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Stability analysis of pearl millet genotypes: An eberhart and Russell model approach

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Abstract

The current study aimed to identify stable genotypes across eight environments, as the performance of genotypes can vary across different locations. A multi-environment experiment was conducted, involving 29 pearl millet genotypes with three replications, at eight locations in India (ARS Mandor, Bikaner, RARI Jaipur, Jamnagar, Hisar, Gwalior, Ranchi, Jammu and Kashmir) for one year (2019). Each location consisted of nine morphological characters. The data were obtained from ICAR-All India Coordinated Research Projects (AICRP) of pearl millet, Agricultural University, Mandor, Rajasthan, India. The stability of genotypes was evaluated using the Eberhart & Russell model (1966). The stability analysis, based on combined ANOVA, indicated significant differences between genotypes (G), environments (E), and genotype x environment interactions (G X E). None of the genotypes were stable for all characters. The results showed that genotypes G14, G12, G10, G19, G11, G15, G21, G23, G20, G29, G27, G22, and G29 were determined to be stable for the majority of pearl millet characters. The adaptability of genotypes to favorable, unfavorable, and stable environments was also assessed.

Keywords: Genotype (G), environments (E), pearl millet, G X E interaction, Eberhart & Russell (1966)

1. Introduction

Pennisetum glaucum (L.) R. Br., commonly known as pearl millet or bajra, belongs to the Poaceae family (Gramineae) and has a chromosome count of $2n = 14$. It is a significant coarse cereal crop cultivated in semi-arid tropical regions, known for its ability to thrive in conditions characterized by light-textured soil, low moisture, nutrient-deficient soil, and temperatures exceeding $40\text{ }^{\circ}\text{C}$. According to Vavilov (1950) [22] and Murdock (1959) [24], pearl millet is believed to have originated in West Africa and subsequently spread to India and other countries. The crop exhibits a protogynous state and relies heavily on cross-pollination (Animasaum *et al.*, 2019) [2]. It is widely grown in India's arid and semi-arid regions and finds diverse applications in both food and non-food sectors. Pearl millet possesses heterozygous and heterogeneous characteristics. India holds the title of the world's largest millets producer, with an annual production exceeding 11 million tons, accounting for approximately 36% of global production. Pearl millet occupies nearly 90% of agricultural land in the country's dry regions, particularly in the states of Rajasthan, Haryana, Maharashtra, Gujarat, and Uttar Pradesh. After rice, wheat, and maize, pearl millet ranks as the fourth most extensively cultivated food crop in India.

Pearl millet often falls short of its actual productivity potential due to several factors. The main reasons for low crop production include the use of unstable varieties/hybrids, inadequate fertilizer management, and limited availability of soil moisture during critical growth stages throughout the growing season. The interaction between a genotype's characteristics and the environment determines its phenotypic expression. Failure to account for the interaction between genotype and environment (G X E) can lead to biased estimations of genetic parameters obtained from a single environment (Kumar *et al.*, 2022) [11]. To gain an objective understanding of how different traits manifest, it is crucial to consider the G X E interaction when estimating various genetic factors. Given these findings, the development of varieties that consistently yield optimal results across seasons and locations, even under moisture stress conditions, becomes imperative. Stability analysis, often conducted by analysing diverse trials, is commonly employed to address this objective.

Breeding programs should prioritize the development of stable and adaptable varieties that can consistently perform well across different environmental conditions, meeting the requirements of producers. Plant breeders now recognize the importance of testing a wide range of potential varieties in diverse locations before selecting promising candidates for release and commercial cultivation (Gupta and Ndoye, 1991) [7]. Several methods have been employed to assess the performance of each variety in different testing environments. Finlay and Wilkinson (1963) [5] used regression analysis to evaluate the stability of barley, considering linear regression with a high mean yield as an indicator of stability (Yates and Cochran, 1938) [23]. According to Eberhart and Russell (1996) [4], a genotype is considered stable when it exhibits unit regression coefficients and a mean yield greater than the overall mean. Various statistical methods, both parametric and non-parametric, have been developed to measure yield stability (Finlay and Wilkinson, 1963; Eberhart and Russell, 1996; Freeman and Perkins, 1971; Hanson, 1970; Tai, 1971; Nassar and Huhn, 1987) [5, 4, 6, 8, 20, 15].

