A-5950
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RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume Issue : ()

AMMI Analysis of Yield Performance in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes for Adaptation to Rainfed Conditions in Andhra Pradesh

L. Madhavilatha, C.V. Chandra Mohan Reddy, M. Shanthi Priya, N. Anuradha,
R. Narasimhulu, Y. Pushpa Reni, C. Kiran Kumar Reddy, M. Hemanth Kumar

10.18805/IJARe.A-5950

ABSTRACT

Background: Foxtail millet is a short duration crop which is suitable for different cropping systems in rainfed farming. Improvement of yields is necessary to achieve profits in rainfed situation which is highly influenced by the high yielding varieties. Genotype by environment interaction (G×E) causes genotypes failure to keep high performance in all environments. Location specific climatic conditions also influence significantly genotype × environment (G×E) interaction, so with the result that identifying stable genotypes for rainfed situations is difficult. The study was conducted with a prime objective to identify stable high yielding foxtail millet genotypes for rainfed cultivation and to identify ideal mega-environments using additive main effects and multiplicative interaction stability model analysis.

Methods: Four prerelease promising foxtail millet genotypes including three released popular check varieties were evaluated across six locations in Andhra Pradesh during *Kharif*, 2018 under rainfed situation.

Result: The culture, SiA 3159 was found to be stable performer across the locations indicating that it is suitable for wide range of environments. In contrast the genotypes SiA 3085 and SiA 3156 showed narrow adaptation, specifically adapted to Anantapur (rainfed situation having scarce rainfall) and Vizianagaram (favorable environments with assured rainfall areas) respectively.

Key words: AMMI analysis, Foxtail millet, Multilocation testing, Stability.

INTRODUCTION

Foxtail millet [*Setaria italica* (L.) P. Beauv.] is one of the world's oldest cultivated crop and ranks second in the world's total production of millets. It is an important staple food for millions of people in southern Europe and Asia (Marathee, 1993). In India the crop area has declined and cultivated in a limited area of around 0.1 million hectares in sporadic patches in the states of Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra, Madhya Pradesh, Uttar Pradesh and North Eastern states with an annual production of 0.29 million tones and productivity of 600 kg /ha (Anand *et al.,* 2020). Millets are known to possess unique features of resilience to adverse environments, especially during drought and infertile soil conditions (Nadeem *et al.,* 2020). Foxtail millet is a short duration crop which is suitable for different cropping systems in rainfed farming. Foxtail millet grains are rich in starch, proteins and lipids as well as vitamins and minerals, which makes it a good source of nutrients in the human diet in many parts of the world, especially in Africa, China and India where food security has always been the primary concern (Bai *et al.,* 2008). Improvement of yields is necessary to achieve profits in rainfed situation which is highly influenced by the high yielding varieties. Development of high yielding varieties has always been the ultimate objective of crop breeders especially those who do research on orphan crops. Although research on the development of high yielding varieties have led to release of a large number of new varieties in different crops, genotype by environment interaction (G × E) causes genotypes failure to keep high performance in all environments (Mohammadi and Nader, 2008). So, yield stability has been considered as important as the yield potential in plant breeding and will be of particular concern by continuing changes in climatic condition (Fasahat *et al.,* 2015). The newly developed genotypes which perform best in advanced yield trials are promoted to MLTs to assess the stable performance and adaptability across different environments. The genotype environment interaction results in complex data which needs an effective statistical analysis tool for better interpretation. Location specific climatic conditions also influence significantly to genotype × environmental (G × E) interaction, so with the result that

Department of Genetics and Plant Breeding, Agricultural Research Station, Tirupati-517 505, Andhra Pradesh, India.

Corresponding Author: L. Madhavilatha, Department of Genetics and Plant Breeding, Agricultural Research Station, Tirupati-517 505, Andhra Pradesh, India. Email: lmlreddy36@gmail.com

How to cite this article: Madhavilatha, L., Reddy, C.V.C.M., Priya, M.S., Anuradha, N., Narasimhulu, R., Reni, Y.P., Reddy, C.K.K. and Kumar, M.H. (2022). AMMI Analysis of Yield Performance in Foxtail Millet [*Setaria italica* (L.) P. Beauv.] Genotypes for Adaptation to Rainfed Conditions in Andhra Pradesh. Indian Journal of Agricultural Research. DOI: 10.18805/IJARe.A-5950.

