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Genetic Diversity of Seed Orchard Crops

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1. Introduction

Different climate types enable local or exotic plantations to be established. Thus, the opportunity to establish stands of high quality and quantity is increasing. In establishing a plantation, it is necessary to select appropriate species, obey improvement principles, consider nursery and plantation techniques, and take into account economic and social issues. Selecting genetically high-quality seed sources and performing plantation improvement studies are of particular importance (Ürgenç, 1982; Alptekin, 1986; Ertekin, 2006). Genetic diversity among seeds is an important aspect of plantation forestry, especially when using improved seeds (e.g., seed orchard crops). Many currently established plantations originated from seed orchard crops. The genetic structure of these plantation forests is the same as the original seed orchard structure; therefore, the rich genetic diversity of natural forests is lacking in new plantation forests. This narrow genetic diversity increases the risk of mass deaths, insect and fungal diseases, and lowers resistance to climate change in the future forest.

Seed orchards are important seed sources and are essential for global tree improvement programs and studies. The primary objective of seed orchards is to produce genetically improved seeds, but they also function as a breeding population. Seed orchards have been established in many countries to produce improved seeds. The first studies using seed orchards were performed in 1934 using a vegetative production technique (Larsen, 1956). Since then, seed orchards have become an important global seed source (Zobel et al., 1958; Faulkner, 1975; Wright, 1976; Zobel and Talbert, 2003).

The genetic quality of seed orchard crops and the vitality and performance of the resulting trees depend on many factors, including clone fertility, genetic diversity, mating design, and combining ability (Hosius et al., 2006; Ertekin, 2010). In seed orchards, some clones produce more flowers or pollen than others. Also, certain genotypes rarely mate because they flower out of synchronization, or because the male and female gametes of different clones contribute differently to the specific seed crops (sexual asymmetry [A_s]) (Müller-Starck et al., 1982; Zobel and Talbert, 2003). Thus, seed orchard crops are generally derived from a limited number of trees. It is reasonable to assume that the seed lot from one crop year does not represent the total gene pool of the respective orchard. It is common to have a small portion of the orchard parents contribute a disproportionately large amount to the orchard crop (El-Kassaby et al., 1989; El-Kassaby and Cook, 1994). This unequal contribution leads to an increase in genetic relatedness and a loss of genetic diversity in seed crops (Kang, 2001).

Therefore, determining the genetic composition of seed orchard crops is important. When establishing new plantations and performing genetic research studies, genetic parameters such as genetic relatedness, inbreeding, and genetic diversity should be measured and monitored in seed orchard crops.

2. Seed orchard

A seed orchard is defined as an area where seeds are mass-produced to increase the genetic quality as quickly and inexpensively as possible (Zobel et al., 1958). It is also defined as a plantation of selected clones or progeny that are isolated or managed to avoid or reduce pollination from outside sources and produce frequent, abundant, and easily harvested seed crops (OECD, 1974; Feilberg and Soegaard, 1975).

The concept of using seed orchards to produce genetically superior seeds was first employed in Europe at the beginning of the last century. In 1906, Gunnar Andersson of Sweden pioneered the vegetative breeding of forest trees. In 1909, Oppermann, Andersson, and Hesselman used elite seeds collected from small natural stands for vegetative breeding and early plantation establishment. These early plantations have been a crucial part of present-day reforestation efforts. The first clonal seed orchards, on the island of Java in the Netherlands, were established to increase the abundance of *Cinchona ledgeriana*, a major source of quinine, in 1880 (Feilberg and Söegaard, 1975). In 1918, Sylvén drew attention to the choice of origin. In 1922, Fabricius coordinated use of the seed orchard with the Forest Trees breeding program. In 1923, Oppermann used seed orchards to propagate *Larix eurolepis*. According to Feilberg and Söegaard (1975), the first forest tree seed orchard was established in 1931 in England with an *L. eurolepis* hybrid. In 1934, Syrach-Larsen established seed orchards using the vegetative technique (Larsen, 1956). At this point, establishing clonal seed orchards as seed sources became globally important (Faulkner, 1975; Wright, 1976; Zobel and Talbert, 2003).

In Europe, establishing clonal seed orchards began immediately after World War II. In Sweden, *Pinus sylvestris* and *Picea abies* clonal seed orchards were established in the 1950s. In Denmark, an *L. eurolepis* clonal seed orchard was established in 1946. In Hungary, *P. sylvestris*, *Larix* spp., *Pinus nigra*, and *Picea* spp. clonal seed orchards were established in 1951. In the United States, *Pinus taeda*, *Pinus elliotti*, and *Pinus echinata* clonal seed orchards were established in 1957. In Finland, clonal seed orchards of *P. sylvestris* and species of *Picea* and *Betula* were established in 1960. In Canada, a *Pseudotsuga* clonal seed orchard was established in 1966. In 1970, *Cryptomeria japonica* and *Pinus densiflora* clonal seed orchards were established in Japan. In 1953, a *Pinus radiata* clonal seed orchard was established in New Zealand.

