

Genetic divergence of lowland rice (*Oryza sativa* L.) genotypes in Uganda

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Forty-eight lowland rice genotypes with two checks were evaluated for their agronomic performance, genetic variability, heritability, and genetic advance for yield and yield contributing traits. Among the tested genotypes SR33859-HB3324-133 (45.7 qha⁻¹), SR33859-HB3324-93 (40.2 qha⁻¹) were the high yielding genotypes above the better check. The analysis of variance showed significant differences for all measured traits and indicating the presence of high genetic variability among genotypes. A highly significant ($P \leq 0.001$) correlations were observed between flag leaf length and plant height ($r_p = 0.76$, $r_g = 0.84$), panicle length and plant height ($r_p = 0.77$, $r_g = 0.90$), and panicle length and flag leaf length ($r_p = 0.75$, $r_g = 0.89$). The estimates of GCV were lower than the respective PCV for all traits, indicating the influence of environmental factors on the expression of the traits. Characters like grain yield (94 %, 90.9), flag leaf length (97 %, 71.6), number of tillers per hill (91 %, 67.2) and plant height (99.0 %, 50.7) showed high heritability coupled with moderate genetic advance as percent of the mean, which suggesting that these traits are controlled by the additive type of gene action and selection could be possible for the improvement of these characters. On the other hand, moderate heritability estimates with low genetic advance as percent of the mean were recorded for flag leaf width and number of days to maturity indicated the presence of non-additive gene effects, and selection for these traits would be poor. As a result, the variability that exists in the germplasm provides an opportunity to use these genotypes in the genetic improvement program.

Key words: rice, variability, GCV, PCV, heritability, genetic advance

INTRODUCTION

Rice (*Oryza sativa* L.) is most commonly produced in Asia, Africa, and Australia (Dogara and Jumare, 2014). It is the third most cultivated cereal crop in the world, after wheat and maize (FAO, 2014). Rice production in Uganda started in 1942, mainly to feed the World War II soldiers. However, due to a number of constraints, production remained minimal until 1974. Today rice is grown mainly by small-scale farmers almost throughout the country, but also by large-scale farmers in few places (Kijima, 2012). Most of the rice production in Uganda is in the Eastern parts of the country, followed by the Western part of Uganda. According to Dewina et al., (2010) rice accounted for 0.42 % of the total production of food crops in Uganda and ranking fifth after maize, cassava, bananas, and beans. Paddy rice production in Uganda ranged from 72,000 to 97,505 hectares with a total yield of 109 to 262,631 thousand tonnes respectively from 2000 to 2017 (FAO, 2018). Since the introduction of upland rice in 2002, farmers producing rice in Uganda increased from 4,000 then to over 35,000 in 2012 (Kijima and Sserunkuuma, 2006). Even though the production of rice in the country is increasing in terms of the

area while the national productivity of the crop doesn't exceed 2.81 tonnes per hectare. According to Akongo, (2017), rice production in the country is constrained by variability in climate, poor market prices, weed infestation, poor seed variety, bird damage, limited knowledge, and declining soil fertility. Creating genetic variability either by crossing and/or introduction would be one of the solutions to increase the chance of selection and success in the breeding program. Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. The success of breeding depends on the extent and the magnitude of variability existing in the germplasm, the heritability of the traits, information on the genetic variability, and degree of transmission of the target traits. The variability available in the population can be partitioned into heritable and non-heritable component viz., phenotypic and genotypic coefficients of variation, heritability, and genetic advance on which selection can be effectively carried out. Heritability is the degree of correspondence between the phenotype and the breeding value of an individual for a particular trait which enables the

breeders to select the elite variety for a character. However, heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance but it fails to indicate the expected genetic progress in one cycle of selection. According to Johnson et al., (1955), high heritability alone is not enough to make an efficient selection, unless the information is accompanied by for substantial amount of genetic advance. As a result, the present investigation was undertaken to assess the agronomic performance, the nature, and magnitude of genetic variability, heritability, and genetic advance among the genotypes for further utilization in breeding programs.