Stability analysis involves examining the regression coefficients or slopes to determine if each variety exhibits stability across different environments or demonstrates responsiveness to environmental variations. The presence of a significant genotype x environment interaction indicates that different genotypes respond differently to environmental changes, implying that the best-performing genotype in one environment may not perform well in another. Understanding the genotype-environment interaction is crucial for breeding improved cultivars that are well-adapted to the prevailing environmental conditions in target locations (Arun Kumar *et al.*, 2020) [3]. When the interaction components are significant and substantially larger than genotypic characteristics, breeders seek varieties with overall adaptability and consistent performance across a range of environments, considering identifiable environmental conditions (Abdelrahman and Abdalla, 2002) [1]. The aim of the study was to assess the stability of several measuring traits of pearl millet in various environments.

2. Material and Methods

The stability analysis utilized a total of twenty-nine genotypes (refer to Table 1), arranged in a randomized block design with three replications. The genotype data were collected from the ICAR-AICRP on Pearl Millet at Agricultural University, Mandor, Rajasthan, India. The multi-environment experiment was conducted at eight locations in India, namely ARS Mandor, Bikaner, RARI Jaipur, Jamnagar, Hisar, Gwalior,

Ranchi, and Jammu-Kashmir, throughout the year 2019. Each location encompassed nine morphological characters, including Grain Yield (kg/net plot), Dry Fodder Yield (kg/net plot), Days to Maturity (days), Days to 50% flowering (days), Plant Height (cm), Panicle Diameter (cm), Panicle Length (cm), 1000-Seed Weight (g), and Population at Harvest (number in net plot). Each character was replicated three times. The collected data were analyzed using R software, employing the linear regression model of stability proposed by Eberhart and Russell (1966) [4].

2.1 Stability analysis

The following model was developed by Eberhart and Russell (1966) [4] to examine the stability of genotypes in various environments:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where, Y_{ij} = mean of the i^{th} genotype at the j^{th} environment,

($i= 1, 2, 3, \dots, g; j= 1, 2, 3, \dots, n$)

b_i = regression coefficient that measures the response of the i^{th} genotype to varying environments,

δ_{ij} = deviation from regression of the i^{th} genotype at the j^{th} environment and

I_j = environmental index

$$I_j = (\sum Y_{ij}/g) - (\sum \sum Y_{ij}/gn), \text{ where } \sum I_j = 0$$

2.2 Stability parameters

Two parameters of stability are calculated: (a) the regression coefficient, which represents the performance of each variety under various environments on the environmental means over all the genotypes. This was estimated as follows:

$$b_i = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

$\sum_j Y_{ij} I_j$ is the sum of products and $\sum_j I_j^2$ is the sum of squares.

(b) Mean square deviations ($S^2 d_i$) from linear regression.

$$S^2 d_i = \frac{\sum_j \delta_{ij}^2}{(n-2)} - \frac{S_e^2}{r}$$

Where, $\sum_j \delta_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_i^2}{g} \right] - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2}$ and S_e^2 = the estimate of pooled error.

Table 1: List of twenty- nine genotype evaluated at eight environments in India

Sr. No.	Genotype code	Genotypes	Sr. No.	Genotype Code	Genotypes
1	G1	HHB272	16	G16	HHB223
2	G2	MPMH21	17	G17	GHB744
3	G3	RHB177	18	G18	GHB732
4	G4	HHB197	19	G19	KBH108
5	G5	GHB538	20	G20	86M86
6	G6	HHB67	21	G21	Kaveri Super Boss
7	G7	AHB1269	22	G22	MP-7792
8	G8	HHB299	23	G23	Proagro9444
9	G9	AHB1200	24	G24	GHB558
10	G10	PB1705	25	G25	Dhanshakti
11	G11	XMT1497	26	G26	ICMV221
12	G12	86M01	27	G27	PusaComposite701
13	G13	GHB905	28	G28	Posa Composite383
14	G14	MPMH17	29	G29	JBV 2
15	G15	RHB173			

3. Result and Discussion

The combined analysis of variance (Table 2) conducted for grain yield and its morphological traits exhibited significant variations among genotypes, environments, and the interaction between genotype and environment. These findings support the suitability of stability analysis. The results observed by Lata *et al.* (2010) [12] and Usharani (2012) [21] were consistent with the present study's outcomes. The genotype by environment interaction was found to be statistically significant for all traits, indicating that all genotypes interacted with environmental variables. Similar significant differences in environments, hybrids, and their interactions were also reported by Sirilene *et al.* (2017) [17].

