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## Assessing diverse cotton germplasm through genetic evaluation and AMMI analysis

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### Abstract

The multi-environment trials (MET) were conducted at various locations of AICRP centers of cotton in 2019-20. In cotton (*Gossypium hirsutum* L.), MET was carried out in different five environments with twenty-two different genotypes for selecting the best genotype and environment. In a simple ANOVA analysis, the genotypes were found significantly different from each other in all five environments. Also, there was significant interaction found in G×E interaction for seed cotton yield. In AMMI analysis, principal component 1 (PC1) expressed about 51.5% of the variation and it was found significant, while PC2 was not found significant so only PC1 was taken under study. Among all the tested genotypes, the genotype GTHV-13/39 (G20) was recorded as the highest yielding genotype and the most stable genotype was GN. Cot. 22 (CC) (G21). But the most ideal genotype was GBHV-203 (G18) in seed cotton yield as well as stability performance in all five environments. Within these five environments, Talod (E3) was observed as the highest yielding environment. The Achhalia (E5) was found as the most stable environment among this environment for seed cotton yield. Thus, our studies suggest that AMMI model is also useful for estimating adaptability of traits other than yield utilized for breeding cotton cultivars.

**Keywords:** AMMI, Biplot, GGE, genotype x environment interaction, seed cotton yield

### 1. Introduction

Cotton is an essential crop required in the production of industrial fiber materials, edible oil, and feed for livestock utilized in many countries of the World. Cotton is grown in more than 100 countries and it is estimated that, the crop is planted on about 2.5 percent of the World's cultivable land (Shiv Sankar and Naidu, 2015) <sup>[13]</sup>. Among these countries, China, USA, Russia, India, Brazil, Pakistan, Turkey, Egypt, Mexico, and Sudan are accounted for 85-90% of the total cotton production (Zeng *et al.*, 2014) <sup>[14]</sup>. Cotton is the most important cash crop in India. India stands first in cotton production in the world and 2<sup>nd</sup> largest exporter of cotton in the World followed by USA. Among the available species of cotton, the *Gossypium hirsutum* is the predominant species, which alone contributes about 90% to the global production. During the current year 2019-20, Gujarat, Maharashtra and Telangana were the major cotton-growing states covering around 71% (86.4 lakh hectares) in area under cotton cultivation and 65% (246 lakh bales) of cotton production in India. The average productivity of India is 524 Kg/ha which is much below compared to World's average of 792 kg/ha (Anonymous, 2019). Cotton contributes 30 % of the GDP of Indian agriculture and 4% of total GDP. Cotton yield is a polygenic complex character that depends on several contributing characters coupled with varying environmental conditions (Khan *et al.*, 2009) <sup>[7]</sup>.

Cotton is also known as “white gold” in farming community. Cotton is also known as the “King of Fibre” crops due to its global importance in agriculture as well as industrial economy. It has high economic values in industry area. In last few years, farmers got high price for cotton, so there is increase in cultivated area of cotton. After developing textile and fiber industries cotton got high economic importance, so there is good demand for high-yielding genotypes of cotton.

The success of any breeding program depends on the extent of genetic diversity present in germplasm. One of the important steps here is to assess the performance of improved

genotypes in multi-environment (multi-location, multi-year or both) trials. It's observed that different varieties are expressed differently in different environments. A specified difference in the environment may produce a differential effect on phenotypes. This inter-play genetic and non-genetic effect causing differential relative performances of genotypes in different environments is called Genotypes × Environment Interaction (GEI). The occurrence of GEI causes difficulty in identifying superior genotypes. Genotype-environment interaction poses a major barrier to the breeder in the process of evolution of improved variety. Environment may cause changes in the genetic constitution of a population by the selection pressure on the population and in the long run may lead to evolutionary changes. Since genotype-environment interaction has masking effect on genotype, it is necessary to estimate the magnitude of this interaction variance to avoid over/ under estimation of genotypic variance in breeding programme (Rao *et al.*, 2004) [11]. The Additive Main effects and Multiplicative Interaction (AMMI) model (Gauch, 1988) [15] is a multivariate data analysis tool for stability analysis that first calculates genotype and environment effect (main and additive) using analysis of variance (ANOVA) and then analyses residual effect (genotype × environment interaction) using principal component analysis (PCA).