MATERIALS AND METHODS

A field experiment was conducted at the National Crops Resources Research Institute (NaCRRI) in Kampala, Uganda in the two cropping seasons of 2015 (referred to as seasons 2015 A and 2015 B) with the objective of evaluating the genetic variability of KAFACI materials for yield and yield related traits. NaCRRI is located at 0° 31' N, 32° 35' E, with a mean altitude of 1150 meters above sea level. The soils are ferralitic (red sandy and clay loams) and have a pH range of 4.9 - 5.0. The average annual rainfall is 1300 mm and maximum and minimum temperature of 28.5 ° C, and 13.0 ° C respectively. A nursery was raised for each genotype and twenty-one days old seedlings of forty-eight genotypes were transplanted in the swamp field in a 6 by 8 alpha lattice design with two replications. The spacing was 20 cm between rows and between plants and 40cm between plots and between blocks with 1 meter between replications. Each treatment was transplanted in plot size of 1.6 m length and 1 m wide. the fertilizers, Diammonium Phosphate

and season were random effects. Means of significant treatments effects were separated using LSD at P≤0.05 level of significance. Correlation analysis was done to determine the relationship among different traits included in the study.

The linear model for the across season analysis was as follows:

$$y_{ijk} = \mu + s_i + g_j + r/b_k + (sxg)_{ji} + e_{ijk}$$

Where, y_{ijk} = observed value from each experimental unit, μ = mean, s_i = effect of the i^{th} season, g_j = effect of j^{th} genotype, r/b_k = effect of replication nested within the k^{th} block, $(sxg)_{ji}$ = interaction effect of j^{th} genotype and the i^{th} season and e_{ijk} = the experimental error. In addition to these, phenotypic, genotypic variance were estimated and genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability in broad sense and genetic advance as percent of mean were calculated as follows; The variance components obtained from the across season analysis result were calculated as;

$V_{ph} = V_G + V_{GS}/r + V_e/rs$; where r and s are the number of replications and seasons respectively.

The phenotypic (PCV) and genotypic (GCV) coefficients of variation were obtained as the ratio of the respective phenotypic ($\sqrt{V_{ph}}$) and the genotypic ($\sqrt{V_G}$) standard deviations to the trait means. Broad sense heritability (H) was estimated as the percentage of the genotypic to the phenotypic variance (V_G/V_{ph}). The genetic advance (GA) and genetic advance as percent of the mean (GAM) expected from selection of the best 5 % of the genotypes were calculated as:

Table1. List of genotypes used for the study

S/No	Designation	S/No	Code	Designation	Code	S/No	Designation	Code
1	SR33859-HB3324-75	17	G1	SR33701-HB3330-73	G17	33	SR34042-HB3368-196	G33
2	SR33859-HB3324-80	18	G2	SR33701-HB3330-78	G18	34	SR34042-HB3368-228	G34
3	SR33859-HB3324-93	19	G3	SR33701-HB3330-86	G19	35	SR34034F3-125	G35
4	SR33859-HB3324-108	20	G4	SR33701-HB3330-90	G20	36	SR34034F3-135	G36
5	SR33859-HB3324-133	21	G5	SR33701-HB3330-95	G21	37	SR34034F3-147	G37
6	SR33859-HB3324-142	22	G6	SR34461-HB3369-54	G22	38	SR34035F3-57	G38
7	SR33686-HB3326-2	23	G7	SR34461-HB3369-65	G23	39	SR34035F3-182	G39
8	SR33686-HB3326-8	24	G8	SR34461-HB3369-67	G24	40	SR34038F3-13	G40
9	SR33686-HB3326-12	25	G9	SR34461-HB3369-105	G25	41	SR34038F3-32	G41
10	SR33686-HB3326-37	26	G10	SR34461-HB3369-108	G26	42	SR34038F3-42	G42
11	SR33698-HB3329-66	27	G11	SR34461-HB3369-118	G27	43	SR34038F3-75	G43
12	SR33698-HB3329-70	28	G12	SR34462-HB3370-64	G28	44	SR34040F3-29	G44
13	SR33701-HB3330-35	29	G13	SR34461-HB3369-120	G29	45	SR34042F3-3	G45
14	SR33701-HB3330-44	30	G14	SR34461-HB3369-139	G30	46	SR34566-7	G46
15	SR33701-HB3330-56	31	G15	SR34042-HB3368-170	G31	47	NERICA-1	G47
16	SR33701-HB3330-71	32	G16	SR34042-HB3368-182	G32	48	IR-64	G48