Submitted: 06-12-2021 **Accepted:** 08-03-2022 **Online:** 11-04-2022

identifying stable genotypes for rainfed situations is difficult. Among all the statistical models propounded for dealing with G × E data, the addictive main effects and multiplicative interactions (AMMI) Model (Zobel *et al.,* 1988) is the best to analyze the stable performance of the entries.

The best practice of AMMI involves (1) Analysis of variance (ANOVA) (2) Model diagnosis (3) Mega-environment delineation (4) agricultural recommendations to exploit both broad and narrow adaptation to increase yields (Gauch, 2013). Therefore in the present study, AMMI stability analysis was utilized for the data collected from Multilocation trial conducted in six locations under rainfed condition during Kharif, 2018. The main objective of the study was to identify high yielding stable foxtail millet genotypes for general and specific adaptation to rainfed conditions and to investigate the mega environment specific genotypes which can be suggested for cultivation under rainfed situations.

MATERIALS AND METHODS

The study was conducted to evaluate seven foxtail millet genotypes developed from Regional Agricultural Research Station, Nandyal in multi-location trial in six locations across Andhra Pradesh in rainfed situation during *Kharif*, 2018. Description of these six locations is given in Table 1. Four promising prerelease foxtail millet cultures (SiA 3159, SiA 4148, SiA 4201 and SiA 4203) were evaluated along with three checks (Suryanandi, SiA 3156 and SiA 3085). Details of these genotypes along with pedigree are given in Table 2. In six locations, experiment was raised during *Kharif*, 2018 in randomized complete block design (RCBD) with three replications. Each plot consisted of ten rows of 3 m length with a spacing of 22.5 cm × 7-10 cm. Recommended package of practices were followed to raise the crop under rainfed situation. Observations were recorded for plant height, number of productive tillers per plant, panicle length and grain yield.

AMMI Model was used to analyze the G × E interactions. The procedures of Ebdon and Gauch (2002 a, b) and Gauch (2013) were used for AMMI Model analysis and accuracy gain. The AMMI Model applies ANOVA to partition the variation into the main effects *viz.,* genotype (g in AMMI), environment (e in AMMI) and GEI and then it applies Principal Components Analysis (PCI) to the data. According to Gauch (2013), model diagnosis is useful to determine the best AMMI model family for a given data set and is advised to use F_R-test (Cornelius, 1993) to assess model diagnosis and to identify significant interaction principal components (IPCs) in the AMMI model using AMMISOFT software for the analysis of the data. AMMI constitutes a model family with AMMI 0 having no IPC, AMMII 1 having 1 IPC, AMMI 2 having 2 IPC and so on up to AMMIF (residual discarded).

The ratio of yield for AMMI winners within each environment (identified in the first column of AMMI ranks) was calculated by dividing the yield for the overall winner (Gauch, 2013). According to Gauch (2013) a ratio of 1 represents a winning genotype across environments. This ratio is an assessment of the importance of narrow adaptation due to GEI effects, with a ratio of ≥1.10 indicative of narrow adaptation.

