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Flowering Phenology in Teak Seed Orchards – Genetic Variation, Measurement and Implications to Seed Orchard Fertility

Vasudeva Ramesh¹ and Rajesh Gunaga²

¹University of Agricultural Sciences, Dharwad, Karnataka,

²Dr. B.S.K. Krishi Vidyapeeth, Dapoli, Maharashtra,
India

1. Introduction

Teak (*Tectona grandis*. Linn. f.) is an important timber species preferred all over the world because of its versatile range of uses (Katwal, 2005). Its matchless timber properties include strength, workability, attractiveness, lightness, resistance to termite, fungus and weather, as well as seasoning capacity without splitting or cracking. Teak occurs in natural forests between 9° to 26° N latitude and 73° to 104° E longitude, which includes southern and central India, Myanmar, Laos People's Democratic Republic and northern Thailand (White, 1991). The species is a dominant component of diverse forest types. For instance in India, teak forests are spread over a large geographic area of 8.9 million ha which range from very-dry to very-moist types. As a consequence, natural populations exhibit great genetic variability for economically important traits (Katwal, 2005). In fact the Indian subcontinent is considered the center of diversity for teak because of the huge genetic variation for economically important traits such as bole form, timber quality, biochemical traits and others (Anmol Kumar et al., 1997). Further teak is emerging as one of the predominant plantation species in the Indian subcontinent as well as in 30 other countries of tropical Asia, Africa and Latin America. Though teak plantations account for 5-8 per cent of the total forest area in the tropics (Ball et al. 1999), about 90 per cent of the quality hardwood plantations for timber production belongs to only teak (Granger, 1998). As per 1990 data, globally, area under teak plantations was 2.2 million ha, with 94 per cent in Tropical Asia, especially in India and Indonesia, followed by Tropical Africa (about 4.5 %) and remaining area in Tropical America (FAO, 1995). Presently about 1.5 million ha of teak plantations exist in India and around 50,000 ha are raised annually (Subramanian et al., 2000). This has resulted in a huge demand for quality planting stocks in astronomical quantities.

Genetic improvement of teak in India, started in the year 1954, has focused mainly on identifying phenotypically superior trees from diverse growing regions and deploying them as vegetatively propagated clones in seed orchards (Gunaga & Vasudeva, 2005). Seed orchard is essentially a collection of phenotypically superior and diverse individuals of a species, which is silviculturally managed to produce genetically superior seed crop through

the process of open pollination (Askew, 1986). Establishment of seed orchards using superior clones from diverse regions has been an important strategy of genetic improvement programme of teak. It is assumed that the offspring developed through a random mating among the superior types would also be genetically superior. The main purpose of establishing seed orchard is to mass-produce such genetically superior seeds, which are easily accessible and collectable. Thus, seed orchards form an important link between on-going tree improvement programme and commercial planting activity. The establishment of seed orchards would be a genetic dead-end unless full potential of an orchard is realized through harvesting of genetically improved seed crops. Unfortunately, low fruit production in clonal seed orchards has been an important limitation in teak improvement programmes of India and worldwide (Gunaga & Vasudeva, 2005; Indira, 2005).

1.1 Importance of flowering in seed orchards and the basic assumptions

The assumption made while establishing a seed orchard is that diverse genotypes are highly compatible and completely overlap in their flowering phenology and the process would lead to big genetic gain. Synchronous flowering among different clones helps to achieve random mating (panmixis) and hence good seed output. Further, it also reduces the foreign pollen contribution in the process of pollination, if any. In general the following requirements are assumed to be fulfilled in an idealized seed orchard (Askew, 1986, Vasudeva et al. 1999)

- The orchard is completely isolated from the influence of undesirable pollen from outside
- Natural self-pollination occurs only in insignificant amounts
- Clones are equally productive in male and female flowers (in case of unisexual species)
- Pollen flight and female flower receptivity coincides especially in monoecious types
- The gamete contributions of the parents are in the same proportions as they were in the orchard
- The pollen contributions to the seed crop are either uniform for all parents or that they are in similar proportions to the seed crop.