Seed orchards are commonly categorized by the first, second, or more advanced generation depending on how many cycles of improvement they have undergone (Zobel and Talbert, 2003). Seed orchards are also grouped by origin type (e.g., tree seed orchard, elite seed orchard, or hybrid seed orchard) according to the purpose or establishment form (Boydak, 1979). Generally, global seed orchards are first generation orchards initiated by parents whose genetic worth is unknown and in which the trees are generally closely spaced to allow for rouging of poor genotypes while maintaining a fully function seed orchard (Zobel and Talbert, 2003).

The optimal number of individuals in an orchard allows for rouging of the poorer genotypes, maintains the desired spacing, and maximizes seed production by having enough high-quality trees with adequate pollination and ensuring a minimum of relatedness (Zobel and Talbert, 2003). Older seed orchards are composed of a smaller number (20-30) of clones, while recently established orchards contain a much larger number of clones and aim to have a combination of maximal breeding progress and strong genetic diversity (Gagov et al., 2004). The correct number of clones to deploy in an orchard is an important consideration (Lindgren and Prescher, 2005). Generally, in orchard design the goal is to minimize selfing, maximize out-crossing and mating of all genotypes, allow for simple and easy establishment and management, and allow for any number of clones/families to fit into the completely randomized block and seeding designs (Schmidt, 1991). Seed orchards should be located within the natural range of the species; however, warmer climates can be advantageous for seed maturation and earlier flowering. Physical isolation from pollen contamination is also beneficial (Sarvas, 1970; Kang, 2001).

3. Genetic diversity in seed orchards

Genetic diversity refers to the richness of genetic information in the gene pool of a specific species. The genetic diversity of a species is shaped by the frequency of genetic change (migration, mutation, or isolation). In different ecosystems, the same species may exist with different genetic constitutions. The size of the gene pool in these populations (according to their degree of inheritance) may be wide or narrow. Forest trees typically have high levels of genetic diversity compared with other species. Also, genetic diversity within a species is often higher than that between populations. Recently, DNA or isozyme markers have been used to analyze genetic diversity. For example, a study performed in Turkey based on fourteen different isoenzyme analyses of black pine identified 92.6% of the total genetic diversity within the population (Yüksek, 1997).

Seed orchards must reflect the genetic diversity of the original population and be sufficiently large to maintain genetic diversity for future generations. If the genetic diversity of a seed orchard crop is maximized, all clones must contribute equally. Unequal gametic contributions can result from an absence of flowering synchronization among the clones (Matziris, 1993). Strong genetic diversity in seed orchard crops can only be attained when all parents contribute equally to the gamete pool.

4. Genetic gain in seed orchards

The primary issues affecting the genetic characteristics of seeds are genetic diversity and genetic gain (Stoehr et al., 2004). Genetic gain is directly related to the genetic diversity and degree of genetic structure transferred from parent to progeny. Kang (2001) stated that there are long- and short-term considerations in practical tree breeding programs. In the short term, forestry practices should result in productive stands that can tolerate changing environmental pressures for the duration of the rotation. Long-term concerns include maintaining reservoirs for genetic variability, which is required for current breeding populations. Short-term genetic gain is typically maximized in clonal forestry and seed orchards. For long-term breeding strategies, breeding and base populations should be managed for sustainable genetic diversity.

The genetic gain obtained from seed orchards is broader than that obtained from natural forests. By using plus trees to establish seed orchards, one can achieve genetic gain in orchard crops. In orchards, the increased combining ability of plus trees increases the genetic gain, which is derived from the additive variance in the referencing population (Kang, 2001). Wright (1976) stated that genetic gain could reach 30% in seed orchards using plus trees. Weir and Zobel (1975) reported a genetic gain from first- to second-generation seed orchards of 35%, exceeding the previously reported values of 10-20%. Matziris (1999) reported that *Pinus halepensis* clonal seed orchards had an increased volume ratio of 21.25%. Öztürk (2003) reported that by using plus trees to select for optimal mass, an 8.1% increase in size could be attained. Moreover, by reducing the number of clones in an orchard and further selecting for optimal characteristics, an additional 5% gain in size could be achieved.

Maximum flowering synchronization and equality, combined with minimal inbreeding and self-pollination, are important for seed orchards to reach their theoretically expected genetic gain and to achieve genetic diversity (Kang, 2001). In particular, flowering synchronization (Fig. 1) among clones in a seed orchard is important for the genetic composition of orchard crops since it affects the genetic exchange between clones. If seeds are collected from clones that lack synchronization, genetic diversity will be below the ideal level, resulting in a panmictic equilibrium (El-Kassaby and Askew, 1991; Kang and Lindgren, 1998).



