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# Stability of Fodder Yield and its Quality Traits in Forage Sorghum

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**Abstract:** The present study was undertaken with a view to know the G × E interactions and stability parameters in newly developed hybrids of forage sorghum for fodder yield and quality traits. The newly developed 60 hybrids, 19 parents and 3 checks were evaluated in a randomized block design with three replications during summer and kharif 2013 with two different dates in each season. Analysis of variance in individual environment as well as on pooled basis revealed highly significant differences among genotypes, parents and hybrids for all the traits. Stability analysis indicated important role of linear and non-linear components in the contribution of total G × E interaction. The linear portion was considerably high for green and dry fodder yield plant$^{-1}$, brix per cent, HCN content and crude protein content. Results revealed that the prediction of performance of genotypes over environments based on regression analysis could be reliable. The magnitude of non-linear component was higher for shoot fly dead heart percentage indicated greater importance of non-linear portion in building-up total G × E interaction for this trait. The hybrid 27A × SRF 323 was more suitable specifically under good farming conditions for green and dry fodder yield plant$^{-1}$ and had significant $b_i$ above unity, non-significant $S^2d_i$ and high mean value. Hybrids 27A × SPV 2113 and 27A × SRF 327 on the other hand were more suitable specifically under poor farming situation for green and dry fodder yield plant$^{-1}$ because, they had high mean, significant $b_i \leq$ unity and non-significant $S^2d_i$. For quality characters viz., HCN content and crude protein content, hybrids 9A × SRF 331 and 104A × SPV 2113 were found stable. Thus, these hybrids can be exploited commercially for high quality fodder after testing in wide range of environments.

**Key words:** Environment, G × E interaction, sorghum bicolor, stability analysis.

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most important cereals of the semi-arid tropics. The major challenge in sorghum research in India is to evolve technologies that will enable transformation of subsistence farming into profitable production. For accomplishing these objectives, it is crucial to enhance the productivity and stability of sorghum, diversification of the genetic base including hybrid cytoplasm, disease and pest resistance, fodder quality, acid and saline soil adaptability, etc. In order to make forage sorghum as an enterprising and remunerative crop, there is an urgent need to initiate research to develop varieties and hybrids having high fodder yield with good quality parameters like juiciness, resistance to insect pest, sweetness, high protein content and minimum toxic constituents like HCN content. For this, it is necessary to screen and develop stable genotypes, which perform more or less uniform under varying environmental conditions. Thus, knowledge of genotype × environment interaction helps the breeder to select high yielding and most stable varieties or hybrids. Crop yield, in which the plant breeder is most interested, is dependent on the genotype, the environment and their interaction. When interaction between genotype and environment exists, ranking of genotypes will be different under different environments (Eberhart and Russell, 1966). Crop production is dependent on the release of such stable hybrids/varieties that gives consistent performance under wide range of agro-climatic conditions. The stability of productivity is therefore very important and hence, it is always desirable to isolate factors manifesting stability with respect to economically important characters. The study of hybrids over environments would give reliable and unbiased estimates of combining ability effects. This study would not only help forage breeders in selecting suitable parents for hybridization, but will also

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provide a continuity towards the evolution of effective breeding procedures to improve productivity of forage sorghum having high nutritive value with low toxicity. Therefore, the present investigation was undertaken to study the stability performance of parents and newly developed forage sorghum hybrids over different environments.

## Materials and Methods

The experimental material that comprised of 82 genotypes including fertile counter parts of four male sterile lines (9A, AKMS 14A, 27A and 104A), 15 males (SRF 317, SRF 321, SRF 323, SRF 327, SRF 328, SRF 330, SRF 331, SRF 332, SRF 334, SRF 335, SRF 336, SRF 337,CSV 15, SPV 1616 and SPV 2113), 60 hybrids and three checks viz., GFS 4, GFS 5 and CSV 21F, were grown in a randomized block design replicated thrice during summer-kharif, 2013 at Sorghum Research Station, S. D. Agricultural University, Deesa, Gujarat. The individual environments were created by sowing in two seasons, i.e., summer and kharif with each season having two different dates of sowing (Summer: 28/02/2013, 14/03/2013 and kharif: 20/07/2013, 05/08/2013) with two different doses of N P K fertilizers (early sowing + 80:40:00, late sowing + 100:50:00). Each genotype was represented by a single row plot of 4.0 metre length. The inter and intra row distances were 30 cm and 7.5 to 10 cm, respectively. All the recommended agronomical practices and plant protection measures were followed to harvest a good crop. Observations were recorded on, green fodder yield plant$^{-1}$ (g), dry fodder yield plant$^{-1}$ (g), shoot fly dead heart percentage, brix (%), HCN content (ppm) and crude protein (%). Five representative plants were selected randomly and tagged from each plot of entry for recording observations and average value plant$^{-1}$ was computed. The statistical analysis for G × E interaction and stability parameters was carried out as suggested by Eberhart and Russell (1966).

