



Fertilizer Response of Traditional Rice Cultivars at Four Different Levels as Analyzed by Multi-Criteria Decision Making Model

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Authors' contributions

This work was carried out in collaboration between all authors. Author ALR designed the study, wrote the protocol, and wrote the first draft of the manuscript. Author UGSA collected and tabulated the data managed the literature searches. Authors ALR and UGSA together analyzed the data. Author SGJNS supervised the study. All authors read and approved the final manuscript.

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ABSTRACT

Aims: to understand the effect of various polygenic traits on grain yield of traditional rice cultivars at four different fertilizer levels namely no fertilizer, x ½ recommended dose (x ½ RD), recommended dose (RD) and x2 recommended dose (x 2 RD).

Study Design: Randomized complete block design with four replicates.

Place and Duration of Study: Faculty of Agriculture, University of Ruhuna, Mapalana, Sri Lanka from 2011 to 2013.

Methodology: Germinated seeds were planted in rows with 15 cm X 20 cm spacing. Experiment was conducted with four replications according to the randomized complete block design and each replicate consisted of three lines. Twenty plants were included in to each line. Data were collected on plant height (cm), number of tillers/plant, number of fertile tillers/plant, panicle length (cm), panicle weight (g), number of spikelets/panicle, number of fertile spikelets/panicle, 100 grain weight (g) and yield/plant (g). Path analysis was conducted to measure the degree of association between variables (traits). Multi-criteria decision-making model was used to rank the studied traditional rice genotypes according to the measured various yield attributing traits and the degree of association of each trait on yield as described by path analysis. Total effects of Path analysis were used

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as criteria weights to quantify the variables (traits). Data matrix was multiplied by the criteria weight to obtain the relative distances and cumulative values of relative distances were used to calculate the ideal distances (Lp). Genotypes were ranked according to the ideal distances (Lp) to understand the effect of fertilizer on yield and yield attributing factors of traditional rice genotypes at each fertilizer level. This procedure was applied separately to all of the four fertilizer levels.

Results: The effects of various yield attributing traits on grain yield/plant were varied with four different levels of fertilizer. The effect of plant height on yield/plant was decreased linearly with the increased fertilizer. The highest effect was recorded by the panicle weight (0.872) at X 2 RD. Plant height (0.215), number of fertile tillers/plant (0.864), panicle length (0.082), and number of fertile spikelets/panicle (0.870) recorded the highest effect on yield/plant at no fertilizer condition.

Conclusion: It emphasized the less fertilizer response of traditional rice genotypes. Excess application of fertilizer badly decreased the effect of yield attributing factors on final yield. Multi-criteria decision making model can be utilized to rank traditional rice genotypes according to their performances at different fertilizer levels.

Keywords: Fertilizer response; path coefficients; traditional rice genotypes; Sri Lanka.

1. INTRODUCTION

Grain yield is a complex polygenic character controlled by many gene interactions with the environment. These polygenic characters are defined as yield components. The selection of parents based on yield alone is often misleading [1]. Knowledge regarding the relative contribution of individual trait to determine the yield may be accomplished by correlation studies [2]. Simple correlation does not provide adequate information about contribution of each factor on the yield [3]. The study of direct and indirect effects of yield components on the yield provides the basis for a successful breeding program [4,5]. Increase of the yield can be more effectively tackled if the effect of yield components on the final yield is known [4]. Determination of closely associated traits on the yield can be done by path analysis. Path co-efficient permits the separation of the correlation co-efficient into components of direct and indirect effect [6,7]. Selection of genotype based on the path coefficient needs a Multi-criteria decision making model [8]. Multi-criteria decision making model (MCDM) is defined as “selection problems” or “mathematical programming problems” and is used to identify the “best” alternative in a set of alternatives. The typical multiple criteria evaluation problem focuses on a set of feasible alternatives and considers more than one criterion to determine a priority ranking for alternative implementation [9]. Compromise programming was used to choose the optimum genotypes from a set of efficient ones as proposed by Zeleny [9]. Compromise programming was initially proposed by Zeleny [10] and subsequently used by many researchers to determine the optimal solution as the one that has the shortest distance to an ideal point where the multiple objectives simultaneously reach their minimal values [11,12]. The ideal point is not practically achievable but may be used as a base point. The algorithm for multi-objective optimization includes a stochastic generating process and a choosing process. The former specify scores of each alternative obtained for each evaluating criterion, estimate maximum and minimum points for each criterion, searches weight vectors in the whole weighting space, and in the latter analytic hierarchy process evaluation model chooses the best solution and rank alternatives on basis of minimum relative distance to the ideal point (The compromise solution). The total value of

