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Fertility Variation and Status Number in Clonal Seed Orchards of *Pinus sylvestris*

Nebi Bilir and Halime Temirağa

Faculty of Forestry, Suleyman Demirel University, Isparta, TR-32260, Turkey

Abstract: The present study was carried out to evaluate fertility variation, status number and gene diversity based on strobili productions in two clonal seed orchards of Scots pine (*Pinus sylvestris* L.). There were large differences among clones for the female and male strobili productions in the orchards. Positive and significant ($p \leq 0.05$) correlations were found between female and male strobili production ($r = 0.76, 0.55$). Female fertility variation (1.03, 1.07) was larger than male fertility variation (1.02, 1.03) in the orchards. The status numbers estimated based on the total fertility were very high (97 and 98% of census numbers). The large fertility variation could be balanced by different treatments such as mixing seed equally from clones or genetic thinning.

Key words: Scots pine, graft, gene diversity, coancestry

INTRODUCTION

Seed orchards are one of the important seed sources for plantation forestry and a link between present and future forests as gene conservation areas. They are becoming gradually more importance for conversion of unproductive forest to productive forest because of its improved seeds. For instance, while the species occupy roughly 750000 ha, of which about 475000 ha are considered to be productive forests, only 10% of the seed demand in the species was supplied (Cengiz, 2003) in from 111 ha of seed orchards in Turkey. New seed orchards have been established according to the "National Tree Breeding and Seed Production Programme" of Turkey (Koski and Antola, 1993). One of the factors that have impact on seed production is the variation in fertility, among and within clones in the orchards (Prescher *et al.*, 2007). Gene diversity in orchard crops is a function of fertility variation and pollen contamination. Many studies were conducted on fertility variation in forest tree species (Bila, 2000; Kang, 2001; Kang and Lindgren, 1998; Bilir *et al.*, 2002, 2004; Varghese *et al.*, 2006) for different purposes such as genetic management of populations (Bila, 2000), breeding (El-Kassaby, 1995; Griffin, 1982; Dutkuner *et al.*, 2008) and gene conservation programs (Kang *et al.*, 2003). Gene diversity is regarded to be of importance for the sustainability of forest ecosystems. Gene diversity in seed orchard crops can play an important role in coping with climate change as it may make the seed crop more robust and more adapted to a range of environments. Gene diversity is one of the relevant considerations when establishing and managing seed orchards (Prescher *et al.*, 2007) and for gene diversity estimates information on fertility variations is

needed (Lindgren and Mullin, 1998). Many studies were carried out on female and male fertility in seed orchards (Kjaer, 1996; Kang and Lindgren, 1998; Nikkanen and Ruotsalainen, 2000). To monitor and determine the genetic diversity of seed crops, some genetic parameters such as genetic relatedness, inbreeding and gene diversity should be calculated.

The present study aimed to evaluate fertility variation among orchard parents and its effect on status number and gene diversity and to contribute breeding programme of the species.

MATERIALS AND METHODS

The study was carried out in two clonal seed orchards of Scots pine (*Pinus sylvestris*). The seed orchards established with originated from plus trees, which were selected from a specific seed stand. The seed orchards were established at Mengen, Bolu (40°56'N, 32°13'E, 850 m) at spacing 7×7 m consisting of 30 clones and 1034 grafts in 1988 and at Taskopru, Kastamonu (41°36'N, 35°05'E, 1500 m) at 6×6 m consisting of 30 clones and 1987 grafts in 1995.

Female and male strobili data were collected on three grafts, chosen at random, from each of twenty two clones of Mengen orchard and twenty five clones of Taskopru orchard in the spring of 2005.