Fig. 1. Optimal flowering synchronization period: maximum pollen accepting period (left) and maximum pollen shedding period (right).

5. Measuring of genetic diversity in seed orchards

5.1 Parental balance and maleness index

The number of female and male flowers, the number of cones, and the conversion rates of flowers to cones in a seed orchard is important information for forest genetic and tree

improvement studies (Matziris, 1997; Kang and Lindgren, 1998; Kang, 2000; Gömöry et al., 2000; Choi et al., 2004; Ertekin, 2006). In seed orchards, it has been shown that some clones produce large numbers of flowers, while others produce very few. Many studies have shown that a small number of clones are often responsible for a large part of clone production in seed orchards. Also, some clones produce more male than female flowers. For example, Ertekin (2006) observed that 33% of the total clone population accounted for 62% of all male flowers and 49% of all female flowers. Also, nine clones accounted for 50% of the total clone production on average for two years in a black pine seed orchard in Turkey (Figs. 2-4). Also, Johsson et al. (1976) showed that in a *P. sylvestris* seed orchard, 25% of the total clones accounted for 62.1% of all male flowers produced and 50.8% of all female flowers produced. Nikkanen and Velling (1987) observed that in a *P. sylvestris* seed orchard, 19% of the total clones accounted for 50% of all male flowers produced, while 35% of the total clones accounted for 50% of all female flowers produced. Kang (2000) found that in a *P. densiflora* seed orchard, 25% of the clones accounted for 37.3% of all male flowers produced and 48.1% of all female flowers produced. Yazdani and Fries (1992) found that in a *Pinus contorta* seed orchard, 23% of the clones accounted for 50% of the total female flower population.

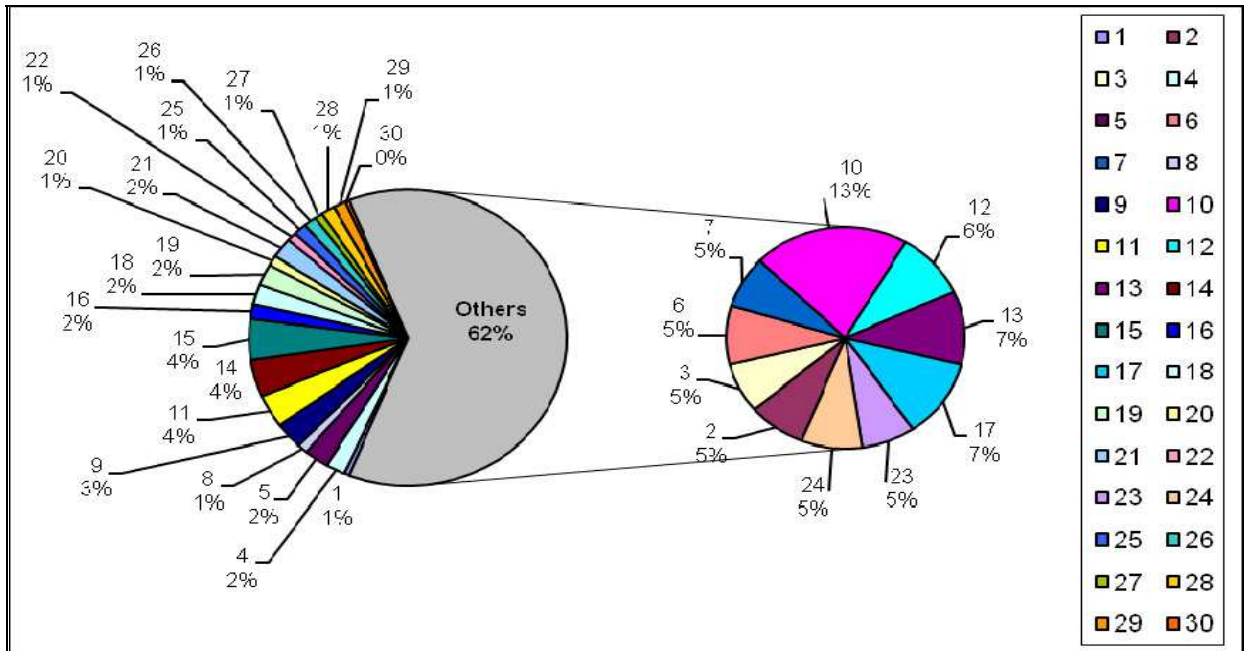


Fig. 2. Clonal contributions to male flower production in a black pine seed orchard in Turkey (Ertekin, 2006).