**2. Materials and Methods**

The present experiment was conducted under multi-environment trials (MET) (multi locations) with twenty-two different genotypes of cotton in five different environments viz. Surat (E1), Bharuch (E2), Talod (E3), Junagadh (E4) and Achhalia (E5) at the AICRPs centers respectively, during 2019-20. For the study of stability analysis twenty-two different genotypes of cotton were selected and the experiment was carried out under a large-scale variety trial (LSVT). The experiment was carried out in simple Randomized Block Design (RBD) with three replications in all five environments. Six traits like seed yield and yield attributing traits viz. lint yield, Ginning Percentage, boll weight, no. of bolls per plant and seed index were taken under study. But, the main trait is seed cotton yield because it is the most important economic trait for the farmer community. So, only this trait was taken under this study. Seed cotton yield was collected from the cotton bolls of some randomly selected plants of cotton and taken their weight in kg.

The combined analysis of variance was proceeded to look at G×E and stability of the genotypes across all environments. The AMMI model, which combines standard analysis of variance with IPC analysis (Zobel *et al.*, 1988) [15], was used to investigate. In AMMI model the contribution of each

genotype and each environment to the G×E interaction is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA1 (Zobel *et al.*, 1988) [15].

$$Y_{ij} = \mu + g_i + l_j + \delta_{ij} \tag{1}$$

Where,

- $Y_{ij}$  = Response of  $i^{th}$  genotype in  $j^{th}$  environment,
- $\mu$  = General mean effect,
- $g_i$  = Effect of  $i^{th}$  genotype,  $I = 1, 2, \dots, k$ ,
- $l_j$  = effect of  $j^{th}$  environment,  $I = 1, 2, \dots, n$
- $\delta_{ij}$  = residual

The residual component can be partitioned into the sum of multiplicative functions of  $i$  and  $j$  (Mandel, 1971) [9]. Thus,

$$Y_{ij} = \mu + g_i + l_j + (\lambda_1 v_{1i} v_{1j} + \lambda_2 v_{2i} v_{2j} + \dots + \lambda_m v_{mi} v_{mj}) = \mu + g_i + l_j + \sum_{m=1}^m \lambda_m v_{mi} v_{mj} + \rho_{ij} \tag{2}$$

where,  $\lambda_m$  is the square root of the eigenvalues for PCA axis  $m$  of the matrix  $E'E$  and  $E$  is the  $k \times n$  matrix,  $v_{mi}$  and  $v_{mj}$  are the elements of the corresponding normalized eigen vectors of the matrices  $EE'$  and  $E'E$ , respectively;  $m$  is the number of axes retained,  $m \leq \min(k, n-1)$ ;  $\rho_{ij}$  is a random error.