the alternative can be calculated based on the weighted sum method given in the following equation [10]:

$$V_{(A)} = \sum_i w_i \cdot v_{i(ai)}$$

Where, w_i is the weight of the criterion i , $v_{i(ai)}$ is the score of the alternative with respect to criterion i and $V_{(A)}$ is the value of the alternative A .

To solve the multi-criterion problem using compromise programming algorithm the values of vectors of ideal points, max and worst values, status of the objective functions, is determined for the variable weights (agronomist preferences). Consequently, this enables determination of ideal distance (L_p) for each genotype. As the scores have different unit, standardization is necessary to convert all scores in the same unit. The difference between the individual and the minimum score is divided by the difference between the maximum and the minimum score. The best strategy has a standardized score of 1 and the worst strategy has a standardized score of 0. Mathematically, the method is expressed for alternative k with respect to criterion j below:

For the case of minimization:

$$STD_{kj} = | (ACT_{kj} - WORST_{kj}) | / | (BEST_{kj} - WORST_{kj}) |$$

For the case of maximization:

$$STD_{kj} = | (BEST_{kj} - ACT_{kj}) | / | (BEST_{kj} - WORST_{kj}) |$$

where, STD_{kj} is the standardized score, ACT_{kj} is the actual score, $WORST_{kj}$ is the worst (minimum) score and $BEST_{kj}$ is the best (maximum) score [10].

In the present study yield and yield attributing characters of hundred traditional rice genotypes were evaluated for their fertilizer response by the multi-criterion decision making model using path coefficients, compromise programming and sensitive analysis.

2. MATERIALS AND METHODS

Hundred traditional rice genotypes obtained from Plant Genetic Resources Center (PGRC) were germinated and planted in nursery beds. Ten day old seedlings were transplanted in the experimental field at the Faculty of Agriculture, Mapalana, Kamburupitiya, Sri Lanka in rows with 15 cm X 20 cm spacing according to the randomized complete block design with four replications and each plot was consisted of 3 lines. Twenty plants were included in to each line. The soil type of the field was low-humic-glay soil with low base saturation. Four different fertilizer levels were applied in to the field which was separated by bunds. Fertilizer levels were: no fertilizer, half of the recommended dose, recommended dose and twice the recommended dose. The recommended fertilizer dose was basal dressing (Urea 50 kg/ha, TSP 62.5kg/ha, MOP 50kg/ha) before planting and top dressings (Urea 37.5Kg/ha) two times at 2 weeks after planting and at 8 weeks after planting.

Weed management and pest management were done to minimize the environmental effect on the final grain yield. Field was properly covered by a birds' nest to minimize the bird attack on the yield.

