Sri Lanka Journal of Food and Agriculture
DOI: http://doi.org/10.4038/sljfa.v8i1-2.109

8 (1-2): 1-18,2022

Sri Lanka Journal of Food and Agriculture (SLJFA)

ISSN: 2424-6913
Journal homepage: www.slcarp.lk

Research Paper

Analysis of genetic variation of growth traits of *Eucalyptus grandis* in a progeny trial at Erabadda, Sri Lanka

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Article History:
Received: 01 April 2022
Revised : 23 June 2022
Accepted: 01 December 2022

Abstract: *Eucalyptus grandis* is important timber species in both forest plantations and home gardens in Sri Lanka's tropical uplands. At present seeds used for *E. grandis* are mainly collected off trees of the local land races, which have been of unverified genetic provenance. In 1995, an *E. grandis* provenance- family trail/ seedling seed orchard was established in intermediate zone, IU3e agro ecological region of Sri Lanka. It comprises 88 families representing 19 Australian provenances. According to the previous studies, at the 27 months ago there were considerable differences among provenanaces and among families within provenanaces in the *E. grandis* provenance- family trail for height, diameter at Brest height (DBH) and tree volume. The natural stand povenanaces from Windsor Tableland (CSIRO No. 18138) and from Atherton (CSIRO No. 16583), both from higher altitude areas in northern Queensland, showed best growth. However, the variation between the families within povenanaces exceeded most of the differences between povenanaces with a family from one of the poorest povenanaces. Kin Kin in Queensland (16892), proving to be second biggest family overall volume. Heritability estimates obtained for height (0.22) Diameter at Brest Height (DBH) (0.12) and volume (0.11) were intermediate to low but still indicate that reasonable genetic gain will be achieved through an open pollinated breeding strategy in Sri Lanka. In the eucalyptus species trail, *E. grandis* showed the best growth at age 27 months of the five species tested. Present study was carried out in Erabadda research plot (2.8 Ha) of Badulla district, Sri Lanka. The study area contains seven different seed sources of *E. grandis*, which were belong in to seventy-two provenances. In this study, several parameters, such as DBH, Height of the tree and volume of the trees were determined. Collected data were analyzed by the Dataplus and GeneStat software's to determine the genetic variance was determine among all varieties of *E. grandis* in the study area. These findings will be useful for the future improvements of *E. grandis* in Sri Lanka.

Keywords: DBH, *Eucalyptus grandis*, Genetic variance, Height, Volume, Heritability, Seed sources

Introduction

Eucalyptus has been proved to be fast growing, multipurpose tree and is now of major socio-economic importance. More than 800 *Eucalyptus* species are available all over the world (Bandara *et.al.*, 2000). Most of them have been domesticated (i.e. *Eucalyptus grandis, Eucalyptus microcorys, Eucalyptus camaldulensis, Eucalyptus robust*). Large scale plantations have been established in the sub-tropical areas such as South Africa, South America and high-altitude areas around the world including high altitude areas of Sri Lankan, Among *Eucalyptus* species, *Eucalyptus grandis* is one of the main commercial forest plantation species in the sub-topical and high-altitude areas in the world including Sri Lanka.

E. grandis is having distinctive flowers and fruits. White color flowers have numerous stamens enclosed in a cap known as an operculum, which is composed of fused sepals, petals or both. Flowers found in clusters of 7-11. Flowers are bisexual, with fertile male and female organs on the same flower. In most of the *Eucalyptus* spp. thus flowers have no petals (Bandara *et.al.*, 2000). The timber of *E. grandis* is pale, relatively soft and less dense than most of the *Eucalyptus*. It finds a wide range of uses including pulp for paper and rayon, charcoal, poles and sawn timber for light construction (Jacobs; 1981). One characteristic of Sri Lankan grown *E. grandis* timber, which limits its quality and value in solid wood applications, is its high incidence of end splitting. This tendency can relegate timber of this species to the "grade two" category and consequently lower market values than other timbers, such as that of *E. microcorys,* which more frequently classes in to the "grade one" category. Other application for this species, include fuel wood production, shade plantings and ornamental plantings (Boland *et al.,* 1984). It makes a good fuel wood, which splits easily when dry.

E. *grandis* is probably the most widely planted species of the eucalyptus for industrial wood production, with an estimated area of plantations of about 2 million hectares in 1987 (Burgess; 1988). Most of these are in Brazil (over 1 million hectares) and South Africa (300,000 ha), but there are also large areas of plantations in Argentina, Australia, India, Uruguay, Zambia, Zimbabwe and other countries. Seed lots from the Coffs Harbor area have generally performed well (Thavananthan Sivananthawer and Ralph Mitloehner, 2011). *E. grandis* has been favored because of its ease of nursery care, rapid early growth, good form, and wood properties suitable for many uses (https://www.fao.org/4/ac121e/ac121e04.htm).
It will generally grow faster than any other tree species on good sites in sub-tropical and warm temperate climates (eg. Barrett *et al.,* 1975 for Zimbabwe).It is not suited to lowland regions of the humid tropics and is susceptible to disease in these environments (Thavananthan Sivananthawer and Ralph Mitloehner, 2011), using mapping based on the limits of climatic tolerance of *E. grandis* derived from its natural distribution, have correctly identified the areas in Africa where the species has succeeded in plantations.

Eucalyptus grandis has proved to be one of the best timber plantation species in Sri Lanka's up-country intermediate and wet zones. In the past, many local and exotic tree species have been tested in these zones. However, most of the natural local tree species have failed to establish and grow well in plantations in early trials which indicated that *E. grandis* was better adapted for plantation establishment compared with several other *Eucalyptus* species such as *E. cloeziana* and *E. pilularis. Eucalyptus grandis* has been used since the early 1900s as a plantation tree species in Sri Lanka, largely for construction timber and fuel wood. *E. grandis* has been established by both the public and private sectors. During the past century, there are more than 10,000 ha *E. grandis* being raised by the Forestry Department of Sri Lanka, and a significant though unknown area has been established by the tea estate sector and in farm home gardens (Bandarathilake, 1999). *Eucalyptus* species are planted throughout the country (Bandarathilake, 1999). The total extent of eucalypt plantations raised in various parts of the country to 1991 amounts to 29,600 ha. This is included over 2700 ha of *E. grandis*. According to mean annual rainfall and the altitude, the planting areas can be categorized in to three agro-climatic regions, i.e. Intermediate zone, Wet zone and upcountry.