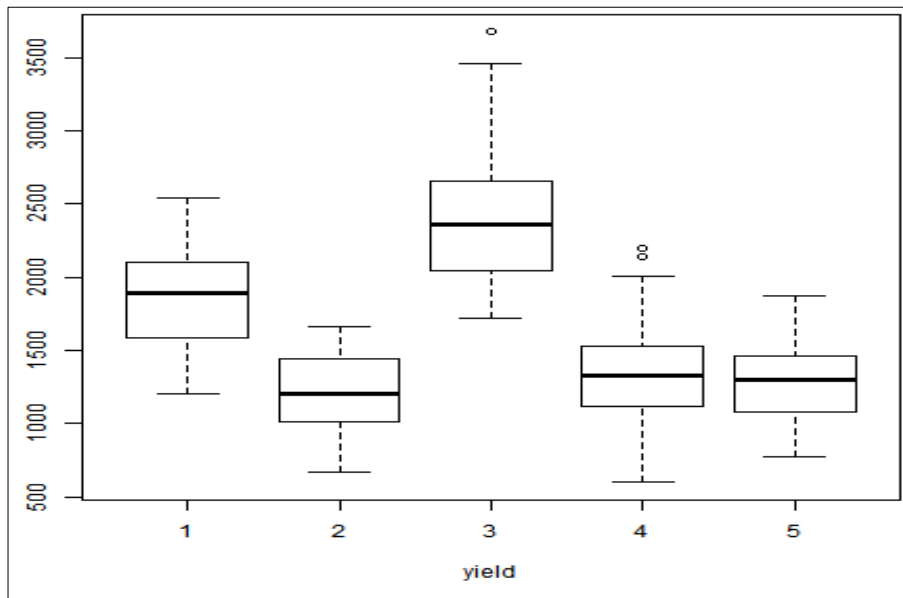
**3. Result and Discussion**

**3.1 Assumption for Normality test and ANOVA**

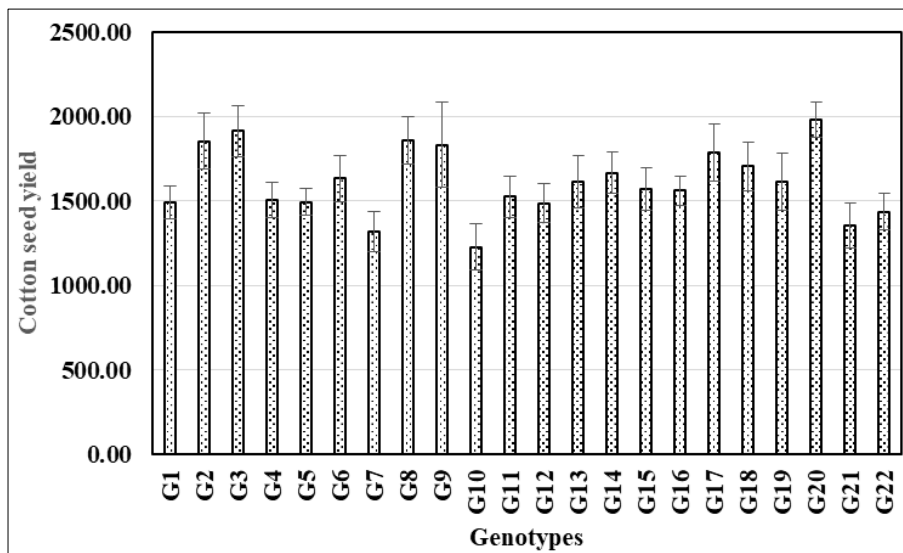
In order to check the assumption of AMMI and ANOVA, Shapiro-Wilk's normality of the error (1995) [12] and Bartlett's homogeneous variance of errors (1937) for the seed cotton yield allowed preceding the individual ANOVA in each of five environments. Similarly, assessment of the Hartley's  $F_{max}$  test (1950) [5] indicated homogeneous error variances among the evaluated environments that allowed pooled ANOVA. It shows that the assumption is valid for homogeneous variance and normality of the error accordingly the ANOVA could be validated. Generally, the box plot was used for graphical representation to test for the normality. Boxplot encodes five characteristics of the distribution of data by showing their position and length. The box plot uses the median, the approximate quartiles and the lowest and highest data points of a distribution of data values. The analysis has been carried out with the help of STAR software. It shows that the assumption of homogeneous variance and normality of the error was proved.

**Table 1:** Descriptive Statistics for cotton seed yield

Cotton seed yield						
	E1	E2	E3	E4	E5	Pooled
<b>Descriptive statistics</b>						
Mean	1866.18	1206.46	2387.46	1325.77	1264.68	1611.59
SD	171.16	143.09	148.45	173.52	149.53	239.99
CV	9.17	11.86	6.22	13.09	11.82	14.89
SE(m)	98.82	82.61	85.71	100.18	86.33	107.33
CD (0.05)	282.03	235.78	244.61	285.91	246.38	301.84
<b>Genetic parameters</b>						
GCV	14.87	16.68	16.29	20.46	16.40	10.52
PCV	17.47	20.47	17.44	24.29	20.22	18.23
ECV	9.17	11.86	6.22	13.09	11.82	14.89
$h^2$	72.44	66.43	87.29	70.96	65.80	33.30
GA	486.54	337.95	748.71	470.65	346.57	201.61
GA % of mean	26.07	28.01	31.36	35.50	27.40	12.51