RESULTS AND DISCUSSION

ANOVA and identification of AMMI Model families

Analysis of variance for grain yield using AMMI model is presented in Table 3. The main effects genotype (G), environmental (E) and their interaction (GEI) components were statistically significant at $p \leq 0.001$. The environmental component showed the largest proportion of variation 62.38% followed by G × E interaction components (25.02%) and least variation by genotypic component (4.42%). The large variation for environments indicated that the environments were diverse with large differences among environmental means causing most of the variation in grain yield which is in harmony with the findings of Molla *et al.* (2013). The variation due to GEI was higher than genotype variation indicating that there were substantial genotypic responses across environments. Presence of significant GEI was also reported earlier by Misra *et al.* (2009). The total variation of GEI consists of GEI_N and GEI_S with GEI_N estimated simply by multiplying the error mean square by the number of degrees of freedom of GEI and GEI_S obtained by subtracting GEI_N from GEI (Gauch, 2013). The GEI effects were partitioned into four IPCs (IPC 1, IPC 2, IPC 3 and IPC 4). IPC 1, IPC 2 and IPC 3 were found to the significant at $P \leq 0.001$ for grain yield in different environments under rainfed conditions. In terms of contribution to the total GEI for grain yield IPC 1 alone contributed to 59.07%, (IPC 1 and IPC 2 cumulatively contributed 84.84%) and IPC 1 to IPC 3 contributed 94.94%. Based on statistical and practical considerations model evaluation is essential to determine the best AMMI Model family for grain yield. Three AMMI model families were identified based on the FR-test at $P \leq 0.01$ for grain yield in the different environments (Table 3). The AMMI model captured 88.33% of the GEIs (GEI Signal) and 11.67 of the GEI_N (GEI Noise). Sum of squares for GEI_S and GEI_N was 5 fold and 0.66 fold respectively that of genotype main effect. The results show that the AMMI model as used in this study was appropriate and worthwhile, since the SS for GEI_S and also SS for GEI are not buries in GEI_N. AMMI is not a single model; rather it constitutes a model family, AMMI0 to AMMIF. AMMI0 captures no GEI_N and GEI_S whereas AMMIF, the full model equals the actual data so it has no residual and captures all GEI_N and $GEI_{S.}$ Therefore, model selection is one of the most important steps in AMMI analysis. Model diagnosis provides cues for selecting the best model for a given dataset (Gauch, 2013). The results clearly indicate that IPC1, IPC2 and IPC3 represent the AMMI model families AMMI 1, AMMI 2 and AMMI 3 respectively, cumulatively covering 94.94% of the GEI variation and 107.47% of the GEIs variation. This indicates the AMMI biplot model is the best fit for the data set which is in agreement with Naveed *et al.* (2007). In AMMI

Table 1: Description of locations used for the evaluation of foxtail millet genotypes.

Location	Latitude and Longitude	Environment code	EC dS/m	PH	Mean yield q/ha
Utukur	14° 45′ 78° 81′	UTK 1	0.67	7.8	27.67
Perumallapalle	13° 37′ 79° 25′	PMP 2	0.32	7.8	16.34
Anantapur	14° 41′ 77° 40′	ANT 3	0.85	6.2	22.59
Lam	16° 10′ 80° 43′	LAG 4	0.16	7.4	11.93
Vizianagaram	18° 7′ 83° 23′	VIN 5	0.25	7.2	29.04
Nandyala	15° 46′ 78° 48′	NDL 6	0.25	8.2	25.55

Table 2: List of foxtail millet genotypes and their parentage used in the study.

Genotype	Parcentage
SiA 4201	SiA 2884 × GS-445
SiA 3156	Selection from SiA 2871
SiA 4148	SiA 3088 × SiA 3075
SiA 4203	SiA 2723 × GS-445
SiA 3085	Selection from SiA 2644
SiA 3159	Srilakshmi × SiA 1378
Suryanandi	Selection from SiA 1244

biplot 1 IPC1 scores of genotypes and environments are plotted against their respective means, the plot is helpful in visualizing the average productivity of the genotypes, environments and their interaction for all possible genotype-environment combinations (Fig 1). Genotypes that group together have similar adaptation while environments which group together influence the genotypes in the same way. AMMI2 model family delineated three mega-environments with three winner genotypes namely SiA 3159, SiA 3085 and SiA 4203 (Table 4). AMMI biplot2 shows the GE interaction patterns beyond those captured in an ordinary AMMI1 biplot, helps in visual interpretation of the GEI patterns and identification of the genotypes or locations that exhibits a low, medium or high level of interaction effects (Fig 2). Genotypes near the origin are non-sensitive to environmental interactive forces and those distant from the origin are sensitive to environment and have large interactions. The points of either genotypes or environments that are close to each other have similar interaction patterns, while those distant from each other have different interaction patterns (Krishnamurthy *et al.,* 2021 and Simon *et al.,* 2018).