## Results and Discussion

A variety does not perform consistently in different agro-climatic situations because of genotype environment interactions. This type of situation poses serious difficulty to plant breeders in making proper assessment of varieties when the same are compared over a series of environments. The G × E interactions had been emphasized by Johnson *et al*. (1955) in selection of soybean. Comstock and Moll (1963) statistically confirmed that large G × E interaction could reduce progress from selection. Hence, knowledge of kind and magnitude of G × E interaction has become essential to plant breeders in taking the decisions concerning breeding methods. Even though, stratification of the environment to reduce the G × E interaction and enhance the precision in selection, the interaction of genotype with location in a sub region and with environments within the same year remains very large (Allard and Bradshaw, 1964). Factors responsible for interaction, can be reduced materially up to certain limit in the field experiments (Sprague, 1966). In the present study, the analysis of variance revealed that genotypic component was significant for all characters, which indicated genotypic differences among genotypes tested in different types of environments exists. The environment component was also significant. The G × E interaction was significant for most of the traits. Significant G × E interaction indicated that the genotypes interacted considerably with the changing environmental conditions. Further, G × E interaction component was also significant when tested against pooled deviation and this revealed that the major components for differences in stability were due to the deviation from linear function (Table 1). The prediction of performance of genotypes over the environments, based on regression analysis for these traits may also be very appropriate. This was in accordance with the previous reports on forage sorghum [Patil *et al*. (2006); Narayan (2009) and Ghazy, Mona *et al*. (2012)]. However, the linear component of G × E interaction was significant for brix per cent, HCN content and crude protein content (Narayan, 2009; Umakanth *et al*., 2012). This indicated that genotypes did differ genetically in their response to different environment, while, the significant linear component of G × E interaction revealed that the regression coefficient of some hybrids had more or less than unity ($b_i = 1$) and some hybrids were more stable than other over the environments. The linear portion of environment was considerably high for green fodder yield plant$^{-1}$, dry fodder yield plant$^{-1}$, brix per cent, HCN content and crude protein content. This reflected greater importance of linear portion in building up total G × E interactions and the possibility

*Table 1. Analysis of variance for phenotypic stability for fodder yield and quality characters in forage sorghum*

| Source of variation | d.f. | Green fodder yield plant$^{-1}$ (g) | Dry fodder yield plant$^{-1}$ (g) | Crude protein (%) | Shoot fly dead heart (%) | Brix (%) | HCN (ppm) |
|---|---|---|---|---|---|---|---|
| Genotypes (G) | 81 | 31221.708** | 3092.642** | 2.618** | 16.269** | 13.514** | 1267.460** |
| Environments (E) | 3 | 94314.461** | 8692.615** | 0.962** | 712.394** | 35.876** | 128.657** |
| G × E | 243 | 8856.271** | 831.236** | 0.078 | 3.136** | 2.207** | 6.282 |
| E + (G × E) | 246 | 9898.444 | 927.107 | 0.089 | 11.786** | 2.617** | 7.774** |
| Environments (linear) | 1 | 282959.720** | 26080.000** | 2.897** | 2137.193** | 107.641** | 385.159** |
| G × E (linear) | 81 | 10309.156 | 947.829 | 0.143** | 2.838 | 5.810** | 10.136** |
| Pooled deviation | 164 | 8030.584** | 763.501** | 0.046 | 3.245** | 0.400** | 4.306 |
| Pooled error | 648 | 644.722 | 52.998 | 0.254 | 0.670 | 0.383 | 29.346 |

*, **: Significant at 5 and 1 per cent levels of significance, respectively.

of prediction across the environments for these characters. The high linear portion of environment for green fodder yield plant$^{-1}$, dry fodder yield plant$^{-1}$, brix per cent, HCN content were also observed by earlier research workers [Patil *et al*. (2006); Mungra *et al*. (2011); Umakanth *et al*. (2012)].

