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Original Research Article

PERFORMANCE EVALUATION OF UPLAND COTTON GENOTYPES IN TERMS OF SEED COTTON YIELD UNDER INCONSISTENT ENVIRONMENTAL CONDITIONS

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Abstract: *Yield constancy is a crucial characteristic for a variety to become popular among growers. To study this aspect, the present trial was carried out at seven locations in the cotton belt of Punjab during 2020-21. Twenty-five upland cotton strains from different breeding stations were tested along with the standard variety CIM-602. The main objective was to choose super-yielding plus stable strains. Maximum variability due to environments (65%) followed by GEI (22.8%) was observed. The first two interaction principal components (IPC) were squeezed with 72.3% of cumulative variability due to GEI. The analysis of additive main effects and multiplicative interaction (AMMI) diagnosed AMMI5 as an appropriate model. Strain CKC-5 gave maximum mean yield (1812kg ha-1) and winner in all AMMI models. Test sites were split into two mega environments (ME). ENT7 (CRS Faisalabad) site was bearing the highest mean seed cotton yield of (2532kg ha-1) with the biggest (52.18) IPC1 score. The correlation between sites and IPC1 scores was (0.68) as recorded by AMMI analysis. AMMI1 ranks depicted that (PCI2) CIM-875 bears yield advantage of (29.09%) at ENT6 (Vehari) site over (trial winner strain CKC-5) due to micro adaptations. Genotype Selection Index (GSI) discriminated strain BS-J5 as yielder cum stable one with the least GSI value. Approval of this strain for general cultivation from the respective forum may boost cotton production in the province.*

Keywords: Genotype Selection Index, Interaction principal components, Micro adaptations, Upland cotton, Yield constancy

Introduction

Cotton is a life line of our economy. It provides lint to the textile sector, the main component of national exports. Approximately two per cent of our GDP is intemperately dependent on cotton (Sial *et al*., 2014). Its economic impact is nearly six hundred billion U.S dollars worldwide (Ashraf *et al*., 2018). Cotton seed is also a valuable source of edible oil for the rapidly growing population. The cotton-growing belt consisting of central and south Punjab remained a major production hub in the past, but production is declining each year drastically. The main reason for this trend is changing environment and uneven performance of cotton cultivars in a new scenario. Testing of elite strains under diversified agro-climatic conditions is a prerequisite to assessing yield stability (Farshadfar *et al*., 2012). Significant GEI interaction in polygenic traits like yield can influence the performance of cultivars in erratic environments (Gurmu *et al*., 2009). Generally, GEI impact is more significant on yield, as it is a quantitative character with a low heritability value. Thus, seed cotton yield is dependent on genotypes, environment and GEI.

In conclusion, yield plus stability must be explored together in experiments to exploit the positive effect of GEI and effective and refined selection of genotypes (El-Hashash *et al*., 2019). If the GEI portion of variability is significant, then selecting genotypes merely on a yield basis is ineffective and misleading (Sharifi *et al*., 2017). Side effects of high GEI result in a poor link between phenotypic into the genotypic look and biased heritability estimates

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(Alghamdi, 2004; Khalid and Amjad, 2018; Khalid and Amjad, 2019).

Researchers use different biometrical methods to explore GEI. Additive main effects and multiplicative interaction (AMMI) are prominent among them, as they partitioned the GEI component of variation and calculated direct effects by genotypes (Ebdon and Gauch, 2002). Kandus *et al.*, (2010) concluded that AMMI analysis was an efficient method to assess the magnitude of the GEI in field experiments. Stability is rarely used as the sole selection indicator in field trials because mostly stable varieties do not prove performers in terms of mean yield (Mohammadi and Amri, 2007). Genotype Selection Index (GSI), as a new tool, was efficient in selection. It combines mean yield and AMMI stability value (ASV) to single non-parametric criteria, which generates sufficient information for the selection of novel plant material (Gridhar *et al*.,2016). The main purpose of the current experiment was to know the adaptation of cotton strains using the AMMI method and to quantify the magnitude of the GEI segment of variation. Further, to pinpoint mega environments, choose the winner genotype in each mega environment, and select yielder cum stable cotton trains. Such genotypes are probably hoping for a cotton revival in the Punjab belt.

