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RESEARCH ARTICLE

Genetic parameters and correlations of yield attributing characteristics of weedy rice in Sri Lanka

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Abstract: Weedy rice possesses a high diversity in yield attributing characteristics and is an important resource for rice improvement programmes. The present investigation was carried out to estimate the genetic parameters and the correlations of yield attributing characteristics of weedy rice using 370 weedy rice accessions in Sri Lanka. Analysis of variance revealed significant differences ($p < 0.05$) among the weedy rice accessions for all the characteristics studied, implying the presence of a substantial amount of genetic variability and scope for selection. Shattering percentage, total number of spikelets per plant and the number of filled seeds per panicle exhibited high genotypic and phenotypic coefficients of variation. The degree of difference between phenotypic and genotypic coefficients of variation was relatively low for all the characteristics, except for the total number of spikelets per panicle, indicating comparatively less environmental influence. Very high heritability values coupled with very high genetic advance were observed for the shattering percentage, total number of spikelets per plant and the number of filled seeds per panicle. High heritability values coupled with high genetic advance were recorded for height at the booting stage, number of panicles per plant and tiller number at the seedling and booting stages suggesting the prevalence of additive gene action in the expression of these characteristics and the possible selection for effective improvement based on their phenotypic performance. Correlation studies showed that simply selecting comparatively taller plants with long seeds would identify high yielding weedy rice plants, which may be used in rice improvement programmes.

Keywords: Genotypic variance, heritability, *Oryza sativa* L., phenotypic variance, rice improvement programmes, weedy rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the major staple food crops in the world and is particularly important in Asia where approximately 90 % of world's rice is produced and consumed (Khush, 2004; Zeigler & Barclay, 2008). Improving the productivity of rice has become of immense importance to feed nearly half of the world's population. Rice genetic resource is the primary material for rice improvement. Utilizing this genetic resource in rice genetic improvement programmes for increasing the yield, incorporating resistance to biotic and abiotic stresses and improving grain quality is important. Cultivated rice has undergone intensive selection during its domestication and genetic improvement. Moreover, modern rice improvement programmes continuously select desirable characteristics under highly controlled conditions to achieve an ideotype, which exacerbates the reduction in the gene pool of cultivars (McCouch, 2004). Consequently, the genomic regions controlling the traits of economic importance are expected to be identified by this selection. The resulting narrow genetic base would lead to cultivars lacking resistance to new pests and diseases and tolerance to unfavourable environmental conditions. To breed new varieties in order to face the effects of global climate change and other challenges, the gene pool of rice cultivars must be broadened by introducing genes from wild or weedy species, landraces and exotic germplasm into breeding lines.

Weedy rice (*Oryza sativa* L. *f. spontanea*), botanically classified as the same species as cultivated rice of the family Poaceae is a weed accompanying cultivated rice and is widely distributed in rice growing areas all over the world (Ferrero *et al*., 1999; Mortimer *et al*., 2000). In regions of rice cultivation such as Asia and Latin America where native *Oryza* species occur, weedy rice may have arisen through a continual process of gene flow between

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the cultivated crop and neighbouring wild populations (Olsen *et al*., 2007). In the past, gene flow has apparently moved predominantly from the in-breeding cultivars to the out-breeding weeds as these weeds are more receptive to pollens from outside. Therefore, weedy rice may be a useful source of genes for improving cultivars in the future (Vaughan & Morishima, 2003).

Weedy rice appears to possess a wide variation in the characteristics. It generally grows faster with better use of the available N; produces comparatively more tillers, panicles and biomass in general; shatters early; has comparatively better resistance to adverse dry conditions; and possesses long dormancy in soil (Cohn, 2002; Gu *et al.,* 2003). As weedy rice is considered a natural hybrid between cultivated rice and wild rice, it may be used as a bridge to transfer genes to cultivated rice from its secondary gene pool. The genetic diversity of weedy rice can be a driving force in domestication and represents a potential source for cultivated rice improvement (Chen *et al*., 2001).