Data were collected on plant height (cm), number of tillers/plant, number of fertile tillers/plant, panicle length (cm), panicle weight (g), number of spikelets/panicle, number of fertile spikelets/panicle, 100 grain weight (g) and yield/plant (g). Total effect of yield attributing traits on grain yield was estimated by path analysis. Path analysis was done by IBM SPSS AMOS statistical software [13]. Total effects were used as the criterion weight of individual trait. Finally, a sensitivity analysis was carried out by changing weights of different criteria so that the role of each criterion on the selection of alternatives can be understood. First, data matrix was obtained by using standardized scores of each parameter. Data matrix was multiplied by the criterion weight to obtain the relative distances and cumulative values of relative distances were used to calculate the ideal distance (L_p). Genotypes were ranked according to the ideal distances (L_p) to understand the effect of fertilizer on yield and yield attributing factors of traditional rice genotypes at each fertilizer level. Above procedure was done for each genotype at four fertilizer levels separately to understand the changing pattern of effect of yield attributing factors on the final yield at different fertilizer levels.

3. RESULTS AND DISCUSSION

According to the path analysis, different parameters scored maximum effect on yield at different fertilizer levels. Out of nine considered parameters 4 parameters recorded the maximum effect on the yield at no fertilizer level. Only one parameter recorded the maximum effect on yield at no fertilizer level and two each parameters recorded the maximum effect at $\frac{1}{2}$ RD, RD levels. Effect of plant height (cm), number of fertile tillers/plant, panicle length (cm), and number of fertile spikelets/panicle recorded the highest effect on the grain yield at no fertilizer level and, number of spikelets/panicle and filled grain percentage were higher at the $\frac{1}{2}$ of the RD. The only parameter which recorded the highest effect on the final grain yield at XRD was panicle weight (Table 1).

The total effect of any parameter on yield/plant didn't show linear increase with the fertilizer. The effect of plant height on yield/plant was decreased linearly with the fertilizer (Table 1). Plant height was affected by many factors such as planting method, plant density and fertilizer application [14,15]. In traditional rice genotypes the highest effect of plant height on yield was recorded at no fertilizer level. This might be the reason that traditional rice genotypes are said to be less responsive for fertilizer [16].

Tiller number under field conditions changed according to the species, strength of plant, sunlight, nutrition, the duration in which the field stayed under water, the level of water and the plant density [17]. The highest effect of number of tillers/plant on the yield recorded at the RD level. However at the RD level only the number of tillers/plant and the 100 grain weight recorded the highest effect on the yield. Cheng et al. [18] reported positive direct effect of 1000-grain weight on grain yield. The highest total effect of the 100 grain weight on the yield was 0.514 at RD level while the minimum value was .101 at X2 RD level.

Positive direct effect of number of productive tillers and biological yield on grain yield have been reported in rice [19,20]. In the present study, number of fertile tillers/plant (0.864) and number of fertile spikelets/ panicle (0.870) recorded the highest effects on yield/plant at no fertilizer conditions. It emphasizes that the effects of fertile tillers/plant and spikelets/panicle on the yield will not be increased with the fertilizer. This has been concluded by Selvaraj et al. [1] where they reported that the genetic effect of fertile tillers/plant and spikelets/panicle were strong rather than the environmental effect.

The number of spikelets/panicle recorded the highest effect (0.643) on yield/plant at X ½ RD (Table 1). Grain number/panicle which partially determined by the number of spikelets/panicle was affected by the environmental and cultivation factors [21,17,22].

Table 1. Total effects of yield attributing traits on grain yield/plant of evaluated traditional rice genotypes at four levels of fertilizer is used as criteria weights of MCDM

Traits	Criteria weights			
	No fert	X1/2 RD	RD	X2 RD
Plant height (cm)	0.215	0.200	0.072	0.058
Number of tillers/plant	0.571	0.387	0.573	0.367
Number of fertile tillers/plant	0.864	0.188	0.297	0.338
Panicle length (cm)	0.082	0.074	0.030	0.058
Panicle weight (g)	0.305	0.090	0.136	0.872
Number of spikelets/panicle	0.370	0.643	0.513	0.168
Number of fertile spikelets/ panicle	0.870	0.595	0.819	0.114
Filled grain percentage	0.141	0.343	0.066	0.187
100 grain weight (g)	0.260	0.416	0.514	0.101
Yield (g/plant)	1.000	1.000	1.000	1.000

Number of fertile spikelets/ panicle (0.819) recorded the highest effect on yield/plant at RD, but its magnitude was not so high as at no fertilizer (0.870) condition. Number of grains/panicle had the highest positive direct effect (0.1486) on grain yield followed by 1000 grain weight [23]. Except at no fertilizer level, effect of fertile spikelet per panicle on grain yield was comparatively higher at any fertilizer level.