Material and methods

The current trial was sown at seven central plus south Punjab, Pakistan regions during 2020-21 (Table-1). 25 candidate cotton cultivars evolved by reputed public and private research centres, plus one standard variety CIM-602 were planned for the study. Sowing was completed in May by adopting the Randomized Complete Block Design (RCBD) protocol with 3 replications. Each test entry comprised 7.65 m long 4 lines and 0.75 m distance between lines. One line was skipped after each plot for ease in recording observations. Manual thinning kept a distance of 0.3 m between plants in each line. Pre emergence weedicide was applied within 24 hours after sowing.

Table-1 Detail of seven environments plus twenty-five cotton strains under study

Seven Environments			**Twenty-five Cotton Strains inclusive one check variety**					
S.N	**Code**	**Description**	**S.N**	**Code**	**Description**	**S.N**	**Code**	**Description**
1	ENT1	Central Cotton Research Inst. Multan.	1	PC09	SLH-33	**15**	**CHEK**	**CIM-602 (Stnd)**
			2	PC10	Eye-22	16	PC24	Rawal-111
2	ENT2	Cotton Research Institute, Multan.	3	PC11	CKC-5	17	PC25	CIM-785
			4	PC12	CIM-875	18	PC26	NIA-89
3	ENT3	Cotton Research Station, Bahawalpur.	5	PC13	ASLP-709	19	PC27	WEAL-AG-9
			6	PC14	IR-NIBGE-14	20	PC28	VH-418
4	ENT4	Cotton Research Station, Sahiwal.	7	PC15	YBG-2222	21	PC29	Sayban-209
			8	PC16	Diamond-2	22	PC30	Cyto-537
5	ENT5	Cotton Research Station, Khanpur.	9	PC17	FH-494	23	PC32	RH-King-20
			10	PC18	WEAL-AG-CKC-301	24	PC33	Eagle-4
6	ENT6	Cotton Research Station, Vehari.	11	PC19	FH-498	25	PC34	BH-225
			12	PC20	BS-J5			
7	ENT7	Cotton Research Station, Faisalabad.	13	PC21	NIAB-484			
			14	PC22	NS-211			

Other recommended crop husbandry and insect pest management operation were carried out throughout cropping season among test entries in even ways to minimize any manmade bias. When maximum bolls were opened at the end of October, picking was done after 10 am by employing female labour. After cleaning trash seed cotton picked from each plot was weighed with electronic balance and plot yield was converted to the standard form of kg ha^{-1} for comparison and analysis.

Data analysis

Each plot's seed cotton yield data were put for the Analysis of Variance (ANOVA) technique (Steel *et al.*, 1997). This technique can capture main effects due to genotypes and environment but cannot do anything with multiplicative effects if present. This GEI portion of variability can further be analyzed by using Principal Component Analysis (PCA) method. In the present study, data were analyzed by Additive Main effects and Multiplicative Interaction (AMMI) protocol proposed by Gauch (2013). This technique is a novel combination of ANOVA and PCA, developed to handle both bottlenecks as mentioned above Captured amount of GEI was split into various Interaction Principal Components (IPC) as per the protocol of PCA. A minute portion of GEI was leftover during this analysis and treated as residual. A particular F-test (F Ratio), was employed to determine the significance of (IPC) in a specific Degree of Freedom (DF) in AMMI analysis (Cornelius *et al.*, 1992). AMMISOFT version 1.0 computer software was used for AMMI analysis in the present study. The biometric AMMI equation is as described under.

$$Y_{ge}=\mu+\alpha_{g}+\beta_{e}+\Sigma_{n}\lambda_{n}\gamma_{gn}\delta_{en}+\rho_{ge}$$

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Whereas: Y_{ge} denotes the yield of genotype (g) in an environment (e) μ denotes grand mean α_g denotes mean deviation due to genotype (g) β_e denotes mean deviation from particular environment mean. λ_n denotes a singular value for IPC(n) γ_{gn} represents a particular genotype (g) eigenvector value to IPC(n) δ_{en} denotes the value of eigenvector due to the environment for IPC(n) ρ_{ge} denotes the leftover portion of GEI.