Development of high yielding varieties through genetic improvement requires knowledge on the nature and the magnitude of genetic variation governing the inheritance of quantitative characteristics, particularly yield and yield attributing characteristics. The understanding of genetic variability present in a given crop species for the traits under improvement is imperative for the success of any plant breeding programme (Sankar *et al*., 2006).The parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic. Heritability (h^2) of a characteristic is important in determining its response to selection. Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding programme (Akinwale *et al*., 2011). Heritability coupled with high genetic advance (GA) would be more useful in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits (Singh *et al*., 2011). The determination of correlation coefficients between various characteristics helps to obtain the best combinations of attributes in crops for achieving comparatively higher return per unit area. In addition, it is important to know how the improvement or the change of one characteristic causes simultaneous changes in other characteristics. However, literature on these aspects of weedy rice to examine its potential use in rice improvement programmes is lacking. Thus the present investigation was undertaken to study the genetic parameters such as GCV, PCV, h^2 and GA with respect to yield attributing characteristics and correlations among them in weedy rice populations of Sri Lanka.

METHODS AND MATERIALS

Plant materials

The experimental material used in the study consisted of 370 weedy rice accessions collected from 29 locations (Annex 1) with at least 10 different accessions from each location. All the accessions were confirmed to be weedy rice as each of them possessed typical weedy rice characteristics such as early shattering, seeds with long awns, high percentage of empty seeds and relatively faster plant growth with profuse tillering. The natural weedy rice population in Sri Lanka was well represented by these 370 accessions, although this does not mean that there are 370 different weedy rice varieties in the Sri Lankan weedy rice population. The characteristics of the 370 weedy rice accessions are already catalogued and the accessions are preserved at -20 ºC and maintained at the Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna for future verifications. Also, molecular characterization of the above accessions carried out at Fudan University, Shanghai, China confirmed that the accessions were genetically different (He *et al*., 2014) and thus, a set of seed samples has also been conserved at their germplasm conservation laboratory for future verifications. Although there may be duplications within the 370 accessions, identification of these duplications was not possible at this stage and the existing genetic diversity within the weedy rice population in Sri Lanka was considered to be adequately represented by the sample even with duplications.

Establishment and maintenance of the experiment

The mature seeds of weedy rice accessions were collected separately and hundred seeds from each accession were germinated in transparent dishes (bottom lined with moist filter papers). Seeds of the weedy rice samples were placed in an oven (~55 °C) for 5 - 7 days to break the seed dormancy, and presoaked in tap water for 24 hrs before they were sown in petri dishes. After 14 days, seedlings from each accession (treatment) were transplanted in the research field (longitude 6^0 3’ 21.07”, latitude 80^0 33’ 37.37”) at the Faculty of Agriculture, University of Ruhuna, Mapalana, Kamburupitiya in a randomized complete block design (RCBD) with three replications during the 2009/2010 Maha season. In each plot, 25 weedy rice seedlings (14 day old) from the same accession were planted in 5 rows with a spacing of 25 cm between rows and 20 cm within rows. To avoid the border effect, only the nine plants in the middle of the plot were characterized.

All the management practices including fertilizer application, pest and disease management etc., were performed according to the recommendations given for cultivated rice by the Department of Agriculture, Sri Lanka. Weeds occurring in the plots were hand-removed periodically.

Morphological characterization

The observations were taken on 13 quantitative characteristics *viz*., plant height at seedling and booting stages, number of tillers per plant at seedling and booting stages, number of panicles per plant, panicle length, shattering percentage, filled seeds per panicle, total number of seeds per panicle, total number of seeds per plant, seed length, seed width and 1000-seed weight (Table 1). The plants were chosen randomly from each plot excluding the border plants and the data were recorded on their corresponding growth stages following the guidelines of Descriptors for Rice, *Oryza sativa* L., published by the International Rice Research Institute (IRRI, 1980).

Table 1: Yield attributing characteristics studied and the methods of their measurement in weedy rice