The highest effect on the yield was recorded by the panicle weight (0.872) at X 2RD but there was no linear relationship of the panicle weight with the fertilizer application. However panicle length has a minimum effect on the final grain yield at any fertilizer level hence panicle length will not be a good parameter for genotype selection.

Path coefficient analysis furnishes information of influence of each contributing trait to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution [24]. For the selection of the best compromise genotypes data were maximized and standardized. The total effect of the each parameter on the yield was considered as the criteria weight set for each trait. The use of phenotypic and/or genotypic direct effects (path coefficient) as economic weights (criterion weights), serve as an effective selection criterion in multivariate analysis. Standardized data set and criterion weights enable determination of ideal distance (Lp) for each genotype.

Crop yields world-wide have continuously increased, partly because of the increase in fertilizer nutrient input, especially N fertilizer [25]. To maximize grain yield, farmers often apply more N fertilizer than the minimum requirement for maximum crop growth [26]. According to the results of the present study majority of the yield determination factors of traditional rice genotypes have the highest effect on yield at no fertilizer level. There is no prominent effect of fertilizer on yield determination of traditional rice genotypes.

However considering various criteria (traits) traditional rice genotypes were ranked for the fitness of the farmer field. Here the genotype with minimum Lp distance was considered as the best genotype for cultivation. Cultivar Hondarawala was the best genotype (Rank 1)

among hundred traditional rice cultivars at no fertilizer and X 2 RD fertilizer levels. Cultivar Jamis wee II and Karayal III were the best genotypes at x ½ RD and 2 RD. Cultivar Bathkiri el recorded the second place among 100 traditional rice genotypes at no fertilizer and RD of fertilizer and it was fallen in to 5th place at x ½ RD and X 2 RD.

Cultivar *Gunarathna*, *Kokuvellai*, *Kotathavalu*, *Lumbini II*, *Madoluwa*, *Pokuru samba* and *Sudu Karayal* linearly increased their rank with the increase of fertilizer. Perversely cultivar *BG 35-7*, *Chinnapodiyen*, *Geeraga Samba*, *Maha Murunga Badulla*, *Miti Riyan*, *Sudu wee Rathnapura* and *Yakada wee II* decreased their ranking with the increased fertilizer (Table 2). The best rice genotypes performed well at each fertilizer level according to multi-criteria decision-making model gives the information on their fertilizer response on final grain yield (Table 3).

Table 2. Ranking traditional rice cultivars according to compromise distances (Lp) at four levels of fertilizer