The stability parameter $b_i$ and $S^2d_i$ were computed for all parents and hybrids as per Eberhart and Russell (1966) to identify stable parents and crosses for different characters. From the present investigation, it was clear that none of the genotypes was stable for all the traits (Table 2). With regard to green fodder yield plant$^{-1}$, total four parents exhibited higher mean than their general mean (389.10 g), among those, SRF 317, SRF 323 and CSV 15 reflected below average stability and unpredictable performance over the environments because the $b_i$ values were above unity with significant non-linear component. None of the stable parent was found to be specifically good under average response to environments for this trait. The hybrids 27A × SPV 2113 and 27A × SRF 323 had high mean and $S^2d_i$ value non-significant which showed their stability in the poor ($b_i$ = -0.55*) and the favorable ($b_i$ = 3.49*) environments, respectively. The above results are in conformity with the findings of Narayan (2009); Patel and Patel (2010); Kher *et al*. (2008); Yadav *et al*. (2010); Vange *et al*. (2014) and Shiri (2016). For dry fodder yield, three hybrids viz., 9A × SRF 328, 14A × SPV 2113 and 104A × SPV 2113 had high mean than population mean, non-significant regression coefficient ($b_i$ = 1) and significant deviation from regression. Therefore, these hybrids produced more dry fodder yield plant$^{-1}$ in average environments with unpredictable performance. The hybrids 27A × SRF 323 and 9A × SRF 334 that showed above average dry fodder yield plant$^{-1}$ with high mean, significant regression coefficient ($b_i$ > 1) and non-significant $S^2d_i$ value. Thus, these hybrids may be good donor for stability for this trait. Further, the hybrid 27A × SRF 327 with significant regression below unity ($b_i$ < 1) and non-significant deviation from regression produced more dry fodder yield plant$^{-1}$ in poor environments as reported by Narayan, 2009; Yadav *et al.,* 2010 and Ghazy, Mona *et al.,* 2012.

With respect to shoot fly dead heart percentage four parental lines viz., SRF 335, 104A, SRF 334, SRF 336 and 10 hybrids, 104A × SRF 335, 27A × SRF 323, 27A × SRF 321, 27A × SRF 337, 104A × SRF 331, 14A × SRF 317, 9A × SPV 2113, 104A × SRF 317, 104A × SRF 328 and 9A × SRF 323 exhibited lower population mean, significant regression coefficient ($b_i$ > 1) and least deviation from regression and reflected stable performance in favorable environments for tolerance to shoot fly reflecting. None of the parents and hybrids exhibited average stability for this character. Whereas, the hybrids 9A × SRF 321, 104A × SRF 336, 14A × SRF 321 and 9A × SRF 335 proved to be an above average responder with high stability in poor environment for this trait with less infestation of shoot fly, significant regression coefficient ($b_i$ < 1) and non-significant $S^2d_i$. Further, the parent 9A , check CSV 21F and GFS 5 proved to be an above average responder with high stability in poor environment as they exhibited low mean, significant regression coefficient ($b_i$ < 1) and non-significant deviation from regression as also reported by Nagare, 2010 and Aruna *et al.,* 2011.

*Table 2. Estimates of stability parameters for leaf width, leaf length, green and dry fodder yield plant*$^{-1}$