Trait	Method of measurement
Plant height at seedling stage (cm)	Height from ground level to the tip of the leaf of the tallest tiller at three weeks after transplanting
Plant height at booting stage (cm)	Height from ground level to the tip of the leaf of the tallest tiller at twelve weeks after transplanting
Number of tillers per plant at seedling stage	Total number of tillers of each plant at three weeks after transplanting
Number of tillers per plant at booting stage	Total number of tillers of each plant at twelve weeks after transplanting
Number of panicles per plant	Counted the total number of panicles of each plant at maturity
Panicle length (cm)	Total length from base to the tip of all the panicles per plant/number of panicles per plant
Seed shattering %	(Number of seeds shattered by hand press per plant/ total number of seeds per plant) x 100
Total number of spikelets per panicle	Number of spikelets per all the panicles per plant/number of panicles per plant
Total number of spikelets per plant	Number of spikelets per all plants per plot/ number of plants per plot
Number of filled seeds per panicle	Number of filled seeds per plant/ total number of panicles per plant
Seed length (mm)	Length of 10 measured filled seeds/10
Seed width (mm)	Width of 10 measured filled seeds/10
1000-seed weight (g)	(Weight of filled seeds from 9 measured plants/ number of filled seeds of 9 plants) x1000

Weedy rice shows high shattering at the maturity stage. Therefore, to minimize the external effects on shattering by data collectors, the plant height was recorded along with tillering at the seedling and booting stages, which are considered as standard stages for recording tillering and plant height. No ample variation was observed for the days to maturity among accessions at the time they were collected, and all the accessions had matured around 108 days. Thus, in the experimental plots, accessions took only 12 wks (84 days) on average from planting in the nursery to booting.

Data analysis

Analysis of variance was done for all the traits according to the model proposed by Panse and Sukhatme (1967). This is a fixed effect model and weedy rice accessions (treatments) were considered fixed as they are reproducible. Genotypic and environmental variances were estimated using the formulae for expected variances in the model and the phenotypic variance was estimated as the sum of genotypic and environmental variances. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formulae given by Burton (1952), and heritability in broad sense [h^2 (bs)] was calculated by the formula given by Lush (1949) as suggested by Johnson *et al.* (1955) according to the following equations;

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 \mathrm{p}}}{\bar{\mathrm{X}}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 \mathrm{g}}}{\bar{\mathrm{X}}} \times 100$$

$$\text{Broad sense heritability } [h^2(\mathrm{bs})] = \frac{\sigma^2 \mathrm{g}}{\sigma^2 \mathrm{p}} \times 100$$

where,

$\bar{X}$ = Mean of the characteristic
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

From the heritability estimates, the genetic advance (GA) was estimated by the formula given by Johnson *et al.* (1955) as follows;

$$\text{Genetic advance (\% of mean)} = \frac{K\sigma ph^2}{\bar{X}} \times 100$$

where,

$K\sigma ph^2$ = Phenotypic standard deviation
K = Selection differential *i.e.* 2.06 at 5 % selection intensity (Allard, 1960). (Assumed top 5 % selected for all the traits except shattering for which bottom 5 % was selected)
h^2 = Heritability (broad sense)
$\bar{X}$ = Mean of the characteristic

Estimated heritability (broad sense) was classified as low (< 30 %), medium (30 – 60 %) and high (> 60 %) and the range of genetic advance as a percentage of mean was classified as low (< 10 %), moderate (10 – 20 %) and high (> 20 %) as suggested by Johnson *et al*. (1955).

The phenotypic correlation coefficients were computed among all the measured traits using SPSS for Windows Version 17.

RESULTS

Plants derived from the same accession (accessions bred true to type) were sufficiently uniform and no variations were observed among the plants within the accessions for the observed morphological characteristics. However, a high variability between the accessions (treatments) and a sufficient uniformity within the accessions in all the morphological characteristics studied was observed indicating that the accessions are genetically different.

The accessions were morphologically different to each other and could be differentiated visually by a number of morphological traits. For example, the plant height at the booting stage ranged from 54.6 – 127.4 cm and the number of panicles per plant varied from 5 – 21 showing a clear difference among the accessions. Ratnasekera *et al*. (2014) reported significantly high levels of morphological variations among these accessions.

Analysis of variance

The results of the analysis of variance revealed that the accessions displayed significant differences ($p < 0.05$) in their mean performance with respect to all the characteristics studied (Table 2). PCV was higher than GCV for all the characteristics, while the highest PCV and GCV values were recorded for shattering percentage per panicle, and the lowest values were recorded for seed length and seed width, respectively (Table 2).