The analysis of variance using the Eberhart and Russell model indicated highly significant E+ (G X E) interactions for all the studied traits compared to the pooled error, indicating the distinctive influence of environments on phenotypic expression. Each trait showed a substantial mean sum of squares due to linear effects of the environment, indicating significant differences among the selected study environments. Pooled deviations were also highly significant for all the characters which showed that predictable portion formed the major part of the G X E interactions (Table 3). Similar work done by (Matin *et al.*, 2017) [13].

For each of the twenty-nine genotypes, the stability parameters mean, regression coefficient (b_i), and mean square deviation (S^2d_i) from the regression line were evaluated. The results of these evaluations are presented in tables 4a and 4b. It is noteworthy that none of the genotypes were found to be stable across all the studied characters. A genotype can be considered stable if it exhibits a higher mean than the grand mean, a regression coefficient of one, and a non-significant deviation from the regression line. The results indicated that G12, G19 and G20 were stable for six different morphological characters, following G10 and G11 stable for five different characters, G21, G22, G23, G27 and G28 stable for four different characters. Similarly, G14, G15 and G29 were stable for three different characters, G18 was stable for two different characters following G13, G16, G17, G24 and G25 were also stable for different morphological characters. Across the environments, G12 found stable and widely adapted for Grain Yield, Days to 50% flowering, Days to maturity, Plant Height, Panicle Length and Panicle Diameter. The genotype G19 was stable for six morphological characters *viz.* Grain Yield, Days to 50% flowering, Days to maturity, Plant Height, Panicle Diameter, Population at harvest except Dry Fodder Yield, 1000-seed weight and Panicle Length. Similarly, G20 was stable for Grain Yield, Days to 50% flowering, Days to maturity, Panicle Length, Panicle Diameter, Population at harvest except for Dry Fodder Yield, 1000-Seed weight and Plant Height. The G10 was adopted for Grain Yield, Days to 50% flowering, Plant Height, Panicle Diameter, Population at harvest and G11 was stable for Grain Yield, Days to 50% flowering, Days to maturity, Plant

Height, Panicle Diameter. Similarly, G21 was adopted for Dry Fodder Yield, Days to maturity, Plant Height, Panicle Diameter, G22 was stable for Dry Fodder yield, Days to 50% flowering, Days to maturity, Panicle Diameter and G23 was stable for Dry Fodder Yield, Days to maturity, Plant Height, Panicle Diameter. Genotype G27 was adopted for Days to 50% flowering, Days to maturity, Plant Height, Panicle Length and G28 was adopted for Days to 50% flowering, Plant Height, Panicle Length and Population at harvest. G29 was stable for stable for Dry Fodder Yield, Days to 50% flowering, Panicle Length. The genotypes G24, G25 and G26 were stable for Panicle Diameter where G25 was only genotype which was stable for character 1000-seed weight. G14 was stable for Dry Fodder yield, Panicle length, Population at harvest and G15 was stable Dry fodder yield, Days to 50% flowering, Population at harvest. G13, G16, G17 and G18 were adopted for Panicle length, Grain yield, Days to maturity and Population at harvest respectively. Similar findings were shown by Nirmal *et al.* (2019) [16].

According to the methodology followed by Mehra and Ramanujam (1979) [14] and Singh and Singh (1980) [18], twenty- nine genotypes with higher mean values than grand mean were grouped into three based on stability parameters *viz.*, regression coefficient and squared deviation (Table 5). In group I, the genotypes falling in higher mean than grand mean, regression coefficient value around one with non-significant deviation from regression. Under group II, genotypes with less than unity regression value and non-significant squared deviation were taken, indicating adaptability towards unfavourable environments. Again, the genotypes more than the unity regression was also classified under group II indicating the genotypes adaptability towards favourable environments. The genotypes falling in group III cannot be predicted as they exhibit significant squared deviation, irrespective of the regression coefficient values. According to the grouping, the genotype G10 was stable for four characters *viz.*, Grain Yield, Dry Fodder Yield, Panicle Diameter, Population at harvest, as it was placed under group I. Under group II ($b < 1$), G11 was stable in unfavourable environments for three characters *viz.*, Grain Yield, Days to maturity, and Days to 50% flowering. Similarly, G20 was stable for Grain Yield, Days to maturity and Panicle Length. The genotype G28 was under group II ($b > 1$) and was stable in favourable conditions for three environments *viz.*, Days to 50% flowering, Panicle Length, and Population at Harvest. The result were similar to the reports of Kaundal and Sharma (2006) [9] and Arun and Singh (2004) [3]. The overall performance of genotype G11 was found promising with stable performance (group II) and may be used for general cultivation in unfavourable environments. In favourable environments, G28 found to be stable. Not a single genotype was found stable across environments, hence consider the need for environments specific genotype.