| SN | Genotypes | Green fodder yield plant$^{-1}$ (g) | | | Dry fodder yield plant$^{-1}$ (g) | | | Crude protein (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | μ | $b_i$ | $S^2d_i$ | μ | $b_i$ | $S^2d_i$ | μ | $b_i$ | $S^2d_i$ |
| [1] | [2] | [3] | [4] | [5] | [6] | [7] | [8] | [9] | [10] | [11] |
| 1. | 9A | 317.50 | 0.03 | 422.39 | 90.00 | -0.03 | 84.28** | 9.15 | 0.04 | -0.08 |
| 2. | 14A | 247.92 | -1.00 | 1813.59** | 83.33 | -1.00 | 254.21** | 8.21 | -0.31* | -0.08 |
| 3. | 27A | 223.25 | -1.89* | 254.00 | 61.42 | -1.71* | 21.00 | 9.49 | 0.08 | -0.08 |
| 4. | 104A | 341.25 | 3.37 | 6486.02** | 102.67 | 3.25 | 759.02** | 10.1 | 0.60 | -0.04 |
| 5. | SRF 317 | 412.92 | 2.47 | 1600.72** | 133.67 | 2.63 | 141.80** | 7.59 | 1.58 | -0.07 |
| 6. | SRF 321 | 336.08 | -2.93 | 3881.78** | 120.83 | -3.62 | 751.68** | 9.56 | 0.80 | -0.06 |
| 7. | SRF 323 | 423.33 | 2.68 | 4248.24** | 117.92 | 2.54 | 342.64** | 8.41 | 0.43 | -0.06 |
| 8. | SRF 327 | 305.00 | 2.44* | 163.55 | 83.83 | 2.29** | -2.38 | 7.63 | 2.58 | -0.01 |
| 9. | SRF 328 | 354.42 | 0.44 | -129.43 | 115.00 | 0.49 | -13.00 | 8.31 | -0.45 | 0.01 |
| 10. | SRF 330 | 251.25 | 1.40 | 829.31** | 119.58 | 1.92 | 207.59** | 7.85 | 4.88 | 0.02 |
| 11. | SRF 331 | 270.92 | 0.77 | 862.41** | 93.25 | 0.93 | 92.50** | 8.40 | -3.89 | 0.09 |
| 12. | SRF 332 | 333.42 | 1.77 | 12504.03** | 96.58 | 1.49 | 1100.79** | 8.70 | 0.97 | -0.08 |
| 13. | SRF 334 | 239.92 | 0.17 | 3982.22** | 65.83 | 0.07 | 315.59** | 8.54 | 0.18 | 0.12 |
| 14. | SRF 335 | 276.50 | -0.17 | 1502.05** | 99.67 | -0.19 | 199.10** | 8.77 | 2.19 | 0.02 |
| 15. | SRF 336 | 350.92 | 0.16 | 10536.03** | 120.67 | -0.12 | 1193.15** | 8.21 | 0.72 | -0.06 |
| 16. | SRF 337 | 133.42 | 0.38 | 3953.59** | 41.67 | 0.28 | 411.60** | 8.03 | 2.08 | -0.05 |
| 17. | CSV 15 | 401.25 | 3.52 | 16359.96** | 141.17 | 3.89 | 2202.36** | 7.69 | 2.71 | -0.03 |
| 18. | SPV 1616 | 356.83 | -0.86 | 7587.22** | 110.17 | -1.11 | 643.81** | 7.82 | 0.62 | -0.07 |
| 19. | SPV 2113 | 428.92 | -1.65 | 8024.01** | 140.33 | -1.75 | 855.97** | 7.52 | 3.31 | -0.00 |
| 20 | 9A × SRF 317 | 454.17 | 3.50 | 4529.99** | 160.92 | 4.07 | 589.27** | 8.04 | -2.96 | 0.00 |
| 21. | 9A × SRF 321 | 399.17 | -0.42 | 6736.96** | 115.83 | -0.55 | 629.39** | 8.99 | -2.98 | 0.08 |