Although the AMMI method capture and split GEI into different IPC efficiently, it lacks any direct mechanism to determine and pinpoint stable genotypes in multi-location experiments. This concept of AMMI stability value (ASV) was given by Purchase (1997). Genotypes with high ASV values are those that contribute more towards GEI, hence considered unstable ones. The formula of ASV is given under.

$$\mathbf{ASV= SQR\ [\{(SS\ IPC1/SS\ IPC2)\ (IPC1)\}^{2} + \{IPC2\}^{2}]}$$

Whereas: **SQR** indicates square root value, **SS** denotes to sum of squares. **IPC1** denotes Interaction Principal Component 1 value, IPC2 denotes Interaction Principal Component 2 value. Further, it was observed that stable genotypes are not usually the best yielders. Considering this matter a nonparametric criterion of Genotype Selection Index (GSI) was proposed by Farshadfar (2008). This approach combines both mean yield and ASV to select genotypes in multi-site varietal trials. The low value of GSI indicates stable cum yielder genotypes, while higher values put genotypes in the rejected category being non-reliable. GSI formula is as under.

GSI = Rank of ASV + Rank of Y where ASV represents AMMI Stability Value and **Y** denotes to mean yield at all study sites.

Results and discussion

AMMI Analysis

The AMMI Analysis of variance (ANOVA) results across 7 sites depicted significant ($P \leq 0.01$) mean squares (MS) of strains, environment and Strain x Environment (GEI) for seed cotton yield (Table-2). This indicates the generous variation among cotton strains, test sites and strains also depicted uneven performance across test locations for seed cotton yield. Earlier researchers (Kaya *et al.*, 2002; Akande, 2009; Workie *et al.*, 2013) also reported similar results in wheat, cowpea and maize respectively. (Yayis *et al*., 2014) stated that significant results for genotype, locations and GEI on yield in cowpea provide enough ground for further stability analysis.

Genotypes, environment and GEI accounted for 9.2, 65, and 22.8% of the total variation, respectively. This shows the largest portion of SS was due to the environment, hence the importance of multi-environment trials (MET) before variety approval was proved. These findings align with earlier research on the cotton crop by (Khalid et al., 2022; Naveed *et al*., 2007; Riaz *et al*., 2013). Ntawuruhunga *et al.* (2001). Concluded that GEI and environmental effects both influence yield performance in cassava. Greater SS value for GEI than strains additive effects depicted that genotypes responded to environments in an erratic pattern. Zare *et al.* (2012) also reported GEI > genotypes additive effects in barley. Overall, higher treatment effects (97%) compared with error effects (3%) indicated the accuracy and reliability of the MET experiment.

Table-2 AMMI ANOVA for seed cotton yield in 25 strains across 07 locations during 2020-21

S.O.V	**D.F**	**S.S**	**M.S.S**	**The proportion of the sum of squares %**		
				T.V	**A &I. V**	**G.E.I**
Treatments	174	302779704	1740113^{X}	97.0		
Strains	24	28773916	1198913^{X}		9.2	
Environments	6	202769954	33794992^{X}		65.0	
S X E	144	71235833 [Total] 67385286 [Signal] 3850547 [Noise]	494693^{X}		22.8	**100**
IPC-1	29	37250879	1284513^{X}			52.3
IPC-2	27	14264318	528308^{X}			20.0
IPC-3	25	9225893	369036^{X}			13.0
IPC-4	23	5094747	221511^{X}			7.2
IPC-5	21	4821018	229572^{X}			6.8
IPC-Residual	19	578977	30472^{Z}			0.7
Error	350	9358969	26740	3.0		
Blocks x Env.	14	584421	41744^{Z}		0.2	
Pure Error	336	8774548	26115		2.8	
Total	**524**	**312138672**	**595684**	**100**	**100**	

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^{X} Significant at ($P \leq 0.01$) ^{Y} Significant at ($P \leq 0.05$) ^{Z} Non significant

Note. F-test uses error as Blocks X Env found Non-significant at ($P \leq 0.05$)

S.O.V= Source of variance **D.F**= Degree of freedom **S.S**= Sum of squares **M.S.S**= Mean sum of squares **T.V=** Total variance **A &I.V**=Additive and Interaction variance **G.E.I**= Genotype X Environment Interaction

The major portion of GEI (94.59%) comprises signal information and (5.41%) noise. This indicated that PCA can effectively allocate signal information to several IPC, s. AMMI analysis split GEI variation into 5 IPC, s significant at ($P \leq 0.01$) and minute value (0.7%) of GEI was left as residual. The first 2 IPC captured (72.3%) of GEI cumulatively, which was (55.8%) greater than SS for genotypes.