Table 2: combined analysis of variance for nine morphological characters of pearl millet

Mean Sum Square										
SOURCE	df	Grain yield	Dry Fodder Yield	Days to 50% flowering	Days to Maturity	Plant Height	Panicle Length	Panicle Diameter	1000- weed weight	Population at harvest
Genotypes (G)	28	3.81**	21.76**	240.04**	139.35**	5212.67**	88.97**	1.68**	12.16**	426.99**
Environment (E)	7	51.981**	999.34**	1774.65**	5185.92**	167723.4**	413.44**	4.96**	84.75**	70310.15**
G x E	196	0.93**	8.86**	11.46**	17.09**	488.99**	7.78**	0.14**	4.46**	207.40**
Error	464	0.15	0.91	2.65	4.26	65.62	2.76	0.05	0.43	83.93

*: Significant at 5% level;
 **: Significant at 1% level

Table 3: Analysis of variance for grain yield and its attributing components (Eberhart and Russell model, 1966) [4]

Mean Sum Square										
Source	df	Grain yield	Dry Fodder Yield	Days to 50% flowering	Days to Maturity	Plant Height	Panicle Length	Panicle Diameter	1000-Seed weight	Population at harvest
Genotypes (G)	28	1.27**	7.26**	80.01**	46.45**	1737.56**	29.66**	0.56**	4.05**	142.33**
E + (G x E)	203	0.89**	14.34**	24.09**	65.11**	2085.23**	7.26**	0.10**	2.41**	874.91**
E(Linear)	1	121.30**	2331.80**	4140.80**	12100.47**	391354.56**	964.70**	11.57**	197.74**	164057.03**
G x E(Linear)	28	0.17**	3.22**	5.96**	5.93**	446.96**	4.23**	0.04**	1.56**	40.77**
Pooled deviation	174	0.32**	2.81**	3.35**	5.46**	111.68**	2.24**	0.05**	1.42**	71.31**
Pooled error	464	0.05	0.28	0.82	1.42	21	0.92	0.02	0.15	27.66