**Fig 1:** Box plot across five environments depicting the normality of the yield traits



**Fig 2:** Standard error of mean graph of twenty-two genotypes of cotton for seed yield across all locations

The seed cotton yield ranged from 1409 to 2354 kg/ha at Surat (E1), 802 to 1583 kg/ha at Bharuch (E2), 1864 to 3417 kg/ha at Talod (E3), 797 to 2034 kg/ha at Junagadh (E4) and 792 to 1621 kg/ha at Achhalia (E5) environments. Genotype, GISV-310 (2354 kg/ha) had the highest yield, and GSHV-200 (1410 kg/ha) lowest yield at Surat (E1) environment, GISV-316 (1583 kg/ha) had the highest yield and GSHV-200 (802 kg/ha) lowest at Bharuch (E2) environment, GSHV-199 (3417 kg/ha) had the highest yield and GBHV-201 (1864 kg/ha) lowest at Talod (E3) environment, GTHV-13/39 (2032 kg/ha) had highest yield and GSHV-192 (797 kg/ha) lowest at Junagadh (E4) and GTHV-13/39 (1621 kg/ha) highest and GSHV-200 (792 kg/ha) lowest at Achhalia (E5). While the overall mean yield of five environments ranged between 1206 to 2387 kg/ha. Fig 1 indicated that genotype G20 has recorded highest mean value across all five environments and ranked first while G5 has recorded the lowest SE (m) within replication among all the genotype across all environments. Among these different five environments is concern Junagadh (E4) has recorded the highest coefficient of variance in percentage (13.08%) and Talod has recorded the lowest CV% (6.21%). The above data indicated that GTHV-13/39 genotype was the highest yielder in pooled environments among 22

genotypes. Among the five environments, the highest mean seed cotton yield was recorded in Talod. Thus, GTHV-13/39 genotype may be recommended for further utilization as variety/parent in a breeding program for high seed cotton yield. The variation of genotypes was greater than the variation of environments for all five environments. Indicated genotypes have a greater effect on phenotypes than the environment.

In the present study, the estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) indicating that the variation is due to the influence of environment. GCV is more useful for assessing the variability as it depends upon the heritable portion of variability. The estimates of variances due to genotypic, phenotypic and environmental effects for the nineteen characters of cotton showed wide variation among different traits. In the current study, a wide range of phenotypic variability was observed among all the traits studied.

The high heritability estimates are supportive during selection of superior genotypes on the basis of phenotypic performance of quantitative traits. Therefore, for improving these traits the selection will be more effective in early generation on the basis of their performance and can be improved by mass

selection or progeny selection. GCV along with heritability gives the better picture for amount of genetic advance to be expected from selection (Burton, 1952) [3].

Genetic advance is the improvement in the mean of selected families over the base population (Lush, 1949) [8]. Genetic advance when expressed, as percentage over mean is called genetic gain. High heritability accompanied with high genetic advance proves presence of additive gene effects for heritability and confirms the efficiency of selection for the traits under study. Similarly, high heritability accompanied with low genetic advance indicates non additive gene action and proves that high heritability is being exhibited due to favourable influence of environment rather than genotype thus selection for such traits may not be rewarding. Low heritability accompanied with high genetic advance explains that the trait is governed by additive gene effects and low heritability is being exhibited due to high environmental effects thus selection may be effective in such cases.

### 3.2 Pooled and Individual Analysis of variance (ANOVA)

**Table 2:** Analysis of Variation (mean sum of square value) of different genotypes of seed cotton trait in different environments and pooled analysis.

Individual					Pooled		
E1	E2	E3	E4	E5	Genotype	Environment	G × E
260311**	142022**	476041**	250801**	151404**	595265**	17043600**	171329**

\*\* Indicate  $p < 0.01$ , \* indicate  $p < 0.05$

Here, among these twenty-two genotypes environment wise highest and lowest genotype differ, so stability analysis helped to identify the most stable and unstable genotypes among these environments. Moreover, as for as environment is concerned all environments differ significantly with each other for seed cotton yield. Analysis of variation for observed trait revealed that mean square value for yield was recorded

The pooled ANOVA revealed a significant difference among cultivars, environments and a significant G×E interaction (Table 2), which indicates that the environment had an influence over the differentiated performance of the different cultivars and the broad range of variability among them (Anandan *et al.*, 2009) [1]. Analysis of variation for the seed cotton yield (Table 2) also revealed that mean square values of different genotypes among all five environments were highly significant, which indicates that all genotypes performed differently in these environments and these genotypes differs from each other. ANOVA for pooled data across environments reflected that the mean square due to genotype was significant for seed cotton yield. Variation due to genotype and environment interaction was found to be significant for Seed cotton yield, which supports a strong case for AMMI analysis for this trait. The same result was found by (Mudada *et al.*, 2017) [10]. Here we have studied only the main economic character *i.e.* cotton seed yield through AMMI analysis.