For seed orchard crops, parental balance curves are used to characterize high- or low-flowering clones. Ertekin (2010) generated parental balance curves in a three-year study of black pine seed orchards in Turkey. As seen in Fig. 5, the parental balance curves varied between flowerings and years, and did not improve with age. The observed curves for female and male flowering deviated significantly from the ideal situation, and the orchard's clones contributed equally to the gamete pool. Thus, specific clones may consistently produce high- or low-flowering clones based on genetic tendencies. Maternal and paternal genetic contributions can be explained by parental balance curves. A

cumulative contribution curve is often used to quantify fertility variation in forest populations (Griffin, 1982; El-Kassaby and Reynolds, 1990; Adams and Kunze, 1996). Parental balance in seed orchard crops is commonly summarized using cone-yield curves (Griffin, 1982). Using this method, seed orchard clones are ranked from high to low yield, and cumulative percentage calculations are plotted against the total number of clones (Chaisurisri and El-Kassaby, 1993).

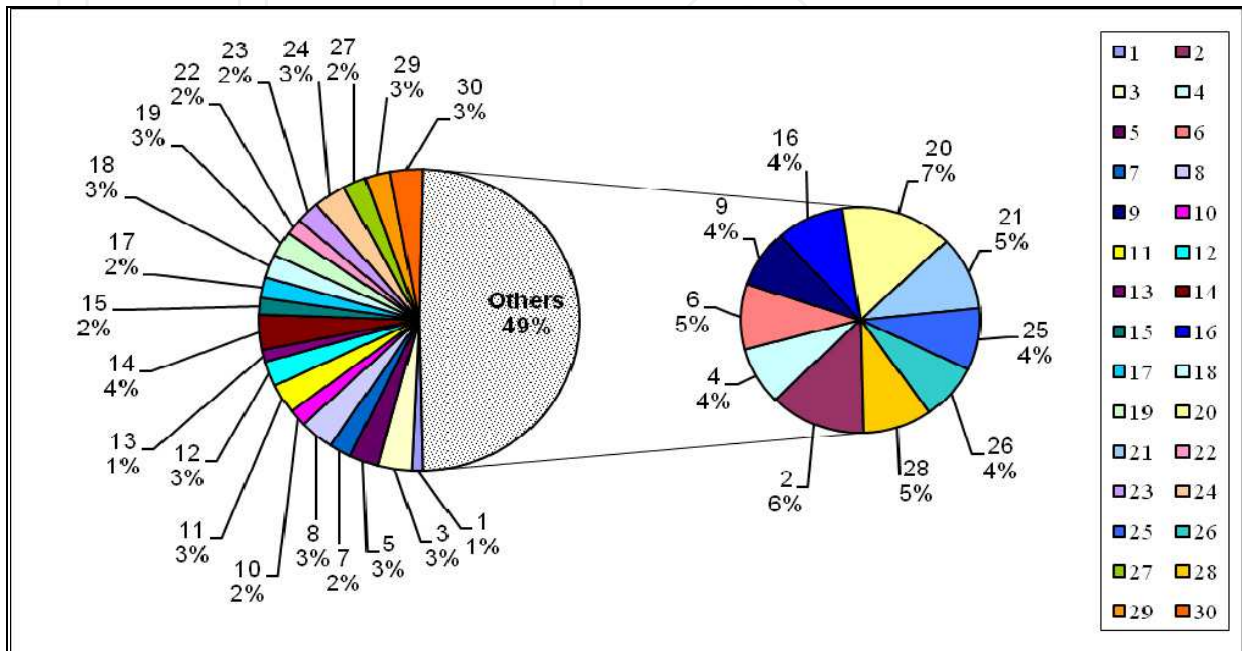


Fig. 3. Clonal contributions to female flower production in a back pine seed orchard in Turkey (Ertekin, 2006).