*: Significant at 5% level; **: Significant at 1% level

Table 4a: Stability parameters for morphological components across environments

varieties	Grain yield			Dry Fodder Yield			Days to 50% flowering			Days to maturity			Plant Height		
	mean	b_i	S^2d_i	mean	b_i	S^2d_i	mean	b_i	S^2d_i	mean	b_i	S^2d_i	mean	b_i	S^2d_i
1	2.07	0.96	0.13	6.33	0.89	2.9	36.33	0.7	0.45	62.43	1.02	0.81	122.25	0.81	12.17
2	2.16	1.15	0.1	6.38	1.03	1.48	37.3	0.7	1.54	63.03	1	5.09	125.59	0.87	24.63
3	2.24	1.24	0.04	6.46	1.04	0.76	35.1	0.56	0.46	61.83	1.1	11.35**	127.62	0.81	31.98
4	2.24	1.2	-1.48	6.72	1.09	-3.84	37.77	1.21	-19.82*	62.63	0.95	-22.82	125.22	0.89	-484.49*
5	2.15	1.26	0.23	6.16	1.03	1.56	36.67	0.78	2.78	61.93	0.94	3.96	126.73	0.93	145.04*
6	2.08	1.12	0.2	6.49	1.08	-0.02	34.83	0.87	3.59	61.67	1.05	8.84*	124.45	0.78	151.59*
7	2.22	0.91	0.23	7.05	0.79	3.54**	41	1.03	6.58**	65.57	1.08	6.1	132.58	0.91	77.27
8	2.36	0.97	0.38	6.45	0.91	2.00*	39.7	1.1	5.37*	64.4	0.95	2.22	124.42	0.77	2.78
9	1.85	0.56	0.23	6.41	0.5	6.77**	39.27	1.02	0.3	64.2	0.98	2.12	125.07	0.81	94.54
10	2.82	1.02	0.14	8.93	1.3	1.96*	40.6	0.98	1.91	64	0.81	4.85	146.25	1.20	21.98
11	2.74	0.83	0.15	7.71	0.96	1.89*	40.17	0.55	2.47	64.43	0.72	3.37	139.05	1.04	8.22
12	2.48	0.6	0.14	7.8	1.2	4.16**	41.5	1.12	0.86	65.1	0.91	1.98	139.09	0.95	79.56
13	2.32	1.06	0.06	6.76	1.2	0.87	38.57	0.88	2.74	63.97	1.09	2.11	127.30	0.89	60.33
14	2.64	1.14	0.47**	7.08	1.07	1.03	37.77	1.16	0.91	63.67	1.11	5.93	128.58	0.89	97.20
15	2.52	1.1	0.51**	7.11	0.97	1.54	39.5	1.18	2.86	64.07	1.09	1.83	136.15	0.87	52.13
16	2.41	1.27	0.23	6.39	1.19	2.59**	37.4	1.05	1.23	62.43	1.03	-0.16	131.32	1.03	267.71**
17	2.14	1.19	0.40**	5.76	1.31	5.81**	41	1.17	3.55	66.17	1.11	3.46	132.90	0.93	167.75**
18	2.57	1.21	0.65**	7.16	1.37	1.76*	40.57	1.19	-0.21	65.2	1.15	3.9	134.12	0.85	161.78*
19	2.77	0.66	0.18	8.44	1.11	6.59**	44.47	1.1	2.14	69.37	1.13	0.72	159.33	1.24	116.78
20	2.53	0.73	0.21	6.83	0.59	5.60**	43.37	1.07	0.41	67	0.88	6.22	142.63	0.98	129.78*
21	2.69	0.9	1.40**	8.23	0.96	7.37**	44.8	1.02	6.99**	68.73	0.87	7.05	154.95	1.35	125.16*
22	2.86	0.9	0.57**	7.28	0.93	1.29	41.27	1.16	-0.7	66.43	1.1	1.79	144.86	0.98	118.92*
23	2.74	1.05	0.46**	7.04	0.77	1.33	40.5	1.18	5.19**	65.13	1.16	2.65	143.05	1.14	64.61
24	2.08	1.29	-0.03	6.8	1.04	1.26	39.37	1.12	1.94	64.7	1.1	9.97*	131.90	0.94	8.40
25	1.7	0.9	0.09	5.78	0.97	0.52	36.77	0.77	7.00**	61.7	1.02	4.22	133.23	1.08	20.55
26	1.69	0.88	0.06	6.4	0.81	1.87*	36.87	0.8	4.88*	63.2	1.12	4.62	135.32	1.02	109.28
27	2.19	1.09	-0.01	6.69	0.92	0.58	40.17	1.13	0.3	64.73	0.87	2.43	153.27	1.30	23.06
28	2.26	1	0.06	7.84	1.17	3.43**	41.63	1.33	0.69	65.13	0.85	4.49	164.37	1.39	40.90
29	2.15	0.8	0.13	7.46	0.82	1.36	40.63	1.09	-0.27	64.83	0.8	-0.37	157.26	1.33	258.09**
mean	2.33			6.96			39.48			64.4			136.86		

