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EVALUATION OF GENOTYPE BY ENVIRONMENT INTERACTION AND ADAPTABILITY FOR GRAIN YIELD IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Rice is a major world staple food crop, and therefore breeding improved varieties is of ultimate importance. Genotype-by-environment analyses are essential to understand the potential performance of the lines over environments. It is essential that a breeder should have an insight on the critical comparison of different stability models. Twenty-three advanced cultures of rice were tested for three consecutive years for yield and its attributes. To study the genotype x environment interactions, the models given by Eberhart and Russell (1966), Finlay and Wilkinson (1963) and Shukla (1972), Wrickes (1962) ecovalance method, sustainability index and AMMI models were used to determine the correlation between different environments and also to partition the sum of squares caused due to genotype x environment. The results revealed that the genotypes viz., NLR 3542, NLR 3573 and NLR 3585 were found to be stable according to Eberhart and Russell whereas NLR 3587 and NLR 3580 were found to be stable as per Wrickes method.

Keywords **:** Genotype by environment interaction, Stability, Rice breeding, Yield Potential

Introduction

Rice is a world staple food, versatile crop, can grow in varied agro climatic conditions throughout the world except Antarctica. Most of the world's annual rice production comes from tropical climate areas including India, Bangladesh and Indonesia. The average world rice productivity reaches about 4.61 tons per hectare (FAO, 2019). To meet the challenges of the ever-increasing world population and climate change, rice production must be increased through breeding programs that have major goals to achieve high yielding cultivars. However, the green revolution in Asia changed the scenario of rice viz., biotic stresses from low to high, genetic potential has become stagnant (Peng and Khush, 2003). Other constraints on rice production in the tropical environment were drought, flooding, and lack of fertile soil. It is therefore challenging to increase the production per hectare from the variety standpoint.

The total area of rice production is ~167 million hectares, of which 15 dan 25% are irrigated and rainfed lowland fields (Dogara and Jumare, 2014). Hence, these two types of rice fields have a great diversity of environmental conditions. Yield is a quantitative trait whose expressions are strongly influenced by environments (Li et al., 2019). For that reason, multi-environment trials (METs) are needed to identify a superior genotype with stable and high yield potential, and as part of the final stages to release a variety. Genotype-by-environment interaction (GEI) is inevitable in plant breeding and crop production (Yan, 2016). The presence of GEI refers to the differential response of genotypes among a range of environments (Kang, 1997). Considering GEI through stability analysis models could facilitate the accurate cultivar recommendation for the target environment (Huang et al., 2021). Stability analyses through univariate stability models have been developed by several workers viz., Finlay and Wilkinson (1963), Eberhart and Russell (1966), Wricke (1962), Shukla (1972) and Perkins and Jinks (1968), In view of the above, the present study has planned to elucidate the stability, agronomic performance of elite rice lines developed for irrigated transplanted conditions at Agricultural Research Station, Nellore, ANGRAU, Andhra Pradesh.

Materials and Methods

The experimental material used for the present study comprising 23 elite rice genotypes (Table 1) developed through pedigree method of plant breeding at Agricultural Research Station, Nellore, ANGRAU, Andhra Pradesh, India. This Research station is situated at an altitude of 20m MSL, $14^{o}21'$N latitude and $79^{o}59'$E longitude having soil type is sandy clay loam. All the rice genotypes were evaluated for grain yield for four consecutive kharif seasons from 2016-2019. The trial was conducted in a randomized block design with three replications having a plot size of $12m^2$ following a spacing of 20cm x 15cm. The need based agronomic and plant protection measures were followed as per the recommendations to raise a healthy crop. The data was recorded on grain yield in all the seasons, replication wise and statistically analysed using different stability models as mentioned here under.

Statistical analyses

GE interaction was quantified using several procedures based on evaluation of genotypes under multiple environments. These methods divided into univariate and multivariate stability statistics. The most widely used univariate methods are based on regressing the mean value of each genotype on the environmental index or marginal means of environments viz., Finlay and Wilkinson (1963), Eberhart and Russell, (1966), Shukla (1972) and Wrike's (1962).