Identification of winner genotypes from the AMMI model family

A mega-environment is defined as a group of locations that consistently shares the best set of genotypes or cultivars across years (Yan and Rajcan, 2002). Mega-environments are distinguished by having different genotype winners. Increasingly complex AMMI models generally have more genotype winners. Winner genotypes identified using the AMMI model family for yield traits are shown in Table 4. Genotypes were listed based on IPC1 scores with the top and bottom order genotypes have contrasting GEI patterns. The AMMI constituted a model family from AMMI 0 to AMMI F with AMMI 0 having one winner genotype in one mega environment whereas the AMMI F consisted five winner genotypes with five mega environments. The genotype SiA 3159 won in all AMMI model families and it also won interms of maximum number of environments with 6,4,3,2,3 and 2 in the AMMI 0, AMMI 1, AMMI 12, AMMI 3, AMMI 4 and AMMI F model families respectively. According to the standard AMMI diagnosis model, an intermediate AMMI model such as AMMI I or AMMI 2 is predicatively accurate. In the present study AMMI1 and AMMI2 delineated three and three mega environments based on IPC 1 and IPC 2 scores respectively with each environment having one genotype. According to AMMI 1 in addition to genotype SiA 3159 the genotype SiA 3085 and SiA 3156 also won in one and one mega environments respectively. Similar results were obtained by Wedajo *et al.* (2018) and Krishnamurthy *et al.* (2017). In the present experiment the AMMI3 model family had the maximum predictive accuracy representing 4 environments with 4 winning genotypes. According to the AMMI 3 model family genotypes SiA 3159, SiA 4201, SiA 4203 and SiA 3085 won in 2, 2, 1 and 2 different mega environments respectively. Among the four genotypes of the AMMI3 model family the genotype SiA 3159 had maximum grain yield of 26.04 q/ha which was more than overall mean yield of 22.19 q/ha under different environments in rainfed conditions. Therefore SiA 3159 is the winning genotype with a ratio of 1.0 is broadly adopted for different environments. In contrast the genotype SiA 3085 and SiA 3156 showed narrow adaptation, specifically adapted to Anantapur (rainfed situation having scarce rainfall) and Vizianagaram (favorable environments with assured rainfall areas) respectively.

Delineation of mega environments based on AMMI

The ranking of the five top performing foxtail millet genotypes across the test environments based on AMMI 1 and AMMI F

Table 3: Analysis of variance for grain yield in foxtail millet genotypes in rainfed conditions across six locations during 2018.

Source of variance	Degrees of freedom	Sum of squares	Mean sum of squares	Proportion of variation			
				Total variation %	Main and interaction variation %	G × E interaction variation %	G × E interaction of signal variation %
Treatment	41	7045.664	171.845***	91.82			
Genotype (G)	6	339.230	56.538***		4.42		
Environment (E)	5	4786.755	957.351***		62.38		
Interaction (G × E)	30	1919.680	63.989***		25.02		
IPC1	10	1133.881	113.388***			59.07	66.87
IPC2	8	494.633	61.829***			25.77	29.17
IPC3	6	193.849	32.308***			10.10	11.43
IPC4	4	70.722	17.681			3.68	4.17
Residual	2	26.594	13.297			1.39	1.57
Error	84	627.329	7.468	8.18			
Blocks/environment	12	22.142	1.845		0.29		
Pure error	72	605.187	8.405		7.89		
Total	125	7672.993	61.384	100	100	100	

***Significant at $p \leq 0.001$.

GEIs or GEI signal = 88.33%; GEI$_N$ or GEI Noise = 11.67%

Table 4: "Winner" genotypes and numbers of mega-environments for the additive main effects and multiplicative interaction (AMMI) model family for foxtail millet genotypes evaluated in six environments in rainfed conditions.

Genotype number	Genotype code	Grain yield (q/ha)	AMMI model family						
			IPC1 score	AMMI0	AMMI1	AMMI2	AMMI3	AMMI4	AMMIF
SiA 3159	3159	26.04	3.19	6	4	3	2	3	2
SiA 4201	4201	21.94	0.32				1		1
SiA 4148	4148	20.90	-0.51					1	1
SiA 4203	4203	21.14	-0.55			1	1	1	1
SiA 3085	3085	22.12	-1.37		1	2	2	1	1
SiA 3156	3156	21.09	-2.29		1				
Mega-environments				1	3	3	4	4	5

The genotype 7 (Suryanandi) never win so not listed.