A wide range of provenances were tested in trails in 13 countries co- ordinated by IUFRO. Results of these trials have demonstrated that significant genetic variation exists within the species between provenance seed lots collected from different locations. The species can attain reproductive maturity as early as age two years from seed. In an *E. grandis* improvement program in Florida, USA, this trait of early maturation enabled turnover of breeding generations of every four years (Meskimen, 1983, Davidson, 1993). Such short cycles enabled rapid genetic gains per unit of time to be achieved. *E. grandis* has been subjected for lot of genetic improvements all over the world, in order to obtain high yield and disease, insects or herbicides resistant.

Genetic improvement of *E*. *grandis* and *E .microcorys* in Sri Lanka started in the late 1980s with establishment of species and provenance trials under the community forestry participatory project. Then in the mid-1990's a breeding program was formulated (Arnold, 1996) and initiated for *E. grandis*. To advance the domestication of other priority *Eucalyptu*s species, *E. microcorys* provenance trial was establishment in the mid-90s. Philips and Weerawardene, 1998 confirmed that *E. grandis* is the most suitable plantation *Eucalyptus* species for Sri Lanka's uplands. *E. grandis* from Ravenshoe, Queensland (CSIRO seed lot 12409) out performed both other *E. grandis* provenances and other *Eucalyptus* species in a trial in the mid country intermediate zone of Sri Lanka (Phillips 1991). In a different species provenance trial in the up country wet zone the same provenance from Ravenshoe also showed the best growth (Phillips; 1991). Other *E. grandis* provenance which has performed well in earlier trails in Sri Lanka's up-country including Bellthorpe Forest, Queensland (CSIRO seed lot 14431) and Baldy Forest, Queensland (CSIRO seed lot 14423) (Phillips, 1991). A breeding strategy was formulated (Arnold; 1994), and initiated by the Forest Department, Sri Lanka, in 1995 to improve *E. grandis* for solid wood production. An *E. grandis* genetic improvement program was initiated in 1995 with the establishment of a first-generation trail. The provenance family trial (first generation trail) and seed production area at Kinigama was established in 1995 in Badulla district, IU3e agro ecological region of Sri Lanka. Based on the 1st generation progeny trail results, the trail has been thinned heavily to convert to a seedling seed orchard (SSO) originally the plot consist 5 trees and 4 out of 5 trees removed and the badly performing families been removed. Accordingly, the trail have been converted to a seedling seed orchard.

The objective of this study is to analyze the genetic variations in the second-generation *Eucalyptus grandis* trial, established in Erabadda, Sri Lanka, in 2007. Growth parameters, including diameter at breast height (DBH), height, and volume, will be assessed at nine years of age (108 months) to evaluate variations among seed sources, families, and individual trees. Additionally, genetic parameters related to growth will be estimated, and breeding options suitable for Sri Lankan climatic conditions will be explored. The findings of this study will contribute to the future improvement of *E. grandis* in Sri Lanka.

Materials and Methods

Genetic material and trail design of the second-generation *Eucalyptus grandis* seed source-family trail

The second generation *Eucalyptus grandis* seed source- family trail/ seedling seeds orchard is established in 2007 at Erabadda (9° 27'N, 81° 12'E) near the town of Welimada in the intermediate zone, up- country, , IU3e agro ecological region of Sri Lanaka, in close proximity to the first generation trail established in 1995 (Bandara *et al*., 2000). The site is approximately 1,350 m above sea level. The second-generation trail included 132 families representing 7 Sri Lankan seed sources (Table 1). Of these, 60 were families from plus trees (i.e. mother plants) selected in various plantations and seed production areas elsewhere in Sri Lanka. The other 72 families were from individual trees selected in first generation Sri Lankan seedling seed orchards; these 72 represented 50 families and 16 of the provenanaces included first generation. Selection of parent trees in the first generation (to provide families for the second generation) was most intensive within the lower ranking families, and less intensive within the highest-ranking families, with a restriction of a maximum of 3 plus- trees from any one first generation family (Bandara *et.al*., 2000). This resulted in 5 families contributing 3 plus- trees, 12 families contributing 2 plus- trees and 33 families each contributing 1 plus- tree.

Table 1. Origins of seed sources and families included in the second-generation *E. grandis* seed source-family trail Erabadda, Sri Lanka, 2007

ID no.	Source#	Location	Latitude (°N)	Longitute (°E)	Altitude (m asl)	No. of families/ seed lots
1	1st generation SSO	Erabadda	6° 53'	80° 52'	1276	72
2	SPA 1	Kinigama	6° 50'	81° 01'	1306	17
3	SPA 2	Erabadda	6° 53'	80° 52'	1370	11
4	Plantation	Kinigama	6° 50'	81° 01'	1306	10
5	Plantation	Erabadda	6° 53'	80° 52'	1250	5
6	Plantation	Rathkarauwa	6° 48'	80° 55'	1319	12
7	Plantation	Galpalama	6° 58'	81° 25'	830	5

Note - #SSO = seedling seed orchard; SPA = Seed production area. SPA 1 was established using mixture of natural provenances seed lots imported from Australia. SPA 2 was developed from mature, visually impressive plantations (thought to originate from locally collected seeds) with heavy thinning to remove inferior trees.

The second-generation trail was designed as a raw-column design for 132 seed lots with 6 replicates and incomplete blocks (rows and columns) using the field trail design software package ALPHA+ (Williams and Talbert, 1993) spacing was 2.0 m between plants within rows. Each seed lot was represented by a 5- tree row plot in each replicate.

Culture

All seedlings for the second-generation trails were propagated at the Forest Departments research nursery at Erabadda, a short distance from the trail site. Seed lots were germinated in the special germination treys, containing a mixture of river sand and compost. Young seedlings were transplanted at the cotyledon plus two leaf pair stage into poly- bags. (15 cm diameter x 22 cm height) filled with media comprising 50% sieved compost and 50% sandy loam soil. The seedlings were planted when they were approximately 30 cm height (at about 4 months after transplanting). Planting was carried out in November at the start of northeast monsoon on 2007. The trail was weeded manually three times per year and consequently weed composition for the E. grandis trees was minimal over the first three years. In December 2008, October 2009 and October 2010 each tree was fertilized with 100g of an NPK fertilizer mixture (1:1:1). First thinning was done 5 years after planting retaining the best 3 tree per 5-row plot based on volume.