| 22. | 9A × SRF 323 | 422.67 | 2.61 | 1086.57** | 135.67 | 3.89 | 347.93** | 8.94 | 3.47 | -0.03 |
| 23. | 9A × SRF 327 | 406.75 | 2.06 | 10129.67** | 135.33 | 2.19 | 1116.40** | 9.48 | -1.90 | 0.00 |
| 24. | 9A × SRF 328 | 470.42 | 1.00 | 14163.14** | 147.42 | 0.95 | 1351.21** | 9.38 | 3.75* | -0.07 |
| 25. | 9A × SRF 330 | 448.33 | 2.72 | 12423.91** | 110.17 | 2.44 | 648.29** | 9.56 | -0.22 | -0.07 |
| 26. | 9A × SRF 331 | 499.50 | -0.12 | 1867.78** | 171.67 | -0.07 | 246.89** | 9.76 | 0.64 | -0.07 |
| 27. | 9A × SRF 332 | 458.67 | -1.06 | 7933.44** | 121.00 | -0.83 | 576.20** | 9.10 | 4.33 | -0.02 |
| 28. | 9A × SRF 334 | 429.33 | 3.67* | 689.29* | 117.92 | 3.45** | 15.38 | 9.40 | -3.18 | 0.01 |
| 29. | 9A × SRF 335 | 412.42 | 1.72 | 19915.40** | 136.42 | 2.06 | 2217.53** | 9.17 | 3.35 | -0.01 |
| 30. | 9A × SRF 336 | 304.00 | 1.24 | 6551.72** | 76.25 | 0.92 | 435.24** | 9.43 | -0.58 | -0.01 |
| 31. | 9A × SRF 337 | 356.92 | 2.38 | 10830.89** | 92.00 | 1.80 | 760.57** | 9.59 | 1.91* | -0.08 |
| 32. | 9A × CSV 15 | 399.25 | 1.46 | 1525.51** | 106.67 | 1.28 | 116.30** | 8.85 | 4.52 | 0.04 |
| 33. | 9A × SPV 1616 | 133.67 | 1.64 | 2411.05** | 33.83 | 1.39 | 146.68** | 8.18 | 1.79 | -0.07 |
| 34. | 9A × SPV 2113 | 526.00 | 1.35 | 18649.44** | 146.92 | 1.47 | 1273.00** | 9.21 | -4.05 | 0.22* |
| 35. | 14A × SRF 317 | 432.00 | -0.53 | 17353.41** | 139.58 | -0.32 | 1977.52** | 8.97 | 5.24 | 0.01 |
| 36. | 14A × SRF 321 | 375.00 | 2.25 | 1439.46** | 98.08 | 1.96 | 58.28* | 8.41 | 2.64 | -0.07 |
| 37. | 14A × SRF 323 | 488.50 | -1.22 | 7905.16** | 131.50 | -0.86 | 536.22** | 8.72 | 0.06* | -0.08 |
| 38. | 14A × SRF 327 | 389.33 | 3.95 | 11534.51** | 113.92 | 3.75 | 979.79** | 7.73 | 5.57 | 0.10 |
| 39. | 14A × SRF 328 | 392.92 | -0.56 | 11885.32** | 133.33 | -0.46 | 1654.29** | 8.70 | -5.65 | 0.19* |
| 40. | 14A × SRF 330 | 480.83 | 0.13 | 4106.66** | 170.25 | 0.04 | 679.62** | 8.93 | 1.09 | -0.04 |
| 41. | 14A × SRF 331 | 366.08 | 0.51 | 23621.97** | 124.08 | 0.83 | 2907.49** | 7.85 | 5.65 | 0.13 |
| 42. | 14A × SRF 332 | 541.25 | 0.24 | 2231.10** | 149.83 | 0.20 | 180.81** | 9.58 | -0.96 | -0.07 |
| 43. | 14A × SRF 334 | 432.33 | 3.42 | 46416.45** | 144.00 | 3.94 | 5093.45** | 9.26 | 0.21* | -0.08 |