AMMI Model diagnosis and Mega Environment delineation

AMMI model diagnosis is crucial to pinpoint the best model for specific data sets and consider biometrical and practical implications. Due to the presence of 5 significant IPC, the AMMI5 model was diagnosed for the current data set. However, Yan and Rajcan (2002) described that the best AMMI model could be suggested baring the first two PCAs. Gauch (2013) in his paper suggested the AMMI1 model as the default, for simplicity and practicable implementations. Agahi *et al.*, (2020) in the spring rape study also used a simpler AMMI1 model. The present study's AMMI1 model delineated 7 test sites into 2 mega Environments ME (Table-3). First (ME) consists of 5 locations and is won by strain CIM-875. The second ME consists of two sites, Faisalabad and Bahawalpur, which was won by strain CKC-5. This strain (CKC-5) was proved the overall winner of the trial, being winning maximum environments in all AMMI models and bearing the highest mean yield (1812kg ha^{-1}). AMMIF model is the last model in the family without any residual and falls near raw data values. Higher AMMI models delineated test sites into many ME, so seldom bear any practical implementation.

Table 3 Victor strains of AMMI model group across 7 locations in Punjab during 2020-21

Strains	AMMI0	AMMI1	AMMI2	AMMI3	AMMI4	AMMI5	AMMIF
CKC-5	7	2	2	2	2	2	2
BH-225							1
BS-J5						1	1
Diamond-2			2	2	2	2	1
NIAB-484					1		1
CIM-875		5	3	2	1	1	1
WEAL-AG-9				1	1	1	1
Mega- Environments	**1**	**2**	**3**	**4**	**5**	**5**	**6**

Mega Environment winners and micro adaptations

The top 5 cotton strains are presented following ranks assessed by the AMMI1 default and AMMIF models (Table 4). AMMIF model represents values at par with raw data and loses any practical implications. Strain (PC11) CKC-5 is ranked in ranking (when sown in ME-2) as per both AMMI & AMMIF models. Similarly (PC12) CIM-875 was the winner and ranked top (when sown in ME-1) as per the AMMI1 model, whereas the AMMIF model lacks any useful signal here.

Table-4 Ranking of best five cotton genotypes as per AMMI1 and AMMIF models in twenty five cotton strains into two Mega- Environments (ME)

Mega Env.	Env. Code	Ratio	AMMI-1 Ranks 1	2	3	4	5	AMMI-F Ranks 1	2	3	4	5
ME-2	ENT7	1	PC11	PC32	PC17	PC29	PC34	PC11	PC32	PC17	PC29	PC34
	ENT3	1	PC11	PC17	PC34	PC20	PC16	PC11	PC09	PC21	PC16	PC18
ME-1	ENT2	1.0084	PC12	PC11	PC30	PC20	PC16	PC34	PC16	PC24	PC27	PC12
	ENT4	1.3030	PC12	PC30	PC27	PC16	PC20	PC12	PC14	PC30	PC15	PC28
	ENT5	1.1729	PC12	PC30	PC27	PC16	PC20	PC20	PC21	PC16	PC24	PC30
	ENT6	1.2909	PC12	PC30	PC27	PC16	PC20	PC16	PC27	PC30	PC28	PC24
	ENT1	1.1059	PC12	PC27	PC30	PC16	PC20	PC27	PC12	PC20	PC19	PC10

The ratio mentioned in (Table-4) indicated the yield advantage of strains ranked top in the AMM1 model when compared to the overall winner (PC11) strain yield at the respective site. So strain (PC12) CIM-875 bears a 30.3% and 29.09% yield edge due to micro adaptations over (PC11) CKC-5 at Sahiwal and Vehari sites respectively. These findings are in line

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with the results by Krishnamurthy *et al.* (2021) on the rice crop.