Table 4b: Stability parameters for morphological components across environments

varieties	Panicle Length			Panicle Diameter			1000-Seed weight			Population at harvest		
	mean	b_i	S^2d_i	mean	b_i	S^2d_i	mean	b_i	S^2d_i	mean	b_i	S^2d_i
1	15.87	0.82	-0.61	2.05	0.67	-0.01	6.78	1.15	0.94*	111.77	0.88	84.12
2	16.33	0.67	1.09	2.07	0.67	0.02	6.15	1.49	1.02*	104.90	1.01	-7.10
3	18.15	0.85	1.60	2.12	1.16	0.03	7.41	0.16	1.06*	108.30	0.88	-1.24
4	18.01	0.81	-3.31	2.16	0.78	-0.09	7.58	1.39	-3.66*	105.87	0.97	-347.52
5	17.44	0.95	-0.15	1.98	1.15	0.03	7.35	1.56	1.26**	107.60	0.92	-18.67
6	16.11	0.96	1.00	1.75	0.73	0.01	6.79	1.54	0.29	105.87	1.03	43.99
7	16.55	1.27	-0.19	2.51	1.04	0.04	7.52	0.75	1.08**	109.40	0.83	1.85
8	18.21	0.68	0.99	2.42	1.21	0.01	7.20	0.65	0.36	106.53	0.99	7.67
9	20.14	1.27	6.60*	2.67	1.49	0.01	7.63	1.29	1.20**	110.33	0.91	52.79
10	18.09	1.13	0.16	2.27	1.03	0.00	7.39	0.07	1.39**	111.17	1.06	8.11
11	17.93	0.78	0.46	2.32	1.31	0.01	6.59	1.37	0.19	112.77	0.97	95.35
12	20.11	1.43	0.48	2.27	0.89	0.02	8.52	0.88	1.53**	110.40	0.89	-13.06
13	19.30	1.03	0.34	2.08	0.72	0.01	6.46	1.32	0.35	104.63	1.09	59.24
14	18.95	1.01	0.86	2.15	1.02	0.03	6.92	1.76	1.62**	110.20	1.02	2.32
15	20.48	0.73	8.55**	1.93	1.00	0.01	7.05	0.32	1.84**	110.03	1.09	4.96
16	17.70	0.55	0.69	2.04	0.65	0.00	6.74	1.33	1.41**	103.90	1.09	-14.24
17	18.22	1.07	0.00	2.14	1.27	0.02	7.37	0.64	3.28**	96.03	0.95	780.05**
18	17.39	1.41	-0.11	1.97	0.55	0.02	7.38	1.53	1.28**	110.03	0.89	-12.53
19	18.76	0.79	2.89	2.57	1.45	0.00	8.02	0.78	2.95**	109.63	0.93	-11.39

20	18.97	0.71	0.12	2.56	1.18	0.00	7.68	0.70	1.00*	108.77	1.05	-10.75
21	21.09	1.23	2.24	2.40	1.28	0.01	7.01	1.10	1.71**	109.97	1.06	-4.56
22	18.01	1.00	-0.18	2.33	0.85	0.00	7.57	0.29	0.76	110.23	1.04	31.77
23	17.92	0.97	-0.13	2.25	0.69	0.00	7.68	1.38	2.12**	107.20	1.14	2.71
24	18.42	0.40	-0.11	2.31	0.80	0.02	7.69	0.59	3.17**	103.63	1.03	25.14
25	17.74	1.00	0.43	2.26	1.14	0.02	8.02	1.35	0.66	106.17	0.97	21.25
26	16.88	0.51	0.25	2.28	1.20	0.01	7.22	0.63	1.79**	107.07	1.00	-19.60
27	21.02	1.73	4.01	2.04	0.45	0.02	6.59	1.38	0.62	106.50	1.13	-6.54
28	21.36	2.02	4.25	2.12	1.93	0.41**	6.21	0.42	0.13	110.27	1.12	-7.06
29	20.94	1.22	2.85	2.05	0.70	0.01	6.51	1.19	1.05*	111.13	1.07	83.64
mean	18.49			2.21			7.21			107.94		

Table 5: Grouping of genotypes based on stability parameters

Sr. No.	Characters	Group I	Group II		Group III
			b<1	b>1	
1	Grain Yield	G10	G11, G12, G20, G19	G16	G4, G17
2	Dry Fodder Yield	G14, G15	G22, G23, G29	Nil	G1, G8, G16, G20
3	Days to 50% Flowering	G10, G19, G20, G29	G11	G12, G15, G18, G22, G27, G28	G4, G26
4	Days to maturity	G7, G12, G22	G11, G20, G21, G27, G29	G17, G18, G19, G23	G3, G6
5	Panicle Height	G11, G12	Nil	G10, G19, G23, G27, G29	G5, G16, G17
6	Panicle Length	G13, G14	G20	G12, G21, G27, G28, G29	Nil
7	Panicle Diameter	G7, G10	G12, G22, G23, G24	G8, G9, G11, G19, G20, G21, G25, G26	Nil
8	1000- seed weight	Nil	Nil	G25	G1, G29
9	Population at Harvest	G10, G14, G15, G20, G21	G3, G7, G18, G19	G28	G17

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