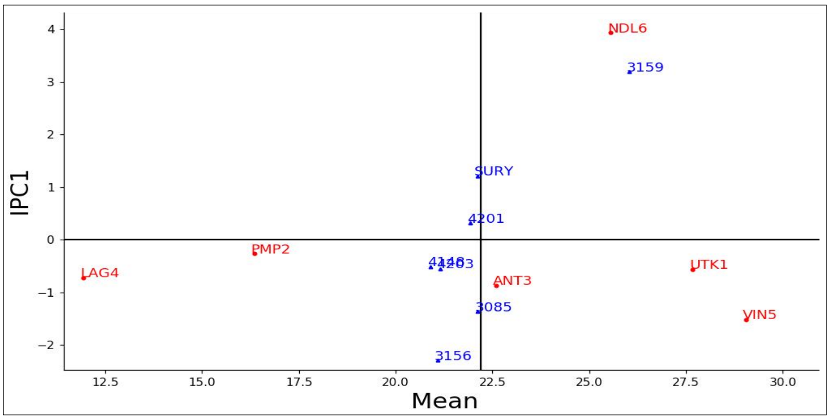

Fig 1: Scattered distribution patterns of 7 foxtail millet genotypes and 6 environments presented in the AMMI model biplot1 with grain mean yield (q/ha).

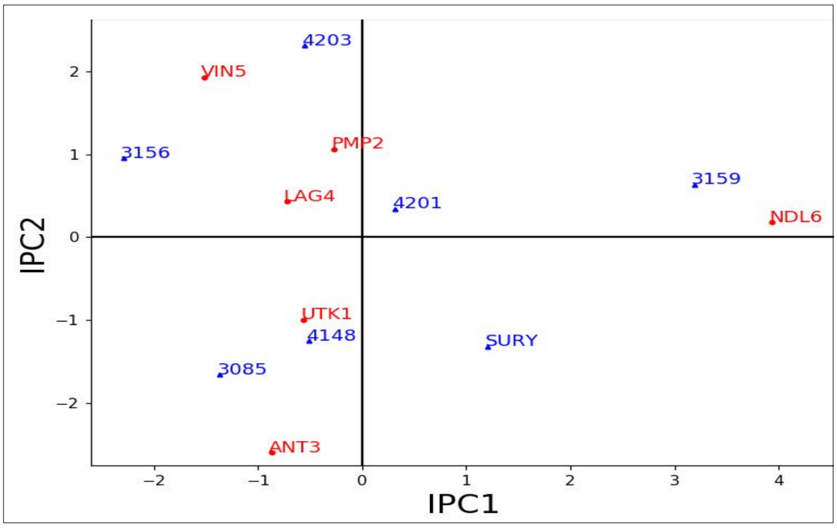

Fig 2: Scattered distribution patterns of 7 foxtail millet genotypes and 6 environments presented in AMMI biplot2 showing IPC1 and IPC2 scores.

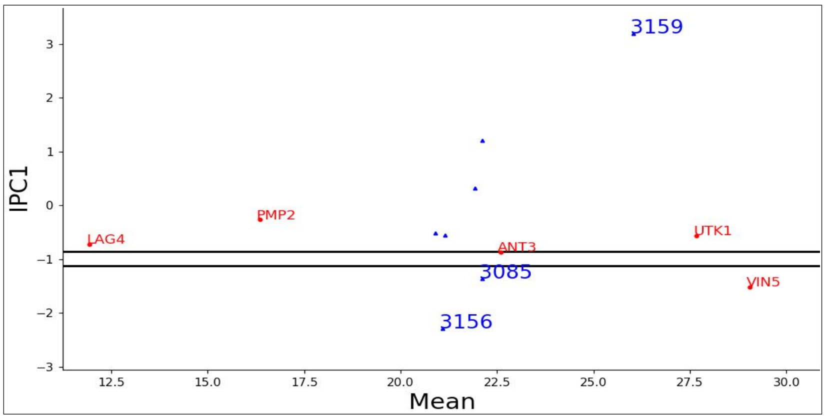

Fig 3: AMMI mega-environment display for 7 foxtail millet genotypes evaluated under 6 environments.