Unfortunately, the above assumptions have not been tested among established clonal seed orchards. It is well known that in a seed orchard, the levels of variation for reproductive traits among the constituent genotypes influence fruit production. Further, the variation in flowering behavior among the clones influence the extent of gene exchange between clones and consequently the genetic composition of the seeds produced (Gunaga & Vasudeva, 2002; Vasudeva et al., 2005). Hence, understanding variation for reproductive phenology is fundamental to the successful operation of any seed orchard. Since superior genotypes identified from diverse regions are used in a clonal seed orchard (CSO), understanding the flowering phenology of the constituent clones becomes imperative to achieve maximum synchrony. A large number of reports is available for temperate species, which document asynchronous flowering among the clones in a seed orchard, especially among monoecious species (Gunaga, 2000; Vasudeva et al., 2001). Any factor that affects the seed production in seed orchards would be a hindrance for logical end of tree improvement programmes (Griffin, 1984). Therefore any variation in flowering phenology within a seed orchard can potentially alter the quantity as well as genetic quality of fruits (Sedgley & Griffin, 1989). Although, there seems to be a direct association between the extent of flowering synchrony among the constituent clones and the fruit production in a seed orchard, surprisingly, there

are very few reports in India that focus on these issues. A few authors, however, have also identified this gap of information earlier (Subramanian et al., 1994; Nagarajan et al., 1996; Radhamani et al., 1998, Gunaga & Vasudeva, 2002). Anmol Kumar (1992) has reported that flowering among local clones belonging to the Maharashtra province of India was early as compared to the clones from other parts (provenance) of India. Rawat et al. (1992) have reported that flowering in teak seed orchard established at New forest, Dehra Dun, Northern India was asynchronous and recognized that these patterns may cause lower fruit production in the seed orchard. A few reports on these lines are also available in south east Asia. For instance, Palupi & Owens (1998) have shown asynchronous flowering among clones of teak at clonal seed orchard established at East Java of Malaysia. A lack of a suitable tool for an objective measurement of flowering synchrony among different clones has also contributed to the negligence!! Hence there is a need for development of objective criteria to evaluate flowering phenological events. In this chapter we firstly bring out patterns genetic variation for reproductive phenology in teak seed orchards; review a novel method of computing the overlap of flowering among individuals in an orchard and discuss its implications to seed orchard fertility from a management perspective.

2. Flowering phenology in teak and its genetic control

Flowering phenological patterns are most diverse and least understood in the tropics (Corlett, 1998). Pattern of flowering is well studied in most of the temperate and sub-temperate species like radiata pine (Griffin, 1984), loblolly pine (Askew, 1986), douglas fir (EL-Kassaby & Askew, 1991), black pine (Matziris, 1994) and *Eucalyptus citriodora* (Verma et al., 1989). Studies of the reproductive biology and pollination in teak (Hedegrat, 1973; Kaosa-ard, 1991) have shown that teak is predominantly an out crossed species and pollinated by insects. Isozyme analysis of seeds from different clones by Kjaer & Suangtho (1995) has confirmed these results. Self-incompatibility and short stigmatic receptive period (which ranges for just about few hours in one morning) are the main reasons for higher out crossing rates (Hedegrat, 1973).

2.1 Variation for flowering phenology among teak clones

Despite extensive planting programmes and the importance of increasing fruit production in seed orchards, little is known about the clonal variation for reproductive biology of teak. To use floral traits as a criterion while selecting the clones, it is essential to understand their genetic control. Hence, in order to achieve better genetic gain, it is imperative to assess variation and genetic control of the floral and fecundity traits in an orchard. However, in general, reproductive traits have been consistently ignored while selecting plus trees of teak as well as while upgrading the existing seed orchards. There is only one report on the extent of genetic control of floral features in teak (Hanumatha et al., 2001). Perhaps the only study that focuses on estimating the genetic parameters of flowering phenophases in teak was published by Gunaga & Vasudeva (2005). In their study the authors have assessed the clonal variation for flowering phenology and estimated the extent of genetic control over flowering phenophases. Phenophases of 407 rametes of 24 teak clones arising from diverse regions of southern India were monitored every week in a 19-year-old-teak CSO of southern India. The passport data on the clones used in the study are provided in the Table 1. The time taken for commencement of flower buds, flowering and peak flowering were calculated as the number of days from 1st January to the date of their first appearance on every tree. Peak

flowering was defined as the time when approximately 75 per cent of the flowers on a tree are in bloom. Duration of all phenophases was considered as total number of days of respective events.