Collection of Data

All trees of 2nd generation E. grandis trail at Erabadda, were assessed at approximately 9 years age, for height and diameter at breast height (DBH). Height was estimated to nearest 0.1 m using a Suunto clinometers and a 25 m tape and DBH was measured to the nearest mm with a DBH tape. DBH, height and volume will analyze at 9 years age. In order to determine the variations in-between seed sources, families and individual trees. Estimate the genetic parameters of growth. Moreover, to discuss the breeding options of E. grandis, which are suitable for Sri Lankan climatic conditions. Although from year, 2010 to 2015 (seven years including 2016) height and diameter at breast height (DBH) data were used for the analysis in order to compare the genetic variation of growth traits in the trail from3 years to 8 years of age.

Analysis

The software package DataPlus (Williams et al., 2000) was used to pre-processing the data and screen for incorrect entries and layout values. Extreme outliers were excluded from the analyses. The tree height and DBH data from each assessment (data belongs to seven years (from 2010- 2016) were used to calculate individual tree volume indices (in dm3) using a conical volume equation as follows.

VOL = π x (DBH/ 2) x HT/ 3 (Williams et al; 2000)

Where

VOL = conical index of over bark tree volume (dm3)

DBH = diameter at breast height (1.3 m) over bark (dm)

HT = total tree height (dm)

Π = the constant pi = 3.141593 (6 decimal places)

Hereafter, the terms volume and tree volume are taken to represent individual tree volume index.

For analysis of variance to examine the significance of differences among, seed sources and families for the data were reduced to plot mean values. Data were then analyzed procedures described by Williams et al., 2002, based on the following linear model:

Y_{ijklm} = μ + Ri + Tj(i)+ Ck(i) + Sl + Fm(i) + eijklm

Y_{ijklm} = the plot mean of family m within seed I in column k and row j of replicate I; μ= the overall mean;

R_i= fixed effect of replicateI;

$T_{j(i)}$ = random effect of row j within replicateI;

$C_{k(i)}$ = random effect of column kwithin replicate I;

Sl = fixed effect of seed source I;

$F_{m(i)}$ =random effect of family m which is nested within seed source I;

e_{ijklm} = random residual error with a mean of zero.

The REML procedure in GENESTAT statistical software was used to obtain estimates of trail means for each seed source, along with standard errors for differences between these means.

Genetic parameters

Preliminary estimation of variance components for genetic parameter computation was carried out using the full data set (all seed sources and families) by mixed modal analyses, with replicates and seed sources included as fixed effects and families within seed sources as random effects (Williams et al., 2000). This analysis was conducted using REML procedure in GENESTAT 5.3.2.

Heritability

The mean within seed source family variance components were used to estimate mean within seed source individual tree heritabilities (denoted hi2) as follows.

$h_i^2 = 1/r \times \sigma_f^2 / \sigma^2_p$ (Williams *et al.*, 2000)

Where:

r = coefficient of relationship

σ_f^2 = variance between families within seed source

σ^2_p = phenotypic variance

$\sigma^2_p = \sigma_f^2 + \sigma_m^2 + \sigma_t^2$ (Williams *et al*; 2000)

Where:

σ_m^2 = variance between plots

σ_t^2 = variance between trees within plots

The coefficient of relationship used in computation of these individual tree heritabilities was taken as 0.25as appropriate for half- sib families with some allowance for imperfect outcrossing, such as selfing and cross- pollination among related individuals.Genetic correlation between traits was calculated using covariance's obtained following methodology described by Williams et al. (2002).

Phenotypic correlations

The correlation procedure (PROC CORR) in Genestat was used to obtain phenotypic correlations and the significance of these, between the parameters of individual tree volume at different ages, using individual tree rather than plot mean data. The coefficient of weight used in computation of correlation between the traits was 5.5.

Selection

A selection index was calculated using the select 1.gen and select 2.gen programs produced by dataplus. The index was based on height and DBH, with economic weight of 1 and 2, respectively to reflect the greater importance of DBH in determining volume. An index coefficient of 1 was used (Cotterill and Dean, 1990). The trees were ranked on the selection index and the best trees identified.

Results

At nine years of age, the trees in the trial had an average individual DBH of 15.4 cm, height of 9.9 m, and volume of 71.7 dm^3 per tree. Table 2 present the significant differences in DBH, height, and tree volume among the seven seed sources and seed lots in the study area.

Table 2. Significant differences of DBH, HT and tree volume among seed sources and seed lots in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

No	Trait	d.f.	Mean square	Variance ratio	significance level
01	**DBH 10**				
	Seed source	6	7.117	4.75	P < 0.001
	Family/ seedlot	125	1.883	1.26	0.042
02	**DBH 11**				
	Seed source	6	17.982	4.64	P < 0.001
	Family/ seedlot	125	5.429	1.4	0.005
03	**DBH 12**				
	Seed source	6	27.468	5.76	P < 0.001
	Family/ seedlot	125	6.414	1.35	0.012
04	**DBH 13**				
	Seed source	6	37.534	6.18	P < 0.001
	Family/ seedlot	125	7.552	1.24	0.05
05	**DBH 14**				
	Seed source	6	47.52	6.9	P < 0.001
	Family/ seedlot	125	9.076	1.32	0.018