Fertility variation and status number: In this study, fertility variation is estimated based on the variation in strobilus production among individuals in the populations. The fertility variation for female (ψ_f) and male (ψ_m) were estimated by Kang and Lindgren (1999) as:

$$\psi_f = N \sum_{i=1}^N \left(\frac{f_i}{\sum f_i} \right)^2 = CV_f^2 + 1 \quad (1a)$$

$$\psi_m = N \sum_{i=1}^N \left(\frac{m_i}{\sum m_i} \right)^2 = CV_m^2 + 1 \quad (1b)$$

where, N is the census number, f_i is the number of female strobili of the i th individual, m_i is the number of male strobili of the i th individual and CV_f and CV_m are the coefficients of variation in female and male strobilus production among individuals.

Total fertility variation (Ψ) was calculated by Kang and Lindgren (1999) as :

$$\Psi = N \sum_{i=1}^N \left(\frac{0.5f_i}{\sum f_i} + \frac{0.5m_i}{\sum m_i} \right)^2 \quad (2)$$

$$= 0.25 \left[N \sum_{i=1}^N \frac{f_i^2}{\sum f_i} + N \sum_{i=1}^N \frac{m_i^2}{\sum m_i} + N \sum_{i=1}^N \frac{2m_i f_i}{\sum m_i * \sum f_i} \right]$$

where, N is the census number, f_i and m_i are the numbers of female and male strobili of the i th individual, respectively.

The status numbers of female ($N_{s(f)}$) and male parents ($N_{s(m)}$) are calculated based on female fertility variation (ψ_f), male fertility variation (ψ_m) and the census number (N) by Lindgren *et al.* (1996) as:

$$N_{s(f)} = N/\psi_f \quad (3a)$$

$$N_{s(m)} = N/\psi_m \quad (3b)$$

Status number on total fertility was calculated following Kang (2001) and as:

$$N_s = \frac{4N}{[\Psi_f + \Psi_m + 2 + 2r\sqrt{(\Psi_f - 1)(\Psi_m - 1)}]} \quad (4)$$

where, ψ_f and ψ_m are the fertility variations of female and male parents, respectively and r is the correlation

coefficient between female and male strobilus production. Relative status number (N_r) was calculated as $N_r = N_s/N$ (Lindgren *et al.*, 1996).

RESULTS AND DISCUSSION

Female and male strobilus production: The average, coefficient of variation, ranges of female and male strobilus production and phenotypic correlation coefficients between female and male strobili were given in Table 1.

Clonal averages of female and male strobili were 150.4 and 371 in Mengen orchard and 179.8 and 238.5 in Taskopru orchard, respectively (Table 1). There were large variations in strobilus production among clones in the orchards (Fig. 1).

The variations of female strobili production were higher than that of male strobili. Large clonal differences in female and male fertility have been reported in seed orchards (Kjaer, 1996; Kang and Lindgren, 1998; Nikkanen and Ruotsalainen, 2000). Differences in gamete contribution among clones could be genetic (Eriksson *et al.*, 1973), environmental (Hedegart, 1976) and management of orchard (Zobel and Talbert, 1984). Thus, could also be other factors such as age and the associated tree size (Bilir *et al.*, 2006), or seed orchard locations and years (Lindgren *et al.*, 1977). For instance, averages of female and male strobili production were reported 201.4 and 531.3 at 16 years (Bilir *et al.*, 2002) and 254.3 and 724.3 at 19 years (Dutkuner *et al.*, 2008) in a Turkish Scots pine seed orchard.

Broad-sense heritability was very low (<0.16) in Turkish scots pine seed orchards. It means that to create desirable characters in seed orchard trees, there ought to be a large potential of management, which affects “the environment” (Bilir *et al.*, 2006).