Sl. No	Teak Clone I.D.	Provenance of the clone	Latitude (North)	Longitude (east)	Altitude (meters a msl)
1	MYHD1	North	15° 17'	74° 38'	573
2	MYHD2	North	15° 17'	74° 38'	573
3	MYHD3	North	15° 17'	74° 38'	573
4	MYHD4	North	15° 17'	74° 38'	573
5	MYHV1	North	15° 06'	74° 36'	570
6	MYHV3	North	15° 06'	74° 36'	570
7	MYHV4	North	15° 06'	74° 36'	570
8	MYHV5	North	15° 06'	74° 36'	570
9	MYHV6	North	15° 06'	74° 36'	570
10	MYHV7	North	15° 06'	74° 36'	570
11	MyHaK1	North	15° 11'	74° 41'	500
12	MyHaK2	North	15° 11'	74° 41'	500
13	MyHaK3	North	15° 11'	74° 41'	500
14	MYS A1	Central	13° 53'	74° 28'	571
15	MYS A2	Central	13° 53'	74° 28'	571
16	MYSS2	Central	13° 53'	74° 28'	571
17	MyBL1	Central	13° 40'	75° 39'	571
18	MYHuT1	South	12° 13'	76° 00'	850
19	MYHuT2	South	12° 13'	76° 00'	850
20	MYHuT3	South	12° 13'	76° 00'	850
21	MYHuT6	South	12° 13'	76° 00'	850
22	MYHuT7	South	12° 13'	76° 00'	850
23	MYHuT8	South	12° 13'	76° 00'	850
24	MyMK3	South	11° 55'	76° 11'	690

Table 1. Passport data of teak clones of a Clonal Seed Orchard (CSO) in Karnataka, southern India.

2.2 Influence of provenance on flowering phenology among teak clones

Generally in South Indian conditions, the period of 'flowering' to 'fruit maturity' in teak takes about nine months. Flower buds appear during April, coinciding with the on-set of monsoon showers, and continue through August. However, Palupi & Owens (1998) have shown that among the teak clones of East Java, flower initiation started from January through middle of February, while the initiation of peak flowering varied from mid January to March first week. Blooming in a clonal seed orchard of south India started in the second week of May and continued until fourth week of September, with peak flowering from fourth week of May to second week of September (Gunaga & Vasudeva, 2005). Thus huge variations for flowering phenology naturally occur in the populations of Teak.

Reports from a wide range of commercial tree species of temperate regions has shown that the variation for time of flowering is genetically based (Griffin, 1984 in Radiata pine; Askew, 1986 in loblolly pine; EL-Kassaby & Askew, 1991 in Douglas fir; Matziris, 1994 in Black pine and Verma et al., 1999 in *Eucalyptus citriodora*). Similarly, as shown by Gunaga & Vasudeva (2005), large genetic variation occurs among teak clones for different flowering phenophases (Figure 1). A few other authors have also reported clonal variation in flowering pattern of teak. Anmol Kumar (1992) reported that flowering among local clones belonging to Maharashtra, Central India, was early when compared to the clones from other states. Drastic variation for flowering among clones in a 10-year old model teak seed orchard in Dehra Dun, Northern India was reported by Rawat et al. (1992).