06	**DBH 15**				
	Seed source	6	62.153	8.35	P < 0.001
	Family/ seedlot	125	9.934	1.34	0.014
07	**DBH 16**				
	Seed source	6	94.909	9.65	P < 0.001
	Family/ seedlot	125	13.082	1.33	0.014
08	**HT 2010**				
	Seed source	6	7.671	4.47	P < 0.001
	Family/ seedlot	125	2.194	1.28	0.032
09	**HT 2011**				
	Seed source	6	31.285	4.74	P < 0.001
	Family/ seedlot	125	7.769	1.18	0.11
10	**HT 2012**				
	Seed source	6	31.831	3.94	P < 0.001
	Family/ seedlot	125	9.731	1.21	0.079
11	**HT 2013**				
	Seed source	6	27.02	3	P = 0.007
	Family/ seedlot	125	10.941	1.21	0.071
12	**HT 2014**				
	Seed source	6	32.747	3.33	P = 0.003
	Family/ seedlot	125	11.533	1.17	0.115
13	**HT 2015**				
	Seed source	6	40.52	3.64	P = 0.001
	Family/ seedlot	125	13.26	1.19	0.091
14	**HT 2016**				
	Seed source	6	56.782	6.35	P < 0.001
	Family/ seedlot	125	10.533	1.18	0.108
15	**Vol. 2010**				
	Seed source	6	62.86	2.53	P = 0.020
	Family/ seedlot	125	26	1.05	0.358
16	**Vol. 2011**				
	Seed source	6	1619.7	3.63	P = 0.002
	Family/ seedlot	125	460.4	1.03	0.399
17	**Vol. 2012**				
	Seed source	6	3417.9	4.04	P < 0.001
	Family/ seedlot	125	884.6	1.05	0.361
18	**Vol. 2013**				
	Seed source	6	7317	4.37	P < 0.001
	Family/ seedlot	125	1872	1.12	0.197
19	**Vol. 2014**				
	Seed source	6	16568	5.54	P < 0.01
	Family/ seedlot	125	3987	1.24	0.112
20	**Vol. 2015**				
	Seed source	6	30446	6.52	P < 0.001
	Family/ seedlot	125	6077	1.3	0.023

21	**Vol. 2016**				
	Seed source	6	19876	5.98	P < 0.01
	Family/ seedlot	125	4356	1.26	0.098

Following graphs are showing the differences of DBH, height and tree volume, in between seven seed sources, available in study area at 9 years ages. As well as the range from maximum to minimum, value.

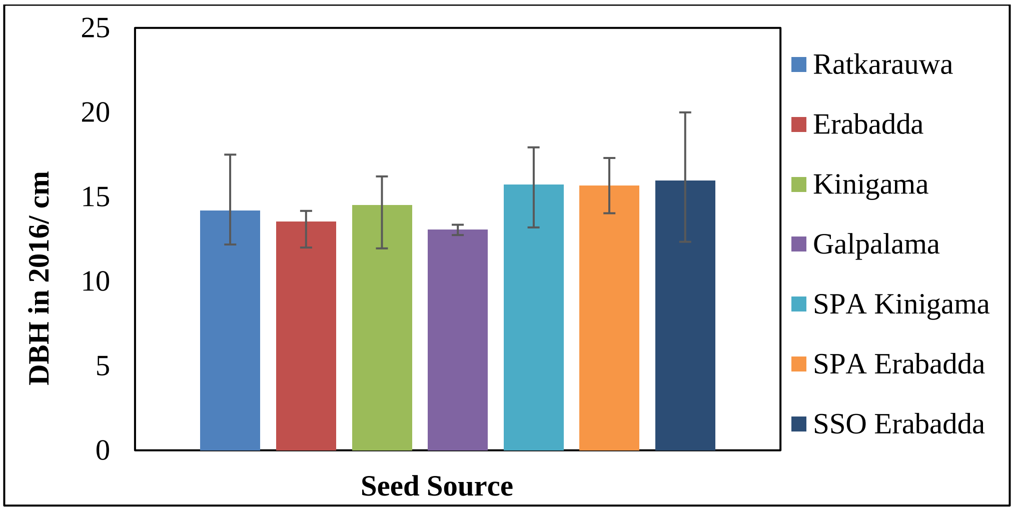

Figure 1. The graph of DBH in 2016 vs. Seed source in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

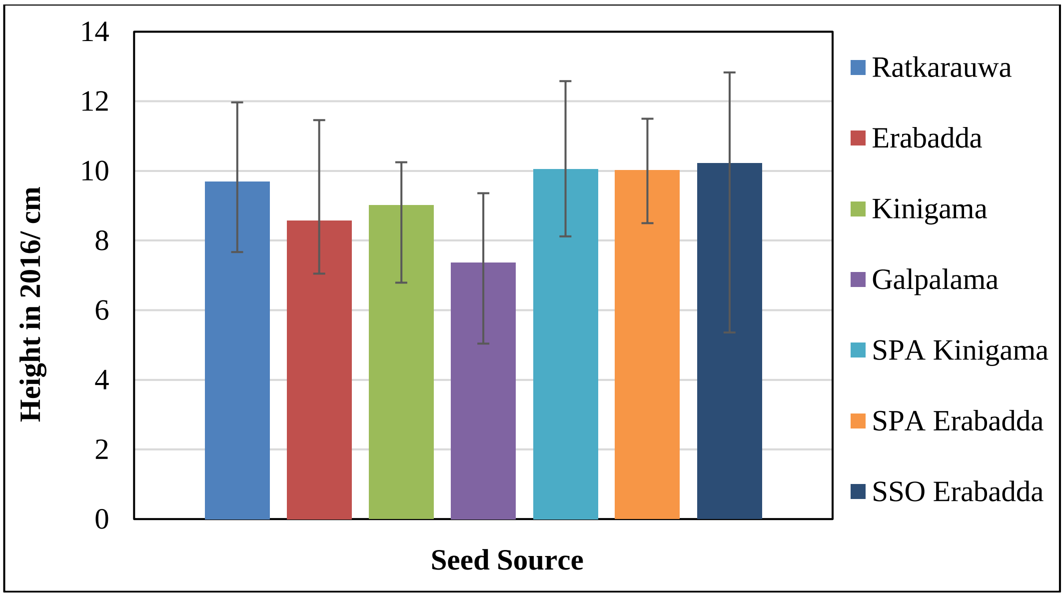

Figure 2. The graph of Height in 2016 vs. Seed source in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