*Table 2. Contd..*

| SN | Genotypes | Green fodder yield plant$^{-1}$ (g) | | | Dry fodder yield plant$^{-1}$ (g) | | | Crude protein (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | μ | $b_i$ | $S^2d_i$ | μ | $b_i$ | $S^2d_i$ | μ | $b_i$ | $S^2d_i$ |
| [1] | [2] | [3] | [4] | [5] | [6] | [7] | [8] | [9] | [10] | [11] |
| 44. | 14A × SRF 335 | 504.33 | -0.16 | 38243.64** | 164.42 | 0.16 | 4545.94** | 8.42 | -0.26 | -0.07 |
| 45. | 14A × SRF 336 | 398.83 | -1.22 | 21675.54** | 136.83 | -0.86 | 2201.08** | 9.44 | -0.34 | -0.08 |
| 46. | 14A × SRF 337 | 381.58 | 1.52 | 3260.45** | 104.67 | 1.35 | 279.16** | 8.51 | 1.68 | -0.06 |
| 47. | 14A × CSV 15 | 410.33 | -0.50 | 2992.40** | 118.83 | -0.40 | 277.79** | 8.64 | 1.25 | -0.08 |
| 48. | 14A ×SPV 1616 | 354.83 | 1.60 | 371.48 | 81.58 | 1.08 | 5.03 | 8.74 | 0.84* | -0.08 |
| 49. | 14A × SPV 2113 | 474.25 | 1.35 | 7079.15** | 119.58 | 1.20 | 511.62** | 7.32 | 1.33 | -0.05 |
| 50. | 27A × SRF 317 | 545.42 | -3.30 | 11718.57** | 134.50 | -2.68 | 692.68** | 8.99 | 0.99 | -0.08 |
| 51. | 27A × SRF 321 | 326.83 | 2.01 | 657.54* | 111.42 | 2.25* | 61.31* | 8.82 | 0.63 | -0.08 |
| 52. | 27A × SRF 323 | 481.83 | 3.49** | -116.23 | 155.50 | 3.79** | -10.98 | 8.66 | 0.65 | -0.08 |
| 53. | 27A × SRF 327 | 471.75 | -2.33* | 681.88* | 126.42 | -2.07* | 28.38 | 9.54 | 1.26* | -0.08 |
| 54. | 27A × SRF 328 | 392.42 | 1.94 | 1186.51** | 99.42 | 1.75 | 38.32* | 7.62 | 2.00 | -0.07 |
| 55. | 27A × SRF 330 | 380.00 | -2.03* | 100.03 | 100.25 | -1.77** | -13.69 | 9.55 | 2.04* | -0.08 |
| 56. | 27A × SRF 331 | 390.17 | -0.29 | 3619.09** | 106.75 | -0.27 | 207.53** | 7.73 | 2.16 | -0.07 |
| 57. | 27A × SRF 332 | 415.17 | -0.10 | 1088.56** | 105.17 | -0.10 | 40.43* | 7.84 | 1.96* | -0.08 |
| 58. | 27A × SRF 334 | 472.33 | 3.85 | 17898.10** | 130.42 | 3.28 | 1660.64** | 9.26 | 0.93 | -0.08 |
| 59. | 27A × SRF 335 | 365.33 | 2.64 | 7047.89** | 123.08 | 3.05 | 765.23** | 7.72 | 0.91** | -0.08 |
| 60. | 27A × SRF 336 | 380.75 | 2.74 | 3047.41** | 122.00 | 2.84 | 390.34** | 8.56 | 0.79* | -0.08 |
| 61. | 27A × SRF 337 | 422.92 | 1.13 | 45220.65** | 107.42 | 0.68 | 2735.47** | 9.60 | -0.35 | -0.04 |
| 62. | 27A × CSV 15 | 448.75 | -0.19 | 6627.90** | 119.00 | -0.42 | 468.20** | 7.94 | 0.54 | 0.00 |
| 63. | 27A × SPV 1616 | 441.92 | 1.69 | 12030.48** | 134.58 | 1.49 | 1187.17** | 8.01 | 1.23 | -0.06 |
| 64. | 27A × SPV 2113 | 413.25 | -0.55* | 210.02 | 105.58 | -0.44* | -2.35 | 9.51 | 1.04** | -0.08 |
| 65. | 104A × SRF 317 | 419.25 | -0.10 | 3163.04** | 123.00 | -0.21 | 271.09** | 7.43 | 1.01 | -0.07 |
| 66. | 104A × SRF 321 | 443.25 | 0.76 | 14851.25** | 108.25 | 0.49 | 956.25** | 9.71 | 1.37 | -0.07 |
| 67. | 104A × SRF 323 | 388.83 | -0.07 | 9880.10** | 106.00 | 0.27 | 517.95** | 9.18 | 1.14* | -0.08 |
| 68. | 104A × SRF 327 | 437.17 | 0.79 | 2746.15** | 130.75 | 0.85 | 235.20** | 7.66 | 1.16 | -0.07 |
| 69. | 104A × SRF 328 | 490.42 | 3.85* | 897.79** | 135.17 | 3.21* | 145.41** | 9.60 | 0.88 | -0.06 |
| 70. | 104A × SRF 330 | 367.08 | 1.70 | 14377.94** | 100.33 | 1.37 | 1169.97** | 9.74 | 0.19 | -0.05 |
| 71. | 104A × SRF 331 | 438.50 | 2.70 | 8016.20** | 128.50 | 2.49 | 846.83** | 9.77 | 2.55* | -0.07 |
| 72. | 104A × SRF 332 | 456.42 | 3.14 | 15728.71** | 155.92 | 3.17 | 1003.85** | 9.94 | 1.15 | -0.07 |
| 73. | 104A × SRF 334 | 329.50 | -0.34 | 1599.65** | 89.00 | -0.29 | 94.61** | 8.20 | 0.74 | -0.07 |
| 74. | 104A × SRF 335 | 358.08 | -1.52 | 4412.01** | 119.42 | -1.81 | 376.64** | 8.74 | 2.56 | -0.02 |
| 75. | 104A × SRF 336 | 319.00 | 2.15 | 3076.35** | 113.42 | 2.43 | 426.02** | 6.64 | 0.78 | -0.06 |
| 76. | 104A × SRF 337 | 294.83 | 1.93 | 3296.20** | 89.25 | 1.94 | 415.08** | 8.14 | 0.68 | -0.07 |
| 77. | 104A × CSV 15 | 450.67 | 2.84 | 26440.75** | 135.75 | 2.66 | 2653.12** | 7.40 | 1.64 | -0.07 |
| 78. | 104A × SPV 1616 | 472.08 | 3.21 | 7246.38** | 131.17 | 2.79 | 711.38** | 7.31 | 2.53* | -0.07 |
| 79. | 104A × SPV 2113 | 529.75 | 0.81 | 2539.63** | 145.67 | 0.70 | 192.56** | 9.71 | 1.27 | 0.05 |
| 80. | GFS 4 check | 84.00 | -0.16 | 2177.03** | 25.08 | -0.18 | 162.51** | 7.08 | 0.94 | -0.07 |
| 81. | GFS 5 check | 390.17 | 0.68 | 5090.69** | 138.33 | 0.84 | 820.51** | 9.52 | -0.90 | -0.05 |
| 82. | CSV 21F check | 340.00 | 3.36** | -127.30 | 116.17 | 3.57** | -10.71 | 9.59 | 0.14 | -0.07 |
| | Mean | 389.10 | 1.00 | - | 116.45 | 1.00 | - | 8.67 | 1.00 | - |
| | S.Em.± | 0.52 | 0.15 | - | 0.16 | 0.15 | - | 0.12 | 0.11 | - |

*, ** Significant at 5 and 1 per cent levels of significance, respectively.