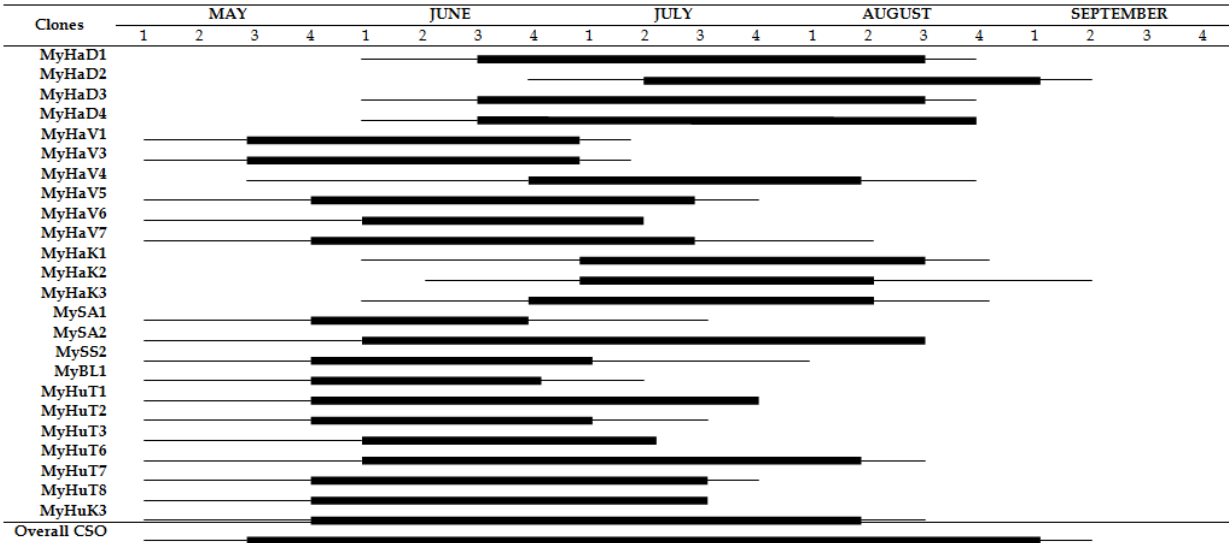


Fig. 1. Phenogram showing clonal variation for duration of flowering (thin line) and peak flowering (bold line) in a clonal seed orchard (CSO) of teak in southern India.

Provenance	Flowering initiation		Peak flowering initiation		Duration of flowering		Duration of peak flowering	
	Mean	±SD	Mean	±SD	Mean	±SD	Mean	±SD
Northern	184.78	24.04	207.11	21.78	51.79	15.89	15.57	7.56
Central	147.50	10.15	174.78	13.55	57.09	12.11	16.24	8.9
Southern	152.18	15.05	178.27	18.29	54.75	11.58	17.23	9.26
F Ratio	114.85		97.30		3.05		1.24	
P. level	<0.001		<0.01		NS		NS	
CV (%)	12.25		10.26		27.86		50.56	

Table 2. Provenance variation for time of budding, flowering, peak flowering (expressed as number of days from 1st January 1999) and duration of flowering and peak flowering (number of days) in the Clonal Seed Orchard of teak. NS= non-significant. CV = Coefficient of variation.

Interestingly, Gunaga & Vasudeva (2005) have also shown strong provenance influence on flowering phenology among the clones of a CSO. Teak clones from central and southern Indian provenances were early in commencement of flower buds, flowers, and

peak flowering (by about 30-40 days) when compared to clones from northern provenance (Table 2; Figure 2). In their study, clearly two peaks for flowering among teak clones were observed -the first, during May to June corresponding mainly to the Central and Southern clones; the second, during July corresponding to those from northern clones (Figure 2). However, duration of flowering and peak flowering among clones of different provenances did not differ. Clearly, a significant proportion of rametes of clones from southern and central regions escaped peak rainfall period in the orchard when compared to those from northern region (Figure 2). Perhaps this is the first empirical evidence among the CSOs of teak in India confirms that clones of diverse origin do not contribute equally to the resultant seed crop. Such genetically based geographical variation in phenology is shown to occur in several plant species. For instance, Yanninen et al. (1988) have shown that northern and southern clones of *Viccinium myrtillus* differ in their spring and autumn phenology. Female flower production in loblolly pine varied between Texas and Arkansas sources (Richmond & Mc Kinley, 1986). Weinstein (1989) reported that the development of flower and the vegetative bud in *Pinus halepensis* and *P. brutia* showed differences among altitudinal races.

2.3 Estimation of genetic parameters for flowering phenophases

Though flowering phenology has been the most conserved life history trait, estimates of genetic parameters such as heritability has been attempted only for few timber species. Gunaga & Vasudeva (2005) have adopted an Analysis of Variance (ANOVA) approach to decompose total variability in flowering phenology into genetic and environmental components using the following model:

Sl.no	Source	d.f.	Expected mean square
1	Between clones	(c-1)	$\sigma^2 + n_0 \sigma^2_c$
2	Error	$\sum (n_i-1)$	σ^2

Where,

- c = number of clones
- σ^2 = sum of squares due to error
- σ^2_c = sum of squares due to clones (genotypic variance)
- $n_0 = \sum n_i - \{ \sum (n_i-1) / n_i \}$ as suggested by Kedharnath (1982)
- n_i = number of rametes of i^{th} clone

From this analysis, following genetic parameters were estimated:

Heritability

Broad sense heritability

$$(H_1^2) = \frac{\sigma_c^2}{(\sigma_c^2 + \sigma^2)}$$

(Individual ramete basis)

Broad sense heritability

$$(H_2^2) = \frac{\sigma_c^2}{(\sigma_c^2 + \sigma^2 / n_0)}$$

(Clonal mean basis)

following Matziris (1994).