Genotype	No fert.		X1/2 RD		RD		X2 RD	
	Lp	Rank	Lp	Rank	Lp	Rank	Lp	Rank
<i>A 6-10-37</i>	2.358	22	1.632	14	1.905	16	2.509	89
<i>Akuramboda</i>	2.487	27	2.373	59	1.774	13	1.607	24
<i>Bala Ma wee I</i>	2.500	29	2.334	57	2.156	25	1.508	17
<i>Bala Ma wee II</i>	2.166	16	1.958	31	2.188	28	2.052	63
<i>Balakara</i>	3.510	86	3.120	97	2.869	84	2.488	86
<i>Bathkiri el</i>	0.685	2	1.341	5	0.803	2	1.103	5
<i>BG 34-8</i>	2.939	54	2.407	61	2.431	53	2.230	75
<i>BG 35-2</i>	2.724	39	2.116	43	2.788	77	2.121	70
<i>BG 35-7</i>	2.479	26	2.086	41	2.490	59	2.069	65
<i>Buruma Thavalu</i>	3.101	63	2.684	81	2.556	67	2.501	88
<i>Chinnapodiyen</i>	3.188	70	2.687	82	2.912	87	2.684	94
<i>Dandumara</i>	2.035	12	1.986	34	1.709	11	1.178	7
<i>Dena wee</i>	3.116	64	2.570	71	2.979	90	2.320	80
<i>Dewaredderi</i>	3.539	88	2.078	40	1.915	17	1.634	26
<i>Dik wee 328</i>	3.282	77	1.910	28	0.970	3	2.140	73
<i>Dingiri Menika</i>	2.976	56	1.944	30	2.209	30	2.313	78
<i>EAT Samba</i>	1.078	3	1.940	29	2.263	34	1.480	15
<i>Gangala</i>	1.528	6	1.832	22	2.394	50	1.793	40
<i>Geeraga Samba</i>	2.957	55	2.582	72	2.748	76	2.680	93
<i>Giress</i>	3.121	65	1.883	26	2.389	49	1.735	34
<i>Gunaratna</i>	2.981	58	2.752	84	2.605	70	1.984	52
<i>H 10</i>	2.808	47	1.977	33	2.648	71	1.877	42
<i>Halabewa</i>	3.715	93	2.681	79	2.838	82	2.082	66
<i>Handiran</i>	3.274	75	2.246	50	2.493	61	1.582	23
<i>Heendik wee</i>	2.794	46	2.684	80	1.681	10	1.886	44
<i>Heendikki</i>	1.961	10	2.395	60	2.528	65	2.045	62
<i>Heenpodi wee</i>	2.854	49	2.408	62	2.508	62	2.518	91
<i>Herath Banda</i>	3.523	87	0.963	2	3.083	92	2.402	84
<i>Hondarawala</i>	0.591	1	2.254	51	1.481	8	0.281	1
<i>Induru Karayal</i>	2.730	41	2.597	74	2.667	72	2.020	57
<i>Ingrisi wee</i>	3.197	71	2.637	76	2.492	60	1.558	20
<i>Jamis wee I</i>	2.239	17	1.827	21	1.926	18	2.089	68
<i>Jamis wee II</i>	1.563	7	0.517	1	1.193	4	1.211	8
<i>Kaharamana I</i>	3.169	68	2.060	36	2.524	64	2.020	58