AMMI Biplot analysis

The mean seed cotton yield across test sites and PCA1 scores for both strains and environments were plotted in the biplots (Figure-1). If any strain or environment with an IPC1 value near zero, it was marked as stable through diverse environments with less contribution towards GEI. Conversely, genotypes bearing high values for IPC1 scores were ranked as explicitly fitted to particular environments (Abdi and Williams, 2010; Askari *et al*., 2017; Malik and Rasheed, 2022). Accordingly (ENT7) Faisalabad site was high yielding (2532 kg ha^{-1}) but with a high IPC1 score (52.18), so ranked an unsuitable site for cotton testing experiments. Winning strain (PC11) CKC-5 is adapted explicitly to (ENT7) Faisalabad and (ENT3) Bahawalpur locations. ENT3 (CRS Bahawalpur) was found ideal test site followed by ENT2 (CRI Multan) being the least contribution towards GEI (Figure-1).PC18 (WEAL-AG-CKC-301) strain was found most stable followed by PC20 (BS-J5) across all test sites. Kumar and Singh (2015) observed similar results during AMMI analysis in maize.

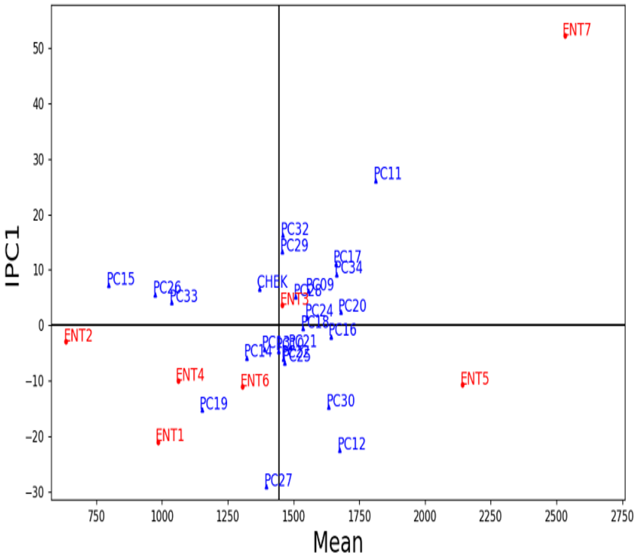

Figure-1: AMMI Biplot showing Seed cotton yield in abscissa & IPC1 interaction score value in ordinate for both environments and genotypes.

In AMMI biplot versus both IPC scores on the opposite axis (Figure-2) revealed that ENT2 (CRI Multan) and ENT3 (CRS Bahawalpur) are near ideal sites for cotton MET experiments in Punjab, while ENT1, ENT5 and ENT7 are located at the periphery of biplot and bearing higher contents of GEI are not suitable for cotton trials. ENT6 (CRS Vehari) was the average site for such cotton trials. Similarly, genotypes at the biplot's centre are stable yielders across test sites and bear the least GEI. These results were also stated by earlier researchers (Bose *et al.*, 2014; Sumathi *et al.*, 2017).

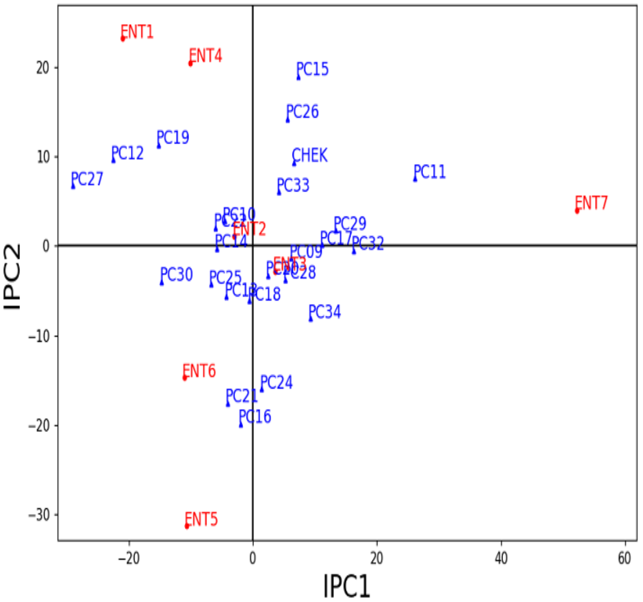

Figure 2: AMMI Biplot showing seed cotton yield of interaction scores IPC1 vs IPC2 values plotted on opposite axes.