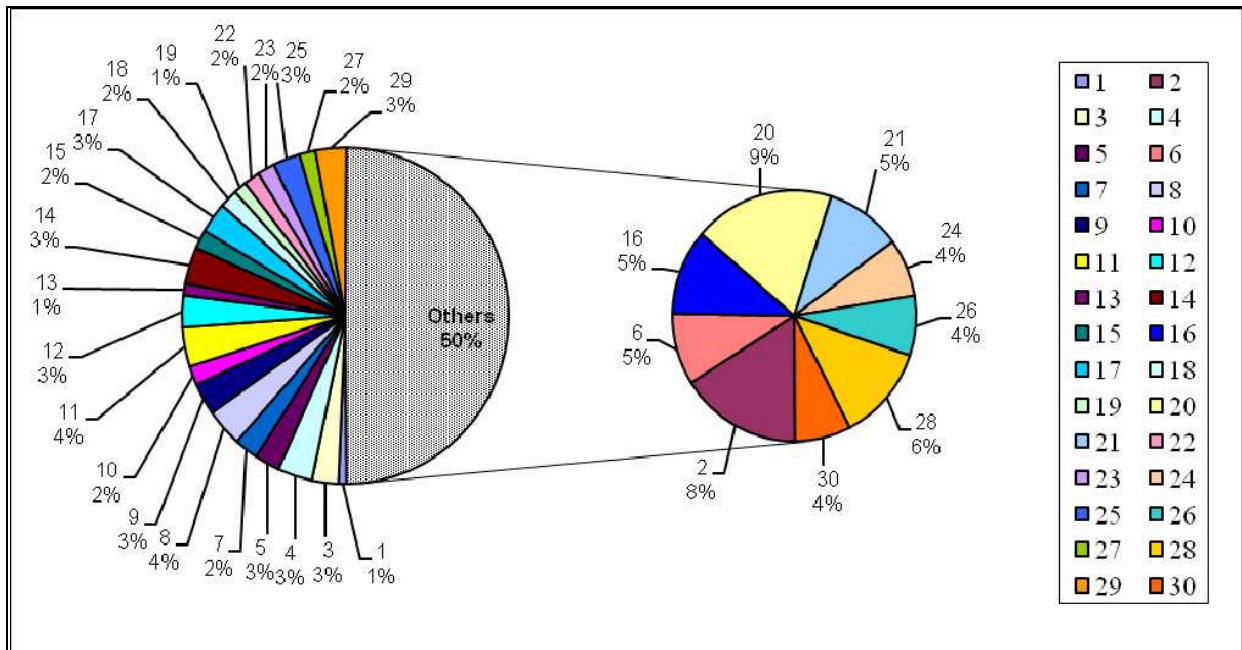


Fig. 4. Clonal contributions to cone production in a back pine seed orchard in Turkey (Ertekin, 2006).

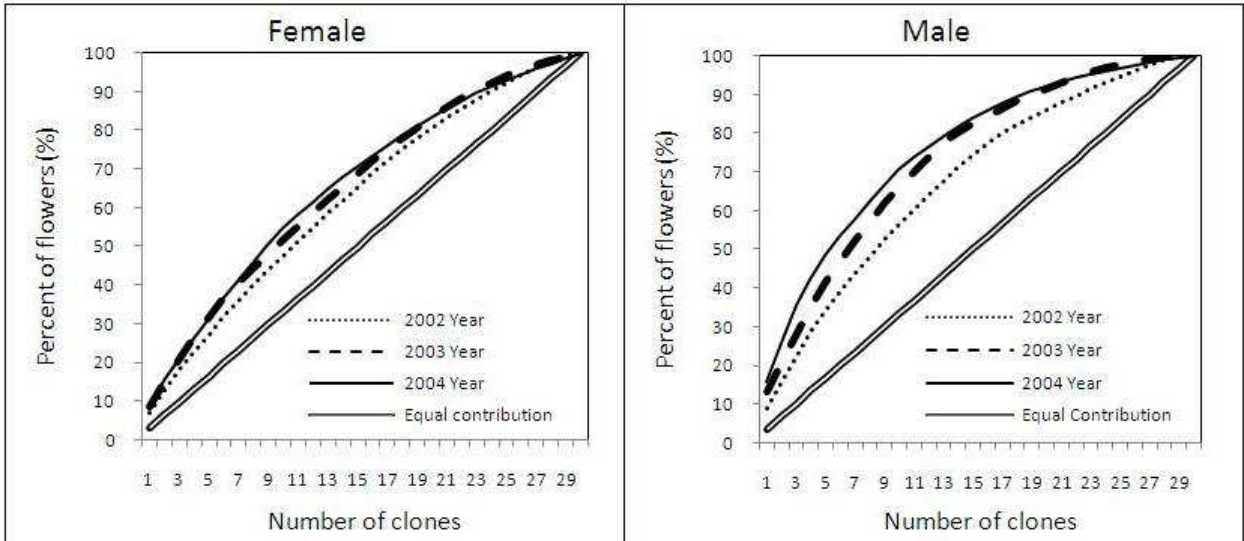


Fig. 5. Parental balance curves for female and male flowers with equal clone contributions (Ertekin, 2010).

To characterize A_s among the clones, the M_i was used. The M_i is defined as the proportion of a clone’s reproductive success that is transmitted through its pollen (Kang, 2000). The M_i (based on flower production) was estimated as follows (Choi, 2004):

$$M_i = \frac{m_i}{(m_i + f_i)} \tag{1}$$

where m_i and f_i are the number of male and female flowers in i^{th} clones, respectively.

A high M_i indicates that a clone is contributing more paternally than maternally (Choi, 2004). Most studies have reported an M_i ranging from 0.2 to 0.8 (Burczyk and Chalupka, 1997; Kang, 2000). An M_i near 0.5 indicates nearly equal female and male fertility. If a small number of clones accounts for a large percentage of the male flowers produced in an orchard, self-pollination may be increased. In this case, sexual asymmetry may reduce the number of homozygotes in an orchard from that expected under Hardy-Weinberg equilibrium and mask the effects of inbreeding (Kang, 2000). To avoid this situation, management activities such as supplemental mass pollination, hormonal treatments, or pruning ramets from high-producing clones could be implemented in these orchards (Ertekin, 2010).