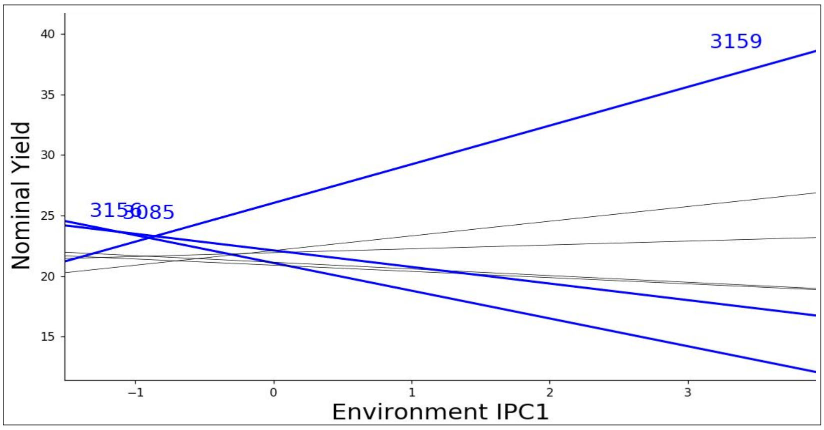

Fig 4: Adaptive responses for foxtail millet genotypes according to the AMMI1 model.

Table 5: Ranking table showing the top 5 foxtail millet genotypes according to AMMI I and AMMIF model families.

Mega-environment	Environment code	IPCI score	Ratio	AMMI I ranks					AMMI F ranks				
				1	2	3	4	5	1	2	3	4	5
ME-1	NDL 6	3.935	1.000	SiA 3159	Suryanandi	SiA 4201	SiA 4203	SiA 4148	SiA 3159	Suryanandi	SiA 4201	SiA 4203	SiA 4148
	PMP 2	-0.267	1.000	SiA 3159	SiA 3085	SiA 4201	Suryanandi	SiA 3156	SiA 3159	SiA 4201	SiA 3156	SiA 3085	SiA 4203
	UTK 1	-0.560	1.000	SiA 3159	SiA 3085	SiA 3156	SiA 4201	SiA 4203	SiA 4148	SiA 4201	SiA 3159	SiA 3085	Suryanandi
	LAG 4	-0.725	1.000	SiA 3159	SiA 3085	SiA 3156	SiA 4201	SiA 4203	SiA 4201	SiA 3085	SiA 3159	SiA 4203	SiA 3156
ME-2	ANT 3	-0.866	1.002	SiA 3085	SiA 3159	SiA 3156	SiA 4201	SiA 4203	SiA 3085	Suryanandi	SiA 4148	SiA 3159	SiA 3156
ME-3	VIN 5	-1.516	1.120	SiA 3156	SiA 3085	SiA 4203	SiA 4148	SiA 4201	SiA 4203	SiA 3156	SiA 3159	SiA 4148	SiA 3085

ranking is presented in Table 5. The environments in the table are listed based on the IPC1 scores with the top and bottom ordered environments have contrasting GEI patterns. According to AMMI1 model 6 environments were delineated into 3 mega environments. The first mega environment was the largest and consisted of 4 different environments (Fig 3). The second mega environment consisted of single environment namely ANT 3 as did the third mega environment VIN 5. AMMIF delineated five mega environments with five genotypes. Adaptive responses for foxtail millet genotypes according to the AMMI model are shown in Fig 4. According to the AMMI1 model genotype SiA 3159 was the winner genotype in four environments of mega environment 1 (Fig 4). This is an ideal genotype in terms of high performance and stability over rainfed areas in comparison to the other genotypes. Similar results were observed in studies by Bose *et al.* (2014) and Reza and Mohammad (2020). The genotype SiA 3159 may be given as minikits for testing in farmers' fields in different zones of Andhra Pradesh. Recently released promising varieties SiA 3085 and SiA 3156 were included as checks in the study were ranked second and won in one environment each.

CONCLUSION

Foxtail millet is a minor millet crop in India cultivated in limited areas having strong adaptability to rainfed areas with minimum yields. In the recent past the area under this crop is increasing which necessitates to develop new high yielding varieties. Under rainfed situations, for making this crop as a remunerative, the varieties should have better adaptability for various environments. Experimental results revealed significant differences among genotype (G), environment (E) and their interaction (GEI) components. SiA 3159 was emerged as winner genotype in four environments of mega environment 1. This is an ideal genotype in terms of high performance and stability over rainfed areas in comparison to the other genotypes. The genotype SiA 3159 suggested for testing minikits in farmers' fields in different zones of Andhra Pradesh.

Conflict of interest: None.

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