(DAP) (18-46-0) at a rate of 0.96 kg and urea (46-0-0) 1.7 kg/experimental area were used. Half of the Urea and the DAP fertilizer were applied during transplanting. The remaining half urea fertilizer was applied four weeks after transplanting as top dressing to all plots. Weeding and other cultural practices were conducted as needed. Data collection was done according to the standard evaluation system for rice described by (IRRI, 2014). Data were collected on five randomly selected and tagged plants for number of tillers per hill, plant height (cm), flag leaf length, flag leaf width, panicle length (cm) while, number of days to heading, number of days to maturity and grain yield (kg ha⁻¹) were recorded on plot basis. The data collected on above mentioned traits were subjected to alpha lattice restricted maximum likelihood (REML) analysis in GenStat 12th edition software package (Payne et al., 2009). The genotypes were considered a fixed effect while blocks, replications

$GA = K * (\sqrt{V_{ph}}) * H$ and $GAM = GA/x * 100$; where GA= genetic advance; H= heritability; GAM= genetic advance as percent of the mean; K= selection intensity of 5%=2.06 and $\sqrt{V_{ph}}$ =phenotypic standard deviation.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance across seasons revealed highly significant differences ($P \leq 0.001$) among genotypes for number of tillers per hill, number of days to 50 % heading, number of heading to maturity, panicle length and grain yield while significant at ($P \leq 0.01$) for flag leaf length and flag leaf width (Table 2). Genotype-by-season interaction effect was significant ($P \leq 0.001$) for number of days to maturity and plant height and

Table 2. Combined analysis of variance for grain yield and agronomic traits of 48 lowland rice genotypes evaluated in 2015 A and B cropping seasons at NaCRRRI

SOV	df	TL	DH	DM	PH	FLL	FLW	PL	GY
Rep	1	3.33ns	21.33*	8.76ns	299.90***	57.54***	0.021***	4.29ns	25.89ns
Rep/block	14	10.91**	37.81***	5.87ns	74.64***	10.69**	0.044**	2.48ns	54.05***
Genotypes (G)	47	35.26***	153.38***	33.83***	421.06***	54.42**	0.063**	10.70***	176.01***
Year (Y)	1	2.96ns	13.31ns	11.45ns	6.90 ns	19.35**	0.962**	8.07**	175.14***
G*Y	47	4.28ns	2.02ns	21.74***	3.96***	1.01 ns	0.052 ns	0.72ns	16.15**
Residual	81	5.61	4.4	5.57	17.06	4.34	0.011	1.55	8.26
Total	191	12.94	43.06	16.57	118.9	16.67	0.040	3.71	55.80
Mean		17.09	81.30	113.47	82.77	20.90	1.47	18.33	29.18
CV		13.86	2.58	2.08	4.99	9.97	7.14	6.79	9.85
LSD (5%)		4.73	2.96	3.33	5.82	4.16	0.17	2.48	5.74

, * Significant at 1 % and 0.1 % respectively, NS= Non- significant, TL= number of tillers, DH= number of days to heading, DM=number of days to maturity, PH= Plant height, FLL= flag leaf length, FLW= Flag leaf width, PL=Panicule length and GY= Grain yield (Quintal ha⁻¹)

significant difference ($P \leq 0.01$) for grain yield. There were no significant interactions among genotypes and seasons for tiller numbers per hill, number of days to heading, flag leaf length, flag leaf width and panicle length.