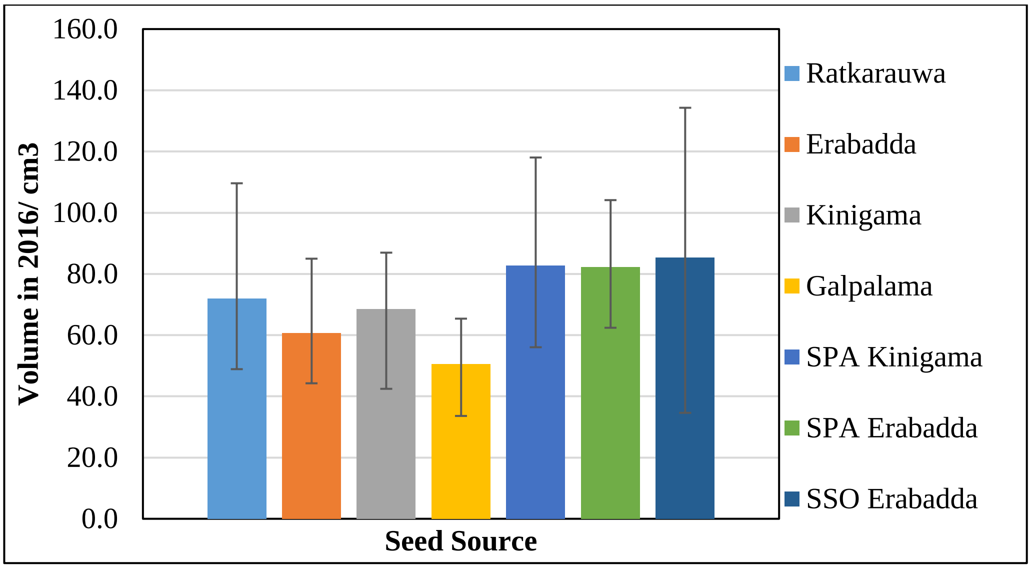

Figure 3. The graph of Volume in 2016 vs. Seed source in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

Seed sources also deferred significantly ($P < 0.001$) provenances for growth (individual tree volume) at the age of assessment with the growth at all assessment ages being that of Erabadda SSO; at the age 9 years its average tree volume was 85.4 dm^3. The seed source with the lowest growth was Galpalama plantation, which had an average tree volume at the age 9 years of just 50.6 dm^3. The average growth improved source as a group (the SSO and two SPAs) at 83.4 dm^3/ tree was significantly better than that of the combined unimproved sources (plantation sources) which had averaged just 63.0 dm^3/ tree. Even the best of unimproved sources, Rathkarauwa plantation with average tree volume of 72.0 dm^3 at 9 years, had markedly lower growth than that of the lowest ranked improved source. SPA Erabadda with average tree volume of 82.2 dm^3 at 9 years (Table 3).

Table 3. Seed source mean for DBH, HT and tree volume index (Vol.) at age 5 and 9 in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007 – seed sources are listed order (descending) by mean tree volume at 2016

Seed source	**No. of Families#**	**DBH 2012 (cm)**	**HT 2012 (cm)**	**Vol. 2012 (cm^3)**	**DBH 2016 (cm)**	**HT 2016 (cm)**	**Vol. 2016 (cm^3)**	**Rank - Vol. in 2016**
SSO - Erabadda	72	8.01	9.58	38.6	15.96	10.22	85.36	1
SPA – Kinigama	17	7.71	9.13	35.8	15.73	10.05	82.73	2
SPA – Erabadda	11	7.6	9.15	32.3	15.67	10.02	82.17	3
Rathkarauwa	12	7.58	9.24	34.7	14.19	9.7	72.03	4
Kinigama	10	7.08	8.65	29.3	14.53	9.02	68.59	5
Erabadda	5	6.43	7.76	20.4	13.53	8.57	60.68	6
Galpalama	5	6.41	7.91	20.7	13.08	7.37	50.54	7
Average - improved sources (SSO + SPA)	100	7.77	9.29	35.57	15.79	10.10	83.42	
Average - unimproved sources	32	6.88	8.39	26.28	13.83	8.67	62.96	

Trial average	132	7.26	8.77	30.26	14.67	9.28	71.73

According to above graphs the highest DBH, height and tree volume was recorded in SSO Erabadda seed source. Second highest was recorded in SPA Kinigama seed source. However, the deference in-between maximum to minimum value is high in SSO Erabadda compared with SPA Kinigama. As well as minimum level of SSO Erabadda parameters are lower than SPA Kinigama seed source.

Variations among families

All the best families for individual tree volume (at age 9 years) were improved sources, and dominated by Erabadda SSO families. Of top 10 families, when ranked by averaged tree volume at the age 9 years, all ten families were from the improved sources, and of the top 50 families, 46 were from Erabadda SSO, just 4 were from Erabadda SPA. There was no family from, Kinigama SPA or plantation plus – trees. But not all families from improved sources performed well; of the 32 lowest ranked families 4 and 11 were from Kinigama and Erabadda SPAs, respectively. The rest 32 were from plantation plus- trees.

Table 4. Statistics from the top ranked 10, 20, 30, 40 and families (ranked by volume in 2016) in second generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

Family grouping	**Trait average**				**Number of families in group by seed source**			
	Vol 2 yr	**Vol 5 yr**	**Vol 7 yr**	**Vol 9 yr**	**SSO - Erabadda**	**SPA – Kinigama**	**SPA – Erabadda**	**plantation plus-trees**
Ranks 1to 10	5.31	38.84	132.21	44.49	9	1	0	0
Ranks 11to 20	3.85	32.24	110.91	44.15	10	0	0	0
Ranks 21to 30	4.3	30.11	103.39	41.2	10	0	0	0
Ranks 31to 40	3.92	31.33	98.23	39.72	8	2	0	0
Ranks 41to 50	3.85	27.7	91.88	37.86	9	1	0	0
Ranks 51to 100	3.35	25.93	78.44	35.08	26	9	0	0
Ranks 101 to 132	2.38	18.32	55.95		0	4	11	32
all families-trail average/ number of families	3.45	26.4	84.06	71.7	72	17	11	32

Heritability

The heritability estimated for height was low at 0.007. However, those for DBH and volume were relatively moderate at 0.068 and 0.101, respectively.

Table 5. Statistics from the heritability's of DBH. HT and volume in 9years age in second-generation *E. grandis* seed source family trail established at Erabadda, Sri Lanka in 2007

Trait	**h mean**	**σ2 t**	**σ2 m**	**σ2 f**	**h2**
DBH	2.406	14.142	1.479	0.434	0.068
HT	5	109.599	-14.757	0.278	0.007
Vol.	2.406	17160.12	281.005	732.114	0.101

Selection

The best 100 trees identified by the combined index on DBH and volume are shown in Table 5. The selection index values were adjusted for replicate and incomplete block (repl. Column) effects.