Eberhart and Russell model of stability analysis

This method provides the linear regression coefficient, b, as an indication of the genotype response to the environmental index and the deviation from regression mean square, S^2 d, as a criterion of stability as suggested by Beker and Leon (1988). According to this method, the genotype is considered to be stable if its response to environmental index is parallel to the mean response of all tested genotypes, and its deviation from regression model is as minimum as possible. If the regression coefficient (b value) is not significantly different from unity, the genotype is considered to be adapted to all environments. If the genotype has significant b value greater than one is more responsive to high yielding environments, whereas any genotype with significant b value less than one is adapted to low yielding environments.

$$Yi\,j = \mu 1 + \beta i\ Ij + \delta ij$$

where Yi j the variety mean of the ith variety at the jth environment (i =1, 2… t and j=1, 2…s), µ1 is the mean of the ith variety over all environments**,** βi is the regression coefficient that measures the response of the ith variety to varying environments, Ij is the environmental index obtained as the mean of all varieties at the jth environment minus the grand mean, and δij is the deviation from regression of the ith variety at the jth environment.

Wrike's ecovalance method of stability analysis

The term eco-valence is used for the relative contribution of genotype 'I' to the overall genotype-environment interaction. According to Wricke (1962), ecovalence (Wi) of a genotype was estimated as:

$$Wi = \sum_j \left(Yij - \frac{Yi}{n} - \frac{Yj}{n} + - \frac{Y..}{gn} \right)^2$$

Wi = where Yij = mean of ith genotype in jth environment;

Yi . = total of ith genotype over environments;

Y. j. = total of jth environment over all genotypes; and

Y.. = grand total.

The minimum Wi^2 value indicates the stable performance of the genotypes.

Finlay and Wilkinson's method of stability analysis

It is a popular statistical technique used to compare the yield performance of a set of genotypes grown at several years /seasons. This involves computing the regression on yield of individual genotypes on the mean yield of all the genotypes for each site/season. These regressions had a high degree of linearity and have been used as a measure of the adaptability of the genotypes.

Rij=a1+bimj where ai= intercept value, is analogous to equation reported for joint regression analysis of adaptation.

Shukla model of stability analysis

The concept of partitioning of GEI sum of square into variance components $\left(\sigma_i^2\right)$ corresponding to each of the genotypes was proposed by Shukla (1972). According to this, a genotype is stable, if its stability variance $\left(\sigma_i^2\right)$ is equal to environmental variance $\left(\sigma_0^2\right)$, which mean that Sh-σ_i^2 = 0. A relatively large value of σ_i^2 indicate higher instability of genotype 'i', whereas stable genotypes are those having minimum stability variance (σ_i^2). This approach is considered of practical importance because it identifies environmental factors that contribute to the heterogeneity in the GEI.

AMMI Model of stability analysis

AMMI model is a Multivariate analysis of GE interaction is an alternative and complementary method for evaluating genotype stability (Crossa, 1990). It combines ANOVA for main effects of the genotype and environment with principal components analysis of GE interactions (Zobel *et al.*, 1988, Gauch 2006). The results of AMMI provide genotypes' yield stability under different environments and facilitate the precise selection of the best-performing genotypes for the environment under study. This method extracts genotype and environment main effects and uses interaction principal components (IPCs) to explain patterns in the GE interaction or residual matrix, which provides a multiplicative model (Romagosa and Fox, 1993). The AMMI model was as follows:

$$Y_{ij} + \mu + \alpha_i + \beta_j + \sum_{k=1} \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_{ij}$$

where, Y_{ij} is the yield of *i*th genotype in *j*th environment over all replications, μ is the grand mean, α_i is the *i*th genotype mean deviation (genotype mean minus grand mean), β_j is the *j*th environment mean deviation, λ_k is the singular value for IPC axis *k*, γ_{ik} is the *i*th genotype eigenvector value for IPC axis *k*, δ_{jk} is the *j*th environment eigenvector value for IPC axis *k*, and ε_{ij} is the error term.

Results and Discussion

In the present study a total of 23 genotypes were evaluated for four consecutive years. The results revealed that the mean grain yield of the genotypes ranged from 5255 kg/ha (NLR 3584) to 6749 kg/ha (NLR 3587) across diverse environments. Six genotypes viz., NLR 3592, NLR 3585, NLR 3586, NLR 3587, NLR 3590 and NLR 3595 recorded high mean yield than the popular rice variety NLR 33892 in southern zone of Andhra Pradesh. The results of individual stability models were discussed here under.