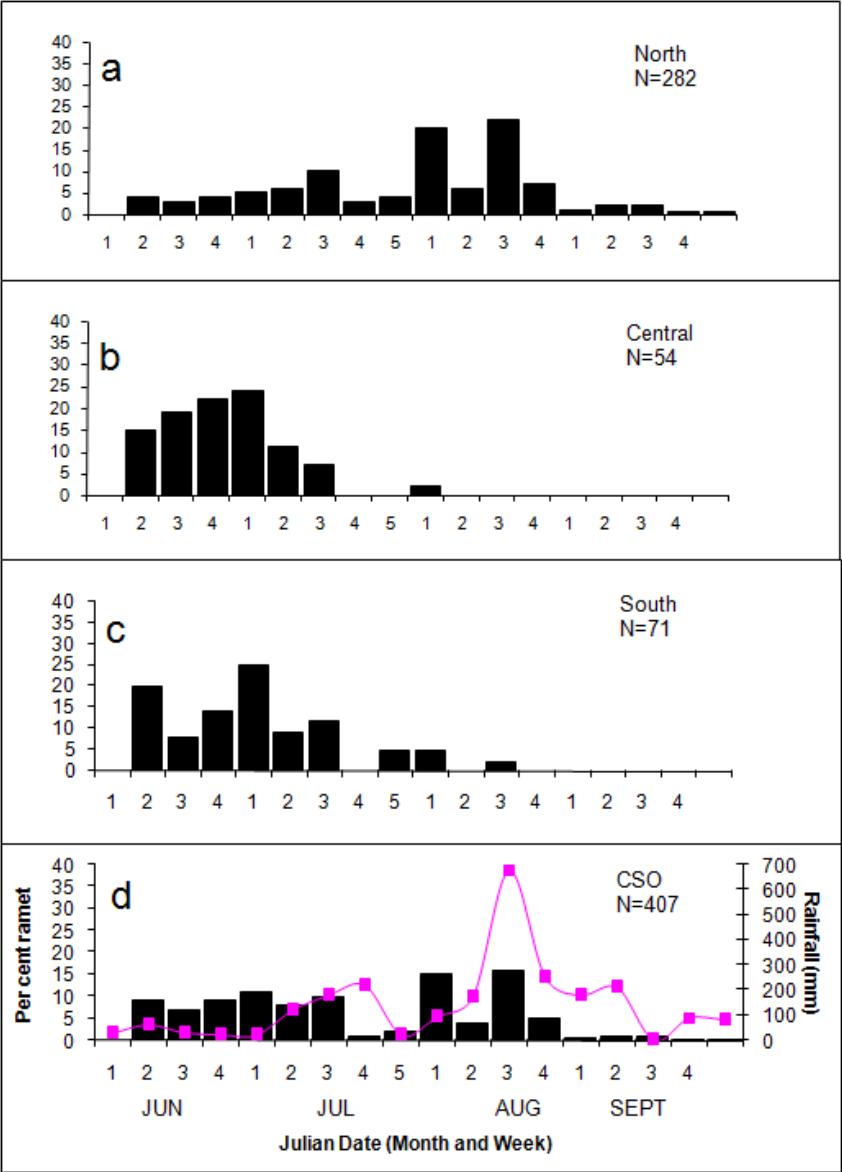


Fig. 2. Distribution of teak ramets of 24 clones from different provenances (a-c) and from overall CSO (d) with respect to initiation of flowering across time. Y- axis represents the per cent ramets in each class. The red line in panel (d) suggests the rainfall pattern in the CSO located in southern India. N= total number of ramets.

Standard error for heritability on individual ramete basis was calculated as follows (Kedharnath, 1982):

$$SEH_1^2 = \frac{2(n-1) \left(1 - H_1^2\right)^2 \left\{1 + (n_0 - 1) H_1^2\right\}}{n_0^2(n-c) (c-1)}$$

Where,

- c = number of clones
- n_0 = Coefficient of σ_c^2
- n = Total number of observation

The authors have shpwn that among the different flowering phenophases commencement of flower buds, flowering and that of peak flowering recorded high heritabilities on individual tree basis ($h^2_1= 0.734, 0.637$ and 0.709 , respectively; Table 4). The values on clonal mean basis were much higher. The low values of standard errors of h^2_1 indicate that these estimates were reliable. However, the duration of flowering and peak flowering were strongly influenced by environmental factors and hence weakly inherited ($h^2_1 = 0.03$ and 0.004 , respectively). These results are in complete agreement with Matziris (1994) who reported that in black pine, the heritabilities on individual tree basis were high for the initiation of male flowering and female receptivity, while that for the duration of flowering stages were lower. Matziris (1997) reported that heritability for female flowering initiation in Aleppo Pine was high.