Table 6. The best 100 *E. grandis* trees in the seed source family trail established at Erabadda, Sri Lanka in 2007 based on block- adjusted index

Rank	**Replicate**	**Row**	**Column**	**Tree**	**Seed lot**	**Region**	**v1**	**v2**	**Selection index**
1	4	1	1	4	123	sso erabedda	41.44	1697.71	1828.16
2	3	11	1	5	70	sso erabedda	49.5	1646.49	1775.99
3	2	3	2	4	108	sso erabedda	42.34	1466.09	1580.85
4	1	1	8	2	108	sso erabedda	41.84	1458.48	1572.55
5	3	11	1	2	70	sso erabedda	46.9	1443.71	1558.38
6	2	6	4	2	120	sso erabedda	42.93	1443.55	1556.94
7	1	11	1	2	54	spa kinigama	43.37	1417.33	1529.04
8	2	11	3	2	70	sso erabedda	46.43	1407.02	1519
9	1	10	3	2	80	sso erabedda	44.53	1390.32	1500.54
10	2	3	1	1	97	sso erabedda	45.62	1355.49	1463.66
11	3	6	5	4	97	sso erabedda	44.53	1298.09	1401.95
12	2	11	3	4	70	sso erabedda	44.53	1286.06	1389.08
13	4	2	3	1	120	sso erabedda	41.74	1275.37	1376.77
14	5	7	4	4	123	sso erabedda	39	1275.95	1376.5
15	2	3	1	4	97	sso erabedda	43.92	1271.95	1373.81
16	4	6	4	3	97	sso erabedda	44.56	1256.26	1357.24
17	3	6	2	5	108	sso erabedda	39.69	1252.81	1351.99
18	4	5	12	5	70	sso erabedda	43.84	1226.08	1324.74
19	6	2	10	4	108	sso erabedda	41.46	1212.83	1309.82
20	3	6	2	3	108	sso erabedda	38.19	1206.24	1301.73
21	1	1	8	1	108	sso erabedda	37.84	1178.01	1271.44
22	3	11	1	3	70	sso erabedda	43	1176.11	1271.05
23	6	7	8	4	70	sso erabedda	42.38	1172.63	1267.14
24	1	7	4	3	70	sso erabedda	41.55	1166.95	1260.8
25	4	6	4	1	97	sso erabedda	43.26	1157.22	1250.94
26	5	2	11	5	70	sso erabedda	42.93	1153.38	1246.73
27	1	7	7	5	120	sso erabedda	38.95	1148.95	1240.73
28	1	1	8	4	108	sso erabedda	36.74	1148.36	1239.39
29	5	6	1	5	97	sso erabedda	43.47	1144.54	1237.45
30	1	8	5	3	97	sso erabedda	41.92	1143.93	1236.31
31	5	11	8	4	54	spa kinigama	42.5	1137.58	1229.7
32	3	1	3	5	40	spa kinigama	36.46	1136.84	1226.99
33	3	6	5	1	97	sso erabedda	40.03	1133.72	1224.79
34	4	11	11	1	108	sso erabedda	40.83	1130.39	1221.49
35	4	5	12	4	70	sso erabedda	41.24	1125.86	1216.77
36	4	11	11	3	108	sso erabedda	38.83	1115.4	1204.82
37	6	11	10	5	80	sso erabedda	42.82	1111.72	1202.16
38	1	1	2	4	116	sso erabedda	35.46	1106.07	1193.77
39	5	6	1	2	97	sso erabedda	41.97	1097.63	1186.83
40	4	2	1	2	131	sso erabedda	37.01	1098.41	1186.07
41	1	1	11	1	81	sso erabedda	36.17	1097.06	1184.36
42	1	9	1	1	109	sso erabedda	36.07	1095.29	1182.44

43	4	6	4	4	97	sso erabedda	40.86	1093.84	1182.42
44	3	9	5	2	80	sso erabedda	40.06	1093	1181.26
45	2	7	7	1	80	sso erabedda	40.06	1086.84	1174.68
46	2	2	12	2	40	spa kinigama	36.07	1082.4	1168.66
47	2	8	3	4	105	sso erabedda	34.77	1071.34	1156.42
48	3	11	3	2	116	sso erabedda	36.19	1054.26	1138.62
49	3	6	5	3	97	sso erabedda	38.73	1045.91	1130.5
50	6	7	11	3	97	sso erabedda	39.61	1039.81	1124.26
51	3	6	2	2	108	sso erabedda	36.19	1037.07	1120.24
52	2	4	2	3	130	sso erabedda	29.41	1036.8	1117.78
53	6	7	8	1	70	sso erabedda	37.68	1033.57	1116.97
54	2	1	3	1	109	sso erabedda	34.57	1033.31	1115.7
55	5	6	1	3	97	sso erabedda	39.47	1026.79	1110.3
56	1	1	5	3	130	sso erabedda	27.35	1029.7	1109.53
57	3	11	12	3	54	spa kinigama	35.58	1021.2	1103.07
58	1	7	4	2	70	sso erabedda	37.95	1019.12	1101.61
59	6	7	11	2	97	sso erabedda	39.61	1011.78	1094.3
60	4	7	5	1	80	sso erabedda	38.99	1009.28	1091.42
61	2	3	2	1	108	sso erabedda	35.04	1009.2	1090.08
62	2	9	12	1	54	spa kinigama	35.68	999.96	1080.4
63	5	4	1	5	109	sso erabedda	36.24	997.76	1078.23
64	4	11	11	5	108	sso erabedda	35.93	997.8	1078.18
65	5	3	4	2	80	sso erabedda	40.15	989.99	1071.17
66	6	8	5	4	54	spa kinigama	37.43	989.32	1069.58
67	1	5	2	5	117	sso erabedda	30.17	983.82	1061.39
68	1	11	1	5	54	spa kinigama	35.57	981.76	1060.91
69	1	7	4	5	70	sso erabedda	36.75	976.8	1055.99
70	5	6	1	4	97	sso erabedda	37.97	975.35	1054.83
71	2	11	3	5	70	sso erabedda	39.03	973.1	1052.76
72	1	8	5	1	97	sso erabedda	38.02	968.49	1047.51
73	1	8	5	2	97	sso erabedda	37.42	965.7	1044.33
74	2	4	3	2	43	spa kinigama	31.27	966.25	1042.96
75	6	7	5	1	102	sso erabedda	39.94	961.84	1041.01
76	2	7	7	3	80	sso erabedda	37.66	960.47	1038.82
77	1	1	2	1	116	sso erabedda	33.96	960.03	1037.17
78	2	10	11	1	116	sso erabedda	35.43	958.01	1035.48
79	1	1	5	1	130	sso erabedda	26.15	959.89	1034.52
80	3	9	12	3	92	sso erabedda	32.44	956.23	1032.61
81	4	2	3	3	120	sso erabedda	34.74	955.48	1032.55
82	1	7	5	4	40	spa kinigama	33.13	954.23	1030.7
83	6	9	6	4	116	sso erabedda	37.45	949.6	1027.13
84	1	7	7	3	120	sso erabedda	34.35	950.34	1026.93
85	3	9	5	3	80	sso erabedda	36.76	947.13	1024.27
86	5	2	11	2	70	sso erabedda	35.93	945.24	1021.99
87	4	1	6	3	41	spa kinigama	33.39	939.76	1015.31
88	2	4	2	5	130	sso erabedda	27.01	941.48	1015.11
89	6	2	10	1	108	sso erabedda	31.86	939.08	1014.1
90	4	7	5	4	80	sso erabedda	37.49	936.87	1013.53
91	5	3	3	2	131	sso erabedda	37.21	936.16	1012.68
92	1	4	1	1	107	sso erabedda	27.82	938.74	1012.45