Eberhart and Russell model of stability analysis

In the present study, the results indicated that the genotypes *viz*, NLR 3542, NLR 3573and NLR 3585 recorded the regression coefficient value near to unity. Hence, the performance of these genotypes can be improved by adopting suitable agronomic management practices and also can be utilized in the crossing programme as one of the parents to breed for high mean yield with well adaptability. NLR 3585 exhibited good yield potential along with stable nature. However, none of the genotypes recorded superior yield coupled with unit regression and less S^2di values. Ramezani, Ahmad and Torabi, Masoud. (2011), Manjunatha *et al* (2018), Shreshta *et al.* (2020), Rawte *et al* (2021) and Quadri *et al* (2023) reported similar results in rice for grain yield.

Wrike's ecovalance method of stability analysis

The minimum Wi^2 (Ecovalance) value indicates the stable performance of the genotype. According to this method, the genotypes viz., NLR 3587 and NLR 3580 recorded both high grain yield as well as less ecovalence values, hence considered as stable genotypes with respect to yield. Even though the genotypes viz., NLR 3587, NLR 3580 and NLR 3573 had the lowest ecovalance values and therefore would be considered to be the most stable genotypes, but the ranks for these genotypes for yield were 1,15,4 and 17, respectively. These results were in accordance with the earlier findings of Aswidinnoor *et al.* (2023) in rice.

Finlay and Wilkinson's method of stability analysis

In the present study, bi-values ranged from 0.1 to 1.3 for grain yield. This variation in bi-value indicated that genotypes had different responses to environmental changes. According to Finlay and Wilkinson model, ten genotypes with bi-values not significantly different from 1, i.e. NLR 3539, NLR 3545, NLR 3548, NLR 3585, NLR 3586, NLR 3587, NLR 3590, NLR 3595, NLR 3592 and NLR 33892 were identified as stable genotypes that have wide adaptability to all environments because their average yield was higher than environment mean yield. These genotypes don't have deviations from the general response to environment and thus permits a predictable response to environments. The genotype NLR 3590 fall under category above average stability and adapted in marginal environments, while rest of the genotypes showed below average stability. Those genotypes with below average stability were sensitive to environmental changes and should be recommended for cultivation under favourable environments only. Aswidinnoor (2023) reported similar results in rice.

Shukla model of stability analysis

The present results indicated that the most stable genotypes were NLR 3586 (Gy:6469 kg/ha, σi^2:0.023), NLR 33892 (Gy:6457 kg/ha, σi^2:0.13), NLR 3587 (Gy:6749 kg/ha, σi^2:0.14), NLR 3592(Gy:6514 kg/ha, σi^2:0.29) and NLR 3589 (Gy:5856 kg/ha, σi^2:0.39) and their respective ranks for grain yield among 23 genotypes were 6, 7 and 1,3 and 11, respectively. The genotypes viz., NLR 3595 (Gy:6481 kg/ha, σi^2:-0.67) and NLR 3590 (Gy:6513 kg/ha, σi^2: 0.56) recorded high yield as well as low σi^2 values, hence considered as stable genotypes. Even though the genotype NLR 3585 and NLR 3359 recorded better yield performance but high σi^2 values, hence, considered as poor stable genotypes. The results were in agreement with the findings of Aswidinnoor (2023).

AMMI Model of Stability analysis

The results of AMMI analysis showed that the first PC $_1$ component of the interaction captured 51.6% of the interaction sum of squares in the total interaction degrees of freedom. Similarly, the second principal component axis explained a further 30.7% of the GEI sum of squares. cumulatively the mean sum of squares for the PC_1 and PC_2 axis were able to explain 82.3% from the total G x E variation. (Table 3). Biplot analysis is the interpretive tool for AMMI Model. It is the resultant from genotype and environmental scores of PC_1 and PC_2 (Hernandez and Crossa, 2000) of AMMI components. The PCA scores in the AMMI analysis indicated the adaptability over the environments. The genotypes close to the origin were not sensitive to the interaction of the environment and the genotypes that were far from the origin were sensitive and had large interaction. NLR 3542 was very close to the axis and found to be the stable genotype in all the environments. whereas NLR 3574, NLR 3592 and NLR 3545 were far away from the axis and found to be the unstable genotypes. Even though NLR 3592 and NLR 3545 recorded high mean yield performance but they were suitable for favourable environments only.