Genotype Selection Index (GSI):

When significant GEI was present, strain selection on a mean yield basis leads to misleading results. AMMI analysis captures GEI efficiently but is unable to find stable genotypes. GSI was found reliable parameter for genotype selection in MET experiments. It is based on the ranks of mean yield and AMMI stability value. GSI ranks are presented in (Table-5). PC20 (BS-J5) was found most stable cum yielder strain with the least GSI value (4) followed by PC18 (WEAL-AG-CKC-301) and PC28 (VH-418) respectively. Contrary to this PC27 (WEAL-AG-9) and PC19 (FH-498) were found most unstable plus poor yielders with the highest GSI value of (43).

Table-5 Classification of cotton strains for mean seed cotton yield (Kgha^{-1}), AMMI Stability Value (ASV) & Genotype Selection Index (GSI)

Strains	Code	Mean Yield	Rank	IPC 1 score	IPC 2 score	ASV	Rank	GSI
SLH-33	PC09	1556	8	6.212	-1.466	16.3	9	17
Eye-22	PC10	1442	17	-4.553	2.710	12.2	3	20
CKC-5	PC11	1812	1	26.167	7.478	68.7	24	25
CIM-875	PC12	1676	3	-22.508	9.644	59.6	23	26

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ASLP-709	PC13	1389	19	-4.229	-5.665	12.4	4	23
IR-NIBGE-14	PC14	1321	21	-5.771	-0.338	15.1	7	28
YBG-2222	PC15	798	25	7.283	18.851	26.8	17	42
Diamond-2	PC16	1642	6	-1.967	-19.931	20.6	15	21
FH-494	PC17	1660	5	11.143	0.118	29.1	18	23
WEAL-AG-CKC-301	PC18	1536	10	-0.540	-6.215	6.4	1	11
FH-498	PC19	1152	22	-15.180	11.279	41.2	21	43
BS-J5	PC20	1679	2	2.400	-3.317	7.1	2	4
NIAB-484	PC21	1490	12	-4.024	-17.629	20.5	14	26
NS-211	PC22	1461	14	-5.984	1.951	15.7	8	22
CIM-602 (Stnd)	**CHEK**	**1370**	**20**	**6.663**	**9.335**	**19.7**	**12**	**32**
Rawal-111	PC24	1552	9	1.458	-16.004	16.5	10	19
CIM-785	PC25	1467	13	-6.696	-4.311	18.0	11	24
NIA-89	PC26	974	24	5.622	14.093	20.4	13	37
WEAL-AG-9	PC27	1397	18	-29.025	6.724	76.1	25	43
VH-418	PC28	1508	11	5.203	-3.814	14.1	6	17
Sayban-209	PC29	1457	16	13.310	1.720	34.8	19	35
Cyto-537	PC30	1634	7	-14.673	-3.995	38.5	20	32
RH-King-20	PC32	1460	15	16.259	-0.564	42.5	22	37
Eagle-4	PC33	1037	23	4.172	6.086	12.5	5	28
BH-225	PC34	1664	4	9.260	-8.148	25.5	16	20

Conclusion

Punjab province was the primary cotton production hub in past decades, but production is declining yearly, posing a severe threat to the national economy. The present study revealed that GEI plays an unavoidable role in MET trials on cotton crops, is necessary for the variety approval process and makes findings complicated and misleading. AMMI analysis captures and elegantly interprets GEI. The main results depicted that ENT2 (CRI Multan) and ENT3 (CRS Bahawalpur) are reliable sites for cotton MET experiments in Punjab. ENT7 (CRS Faisalabad) was found to be an unsuitable testing site in this study due to high interaction contents. Similarly, PC20 (BS-J5) was found to be a stable performer across test sites and a better yielder. Approval of this strain will be helpful for cotton revival in the province.

Conflict of interest

The authors had declared no conflict of interests.

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