5.2 Fertility variation and status number

Fertility variation between clones provides information about genetic diversity in a seed orchard. Fertility variation is measured using the coefficient of variation (CV) and sibling coefficient (Ψ). According to Kang (2001), ψ provides more accurate seed orchard crop genetic diversity information than the CV. The CV (standard deviation divided by the mean) was calculated as follows:

$$CV = \frac{s}{M} = \sqrt{\frac{N \left(N \sum_{i=1}^N P_i^2 - 1 \right)}{N - 1}} \tag{2}$$

where s is the standard deviation, M is the mean, N is the number of the clones, and P_i is the fertility (female or male) of clone i .

The female and male Ψ (Ψ_f and Ψ_m , respectively) were calculated as follows:

$$\psi_f = N \sum_{i=1}^N \left(\frac{f_i}{\sum f_i} \right)^2 = CV_f^2 + 1 \quad (3)$$

$$\psi_m = N \sum_{i=1}^N \left(\frac{m_i}{\sum m_i} \right)^2 = CV_m^2 + 1 \quad (4)$$

where N is the census number and CV_f and CV_m are the CVs for female and male flower production among the clones, respectively.

Generally, fertility variation is small initially then increases in subsequent years (Matziris, 1993; Nikkanen and Ruotsalainen, 2000). Kang et al. (2003) found that fertility differences were slightly larger for males than for females, and suggested that a CV of 100% would be typical in good- or moderate-flowering years for a mature seed orchard.

Status numbers were calculated based on the fertility variation of female and male parents (Lindgren et al., 1996), respectively, as follows:

$$N_{s(f)} = \frac{1}{\sum_i^N f_i^2} \quad (5)$$

$$N_{s(m)} = \frac{1}{\sum_i^N m_i^2} \quad (6)$$

where $N_{s(f)}$ and $N_{s(m)}$ are the N_s for female and males, respectively.

The N_s was calculated as follows, according to the equation of Kang (2001):

$$N_s = \frac{4N}{[\Psi_f + \Psi_m + 2 + 2r\sqrt{(\Psi_f - 1)(\Psi_m - 1)}]} \quad (7)$$

where r is the correlation coefficient between female and male flower production.

If the N_s values for flowering and the number of years were greater than ten, the depletion of genetic diversity in the following generation due to genetic drift and fertility variation would be small, as reported by Kang (2001). Consequently, small numbers of clones produce most of the flowers or seeds in the orchard, resulting in a loss of genetic diversity. Kang et al. (2005) stated that a loss in genetic diversity was expected due to the accumulation of relatedness or fertility variation. A reduction in genetic diversity in orchard crops affects the level of genetic diversity in seedlings and, subsequently, in the plantation forest.

5.3 Relative status number and group coancestry

N_r was calculated as the ratio of N_s to N as follows:

$$N_r = \frac{N_s}{N} \quad (8)$$

N_s was defined as half the inverse of the coancestry group (Lindgren et al., 1996) as follows:

$$N_s = \frac{0.5}{\Theta} \quad \Theta = \frac{1}{2N_s} \quad (9)$$

The expected genetic diversity of seed crops from first-generation seed orchards can be measured relative to the group coancestry of a reference population (Kang, 2001). The relative genetic diversity values, calculated for three years, were high in this seed orchard. Kang and Lindgren (1998) reported that the relative genetic diversity (compared to reference populations) was quite high in first-generation seed orchards.

5.4 Gene diversity and sexual asymmetry

Genetic diversity among seed orchard crops is significantly influenced by the relatedness of orchard clones, parental fertility variation, and pollen contamination. Based on a study of a black pine seed orchard, the top ten cone-producing clones accounted for 33% of all cones produced in year 1, 48% in year 2, and 58% in year 3 (Ertekin, 2006). Based on seed orchard studies, the overall genetic diversity of all clones in the orchard is not represented; thus, the genetic diversity is narrow. Matziris (1993) reported that in an abundant cone production year there was a decrease in the differences between cone-producing clones, and that there was an expansion of the genetic base of seeds from seed orchards.

The expected genetic diversity of seed orchard crops (GD) from first-generation seed orchards can be measured relative to the group coancestry of a reference population. GD is a function of group coancestry (Lacy, 1995) and is inversely proportional to the status number (Kang, 2001), as follows:

$$GD = 1 - \frac{1}{2N_s} \quad (10)$$

A_s was also estimated (Kang and Mullin, 2007) as follows:

$$N_a = \frac{N_{s(f)} + N_{s(m)}}{2} \quad A_s = \frac{(N_{s(c)} - N_a)}{N_a} \quad (11)$$

where $N_{s(f)}$, $N_{s(m)}$, and $N_{s(c)}$ are the N_s for females, males, and clones, respectively, and N_a is the arithmetic mean of the measures ($N_{s(f)}$ and $N_{s(m)}$).