Agronomic performance of rice genotypes

The mean values of genotypes evaluated across seasons under field conditions for agronomic traits is presented in Table 3. The lowest number of tillers per hill were found on genotypes G47 (11.6) and G24 (12.9), while the highest number of tillers was found on G3 (24.4) and G12 (24.1), the overall mean being 17.1 tillers per hill. With an overall mean of 81 days until heading, the earliest heading genotypes were G21 (70 days) and G6 and G9 (71 days), and while genotypes G40 (96 days) was late flowering. In measuring number of days to maturity, the overall mean of 113 days, genotypes G16 (106) followed by G47 (107) days were mature early while genotypes G1 and G36 took long to mature (120) days. There was a difference among genotypes in plant height with an overall mean of 82.8 cm. Genotypes G27 (106.9 cm) and genotype G48 (105.3 cm) were tallest while genotypes G23 (58.9 cm) and G47 (65.7 cm) were the shortest. Genotypes showed long flag leaf were G37 (29.2 cm) and G27 (28.6 cm) and shortest flag leaf was recorded on G47 (15.1 cm) with mean of 20.9 cm. On the other hand, G2 and G21 gave the shortest flag leaf width (1 cm) while G29 was 1.6 cm. The average panicle length was 18.3cm, with the longest panicles recorded on genotypes G27 (22.4 cm) and G1 and G37 (21.6cm). Genotypes G9 and G23 (17.5 cm) and G28 (16.0 cm) had short panicles. An overall mean of 29.2 qha⁻¹ for yield with variation among genotypes, the highest yield was recorded on genotypes, G5 (45.7 qha⁻¹), G3 (40.2 qha⁻¹), G44 (39.1 qha⁻¹). The genotypes with the lowest yield included G3 (17.8 qha⁻¹), followed by G33 (18.8 qha⁻¹).

Genotypic and Phenotypic associations among measured traits

Phenotypic and genotypic correlation of a cross-season evaluation of the introduced rice genotypes for grain yield and other agronomic traits in field conditions is presented in Table 4. The results showed a moderately positively significant ($P \leq 0.001$) correlations between number of tillers per hill and grain yield ($r_p=0.47$ and $r_g=0.58$), number of days to maturity and flag leaf length ($r_p=0.49$, $r_g=0.73$), flag leaf length and number of days to heading (r_p and $r_g=0.43$) and flag leaf width and number of days to heading ($r_p=0.49$, $r_g=0.97$). A highly significant ($P \leq 0.001$) correlations were observed between flag leaf length and plant height ($r_p=0.76$, $r_g=0.84$), panicle length and plant height ($r_p=0.77$, $r_g=0.90$), and

panicle length and flag leaf length ($r_p=0.75$, $r_g=0.89$). Suwansa et al. (2017), Seyoum et al. (2012) and Sravan et al. (2012) had also reported that flag leaf length, number of panicles per plant and number of spikelets per panicle had significant positive phenotypic coefficients affecting grain yield per plant. On the other hand, a low non-significant negative correlation was observed between number of days to heading and grain yield ($r_p=-0.13$, $r_g=-0.07$). Suwansa et al. (2017), also reported similar findings that days to flowering had a significant negative phenotypic correlation with grain yield.

Table 3. The mean performance of the genotypes across two seasons.

Code	TL	DH	DM	PH	FLL	FLW	PL	PB	GY
G1	17.7	86	120	99.3	28.4	1.5	21.6	17.1	23.2
G2	15.4	72	113	68.2	17.6	1.0	18.1	20.8	25.5
G3	24.4	80	113	84.9	18.3	1.1	16.8	15.3	40.2
G4	17.7	73	111	76.5	17.0	1.1	18.9	28.7	33.2
G5	15.8	78	112	80.1	19.4	1.3	19.2	13.8	45.7
G6	14.4	71	108	79.3	18.2	1.1	17.2	18.7	33.4
G7	18.1	77	112	80.1	21.1	1.1	17.7	9.2	34.0
G8	15.1	75	112	79.0	16.6	1.2	17.1	24.8	23.6
G9	20.5	71	111	72.5	16.6	1.1	15.7	12.1	33.0
G10	18.0	80	114	80.3	22.1	1.2	19.6	21.9	34.6
G11	18.0	77	118	79.7	19.7	1.3	18.1	18.1	37.2
G12	24.1	84	114	85.6	24.2	1.2	19.6	11.2	35.8
G13	19.5	83	113	91.8	22.3	1.3	19.6	19.1	36.1
G14	15.5	75	110	76.4	17.1	1.2	17.1	17.9	32.0
G15	15.0	81	113	72.4	18.5	1.2	17.4	16.7	31.2
G16	15.2	77	106	75.2	18.9	1.2	17.3	24.5	25.3
G17	14.8	76	111	92.2	21.2	1.2	19.3	19.5	27.9
G18	19.3	74	116	95.5	25.1	1.4	19.6	13.7	35.2
G19	15.6	78	111	81.5	19.9	1.2	17.3	22.1	21.7
G20	15.7	75	110	83.6	17.9	1.1	17.2	30.1	21.1
G21	17.7	70	113	76.8	18.5	1.0	18.5	25.2	36.9
G22	17.6	79	112	71.2	20.3	1.2	16.7	18.3	26.1
G23	17.5	77	116	58.9	15.3	1.1	15.7	23.0	24.4
G24	12.9	89	115	77.6	20.0	1.5	18.2	13.0	32.7
G25	17.2	83	112	77.9	19.6	1.2	16.9	14.5	27.3
G26	18.9	81	114	93.2	26.5	1.3	21.0	11.5	29.8
G27	20.7	86	113	106.9	28.6	1.4	22.4	12.6	35.9
G28	16.9	87	111	76.2	18.4	1.3	16.0	24.0	37.5
G29	20.9	84	112	90.8	23.9	1.6	19.6	13.2	31.8
G30	13.5	80	117	76.5	21.5	1.4	18.5	21.5	19.6
G31	13.2	82	115	99.8	21.8	1.3	20.7	14.7	29.5
G32	15.8	89	117	87.6	20.2	1.1	18.2	37.3	17.8
G33	14.1	81	113	78.8	16.7	1.2	16.4	36.7	18.8
G34	14.1	83	113	79.9	17.3	1.2	17.9	34.0	19.8