highly significant in all five environments. ANOVA for pooled data across environments reflected that mean square due to genotype was significant for seed cotton yield. Variation due to genotype and environment interaction was found to be significant for Seed cotton yield, which supports a strong case for AMMI analysis for this trait. The same result was found by (Mudada *et al.*, 2017) [10] for this trait.

**Table 3:** Analysis of variation of AMMI model for cotton seed yield

Source	Degrees of freedom	SS	MS
Genotype	21	4166850	198422**
Environment	4	22724800	5681210**
G×E	84	4797200	57109.5*
AMMI1	24	2469140	102881*
AMMI2	22	1120390	50926.7
AMMI3	20	765547	38277.3
AMMI4	18	442122	24562.3
Total	109	31688900	
AMMI scores for genotypes and environments			
Code in Biplot	Genotypes	AMMI1	AMMI2
G1	GISV-298	8.465	-5.476
G2	GISV-310	-6.288	-3.279
G3	GISV-316	-3.256	11.020
G4	GSHV-187	11.300	14.380
G5	GSHV-188	9.777	3.804
G6	GSHV-191	1.049	-1.063
G7	GSHV-192	5.010	-3.861
G8	GSHV-195	-4.577	2.218
G9	GSHV-199	-26.870	-1.756
G10	GSHV-200	-2.399	4.562
G11	GJHV-513	3.485	-8.552
G12	GJHV-520	4.009	-5.671
G13	GJHV-524	-7.523	2.175
G14	GJHV-531	3.631	10.320
G15	GBHV-200	2.020	-14.010
G16	GBHV-201	10.310	-8.650
G17	GBHV-202	-9.486	-4.745
G18	GBHV-203	0.2594	-5.537
G19	GBHV-204	-9.616	4.684

G20	GTHV-13/39	6.352	-1.484
G21	GN. Cot. 22 (CC)	-0.137	7.130
G22	G. Cot. 16 (LC)	4.481	3.788
<b>Environments</b>			
E1	Surat	-4.312	-22.860
E2	Bharuch	21.600	9.673
E3	Talod	-31.130	12.530
E4	Junagadh	10.180	12.270
E5	Achhalia	3.658	-11.620

\*\* Indicate  $p < 0.01$ , \* indicate  $p < 0.05$

The AMMI analysis of variation for seed cotton yield of the twenty-two genotypes tested in five environments showed that 5681210 of the mean sum of square (MS) was attributable to environmental effects, 198422 to genotypic effects, and 57109.50 to GEI effects and their AMMI scores presented in Table 3. The mean square for the IPCA1 (AMMI1) was significant at  $P = 0.01$  but IPCA2 (AMMI2) was non-significant. Therefore, only AMMI1 biplot analysis between main effects and first IPCA was performed. The AMMI analysis of variation for seed yield for all these genotypes in five environments given in Table 3. This finding was in conformity to those of Islam *et al.* (2014) [6].

In the AMMI analysis graph (Figure 3), the relationship between seed cotton yield and AMMI1 scores for twenty-two genotypes across five environments is depicted. Notably, genotypes and environments are positioned in relation to an average yield line, which is indicated by a vertical line. Genotypes and environments to the right of this line demonstrate a seed cotton yield higher than the average, while those on the left indicate yields below average. Remarkably, eleven out of the twenty-two genotypes exhibited notably higher seed cotton yields compared to the general mean. These high-yielding genotypes are: G. Cot. 16 (LC) (G20), GISV-316 (G3), GSHV-195 (G8), GISV-310 (G2), GSHV-199 (G9), GBHV-202 (G17), GBHV-203 (G18), GJHV-531 (G14), GSHV-191 (G6), GBHV-204 (G19), and GJHV-524 (G13). Notably, GBHV-203 (G18) stood out as the most stable genotype among them. Conversely, the remaining genotypes displayed lower seed cotton yields, occupying positions on the left side of the average yield line on the biplot. Regarding the environmental conditions, two test environments stood out for their high-yielding characteristics: Surat (E1) and Talod (E3). Among these, Surat (E1) exhibited the most favourable conditions, being situated closest to the horizontal line (PC1) on the biplot.