Table 2: Analysis of variance for different yield attributing characteristics of weedy rice

Characteristic	Mean sum of squares		CV %
	Treatment	Error	
Height at the seedling stage (cm)	156.647*	26.693	15.543
Height at the booting stage (cm)	599.059*	50.960	16.933
Tiller number at the seedling stage	7.164*	1.215	35.063
Tiller number at the booting stage	28.008*	3.710	27.835
Number of panicles	12.454*	2.245	23.337
Panicle length (cm)	8.137*	2.729	9.761
Shattering percentage per panicle	271.420*	22.982	65.886
Number of filled seeds per panicle	2018.860*	123.816	33.926
Total number of seeds per panicle	2953.940*	1611.499	42.112
Total number of seeds per plant	322875.300*	10276.200	40.095
Seed length (mm)	0.491*	0.119	6.093
Seed width (mm)	0.089*	0.073	9.717
1000-seed weight (g)	17.455*	3.303	11.063

* Significant at p = 0.05 level

Heritability

The characteristics studied in the present investigation expressed low to high broad sense heritability estimates ranging from 7 – 91 % (Table 3). Among the characteristics, the highest heritability was recorded for the total number of seeds per plant followed by the number of filled seeds per panicle, shattering percentage per panicle and plant height at the booting stage. Moderate heritability values were recorded for the panicle length, seed length and 1000-seed weight, while low heritability values were recorded in the total number of seeds per panicle and seed width.

Genetic advance

Genetic advance as a percent of mean was the highest for shattering percentage per panicle followed by the total number of seeds per plant and the number of filled seeds per panicle, while the lowest was recorded for seed width (Table 3).

Correlations among characteristics

Correlation coefficients among nine characteristics of the 370 weedy rice accessions are presented in Table 4. The correlation matrix showed that 1000-seed weight was

Table 3: Genetic parameters of yield attributing characteristics of weedy rice

Characteristic	Mean	Coefficient of variation (%)			Heritability (broad sense) (%)	GA %
		Genotypic	Phenotypic	D[1]		
Height at the seedling stage (cm)	33.24	11.617	14.768	3.151	62	19
Height at the booting stage (cm)	42.16	14.800	16.737	1.937	78	27
Tiller number at seedling stage	3.14	26.969	34.247	7.278	62	44
Tiller number at booting stage	6.92	22.805	27.537	4.732	69	39
Number of panicles per plant	6.42	18.001	23.191	5.190	60	29
Panicle length (cm)	16.92	6.084	9.647	3.563	40	8
Shattering percentage per panicle	7.28	58.340	65.941	7.601	78	106
Total number of spikelets per plant	252.83	38.257	40.099	1.824	91	75
Total number of spikelets per panicle	95.32	19.604	42.052	22.448	22	19
Number of filled seeds per panicle	32.79	30.982	33.882	2.900	84	58
Seed length (mm)	5.66	4.357	6.095	1.743	51	6
Seed width (mm)	2.79	2.521	9.600	7.079	7	1
1000-seed weight (g)	16.42	8.410	10.966	2.556	59	13

[1] Difference between phenotypic and genotypic coefficients of variation

Table 4: Correlation coefficients among yield attributing characteristics of weedy rice

Characteristic[1]	HT-S	HT-B	TIL-S	TIL-B	PNNO	FSD/PN	TSD/PL	SDL	SDWT
HT-S	1								
HT-B	0.767*	1							
TIL-S	- 0.144	- 0.169	1						
TIL-B	- 0.256	- 0.265	0.652*	1					
PNNO	- 0.143	- 0.134	0.366*	0.615*	1				
FSD/PN	0.462*	0.516*	- 0.098	- 0.183	- 0.014	1			
TSD/PL	0.292	0.361*	0.037	0.116	0.438*	0.69*	1		
SDL	0.208	0.248	0.155	0.007	- 0.004	0.115	0.01	1	
SDWT	0.547*	0.583*	0.007	- 0.174	- 0.062	0.338*	0.202	0.647*	1

* Significant at p = 0.05 level

[1] HT-S: Height at the seedling stage; HT-B: Height at the booting stage; TIL-S: Number of tillers at the seedling stage; TIL-B: Number of tillers at the booting stage; PNNO: Number of panicles/plant; FSD/PN: Number of filled seeds per panicle; TSD/PL: Total number of seeds per plant; SDL: Seed Length; SDWT: 1000-Seed weight

positively and significantly ($p < 0.005$) associated with the seed length, height at the seedling and booting stages and the number of filled seeds per panicle. The number of panicles was positively and significantly associated with the number of tillers at the seedling and booting stages. The total number of seeds per plant showed a positive and significant correlation with the height at the booting stage, number of panicles and the number of filled seeds per panicle.