G35	14.2	84	112	79.3	18.2	1.2	17.3	42.9	22.7
G36	17.8	79	120	92.3	27.2	1.3	18.8	28.6	24.8
G37	17.0	82	111	102.8	29.2	1.2	21.6	21.0	24.3
G38	21.5	90	117	89.0	25.9	1.3	20.5	16.8	30.9
G39	19.9	92	117	78.3	20.5	1.3	20.2	18.8	34.5
G40	19.4	96	116	88.5	24.8	1.2	19.7	18.6	21.1
G41	13.7	88	116	74.6	19.5	1.1	16.3	18.5	21.0
G42	23.5	93	115	76.8	22.8	1.4	16.5	19.8	36.6
G43	21.6	90	115	78.0	22.2	1.2	19.2	22.6	28.3
G44	15.8	81	115	101.3	22.9	1.5	19.7	33.1	39.1
G45	15.7	88	112	74.1	15.5	1.3	17.3	28.5	20.9
G46	14.7	89	113	77.9	26.9	1.3	17.1	28.5	21.7
G47	11.6	74	107	65.7	15.1	1.1	16.4	61.0	20.1
G48	13.5	88	117	105.3	24.2	1.4	18.9	18.9	34.4

TL= number of tillers, DH= number of days to heading, DM=number of days to maturity, PH= Plant height, FLL= flag leaf length, FLW= Flag leaf width, PL=Panicle length, PB= panicle blast and GY= Grain yield (Quintal ha⁻¹)

tillers per hill (35.9 %), flag leaf length (35.7 %) and plant height (24.9 %). In line with this, the maximum genetic coefficient of variation was also recorded for grain yield (44.9 %) followed by flag leaf length (35.2 %) and number of tillers per hill (34.2 %). Senapati and Kumar (2015), Suwansa et al. (2017), Biswaranjan et al. (2018), Nikki and Parmar (2020) had also reported high phenotypic and genetic coefficients of variation for grain yield per plant, number of panicles per plant, and number of spikelets per panicle. On the other hand, the smallest phenotypic (5.6 %) and genotypic coefficients of variations (4.7 %) were recorded on number of days to maturity and number of days to heading 15.3 % and 15.2 % respectively. Estimation of the extent of heritability enables breeders to know the extent of which improvement is possible through selection. According to Burton (1952) genetic advance in combination with heritability gives a more reliable index for selection of traits than heritability alone. High degree of heritability was recorded for all measured traits in this study. It ranged from 63.0 % for flag leaf width

Table 4. Estimate of phenotypic and genotypic correlations of 48 rice genotypes evaluated at NaCRRI, Uganda in 2015 A and B cropping seasons