Based on the PC_1 and PC_2 values, ASV and YSI values, out of 23 genotypes studied in the present experiment the genotype NLR 3587 recorded high yield coupled with low PC_1 and PC_2, ASV and relative stability index of 1 followed by NLR 3580 and NLR 3590. These genotypes were found to be stable genotypes. Similar results were already reported by Satato *et al* (2016) and Chandramohan *et al* (2023) in rice.

Agronomic performance:

The average agronomic performance and yield components across four seasons are shown in Table 3. Large phenotypic variations were recorded for all the traits. Out of 23 genotypes selected for study, 13 genotypes were of long duration with NLR 33892 as check and 8 genotypes are of short duration with NLR 34449 as check. The features of all the elite rice genotypes range from 85-128 days for days to 50% flowering, 119-160 days for maturity, 84-108cm plant height, 18.6-23.7cm panicle length, 402-631 ear bearing tillers per sq.m and 5114-6749kg/ha of grain yield. In most of the times, grain yield is largely determined by the trait, average number of productive tillers and length of the panicle. (Li et al., 2003). Slightly tall stature may contribute to higher yields in rice however, very tall plant stature with insufficient strength may leads to lodging.

Out of all the methods tested, the genotypes viz., NLR 3587 and NLR 3590 found to be the stable ones with high yield potential from 4 stability models out of 7 models tested in the present study. These genotypes not only possessing high yield stability but also good agronomic features. Hence, these genotypes may be utilized as parents in the future breeding programmes to get desirable genotypes for both yield and adaptability.

Table 1: Details of the genotypes used for the study

S.No	Genotype	Parentage
1	NLR 3539	(NLR 20083 x NLR 3041)x NLR 34449
2	NLR 3542	NLR 34417 x NLR 34449
3	NLR 3545	NLR 28523 x NLR 3041
4	NLR 3548	NLR 28523 x QR 16
5	NLR 3585	(NLR 34449 x NLR 33358)x (NLR 33892 x NLR 20017)
6	NLR 3586	(NLR 34449 x PS 4)x BCP 2 x BPT 5204
7	NLR 3587	(NLR 20083 x NLR 3041)x NLR 34449
8	NLR 3588	(NLR 34449 x NLR 33358)x (NLR 33892 x NLR 20017)
9	NLR 3589	NLR 28523 x NLR 3041
10	NLR 3590	(NLR 34452 x NLR 33654)x NLR 20017
11	NLR 3592	NLR 9674 x NLR 3041
12	NLR 3595	(NLR 20083 x NLR 3041)x NLR 34449
13	NLR 3600	NLR 28523 x NLR 3041
14	NLR 33892	NLR 27999 x MTU 4870
15	NLR 3571	MDT 6 x NLR 33358

16	NLR 3573	IET 21687 x NLR 40024
17	NLR 3574	NLR 34449 x MTU 1010
18	NLR 3578	IET 21687 x NLR 34449
19	NLR 3579	IET 21687 x NLR 34449
20	NLR 3580	IET 21687 x NLR 34449
21	NLR 3581	IET 21687 x NLR 34449
22	NLR 3584	NLR 145 x NLR 34449
23	NLR 34449	IR 72 x BPT 5204

Table 2: Average yield and stability parameters of 23 rice genotypes evaluated for four seasons