*Table 2. Contd..*

| SN | Genotypes | Shoot fly dead heart (%) | | | Brix (%) | | | HCN (ppm) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | $\mu$ | $b_i$ | $S^2d_i$ | $\mu$ | $b_i$ | $S^2d_i$ | $\mu$ | $b_i$ | $S^2d_i$ |
| [1] | [2] | [12] | [13] | [14] | [15] | [16] | [17] | [18] | [19] | [20] |
| 1. | 9A | 8.69 | 0.99** | -0.19 | 8.73 | 0.32 | -0.06 | 95.68 | 0.54 | -8.38 |
| 2. | 14A | 13.03 | 1.55 | 17.78** | 6.98 | 1.37** | -0.12 | 140.27 | 0.92 | -4.24 |
| 3. | 27A | 11.92 | 2.07 | 29.90** | 6.93 | -0.81 | -0.00 | 112.35 | 1.18* | -9.60 |
| 4. | 104A | 7.21 | 1.01* | 0.05 | 9.65 | 1.97* | -0.02 | 119.79 | 0.95 | -8.27 |
| 5. | SRF 317 | 8.48 | 0.95* | 1.05** | 7.53 | 0.23* | -0.11 | 75.34 | -1.30 | -0.44 |
| 6. | SRF 321 | 6.44 | 0.59 | 6.77** | 8.05 | 0.67* | -0.10 | 102.22 | 0.65 | -7.47 |
| 7. | SRF 323 | 12.33 | 1.53* | 2.16** | 7.03 | -0.62* | -0.06 | 149.04 | 2.84* | -8.08 |
| 8. | SRF 327 | 6.23 | 0.86 | 0.84** | 9.92 | 4.24** | -0.12 | 87.72 | 0.62 | -9.48 |
| 9. | SRF 328 | 9.43 | 1.34* | 0.95** | 6.66 | 0.75 | -0.06 | 101.42 | 0.97 | -2.69 |
| 10. | SRF 330 | 9.73 | 1.57 | 11.84** | 11.75 | 1.14 | 1.10** | 82.61 | 1.65 | -8.05 |
| 11. | SRF 331 | 8.68 | 0.94 | 3.10** | 8.88 | 2.37** | -0.07 | 128.18 | 3.88* | -7.08 |
| 12. | SRF 332 | 9.72 | 0.79 | 3.49** | 8.10 | -0.09 | 0.29* | 111.69 | 0.46 | -7.28 |
| 13. | SRF 334 | 7.58 | 1.14** | 0.11 | 10.59 | 1.41 | 0.10 | 111.07 | 1.19 | 11.59 |
| 14. | SRF 335 | 7.13 | 1.09** | -0.16 | 7.49 | -0.31 | 0.07 | 121.27 | 2.64 | -7.03 |
| 15. | SRF 336 | 8.47 | 1.18* | 0.32 | 8.82 | 0.99 | 0.59** | 98.54 | 2.69* | -9.22 |
| 16. | SRF 337 | 8.54 | 0.83 | 3.87** | 8.18 | -2.92 | 0.99** | 106.18 | -1.19 | -0.79 |
| 17. | CSV 15 | 6.22 | 0.85 | 0.81* | 10.24 | 4.59 | 1.46** | 114.56 | 0.34 | -9.55 |
| 18. | SPV 1616 | 6.57 | 0.88 | 0.99** | 10.84 | 2.04** | -0.07 | 98.72 | 0.34 | -6.21 |
| 19. | SPV 2113 | 9.59 | 0.97** | -0.10 | 7.88 | -0.65** | -0.12 | 112.39 | 2.06 | -5.66 |
| 20 | 9A × SRF 317 | 11.81 | 0.14 | 21.29** | 7.42 | -1.19 | 0.03 | 124.02 | 0.51 | -2.99 |
| 21. | 9A × SRF 321 | 7.17 | 0.85* | 0.05 | 7.57 | 0.48 | -0.00 | 122.27 | 3.00 | 3.16 |
| 22. | 9A × SRF 323 | 9.07 | 1.18* | 0.15 | 7.63 | -1.27 | 0.13 | 118.50 | -1.92 | 2.19 |
| 23. | 9A × SRF 327 | 12.87 | 0.58 | 1.82** | 10.11 | -1.08 | 1.04** | 105.76 | 1.58* | -9.29 |
| 24. | 9A × SRF 328 | 13.48 | 0.67 | 3.69** | 7.97 | -1.51** | -0.12 | 127.10 | 1.86 | -7.66 |
| 25. | 9A × SRF 330 | 9.53 | 1.02** | -0.14 | 7.93 | -2.38* | 0.12 | 104.82 | 1.45 | -8.74 |
| 26. | 9A × SRF 331 | 8.66 | 0.88 | 0.91** | 8.72 | -3.43 | 1.10** | 94.30 | -1.94 | 2.46 |
| 27. | 9A × SRF 332 | 11.78 | 0.82 | 2.82** | 7.52 | -0.62* | -0.11 | 117.28 | 0.25** | -9.76 |
| 28. | 9A × SRF 334 | 9.60 | 0.80 | 2.26** | 7.29 | -1.40* | -0.08 | 121.66 | 1.76 | -7.94 |
| 29. | 9A × SRF 335 | 8.99 | 0.95* | 0.08 | 8.22 | -0.29 | -0.08 | 110.99 | 2.20 | -6.98 |
| 30. | 9A × SRF 336 | 7.44 | 1.27 | 4.17** | 8.21 | 0.11 | 0.03 | 94.36 | -0.59 | -5.22 |
| 31. | 9A × SRF 337 | 7.42 | 1.22* | 1.29** | 15.07 | -1.17 | 1.15** | 86.89 | 0.63 | -9.58 |
| 32. | 9A × CSV 15 | 7.79 | 1.21* | 1.00** | 10.27 | -0.52 | 1.86** | 107.84 | 1.22 | -9.38 |
| 33. | 9A × SPV 1616 | 10.99 | 1.73 | 11.25** | 7.78 | -0.05* | -0.12 | 127.04 | 1.50 | -7.50 |
| 34. | 9A × SPV 2113 | 8.20 | 1.10* | 0.18 | 8.51 | 3.30* | 0.07 | 116.07 | 3.22 | -0.91 |
| 35. | 14A × SRF 317 | 9.04 | 1.07** | -0.00 | 10.16 | 0.80 | 0.03 | 119.04 | 0.97** | -9.77 |
| 36. | 14A × SRF 321 | 8.12 | 0.90* | 0.05 | 9.78 | 6.36* | 1.22** | 100.07 | -0.99 | -5.30 |
| 37. | 14A × SRF 323 | 8.59 | 1.04* | 0.63* | 9.68 | 1.30** | -0.11 | 99.11 | 0.45 | -8.55 |
| 38. | 14A × SRF 327 | 10.70 | 1.02** | -0.17 | 7.53 | 1.82* | -0.01 | 142.73 | 0.46* | -9.74 |
| 39. | 14A × SRF 328 | 10.77 | 1.08 | 3.56** | 9.86 | 2.50* | 0.11 | 137.62 | 1.36 | -6.32 |
| 40. | 14A × SRF 330 | 12.64 | 0.61 | 2.39** | 10.21 | 1.11 | 0.05 | 133.36 | 0.27 | -9.15 |
| 41. | 14A × SRF 331 | 8.51 | 1.40 | 4.09** | 9.35 | 4.98** | 0.19 | 135.06 | 0.63* | -9.70 |
| 42. | 14A × SRF 332 | 13.20 | 0.82* | 0.11 | 10.07 | 1.79** | -0.12 | 124.54 | 0.53 | -9.53 |
| 43. | 14A × SRF 334 | 12.67 | 0.72* | 0.47* | 9.36 | 3.89* | 0.30* | 134.87 | 1.38* | -9.51 |