It is reported that fertility variation is higher when seed orchards are young (Kang and Lindgren, 1999; Bila, 2000). In the present study, data on strobilus

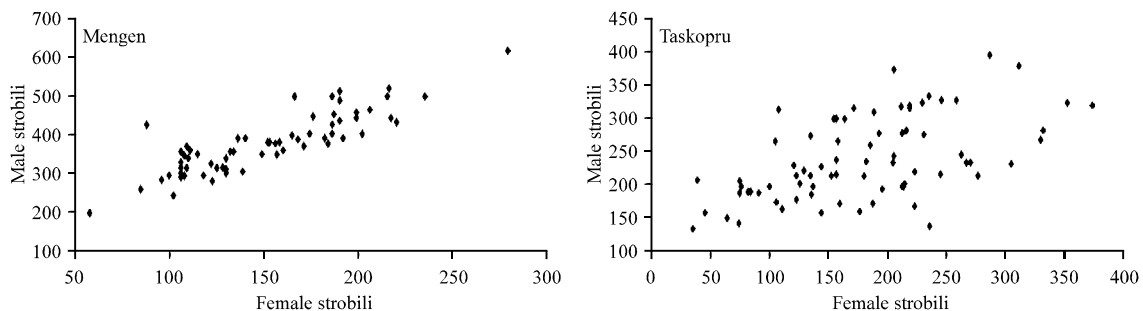


Fig. 1: Relation between female and male strobilus production in the orchards

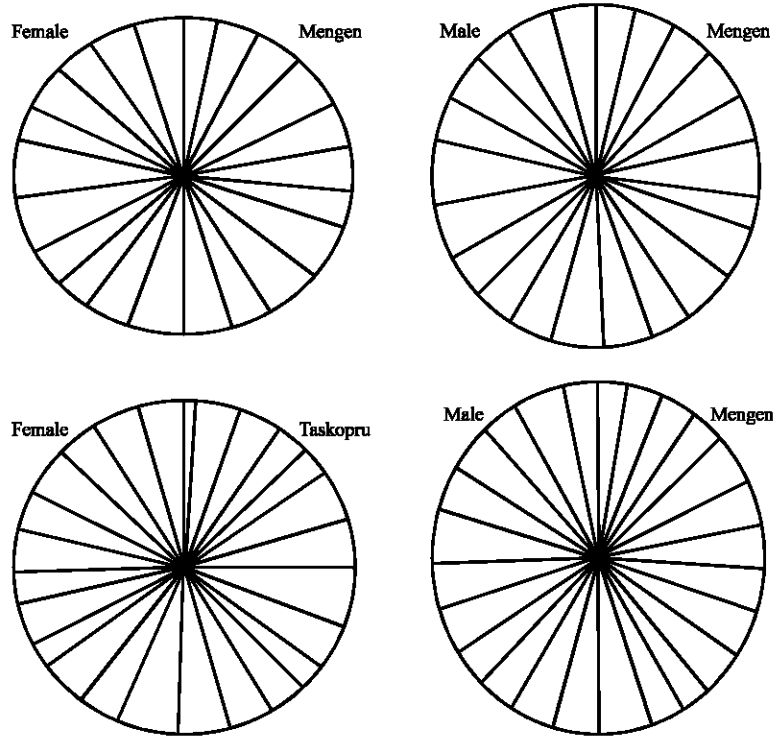


Fig. 2: Parental gamete contribution of clones in the orchards

Table 1: Average, coefficient of variation (CV), range and correlation (r) in female and male strobilus production in the studied seed orchards

Statistics	Seed orchards			
	Mengen		Taskopru	
	Female	Male	Female	Male
Average	150.4	371	179.8	238.5
CV	0.179	0.134	0.257	0.158
Range (clonal)	111-196	253-485	55-267	160-308
Range (individual)	58-279	35-610	35-374	133-394
r ^a	0.763		0.552	

^aPhenotypic correlation coefficient between clonal female and male strobilus production

production were collected from only one year. Kang (2001) reported that clonal fertility was fluctuated over many years in conifer seed orchards.

The most abundant quartile of clones in Mengen orchard produced 28.3% of total female and 32.1%, while they were 31% and 24% in Taskopru orchard, respectively (Fig. 1).

Positive and significant ($p \leq 0.05$) correlations were found between female and male strobilus production in both of the orchards (Table 1, Fig. 2).