Kang and Mullin (2007) stated that A_s theoretically ranges from zero to one, and that an A_s value of zero indicates perfect sexual symmetry. Variation in fertility can be compensated for by intentionally adjusting the number of ramets to manage the orchard. Equal seed harvests or mixing of seeds from consecutive years can be used to reduce the impact of

fertility variation on the diversity of seed orchard crops, since mixing seed crops reduces fertility variation (Kang et al., 2003; Varghese et al., 2000; Ertekin, 2010).

6. Pollen contamination

The flowering phenology of clones in seed orchards allows us to determine the genetic diversity of orchard crops. Xie and Knowles (1994) stated that some clones (those known to be early- or late-flowering) should be removed from seed orchards. Using this method, the risk of self-pollination and pollen contamination can be reduced. Pollen contamination, which directly affects the genetic diversity of seeds, is a major source of gene migration in seed orchards (Adams and Birkes, 1989).

By examining the flowering phenology of specific clones, some variations were identified in the bud burst, pollen shedding, and pollen acceptance of male/female flowers. Similar observations have been made by groups working in various seed orchards, including *P. nigra* (Matziris, 1994; Lario et al., 2001), *P. abies* (Eriksson et al., 1973; Skrøppa and Tuttüren, 1985; Nikkanen, 2001), *P. sylvestris* (Jonsson et al., 1976; Gömöry et al., 2000), *Pinus brutia* (Keskin, 1999), and *Cunninghamia lanceolata* (Zhuowen, 2002) seed orchards. In addition, varying flower development times were observed on the northern or southern branches of the same trees (Ertekin, 2006).

Reynolds and El-Kassaby (1990) reported that the most important indicator of genetic diversity in orchard crops is the flowering quality and harmony of the flowering periods (parental balance). Gömöry et al. (2003) stated that 15% of the total clones in a *P. sylvestris* seed orchard flowered early or late; thus, these clones were not pollinated with the others. These early or late flowering clones pollinated other trees outside the orchard. Thus, pollen contamination is increased in these seed orchards. Pakkanen et al. (2000) found that the pollen contamination rate was 69-71% in a *P. abies* seed orchard.

In a *P. brutia* seed orchard in Turkey, genetic contamination of the orchard by seeds was detected and pollen contamination rates were very high (estimated at 85.7%) (Kaya, 2001). Also, the growth of female flowers before male flowers has been reported in numerous studies. For example, Zhuowen (2002) observed that female flowers were present five to six days before male flowers in a *C. lanceolata* seed orchard. Parantainen and Pulkkinen (2003) stated that female flowers opened three days before male flowers, but ended at the same time in *P. sylvestris* seed orchards. Yazdani and Fries (1992) noted a three- to four-day difference in female and male flower activity in a *P. contorta* seed orchard. Also, Ertekin (2006) observed female flower growth three to four days before male flower growth in a *P. nigra* seed orchard.

The duration of the pollen accepting or shedding periods is as important as the synchronization of flowering for pollen contamination and the genetic diversity of clones.

Matziris (1994) observed that the duration of pollen acceptance was between two and eight days in a *P. nigra* seed orchard. Nikkanen (2001) noted that the duration of the pollen shedding period was five to eight days, while the pollen acceptance period was five to ten days, in a *P. abies* seed orchard. Ertekin (2006) observed that the duration of the pollen shedding period was six to nine days while the pollen acceptance period was six to eight days in *P. nigra*. Therefore, the fertilization period in seed orchards is generally short.

However, within this time period pollen gene exchange in an indoor or outdoor orchard will occur among receptive clones. Pollen contamination also occurs during this time.

Although pollen contamination in seed orchards can be reduced by isolating the orchard, it cannot be completely eliminated. Kang (2001) observed that many of the orchard seeds had unknown fathers from outside sources.

7. Selfing and inbreeding

Selfing is a mating process that occurs by self-pollination among parents of the same genotype. In many forest trees, self-compatibility is necessary for selfing to occur, and it can result in reduced seed germination and growth (Zobel and Talbert, 2003). Selfing in natural populations occurs at a higher frequency than in seed orchards. In seed orchards, ramets of the same clone are scattered and not as close to neighboring trees. Thus, inbreeding is very low because of the mating design. Squillace and Goddard (1982) observed that the yield of selfed seed orchards averaged only 2.5%, lower than the estimates for trees in natural stands. They also noted that selfing had a significant effect on orchard crops since approximately 9.5% of all seeds were self-fertilized. Also, if the self-pollinated offspring survive, the genetic gains are reduced since they are less vigorous than outcrosses. Moreover, Sarvas (1962) stated that inbreeding could result in homozygous lethal genes, causing embryo collapse and empty seeds.