DISCUSSION AND CONCLUSION

Highly significant ($p < 0.05$) mean sums of squares of accessions for all the characteristics indicated that a sufficient amount of variability exists among the accessions for all the traits studied. This allowed the estimation of necessary genetic parameters.

PCV and GCV for all the studied characteristics revealed that there is ample scope for the selection of desirable characteristics from the weedy rice for rice improvement. Selection within the characteristics with high PCV and GCV will be more effective than within those with low PCV and GCV. The shattering percentage gave extremely high PCV and GCV values showing ample scope to select low shattering lines, while the number of spikelets/plant, number of filled grains/panicle and the tiller number at seedling and booting stages had fairly high PCV and GCV values showing promise for selection within these characteristics. However, selection within the rest of the characteristics, particularly within seed characteristics may not be effective as they recorded low PCV and GCV values.

The extent of the environmental influence on any characteristic is indicated by the magnitude of the difference between the PCV and GCV, and hence a small difference between the PCV and GCV indicated the presence of high genetic variability among the accessions and the less influence of environment for the characteristics studied. Under such situations, selection on the basis of phenotype alone can be effective for these traits. The total number of spikelets should never be selected on the basis of phenotype alone as it recorded the highest difference of 22 % between the PCV and GCV. However, the total number of spikelets/plant, seed length and height at booting stage recorded the lowest difference between PCV and GCV (< 1 %) so that the selection for those characteristics may be performed on the basis of phenotype alone. Similar results were observed by Shivani and Reddy (2000) for a number of filled seeds per panicle in rice.

Heritability estimates give an idea of the total variation ascribable to genotypic effects, which is the exploitable portion of variation. All the characteristics except the total number of spikelets/panicle, panicle length and seed characteristics recorded high heritability values showing that those characteristics are less influenced by the environment in their expression and therefore, effective selection within them is desirable. Thus the selection can safely be performed on the basis of phenotypic expression of those characteristics in the individual plant by adopting simple selection methods. High heritability values were reported by Bhatti *et al.* (1998) for the number of spikelets/panicle in rice, in contrary to the present study. Sarawgi *et al.* (2000) has reported high heritability estimates for grain weight in rice. The low broad sense heritability observed for the total number of seeds per panicle and the seed width indicated a high influence of the environment on these traits so that direct selection within these traits will be ineffective.

Heritability value itself does not provide any indication of the degree of genetic progress that would result from selecting the best individuals. Ramanujam and Tirumalachar (1967) discussed the limitations of estimating heritability in broad sense as it includes both additive and non-additive gene effects, and concluded that particularly the heritability estimates in broad sense accompanied with genetic advance would be more reliable. As the weedy rice accessions used to estimate the genotypic variance was fixed and reproducible and the estimation of genotypic variance was not based on parent progeny relationships but based on the variance among accessions, the genetic effects expected in the present study would be a combination of both additive and non-additive.

Very high heritability values coupled with very high genetic advance as a percent of mean were observed for the shattering percentage, total number of spikelets per plant and the number of filled seeds per panicle. In addition, high heritability values along with high genetic advance were recorded for the height at the booting stage, number of panicles per plant and tiller number at seedling and booting stages, suggesting preponderance of additive gene action in the expression of these characteristics. Similar observations have been made by Kundu *et al*. (2008) for the number of grains per panicle and Sankar *et al*. (2006) for plant height, total number of productive tillers per plant, number of grains per panicle and grain yield per plant in rice. However, low genetic advance values were reported for the same characteristics by Babu *et al*. (2011) and Prajapati *et al*. (2011) in rice. In general, the characteristics that show high heritability with high genetic advance are controlled by additive gene action (Panse & Sukhatme, 1967) and such characteristics can be improved through simple or progeny selection methods (Babu *et al*., 2011). The selection for characteristics having high heritability coupled with high genetic advance is expected to accumulate more additive genes leading to further improvement. High heritability coupled with genetic advance was reported by Sarawgi *et al*. (2000) for normalized grain weight and for 100-milled grain weight by Vange (2009) for the days to 50 % flowering and seed yield and by Praveen and Anurag (2010) for the number of spikelets per panicle in rice. Height at the seedling stage exhibited high heritability coupled with moderate genetic advance, suggesting predominance of non-additive gene action in the inheritance of these characteristics showing some promise for improvement through selection.