This result is well in accordance with the results from seed orchards of different forest tree species by Bilir *et al.* (2002), Keskin (1999), Jonsson *et al.* (1976), Bhumibhamon (1978), Burczyk and Chalupka (1997), Nikkanen and Ruotsalainen (2000) and Varghese *et al.*

(2000). However, negative genetic correlations between female and male flowering were reported in different forest tree species by Schultz (1971) and Savolainen *et al.*, (1993). The correlation coefficient between female and male fertility should thus be considered when the total fertility is estimated (Kang, 2001; Kang and El-Kassaby, 2002).

Coefficients of variation of females were higher than those of males in the seed orchards (Table 1). Large differences in the production of female and male strobili among clones were found in seed orchards by Kang (2001) and by Keskin (1999).

Fertility variation and status number: Female (ψ_f), male (ψ_m) and total (Ψ) fertility variation, status number (N_s) and relative status number (N_r) were presented in Table 2. Female fertility variation (ψ_f) was higher than male fertility variation (ψ_m) in the orchards (Table 2). Similar results were also reported by Bilir *et al.* (2002) in a clonal seed orchard of Turkish Scots pine, while it was opposite to Dutkuner *et al.* (2008).

The estimated status numbers were very high in the orchards (Table 2). They were 21.3 (97% of census number) for female parents, 21.6 (98%) for male parents and 21.5 (98%) for total fertility in Mengen orchard and 23.5 (94%), 24.4 (98%) and 24.2 (97%) in Taskopru

Table 2: Fertility variation (t_f and t_m), status number ($N_{s(f)}$ and $N_{s(m)}$) and relative status number ($N_{r(f)}$ and $N_{r(m)}$) in gametic gene pool for female and male parents

Parameters	Seed orchards			
	Mengen (22)*		Taskopru (25)	
	Female	Male	Female	Male
t_f and t_m **	1.03	1.02	1.07	1.03
$N_{s(f)}$ and $N_{s(m)}$	21.3	21.60	23.5	24.40
$N_{r(f)}$ and $N_{r(m)}$	0.97	0.98	0.94	0.98

*Census number of clones (N) in parentheses, **F and m represent female and male, respectively

Table 3: Fertility variation (Ψ), status number (N_s), relative status number (N_r) and relative gene diversity (GD) in total gametic gene pool in the studied seed orchards

Parameters	Seed orchards	
	Mengen (22)*	Taskopru(25)
Ψ	1.023	1.031
N_s	21.500	24.200
N_r	0.980	0.97
GD (= $1-1/(2*N_s)$)	0.977	0.979

Census number (N) in parentheses

orchard, respectively (Table 2, 3). Similar results were also reported by Bilir *et al.* (2002) and Dutkuner *et al.* (2008) in a Turkish Scots pine seed orchard.

Gene Diversity (GD) in seed orchard crop was maintained high (0.977 and 0.979) as seen in Table 3. Maximum gene diversity of seed orchards crop can only be attained when all parents contribute equally to the gamete gene pool (Kang, 2001). The relation between Gene Diversity (GD) and fertility variation (Ψ) and census number of clones (N) can be showed as: $GD = 1-0.5 \Psi/N$. When used many clones in establishment of seed orchard, fertility variation among clones and within clone could be high (e.g., CV).

Relative effective number of clones and the coefficient of variation among clones for ramet numbers were estimated 0.76 and 55.6% in Mengen (Anonymous, 2012) orchard and 0.95 and 23% in Taskopru orchard based on ramet numbers of clones by Bilir and Ulsan (2007). Based on genetic information from progeny tests, new seed orchards will be established in the species according the "Turkish Breeding Programme". Parental trees are selected initially according to their phenotypes for traits such as vigour, form, wood quality or other desired characteristics, which include general adaptability.

CONCLUSION

Genetic information (e.g., genetic value, fertility) could also be used as a criterion of selection for seed production in seed orchards. Equal seed harvest or mixing seed equally from clones may improve the fertility variation and thus status number or balance by different

management treatments such as pruning. It could be also balanced by equal or similar number of grafts each clone.

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