong significant positive genotypic correlation coefficients were estimated between plant height with lateral branches and branch angle (0.84 and 0.69 respectively). This suggests that regarding genotypic correlations, the two characters are good predictors of plant height growth in wild service tree at genotypic level and seedlings with higher number of lateral branches and wider branch angles tend to produce taller trees. Branch angle might be regarded as a non-stable trait which is not significantly varied between adult trees. But it is significantly variable at early growth stages by which other growth characteristics might be soundly influenced. Age-related trends for morphologic characteristics are crucial for developing tree breeding strategy and early selection. A number of studies have documented age-age trends in morphologic characteristics for other woody plant species (PEDERSEN et al., 2007). Very little data have been published regarding time trends in morphological traits for wild service tree. However, a great genetic variation was found between the studied trees and populations based on branch angle of their progenies justifying investigation of their inter-relationship. Collar diameter could be regarded as a secondary important character because of its strong indirect genetic correlation. There are noticeable differences between phenotypic and genotypic correlation coefficients and their components. This may be attributed to early stage data collection or outcrossing generative system of the species. Outcrossing plant species, such as *Sorbus torminalis*, tend to have more genetic variation among its progenies.

Conclusion

Progeny test on two populations of *Sorbus torminalis* revealed significant within and between population genetic variation as well as useful information for early growth stage selection. Estimated heritability values indicated possibilities for improvement by utilizing existing genetic variation in one of the studied populations. The differences in genetic architecture of the two populations might be due to different climatic aspects, which lead to different natural selection intensity as well as differences in pollination pattern and hybridization extent.

Phenotypic correlation and path analysis showed that collar diameter with a positive correlation and relatively strong direct effect on plant height is the best predictor of plant height in wild service tree at phenotypic level, whereas, lateral branches affect plant height mainly indirectly through collar diameter. Significant positive genotypic correlation coefficients were observed between plant height and lateral branches as well as branch angle, suggesting the two characters are good predictors

of plant height growth in wild service tree at genotypic level.

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Genetic Variation in Two Rare Endemic Mexican Trees, *Magnolia sharpii* and *Magnolia schiedeana*

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Abstract

Patterns of genetic variation were examined within two endemic tree species restricted to Mexican cloud forest, *Magnolia sharpii* and *Magnolia schiedeana*. Leaf samples collected from natural populations were analysed using PCR RFLP of cpDNA, Inter-SSR and isozyme genetic markers, which were used to test a series of hypotheses regarding patterns of intraspecific variation within the two species. Genetic diversity esti-

mates derived from Inter-SSR markers (mean S_{pop} of 0.56 and 0.50 for *M. sharpii* and *M. schiedeana* respectively) are comparable to values obtained for other tree species. As predicted on the basis of its larger geographic range, the degree of population differentiation was found to be higher within *M. schiedeana* than *M. sharpii*, with 12.9% and 3.4% of total variation recorded between populations for the two species respectively using isozymes, and 26% and 11% using Inter-SSR markers. Isozyme analyses indicated negative F_{is}

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