The degree of association as measured by correlation coefficients among the traits is an important factor, particularly for economic and complex characteristics such as yield and yield attributing characteristics. Steel and Torrie (1984) have stated that correlations are measures of the intensity of association between the characteristics so that the correlation shows how the improvement in one characteristic will cause simultaneous changes in other characteristics. In the present study, it was found that selection for taller plants at booting stage would also increase the number of filled seeds/panicle, total number of seeds/plant and 1000-seed weight in weedy rice. Such correlations are very useful for yield improvement simply by selecting taller plants at booting stage. In addition, filled seeds/panicle is positively correlated with the total number of seeds/plant and 1000-seed weight, which is positively correlated with seed length. Akinwale *et al*. (2011) reported that the number of grains per panicle had a significant positive correlation with grain yield in rice. Thus, simply selecting taller plants at booting stage with long seeds would identify high yielding weedy rice plants that can be utilized in rice improvement programmes.

Results of the present study highlighted that adequate genetic variability exists in the weedy rice population studied as revealed by the significant substantial variations observed among the accessions for all the characteristics. In general, shattering is considered as an unfavourable trait of weedy rice, which plant breeders wish to eliminate in crop improvement. Hence, selection focused mainly on the total number of seeds per plant and the number of filled seeds per panicle with no shattering would be important as such selected weedy rice plants have a potential use in rice breeding programmes.

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Annex 1: Longitude and latitude of weedy rice collected location, district and the number of samples evaluated

District	Location	No. of samples	Longitude			Latitude		
Ampara	Pothuvil	12	6^0	5’	9.45”	81^0	49’	27.53”
	Thottama	11	7^0	8’	36.1”	81^0	42’	40.8”
	Akkaraipattu	13	7^0	12’	34.8”	81^0	47’	11.5”
	Lahugala	12	6^0	52’	8.3”	81^0	43’	1.8”
Anuradhapura	Saliyapura	14	8^0	23’	48.7”	80^0	26’	39.8”
	Thalawa	15	8^0	12’	10.7”	80^0	20’	17.4”
	Thambuththegama	12	8^0	7’	51.89”	80^0	17’	34.27”
	Nuwarawewa	11	8^0	21’	32.19”	80^0	25’	52.91”
	Mahailluppallama	15	8^0	6’	49.55”	80^0	28’	55.24”
	Medawachchiya	14	8^0	33’	27.5”	80^0	28’	55.9”
	Eppawala	14	8^0	8’	49.57”	80^0	22’	46.24”
	Kekirawa	13	8^0	2’	5.66”	80^0	36’	29.7”
Polonnaruwa	Hingurakgoda	12	8^0	2’	13.3”	80^0	57’	3.4”
	Pulasthigama	15	8^0	1’	31.4”	81^0	4’	50.78”
	Sewagama	14	7^0	58’	39.3”	81^0	1’	52.4”
	Nawanagaraya	11	7^0	54’	43.4”	81^0	0’	44.5”
Puttlam	Thabbowa	12	8^0	3’	49.3”	79^0	55’	25.5”
	Nattabbowa	14	7^0	22’	51.5”	79^0	54’	54”
	Puttalam	12	8^0	2’	34.8”	79^0	54’	55.1”
Matara	Kotapola	11	6^0	15’	42”	80^0	36’	16.8”
	Pitabaddara	15	6^0	8’	27.6”	80^0	28’	47.4”
	Akurugoda	14	6^0	2’	39.3”	80^0	33’	48.3”
	Akuressa	13	6^0	8’	27.9”	80^0	28’	47.7”
	Mulatiyana	12	6^0	9’	21”	80^0	34’	30.5”
	Pasgoda	12	6^0	14’	36.82”	80^0	36’	35.91”
Kurunegala	Kurunegala	10	7^0	28’	30.5”	80^0	22’	14”
	Kuliyapitiya	12	7^0	27’	42.9”	80^0	4’	48.4”
	Mawathagama	14	7^0	26’	43.1”	80^0	25’	47.5”
	Yakwila	11	7^0	23’	59.7”	80^0	2’	52”