93	1	10	3	1	80	sso erabedda	36.73	929.42	1005.33
94	5	5	2	1	40	spa kinigama	33.45	929.93	1004.83
95	3	5	1	1	120	sso erabedda	34.95	925.15	1000.2
96	2	2	3	2	100	sso erabedda	30.19	925.79	999.36
97	5	3	3	1	131	sso erabedda	36.81	920.76	996.09
98	4	9	1	2	40	spa kinigama	33.19	920.36	994.51
99	5	10	12	4	105	sso erabedda	32.91	917.06	990.9
100	5	3	1	1	102	sso erabedda	39.54	913.81	989.54

Table 7. Povenances and families represent in the best 100 *E. grandis* families in the seed source family trail established at Erabadda, Sri Lanka in 2007 by selection index

Seed Sorce	**No. of families**	**Total No. of trees**	**No. of families (%)**	**Total No. of trees (%)**
SSO Erabadda	17	87	81	87
SPA Kinigama	4	13	19	13
Total	**21**	**100**	**100**	**100**

Table 8. Families and trees of deferent seed sources represent in the best 100 *E. grandis* families in the seed source family trail established at Erabadda, Sri Lanka in 2007 by selection index

Seed Source	**Seed lot number**	**No. of trees selected**
SSO Erabadda	123	2
SSO Erabadda	70	15
SSO Erabadda	108	13
SSO Erabadda	120	6
SPA Kinigama	54	6
SSO Erabadda	80	10
SSO Erabadda	97	17
SPA Kinigama	40	5
SSO Erabadda	116	5
SSO Erabadda	131	3
SSO Erabadda	81	1
SSO Erabadda	109	3
SSO Erabadda	105	2
SSO Erabadda	130	4
SSO Erabadda	117	1
SPA Kinigama	43	1
SSO Erabadda	102	2
SSO Erabadda	92	1
SPA Kinigama	41	1
SSO Erabadda	107	1
SSO Erabadda	100	1
Total	**21**	**100**

Selection of the best 100 families based on the DBH and volume combine index at 9 years age provided a reasonably diverse group with respect to provenance and family representation (Table

6).Among seven seed sources SSO Erabadda is representing 81% of families and also 87% of trees among best 100 families. Rest is representing by the SPA Kinigama seed source (Table 7).

The top three seed lots/ families of SSO Erabadda seed source is contributing a total of 45% of trees in the selected 100 trees, remaining 55% of trees were comprised of trees from other 18 families. Among them 15 families are representing five or less trees (Table 6). There were 6 families, which provide more than five trees to the selected group (Table 6). Furthermore, these two provenances provide all the best trees for the selected group. Other five provenances were not representing at all in the selected group

Correlation

Across all families phenotypic correlation between individual trees DBH at different ages were positive and high (favorable correlation) ranging from 0.66 for between DBH in 2016 and DBH in 2010 to 0.96 for between DBH in 2013 and DBH in 2012 (Table 8). The correlation between tree volume at year 9 age with DBH at deferent ages was positive and high (favorable) ranging from 0.69 for between volume in 2016 and DBH in 2010 to 0.92 for between volume in 2016 and DBH in 2016 (Table 8).
Volume of the trees at 9 years age was positive and high (favorable) with height at different ages. It was ranging from 0.67 for between volume in 2016 and height in 2010 to 0.91 for between volume in 2016 and height in 2016 (Table 9). Although correlation between individual trees height at deferent ages were positive and high (favorable) ranging from 0.67 for between height in 2016 and height in 2010 to 0.98 for between height in 2013 and height in 2012 (Table 9).

Table 9. Genetic correlation between DBH and HT with volume in 2016 of second-generation E. grandis seed source family trail established at Erabadda, Sri Lanka in 2007

	Trait														
	DBH 10	**DBH 11**	**DBH 12**	**DBH 13**	**DBH 14**	**DBH 15**	**DBH 16**	**HT 10**	**HT 11**	**HT 12**	**HT 13**	**HT 14**	**HT 15**	**HT 16**	**Vol. 16**
DBH 10	1.000	0.908	0.893	0.852	0.790	0.724	0.657	0.917	0.821	0.809	0.809	0.804	0.779	0.624	0.694
DBH 11		1.00	0.959	0.935	0.885	0.817	0.738	0.878	0.888	0.879	0.878	0.877	0.857	0.741	0.791
DBH 12			1.000	0.963	0.917	0.853	0.778	0.867	0.866	0.866	0.884	0.884	0.871	0.765	0.822
DBH 13				1.000	0.947	0.893	0.826	0.816	0.848	0.853	0.853	0.856	0.854	0.772	0.850
DBH 14					1.000	0.948	0.913	0.736	0.776	0.782	0.786	0.794	0.797	0.794	0.905
DBH 15						1.000	0.931	0.668	0.701	0.708	0.714	0.722	0.734	0.768	0.901
DBH 16							1.000	0.590	0.602	0.604	0.612	0.622	0.648	0.728	0.924
HT 10								1.000	0.86	0.85	0.84	0.84	0.82	0.65	0.667
HT 11									1.000	0.94	0.93	0.92	0.88	0.72	0.699
HT 12										1.000	0.99	0.97	0.92	0.74	0.706
HT 13											1.000	0.97	0.92	0.74	0.71
HT 14												1.000	0.95	0.75	0.721
HT 15													1.000	0.74	0.729
HT 16														1.000	0.905