Selfing is especially important in pine, spruce, and fir species since they are monoic. These species possess certain mechanisms to prevent selfing. For example, male and female flowers occur at different locations on the crown in monoic species. Male flowers occur on the lower crown while female flowers are on the upper crown. Franklin (1971) stated that selfing tended to be greater in the lower crown than the mid or upper crown. However, female and male flowers of seedlings produced by vegetative techniques occur on the end of the same shoot (Fig. 6). In this situation, selfing is unavoidable.

Seed orchards are established to produce genetically superior seeds for plantations. In these orchards, selfing can occur by mating among ramets of the same clone, as well as by self-pollination within individual ramets. Selfing reduces the genetic value of orchard crops. Generally, the selfing rate can be estimated based on isozyme markers (Burczyk, 1991; Harju, 1995; Squillace and Goddard, 1982). If the selfing rate is >10%, the selfed offspring need to be identified and either removed from the orchard or treated by artificial pollenization (El-Kassaby and Ritland, 1986; Kang, 2001).

8. Hermaphroditism in seed orchard

Hermaphroditism (bisexual flowers) means that an organism that has morphologically female and male reproductive organs (strobili) on the same flower bud. In nearly all gymnosperms, male and female strobili occur on the same tree (monoic). Male and female flowers occur at different parts of the crown (female flowers occur on the upper crown and male flowers on the lower crown); moreover, male flowers are borne in clusters at the base of the twig bud while the female flowers are borne in one conelet at the bud apex. However, hermaphroditism occurs in various trees (Zobel and Goddard, 1954; Chamberlain, 1966; Burley, 1976; Matziris, 2002).

In hermaphroditic flowers, the female flowers are at the top while the male flowers are below (Fig. 6). According to Matziris (2002), the cause of this anomaly is not well understood. It has been observed more frequently in plantations of exotic species, possibly due to the lack of adaptability of a species or genotype to a new exotic environment. However, the benefits of hermaphroditism are unknown; thus, further research is required.



Fig. 6. Hermaphroditic flowers of black pine clones at the pollen shedding stage; a female flower (top) has formed on the male flower (base). Also, the selfing risk is quite high.

9. Conclusion

The level of genetic diversity in seed orchards is important to plantation forests because high levels will increase resistance to pests, diseases, or climate change. Some of the clones in seed orchards that produced high numbers of female flowers did not mature to cones because of insect damage, physiological stress, or a lack of fertility synchronization. Generally, clonal variation increased with increases in male flowering. However, if fewer clones produced a large proportion of the male flowers, genetic diversity decreased. If a species is often wind-pollinated, a large amount of pollen will come from outside the seed orchard, widening the genetic diversity but decreasing the genetic gain. Therefore, artificial pollination, thinning, or pruning orchard management techniques can be used. For thinning, low-flowering clones are removed. For pruning, crowns are modified based on the flowering type. These orchard management techniques can increase genetic diversity in seed orchard crops. Strong genetic diversity in seed orchard crops can only be attained when all parents contribute similarly to the gamete pool, which virtually never occurs. Generally, a small portion of the orchard parents contribute a disproportionately large amount to the orchard crop (El-Kassaby et al., 1989; El-Kassaby and Cook, 1994), leading to an accumulation of genetic relatedness and a loss of genetic diversity in seed crops (Kang, 2001). Variations in fertility can be compensated for by intentionally adjusting the number of

ramets. Equal seed harvests, or mixing seeds from consecutive years, can be used to reduce fertility variation.

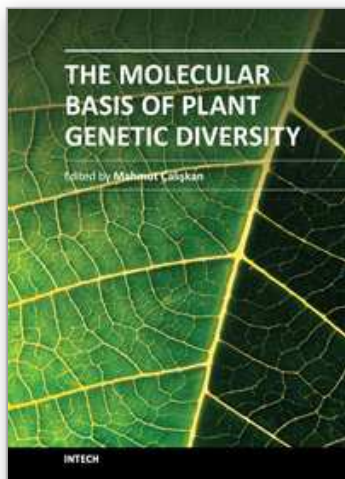
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The Molecular Basis of Plant Genetic Diversity presents chapters revealing the magnitude of genetic variations existing in plant populations. Natural populations contain a considerable genetic variability which provides a genomic flexibility that can be used as a raw material for adaptation to changing environmental conditions. The analysis of genetic diversity provides information about allelic variation at a given locus. The increasing availability of PCR-based molecular markers allows the detailed analyses and evaluation of genetic diversity in plants and also, the detection of genes influencing economically important traits. The purpose of the book is to provide a glimpse into the dynamic process of genetic variation by presenting the thoughts of scientists who are engaged in the generation of new ideas and techniques employed for the assessment of genetic diversity, often from very different perspectives. The book should prove useful to students, researchers, and experts in the area of conservation biology, genetic diversity, and molecular biology.

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