Genotype	No fert.		X1/2 RD		RD		X2 RD	
	Lp	Rank	Lp	Rank	Lp	Rank	Lp	Rank
<i>Kaharamana II</i>	2.307	19	1.393	8	1.463	7	1.952	46
<i>Kahata Samba</i>	1.817	9	1.851	24	1.449	6	1.259	9
<i>Kalu gires</i>	3.081	61	2.976	92	2.822	80	2.131	72
<i>Kalu Karayal</i>	3.129	67	2.545	69	2.122	23	1.499	16
<i>Kaluhandiran</i>	3.650	90	2.861	87	3.188	98	2.510	90
<i>Kalukanda</i>	1.138	4	1.328	4	1.216	5	1.526	19
<i>Karabewa</i>	3.729	94	2.905	88	2.358	45	1.965	51
<i>Karayal I</i>	1.648	8	1.397	9	2.599	69	1.471	13
<i>Karayal II</i>	2.978	57	2.461	65	2.268	36	1.649	28
<i>Karayal III</i>	2.265	18	2.173	47	0.791	1	0.804	2
<i>Kiri Murunga wee</i>	2.754	45	2.490	68	2.732	75	2.230	74
<i>Kiri Naran</i>	3.175	69	1.220	3	2.336	41	1.768	38
<i>Kirikara</i>	3.713	92	2.604	75	2.967	89	1.870	41
<i>Kokuvellai</i>	2.669	36	2.007	35	1.870	15	1.386	11
<i>Kotathavalu I</i>	2.896	52	1.677	19	2.281	37	1.563	21
<i>Kotathavalu II</i>	3.075	60	2.783	85	2.022	20	1.673	30
<i>Kottakaram</i>	2.826	48	1.591	13	2.811	79	1.524	18
<i>Lumbini I</i>	3.216	72	2.438	64	2.448	56	1.042	4
<i>Lumbini II</i>	3.371	81	2.651	78	2.807	78	2.281	77
<i>Madabaru</i>	3.000	59	2.078	39	2.241	33	2.349	81
<i>Madael</i>	2.441	25	1.969	32	2.157	26	1.743	36
<i>Madael Galle</i>	2.417	23	1.375	7	1.762	12	1.958	50
<i>Madael Kalutara</i>	2.016	11	1.675	18	2.529	66	2.724	96
<i>Madoluwa</i>	3.241	74	2.584	73	2.157	27	0.980	3
<i>Maha Murunga</i>	2.528	31	1.633	15	3.163	96	2.895	99
<i>Badulla</i>								
<i>Manchel Perunel</i>	2.935	53	2.065	38	2.443	54	1.906	45
<i>Matara wee</i>	2.548	32	2.061	37	1.959	19	1.425	12
<i>MI 329</i>	3.091	62	2.748	83	2.511	63	2.391	83
<i>Miti Riyan</i>	2.554	33	2.154	46	2.446	55	2.253	76
<i>Mudukiriell</i>	2.744	42	2.330	56	2.209	31	2.413	85
<i>Murunga wee</i>	3.955	99	2.947	91	2.833	81	1.675	31
<i>Murungakayan 101</i>	3.681	91	3.006	94	2.878	85	2.038	60
<i>Murungakayan 3</i>	3.503	85	2.998	93	2.724	74	1.957	49
<i>Muthu Samba</i>	3.312	79	1.840	23	2.147	24	2.808	97
<i>Muthumanikam</i>	2.681	38	1.483	11	1.576	9	1.685	32
<i>Naudu wee</i>	2.496	28	2.799	86	2.333	40	1.573	22
<i>Palasithari 601</i>	2.746	43	2.648	77	2.469	57	1.666	29
<i>Periamorungan</i>	3.927	98	2.945	90	2.850	83	3.137	100
<i>Podi sudu wee</i>	2.047	13	1.355	6	2.306	39	2.128	71
<i>Podisayam</i>	3.310	78	2.470	67	2.668	73	2.086	67
<i>Pokuru Samba</i>	2.334	21	1.671	16	1.778	14	1.476	14
<i>Polayal I</i>	3.281	76	2.552	70	3.188	97	2.315	79
<i>Polayal II</i>	4.014	100	3.415	100	3.329	100	2.724	95
<i>Puwakmalata Samba</i>	3.816	96	3.063	96	2.998	91	2.044	61
<i>Rajes</i>	3.122	66	2.468	66	2.351	43	2.011	55
<i>Ranruwan</i>	3.590	89	3.029	95	2.878	86	2.068	64
<i>Rata wee</i>	2.644	35	2.143	45	2.196	29	1.620	25
<i>Seeraga Samba</i>	2.754	44	1.673	17	2.350	42	1.956	47