Variable	Variance		h^2_1	$\pm SE(h^2_1)$	h^2_2
	σ^2_p	σ^2_c			
Commencement of flower buds	676.09	496.57	0.734	0.0171	0.979
Commencement of flowering	830.39	529.21	0.637	0.0218	0.967
Commencement of peak flowering	629.97	446.88	0.709	0.0184	0.976
Duration of Flowering	224.22	6.80	0.030	0.0213	0.344
Duration of peak flowering	65.09	0.27	0.004	0.0187	0.064

- σ^2_p
- = Phenotypic variance
- σ^2_c
- = Variation due to clones
- h^2_1
- = Heritability on individual tree basis
- h^2_2
- = Heritability on clonal mean basis
- $SE(h^2_1)$
- = Standard error for h^2_1

Table 4. Estimation of components of variance for flowering phenology in clones of teak in a CSO, southern India.

These results suggests that teak clones are genetically predisposed to initiate flowering during the time to which their respective mother plants have been adapted to, while the duration of these events will be under the control of local environmental factors of the orchard. This also suggests that while the time of initiation of phenophases is highly conserved, the duration may be shaped to be plastic such that maximum reproductive success could be obtained. Hence, the results of the present study could be extrapolated and used as indicator to select clones for future seed orchards such that their flowering time could be properly matched. Further, it also hints that the duration of flowering is more amenable for modification through silvicultural practices to suit to the needs of the orchard manager such that maximum flowering synchrony can be obtained.

3. Measures of synchronous flowering

Till recently, reproductive phenologies were qualitatively described as phenograms developed by Mahall & Bormann (1978) which were nothing but bands on a time line. This technique was readily adaptable to display the synchrony patterns male and female flowering in conifers. However it only provided a qualitative idea about synchrony and was impractical to be adopted whenever large number of clones is to be included. Askew and Blush (1990) have developed an index to measure the overlap between male and female flowering synchrony in monoecious loblolly pine. However, their measure doesn't correspond to species with bisexual perfect flowers such as teak. Evaluating the

effectiveness of gamete exchange in a cross pollinated species requires a standard measure of the relative probabilities of crossing between all possible pairs of parents or clones. A quantitative index should have the following criteria:

1. The index should be based on simple observations that could be taken even by a field level worker and it should be simple to compute as well as to interpret
2. The index should be able to characterize a teak clone or a group clones with a single value which truthfully depicts its flowering overlap with either one or a group of clones over a time window.
3. The index should be able to be used as a tool routinely even in orchards with large number of clones to track development of young orchards as well as in monitoring the stability of established orchards.
4. The index must reach its maximum value of 1 if the phenograms of two clones are identical.
5. The index must show its minimum value of 0 if the phenograms of two clones are completely dissimilar.
6. If the phenograms of two clones show some overlap the value of the index must lie between 0 and 1.

Gunaga & Vasudeva (2009) have developed a general overlap index to quantify the exact overlap in flowering phenology among different clones. The authors have adopted the principle of computing similarity in species richness proposed by Morisita (1959) and Horn (1966) and extended to the teak seed orchard scenario. The following is the general formula for computing overlap in any phenophase. The time of peak flowering has been shown an example:

$$\text{Overlap Index (C)} = \frac{2 \sum_{t=i}^n (P_{ij} \times P_{ik})}{\left(\sum P_{ij}^2 + \sum P_{ik}^2 \right)}$$

Where,

- P_{ij} = is the proportion of ramets of j^{th} clone in peak flowering for a given period i
 P_{ik} = is the proportion of ramets of k^{th} clone in peak flowering for a given period i
 n = number of weeks in which the flowering was observed.
 $P_{ij} \times P_{ik}$ = the joint probability of flowering by two clones

The index is a simple, useful quantitative expression of phenological relationship among clones. The value of overlap index ranges from 0 *i.e.* when there is no overlap between two clones to 1 *i.e.* when there is full overlap between two clones. A higher value of the overlap index is suggestive of greater overlap. This index can be conveniently adopted to compute overlap of flowering between any two clones or between groups of clones belonging to different provenances or to know the flowering synchrony between a clone and rest of the clones in a CSO. The overlap index of a clone with all other clones of the CSO indicates its potentiality to contribute effectively to the ensuing seed crop.