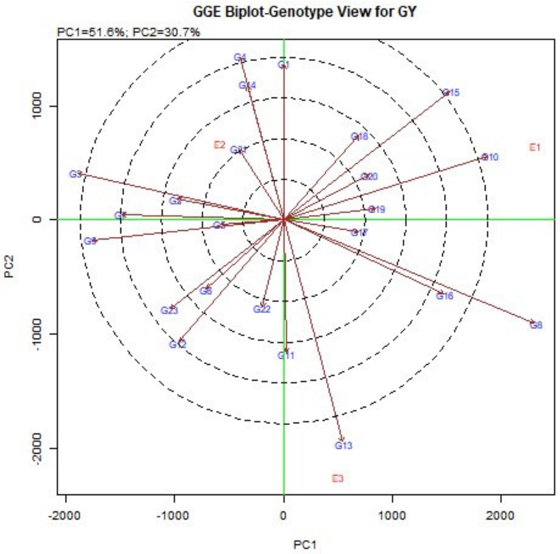
S.No	Genotype	Mean grain yield	CV%	bi	S^2di	Wi^2	σi^2	YSi
1	NLR 3539	6166	30.07	2.10	240802	445.7	1.103	25
2	NLR 3542	5852	11.15	0.13	588407	178.1	-0.869	21
3	NLR 3545	6190	13.48	0.16	1836037	276.7	-1.167	40
4	NLR 3548	6448	12.15	-0.29	298477	368	-1.299	29
5	NLR 3585	6527	27.47	2.38	96655	313.87	1.384	17
6	NLR 3586	6469	18.19	1.02	31309	196.3	0.023	19
7	NLR 3587	6749	14.16	1.13	637398	4.89	0.140	31
8	NLR 3588	5739	24.46	1.82	5902219	150.6	0.824	30
9	NLR 3589	5856	20.98	1.39	672731	134.2	0.391	38
10	NLR 3590	6513	18.16	1.56	2384023	48.37	0.562	32
11	NLR 3592	6514	21.12	1.29	530558	234.6	0.299	20
12	NLR 3595	6481	10.51	0.32	584483	91.07	-0.673	29
13	NLR 3600	5481	6.32	0.05	975785	141.3	-0.949	27
14	NLR 33892	6457	29.6	1.13	259670	634	0.130	24
15	NLR 3571	5841	27.2	2.04	136962	198	1.04	23
16	NLR 3573	5642	14.73	0.79	1788326	75	-0.203	22
17	NLR 3574	5173	19.13	0.65	-39814	219.4	-0.343	2
18	NLR 3578	5623	24.7	1.79	381027	129.4	0.791	30
19	NLR 3579	5480	27.8	1.95	985241	178.5	0.959	24
20	NLR 3580	5763	11.5	0.77	-57657	24.4	-0.228	7
21	NLR 3581	5809	6.4	0.29	2020352	86.2	-0.708	20
22	NLR 3584	5255	13.01	0.52	146812	108	-0.472	12
23	NLR 34449	5114	11.7	0.26	-24352	160.65	-0.736	30

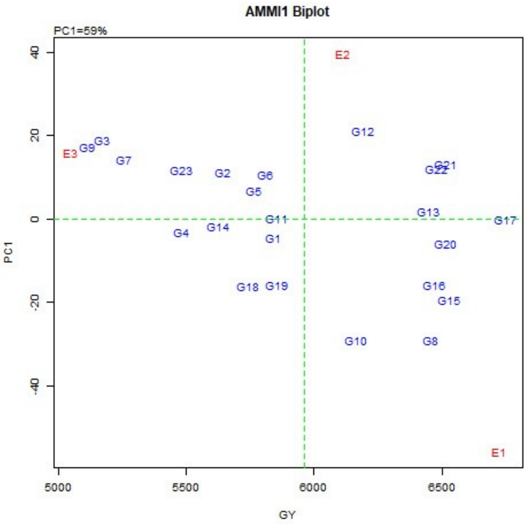
Yi is the average genotype yield across 4, CVi is the coefficient of variations (Francis and Kannenberg, 1978); bi is the regression coefficient of average genotype yield on environmental index (Finlay and Wilkinson, 1963), (,**significantly different from bi = 1.0 at $p < 0.05$ and $p < 0.01$, respectively); s^2 di is the deviation from regression (Eberhart and Russell, 1966) (*,**significantly different from s2 di=0.0 at $p<0.05$ and $p<0.01$, respectively);W^2i is the ecovalence of Wricke (1962). σi^2 is Shukla's stability variance; YSi is yield and stability index (Kang, 1993)