Genotype	No fert.		X1/2 RD		RD		X2 RD	
	Lp	Rank	Lp	Rank	Lp	Rank	Lp	Rank
<i>Batticaloa</i>								
<i>Seevalee Ratnapura</i>	1.354	5	1.532	12	2.575	68	1.126	6
<i>Sinnanayam</i>	2.726	40	2.289	54	2.267	35	1.885	43
<i>Sinnanayan 398</i>	3.406	83	2.270	53	3.098	93	2.361	82
<i>Sirappu Paleusithri</i>	2.438	24	2.429	63	2.305	38	1.994	53
<i>Sudu Goda wee</i>	2.856	50	2.370	58	2.222	32	1.361	10
<i>Sudu Karayal</i>	3.327	80	2.236	49	2.417	52	1.762	37
<i>Sudu wee</i>	2.327	20	2.264	52	2.943	88	1.644	27
<i>Sudu wee Ratnapura</i>	2.103	15	1.454	10	2.389	48	2.112	69
<i>Suduru</i>	3.490	84	3.237	99	3.229	99	1.786	39
<i>Suduru Samba I</i>	3.900	97	3.158	98	3.121	95	2.013	56
<i>Suduru Samba II</i>	3.234	73	2.088	42	2.480	58	2.525	92
<i>Suduru Samba III</i>	2.504	30	1.817	20	2.086	22	2.491	87
<i>Suwanda Samba</i>	2.062	14	2.212	48	2.376	47	1.956	48
<i>Thunmar Hamara</i>	2.679	37	1.864	25	2.025	21	2.008	54
<i>Tissa wee</i>	2.880	51	2.304	55	2.351	44	1.737	35
<i>Wanni Heenati</i>	3.390	82	1.891	27	2.360	46	1.704	33
<i>Yakada wee I</i>	3.813	95	2.936	89	3.110	94	2.030	59
<i>Yakada wee II</i>	2.586	34	2.128	44	2.409	51	2.840	98

Table 3 Best 10 rice genotypes performed well at each fertilizer level according to multi-criteria decision-making model

No fertilizer	X1/2 RD	RD	X2RD
<i>Hondarawala</i>	<i>Jamis wee II</i>	<i>Karayal III</i>	<i>Hondarawala</i>
<i>Bathkiri el</i>	<i>Herath Banda</i>	<i>Bathkiri el</i>	<i>Karayal III</i>
<i>EAT Samba</i>	<i>Kiri Naran</i>	<i>Dik wee 328</i>	<i>Madoluwa</i>
<i>Kalukanda</i>	<i>Kalukanda</i>	<i>Jamis wee II</i>	<i>Lumbini I</i>
<i>Seevalee Ratnapura</i>	<i>Bathkiri el</i>	<i>Kalukanda</i>	<i>Bathkiri el</i>
<i>Gangala</i>	<i>Podi sudu wee</i>	<i>Kahata Samba</i>	<i>Seevalee Ratnapura</i>
<i>Jamis wee II</i>	<i>Madael Galle</i>	<i>Kaharamana II</i>	<i>Dandumara</i>
<i>Karayal I</i>	<i>Kaharamana II</i>	<i>Hondarawala</i>	<i>Jamis wee II</i>
<i>Kahata Samba</i>	<i>Karayal I</i>	<i>Muthumanikam</i>	<i>Kahata Samba</i>
<i>Heendikki</i>	<i>Sudu wee Ratnapura</i>	<i>Heendik wee</i>	<i>Sudu Goda wee</i>

However rice genotypes given in the Table 3 were the best potential rice genotypes suitable for the farmer field according to the multi criteria decision making model.

4. CONCLUSION

Phenotypic and/or genotypic direct effects or path coefficient can be used as an effective selection criterion in multivariate analysis for the evaluation of fertilizer response of traditional rice genotypes. In the same time path coefficients can be utilized as a criterion weight to rank the traditional rice genotypes for the evaluation of traditional rice genotypes for the field fitness. Majority of the yield attributing factors recorded the highest effect on the yield at no fertilizer level. Excessive usage of fertilizer decreased the effect of yield determination factors on the final yield. Recommended fertilizer level increased the effect of

number of tillers/plant and 100-grain weight on the yield. However the best fertilizer level for the individual rice genotype can be decided by the results of the present research.

CONSENT

All authors declare that written informed consent was obtained from the patient for publication of this original research article and accompanying image. A copy of the written consent is available for review by the Editorial office/Chief Editor/Editorial Board members of this journal.

COMPETING INTERESTS

Authors have declared that no competing interests exist

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