Overall, the AMMI analysis provides valuable insights into the yield performance of various genotypes in response to different environments. This information can guide breeding and cultivation strategies to enhance cotton yield in diverse conditions.

Genotypes or environments with larger negative or positive IPCA1 scores have high interaction, while those with IPCA1 scores near zero (close to the horizontal line) have little interaction across environments. Some genotypes, G18, G6 and G21 felt almost on the horizontal line indicating their uniform performance across the environments. These genotypes to be considered as stable against the environments changes. But G21 (low yielding) was most nearer to zero so it indicated most stable genotype among these genotypes on these environments. The genotype, G20 had seed yield on the right half of the mean effect line but with a large positive score on AMMI1. Therefore, there was a positive interaction of G20 with E2, E4 and E5 but negative interaction with E1 and E3. This graph indicated that G3, G8, G2, G9, G17, G13 and G19 which were high seed yielded and most favourable

genotypes for environments E1 and E3. On other side genotypes, G14, G15, G16 and G11 had average or below the average seed yield which was favourable for environments E2, E4 and E5.

Among these, all genotype, the genotype GTHV-13/39 (G20) was recorded as highest yielding genotype and most stable genotype was GN. Cot. 22 (CC) (G21). Within this five environment, Talod (E3) was observed as the highest yielding environment. The Achhalia (E5) was recorded as the most stable environment among this environment for seed cotton yield. AMMI analysis also helps in identifying similar environments and these similar environments may be removed from a multi-location testing programme for saving resources.

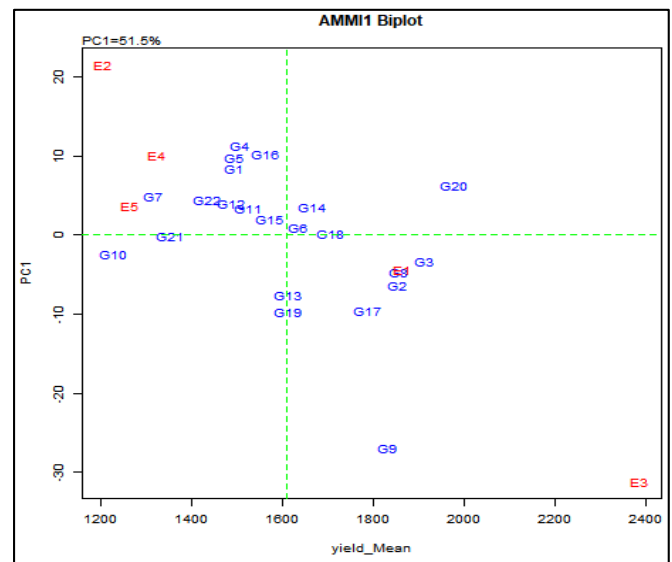


Fig 3: AMMI1 (PC1 vs Mean) graph for seed cotton yield

#### 4. Conclusion

Breeders, geneticists and agronomists are facing major barriers of Genotype-by-Environments (GE) interaction in performance testing of genotypes. The genotype-environment interaction reduces association between phenotypic and genotypic values and leads bias in the estimates of gene effect and combining ability for various characters sensitive to environmental fluctuation. Both yield and stability of performance should be considered jointly to reduce the effect of GE interaction and to make selection of genotypes more precise and refined. The AMMI was quite useful to quantify the GxE interaction and to know the stability and adaptability on the multi environmental trial. The results illustrated that the among these twenty-two genotypes the best ideal genotype is GBHV-203 (G18) with respect to their yield and stability performance in across all environments. The genotype G18 has the high yield than the mean yield and score of PCA1 is mostly near to zero. The highest yielding genotype G20 showed positive interaction in E2, E4 and E5

environments, while negative interaction in E1 and E3 environments. The E5 environment explained less interaction, that why it can be selected as genotype evaluation site for cotton crop. While, the E1 environment has good environments conditions for seed cotton yield as well as less genotypes showed less interaction with environment.

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