An experimental verification of the new method was also reported by Gunaga & Vasudeva (2009). In their study synchrony among clones for peak flowering was assessed through phenograms (Figure 1) as well as through a novel overlap index (Table- 5). The perusal of trend in the phenogram suggests that generally there are two peak periods in flowering. The first peak during early May to July corresponds mainly to the clones of central and southern

Sl. No	Clone ID	With all other clones																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	MyHaD1	0.798																
2	MyHaD2	0.554	0.953	-														
3	MyHaD3	0.701	0.989	0.953	-													
4	MyHaD4	0.702	0.989	0.969	0.995	-												
5	MyHaV1	0.889	0.624	0.424	0.603	0.560	-											
6	MyHaV3	0.830	0.719	0.532	0.695	0.661	0.983	-										
7	MyHaV4	0.546	0.924	0.794	0.910	0.883	0.851	0.906	-									
8	MyHaV5	0.751	0.740	0.550	0.715	0.681	0.973	0.996	0.921	-								
9	MyHaV6	0.862	0.669	0.460	0.641	0.603	0.985	0.982	0.878	0.981	-							
10	MyHaV7	0.714	0.725	0.531	0.697	0.661	0.976	0.988	0.916	0.991	0.985	-						
11	MyHaK1	0.734	0.970	0.991	0.974	0.982	0.504	0.604	0.843	0.617	0.532	0.596	-					
12	MyHaK2	0.626	0.983	0.965	0.990	0.993	0.583	0.680	0.890	0.694	0.615	0.672	0.984	-				
13	MyHaK3	0.720	0.991	0.952	0.998	0.995	0.622	0.715	0.917	0.733	0.659	0.712	0.975	0.991	-			
14	MySA1	0.733	0.719	0.532	0.700	0.660	0.986	0.992	0.907	0.989	0.976	0.983	0.607	0.678	0.717	-		
15	MySA2	0.893	0.738	0.564	0.714	0.676	0.975	0.983	0.922	0.977	0.967	0.983	0.636	0.701	0.731	0.983	-	
16	MySS2	0.483	0.602	0.400	0.573	0.530	0.991	0.968	0.839	0.962	0.981	0.975	0.477	0.550	0.592	0.971	0.969	-
17	MyBL1	0.597	0.663	0.469	0.631	0.595	0.991	0.983	0.871	0.974	0.986	0.983	0.544	0.616	0.653	0.981	0.986	0.989
18	MyHuT1	0.775	0.728	0.551	0.791	0.680	0.974	0.985	0.915	0.983	0.967	0.976	0.629	0.699	0.736	0.988	0.981	0.963
19	MyHuT2	0.637	0.584	0.382	0.553	0.512	0.994	0.975	0.821	0.965	0.977	0.971	0.460	0.536	0.573	0.973	0.967	0.991
20	MyHuT3	0.586	0.619	0.413	0.587	0.547	0.979	0.970	0.850	0.971	0.985	0.983	0.480	0.560	0.603	0.962	0.959	0.986
21	MyHuT6	0.851	0.774	0.608	0.757	0.723	0.962	0.976	0.932	0.970	0.966	0.968	0.679	0.743	0.775	0.980	0.980	0.947
22	MyHuT7	0.730	0.734	0.539	0.704	0.668	0.972	0.986	0.919	0.993	0.983	0.995	0.604	0.678	0.720	0.985	0.978	0.973
23	MyHuT8	0.898	0.793	0.640	0.766	0.740	0.944	0.981	0.933	0.978	0.940	0.963	0.705	0.764	0.786	0.975	0.975	0.926
24	MyHuK3	0.726	0.718	0.528	0.691	0.652	0.985	0.986	0.913	0.987	0.983	0.990	0.599	0.667	0.708	0.993	0.987	0.983

Table 5. Overlap index for peak flowering among 25 clones in a Teak clonal seed orchard at Manch...

column represents the overlap index of that clone with all other clones of the CSO (except with itse...

provenances; the second peak during July to August corresponds to those from northern provenance (also see Figure 2). Table 5 shows the overlap index for peak flowering for all clone pairs of 25 clones in a clonal seed orchard of teak in southern India, Karnataka. It also shows the overlap index of a clone with all other clones of the CSO (except with itself). In nearly a fifth of the bi-clonal interaction with respect to peak flowering period, there was less than 0.6 overlap suggesting a lack of synchrony. In fact in 12.55 per cent of interactions, the overlap was less than 0.5. This suggests a gross violation of basic assumption, of random mating among clones, made while establishing a CSO.