Table 3: Stability parameters and principal components for AMMI model

S.No	Genotype	Grain yield	PC1	PC2	ASV	YSI	RYSI
1	NLR 3571	5841	-4.548	20.672	21.68	25	13
2	NLR 3573	5642	11.210	4.532	16.74	21	17
3	NLR 3574	5173	19.149	7.821	28.62	40	22
4	NLR 3579	5480	-3.113	19.899	20.39	29	20
5	NLR 3580	5763	6.812	0.287	9.8	17	15
6	NLR 3581	5809	10.681	-7.744	17.2	19	14
7	NLR 3584	5255	14.320	0.807	20.6	31	21
8	NLR 33892	6457	-29.030	-21.018	46.73	30	7
9	NLR 34449	5114	17.282	-2.934	25.02	38	23
10	NLR 3539	6166	-29.088	1.736	41.86	32	10
11	NLR 3542	5852	0.260	-20.165	20.16	20	12

12	NLR 3545	6190	21.117	-9.852	31.92	29	9
13	NLR 3548	6448	1.858	-28.916	29.03	27	8
14	NLR 3578	5623	-1.763	17.084	17.27	24	18
15	NLR 3585	6527	-19.268	16.473	32.23	23	2
16	NLR 3586	6469	-15.647	-12.433	25.7	22	6
17	NLR 3587	6749	0.070	3.342	3.34	2	1
18	NLR 3588	5739	-16.007	6.051	23.79	30	16
19	NLR 3589	5856	-15.611	-3.779	22.76	24	11
20	NLR 3590	6513	-5.868	8.315	11.84	7	4
21	NLR 3592	6514	13.263	18.018	26.23	20	3
22	NLR 3595	6481	12.065	-5.775	18.28	12	5
23	NLR 3600	5481	11.851	-12.421	21.08	30	19





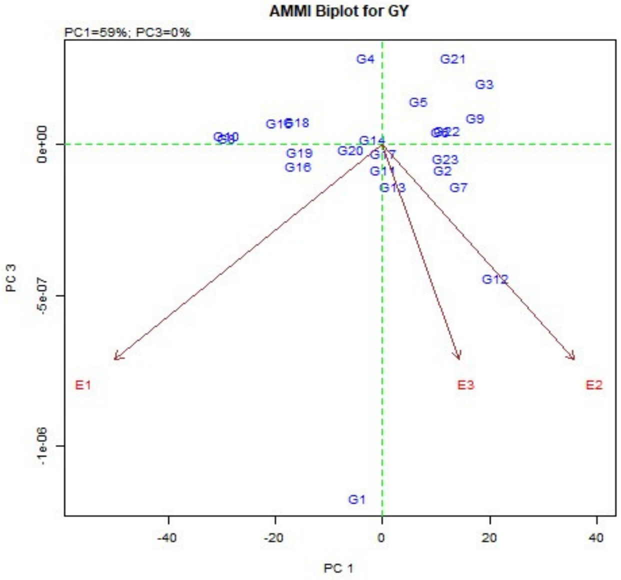


Table 4: Agronomic characters of the genotypes used in the present study

S.No	Genotype	DFF	DM	PH	PI	EBTS	GY
1	NLR 3539	123	154	95.3	20.8	520	6166
2	NLR 3542	124	156	107.9	23.3	545	5852
3	NLR 3545	126	158	103	22.2	476	6190
4	NLR 3548	121	155	97	22.4	518	6448
5	NLR 3585	116	148	84	21.1	542	6527
6	NLR 3586	121	154	94	22	531	6469
7	NLR 3587	124	155	97	20.3	536	6749
8	NLR 3588	122	153	81	18.7	535	5739
9	NLR 3589	128	160	99	23.13	541	5856
10	NLR 3590	126	158	95	21.7	533	6513
11	NLR 3592	119	150	100	23.7	520	6514
12	NLR 3595	118	150	84	18.4	530	6481
13	NLR 3600	120	152	98	23.1	523	5481
14	NLR 33892	125	158	92	23.4	402	5457
15	NLR 3571	87	120	95	22.01	568	5481
16	NLR 3573	89	122	92	21.3	597	5642
17	NLR 3574	92	125	82	18.6	615	5173
18	NLR 3578	85	119	93	21.1	592	5623
19	NLR 3579	88	120	86	19.97	626	5480
20	NLR 3580	89	122	89	20.18	631	5763
21	NLR 3581	93	125	93	21.1	647	5809
22	NLR 3584	92	125	89	22.37	592	5255
23	NLR 34449	93	126	86	19.55	626	5114

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