Discussion

In the second-generation *E. grandis* trail reported here, the best seed sources and families within seed sources for growth represented genetically improved material. The top ranked seed source (by 9 year individual tree volume) was first generation seedling seed orchard, developed from natural stand provenance- family seed lots imported from Australia in the mid- 1990s. the seed sources ranked second and third by 9 year individual tree volume were both formal, manage seed production areas, also developed in the early- mid 1990s; they were established back then to enable rapid development of capacity for production of somewhat improved seeds. The current results validate the effectiveness of approach followed in Sri Lanka for *E. grandis*. The average 9 year volume of trees originating from the seed production areas was over 21.67% greater than that of trees originating from plantation selected plus trees., with trees originating from the first generation seed orchard having about 3% greater volume than those from the seed production areas (Table 3). Despite the superior performance of the improved sources, the first generation Erabadda seed orchard material was notable for the high variability within it. Also, whilst most of the best families originated from this seed orchard source, other families from the same source showed very poor performance. Such results could be used to rogue inferior mother trees from the 1st generation seed orchard, enabling additional genetic gain to realize from that existing seed orchard in the very near future. Whilst the potential of the local *E. grandis* land race could not be discerned by results from the preceding first-generation trail, as reported by Bandara *et.al.,* (2000), this second-generation trail has provided a rigorous elevation of such material. It generally proved markedly inferior (see Table 3), confirming some results from a species- provenance trail established back in 1986 in which volume growth of local land race seed lot of *E. grandis* at age six years was significantly below that of four natural strand *E. grandis* seed lots (Philips and Weerawardane., 1991).Although, a none of the family originating from the local land race material (plantation selected plus- trees) performed well, all were ranked within the last 32 families for volume growth at age 9 years. This one again concurs with conclusions drawn by Matheson and Mullin,1987 and also by Burgess, 1988 that it is inappropriate to judge the merit of *E. grandis* material for a breeding population based solely on its provenance or seed source.

For individual tree volumes, the heritability estimates obtained across all families in the second-generation trail reported here are comparable to those obtained in the first generation SSO, located nearby, at age 2.25 years for volume (0.11) (Bandara *et.al.,* 2000). However, for the subset of 72 first generation SSO families in the second-generation trail, heritabilities for individual tree volume were somewhat higher, ranking up to 0.1 at age 9 years. It was notable that the heritabilities for individual tree volumes, for both the complete set of families and the subset of 72 first generation SSO families, more than from age 5 year (immediately prior to thinning) to age 7 years(about two year after selective within plot thinning). Such selective trails are known to decrease phenotypic variance whilst increasing estimates of genetic variance (Matheson and Raymond, 1984), and thus the thinning is likely a key factor contributing to the somewhat larger heritabilities observed at later age. Even so, the heritabilities in this second-generation Sri Lankan trail generally are within the range of heritabilities reported from work elsewhere on *E. grandis* (see Eldridge *et. al.,* 1993; Leo *et. al.,* 2010), and their magnitude indicates that selection among the second- generation trees in the trail reported, should provide reasonable genetic gains for individual tree volume in the next generation.

The phenotypic and genetic correlations between age 9 and earlier years for volume were all positive (favorable correlations), strong and significant (Table 9). Though these correlations were lowest between age 2 and 8 years, the genetic correlation between these trails for the subset of 72 first generation SSO families in the second- generation trail was still very high at 0.6 , and this suggest good potential for selection on tree volume at age 2 years to provide genetic gains in later stage tree volume. This result concurs with finding from a series of *E. grandis* trails in southern China that a selection age of about 2 to 3 years (for tree volume) would generally provide the optimal selection efficiency for improving later stage tree volume (Leo *et. al.* 2010)

The second- generation *E. grandis* trail reported here has the potential to rapidly provide significant genetic gains for Sri Lankan plantation growers. Re-selection of the superior trees in the Erabadda first generation SSO, based on the results obtained in the second- generation trail, with subsequent additional thinning to remove poorer- performing individual parent trees would serve to increase average genetic quality of bulk seed it produces. But perhaps the best option for rapidly exploiting the potential genetic gains offered by the second generation itself, would be to conduct further selective, intensive thinning of the second-generation trail, with selection both within families and between families, to convert the trail into a second generation SSO. With this latter option, improved seed crops should be available within two years after thinning. An additional option would be selection of the best individual trees from the top 15 or so families in second generation trail for grafting into a clonal seed orchard. Though the latter option could offer a substantial increase in potential gain (see Shelbourne, 1992) it would require considerable additional investment and time delays (perhaps 5 to 6 years) from grafting to abundant seed production.

Each of the options for development of seed capacity production capacity to exploit the genetic gain from the seed generation *E. grandis* trail has its own advantages and limitations. Whether they be genetic gain, time and/or cost. Impotently through, the options are not mutually exclusive and could be pursued simultaneously.

However, significant variation was observed for individual tree volume growth between and within the seed sources included in the second-generation Sri Lankan *E. grandis* trail. Of all the seed sources, the first generation SSO proved significantly superior to unimproved sources for volume growth. Whilst financial benefits from this research could be realized immediately by using the results to guide the choice of seed lots for plantation establishment, greater would be achieved by developing the seed production capacity of second generation trail reported here, through one or more of the seed orchard development options. The markedly superior performances of the first generation seed orchard material over almost all plus- tree selections from local plantations in the trail reported in this study should provide confidence that investments made in Sri Lanka Forest Department's genetic improvement of *E. grandis* is delivering significant gains in volume growth to benefit of Sri Lankan *E. grandis* growers.

According to the present study, the first generation SSO proved significantly superior to unimproved sources for volume growth. The second best seed source was SPA Kinigama, however, the variation of tree volume in this seed source was low compared with SSO Erabadda seed source. Therefore, it suggests the selection of best seeds and selection for breeding from above mentioned first generation SSO and SPA Kinigama seed sources in Sri Lanka.

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