Strong provenance influences on flowering phenology was also observed (Table 6). Comparison of overlap index between groups of clones from different provenances yielded several interesting results (Table 6). The overlap index between northern clones and those from southern was least (0.778); while it was 0.798 between northern clones and those of central. Highest overlap of 0.997 was found between clones of southern and central. Clones from central and southern provenances were early in commencement of flower buds, flowers and peak flowering (by about 30-40 days) when compared to clones from northern provenance (Figure 1). It clearly indicates that a significant proportion of ramets of clones from southern and central provenances escape early showers in the orchard when compared to those from northern provenance.

Overlap of clones of	Index Value
Northern provenances and central provenance	0.778
Northern provenances and southern provenance	0.798
Southern provenances and central provenance	0.997

Table 6. Overlap index for peak flowering between provenances.

Genetically based geographical variation was recorded in the present study and it was also shown to occur in several plant species. Hence, simple geographical continuity of the clonal origin could be considered as thumb rule while selecting right clones for seed orchard. Effimov (1987) has also suggested the selection of plus trees based on synchronized flowering while establishing second-generation clonal seed orchards. In fact in Australia constraints for *Pinus caribaea* seed production has prompted a co-operative arrangement wherein special clonal seed orchards would be established using local clones alone. The overlap index between ‘early flowering clones’ (those clones blooming during May-June month corresponding to Figure 2 b, c) with ‘late flowering clones’ (those bloomed during July to August months corresponding to Figure 2a) was 0.739. This suggested that about 70 per cent synchrony can be expected between clones which flowered early *i.e.* during June month, with clones that flowered late (during July to August; Figure 1). In order to improve the seed production level in CSO, seed orchards need to be established considering the flowering synchrony of the constituent clones.

4. Management implications

Having a measure of flowering synchrony of each clone with the reminder of the clones in the orchard plays an important role in assessing the genetic value of the orchard crop (Askew & Blush, 1990). Rating an entire orchard for its relative degree of flowering synchronization is effective with this new measure. This helps to track the changes in flowering on a quantitative scale through out the orchard life and hence help in evaluating the panmixia/ genetic gain. The index is a simple, useful quantitative expression of

phenological relationship among clones. The overlap index of a clone with all other clones of the CSO indicates its potentiality to contribute effectively to the ensuing seed crop. Assuming there are no variations in the pollen grain fertility, it may also represent a value akin to the general combining ability of a parent. Flowering synchrony and parental balance would influence on panmictic equilibrium (random mating). It may be one of the causes for low fruit production in seed orchards (Gunaga & Vasudeva, 2005). For production of genetically superior seed, abundant and synchronized flowering of all clones in a seed orchard is very necessary, otherwise the seed produced cannot be guaranteed as genetically superior (Rawat et al., 1992). To overcome these problems, selecting a clone with high overlap index to establish future CSOs could be a good practice to increase the panmixis and hence the genetic quality of the seed crop from a CSO.

5. Conclusion

Genetic improvement of teak has focused mainly on identifying phenotypically superior trees from diverse growing regions and deploying them as vegetatively propagated clones in seed orchards. One of the most important aspects in a seed orchard is the synchrony among the clones for reproductive phenology. This will decide the extent of random mating among the constituent clones and hence the genetic gain in the resultant progeny. Although, there seems to be a direct association between the extent of flowering synchrony among the constituent clones and the fruit production in a seed orchard, surprisingly, there are very few reports in India that focus on these issues. A lack of a suitable tool for an objective measurement of flowering synchrony among different clones has also contributed to the negligence!! Hence there is a need for development of objective criteria to evaluate flowering phenological events. The patterns of genetic variation for phenology in teak seed orchards have shown that the reproductive initiation events have a strong genetic basis and show moderately high heritable values. A novel index to measure flowering among individuals in an orchard has been developed and the experimental verification of the same has shown that there is a large asynchrony among the clones guided by the provenance influence.

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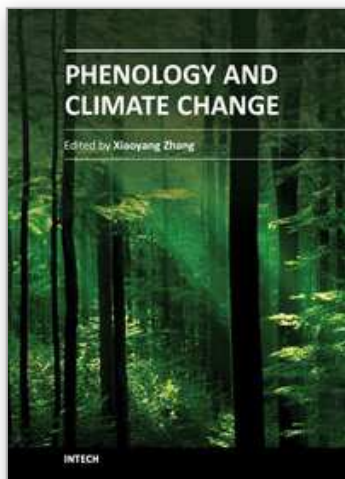
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