		TL	DH	DM	PH	FLL	FLW	PL
DH	rp	0.212						
	rg	0.206						
DM	rp	0.24	0.491***					
	rg	0.311	0.818***					
PH	rp	0.168	0.253	0.356***				
	rg	0.233	0.255	0.385**				
FLL	rp	0.357**	0.434***	0.494***	0.763***			
	rg	0.374	0.432***	0.736***	0.841***			
FLW	rp	0.08	0.496***	0.427**	0.519***	0.563***		
	rg	0.189*	0.978***	0.970***	0.811***	0.947***		
PL	rp	0.259	0.248	0.406**	0.778***	0.758***	0.433**	
	rg	0.287	0.256	0.492***	0.909***	0.895***	0.789***	
GY	rp	0.473***	-0.132	0.016	0.203	0.116	0.213	0.223
	rg	0.589***	-0.074	0.018	0.268*	0.173	0.6171***	0.292

rp= Phenotypic correlation coefficient and rg=genotypic correlation coefficient

Table 5. Phenotypic and genotypic variances, heritability and expected genetic advance of 48 lowland rice genotypes evaluated at NaCRRI over two cropping years

Measured traits	Genetic parameters						
	GV (σ^2g)	PV (σ^2p)	GCV (%)	PCV (%)	H ² (%)	GA (%)	GAM (%)
TL	34.19	37.73	34.22	35.95	0.91	11.48	67.19
DH	152.88	154.99	15.21	15.31	0.99	25.33	31.16
DM	28.40	40.66	4.70	5.62	0.70	9.19	8.10
PH	420.07	426.32	24.76	24.94	0.99	41.97	50.71
FLL	54.17	55.76	35.22	35.74	0.97	14.97	71.62
FLW	0.05	0.08	15.22	19.10	0.63	0.37	25.02
PL	10.52	11.27	17.70	18.31	0.93	6.47	35.28
GY	171.98	182.12	44.94	46.25	0.94	26.29	90.09

GCV= Genetic coefficient of variation, PCV= Phenotypic coefficient of variation, H= Heritability in broad sense, GA=Genetic advance at 5 % selection intensity and GMA=Genetic advance as percent of the mean

Phenotypic and genotypic variances, expected genetic advance and heritability for grain yield and yield agronomic traits of rice genotypes

The phenotypic and genotypic variances and coefficients of variation, heritability in broad sense, genetic advance at 5 % selection intensity and genetic advance as percent of the mean for all measured traits are presented in Table 5. The estimates of PCV and GCV indicated the existence of variability of genotypes included in the study. In general, the phenotypic coefficients of variations were higher than the genotypic coefficients of variations for all measured traits. The largest phenotypic variation was observed for grain yield (46.25 %) followed by number of

to 99.0 % for number of days to heading. High heritability estimates associated with moderate to high genetic gain were observed for grain yield, plant height and flag leaf width. This indicated that the influence of environments on the expression of this traits were low. Low genetic advance as percent of the mean coupled with low estimates of heritability were recorded for number of days to maturity, flag leaf width and number of days to heading, which indicated that the involvement of non-additive gene actions and hence, population improvement approach would be most effective for improvement of these characters. As indicated in Table 5, the presence of sufficient variability in the studied traits showed high possibility to explore the material for further genetic improvement program.

CONCLUSION

The materials used in the study showed a highly significant difference for all measured traits and indicating the presence of substantial genetic variations and thus provide enough scope for selection. Among the tested genotypes SR33859-HB3324-133 (45.7 qha⁻¹), SR33859-HB3324-93 (40.2 qha⁻¹) were the high yielding genotypes above the check and could be further evaluated in different locations and seasons before assuring for production. Moderate to a high degree of heritability estimates and high, GCV and PCV were found for grain yield, number of tillers per hill and flag leaf length which indicating the low or negligible influence of environment in the expression of this traits. The presence of sufficient variability in the studied traits, gives possibilities to explore the material for further genetic improvement program and also to widen the genetic background of various rice genotypes.

AUTHOR CONTRIBUTIONS

Zelalem Zewdu: carried out the whole experiments and generated this manuscript.

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COMPETING INTERESTS

The author declares that they have no conflicts of interest associated with the publication of this article.

ETHICS APPROVAL

Not applicable.

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