*Table 2. Contd..*

| SN | Genotypes | Shoot fly dead heart (%) | | | Brix (%) | | | HCN (ppm) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | $\mu$ | $b_i$ | $S^2d_i$ | $\mu$ | $b_i$ | $S^2d_i$ | $\mu$ | $b_i$ | $S^2d_i$ |
| [1] | [2] | [12] | [13] | [14] | [15] | [16] | [17] | [18] | [19] | [20] |
| 44. | 14A × SRF 335 | 12.57 | 0.38 | 8.75** | 9.18 | 3.35 | 1.03** | 120.76 | 0.33 | -7.42 |
| 45. | 14A × SRF 336 | 12.97 | 1.04** | -0.06 | 13.25 | 2.32 | 0.39* | 130.17 | -0.89 | -4.75 |
| 46. | 14A × SRF 337 | 13.35 | 1.61 | 5.27** | 10.80 | 4.74** | -0.07 | 124.42 | 0.08 | -9.53 |
| 47. | 14A × CSV 15 | 10.16 | 0.27 | 14.81** | 12.06 | 3.92** | 0.02 | 156.90 | 2.57 | 67.84** |
| 48. | 14A ×SPV 1616 | 9.67 | 1.16* | 0.80* | 8.86 | 2.10 | 0.32* | 137.71 | 2.40 | -6.11 |
| 49. | 14A × SPV 2113 | 12.30 | 1.08* | 0.49* | 9.78 | 1.93* | 0.01 | 112.87 | 0.17* | -9.73 |
| 50. | 27A × SRF 317 | 12.80 | 0.87* | 0.80* | 10.64 | 2.69 | 0.83** | 112.97 | 1.81* | -9.25 |
| 51. | 27A × SRF 321 | 7.97 | 1.08* | 0.42 | 8.47 | 3.10* | 0.41* | 120.98 | 2.58 | -6.62 |
| 52. | 27A × SRF 323 | 7.71 | 1.01** | -0.14 | 9.44 | 5.56* | 2.00** | 102.31 | 1.95 | -8.27 |
| 53. | 27A × SRF 327 | 10.19 | 0.74* | 0.54* | 10.77 | 3.94* | 0.96** | 94.70 | -0.63 | -7.70 |
| 54. | 27A × SRF 328 | 11.48 | 0.75 | 1.86** | 8.23 | 0.40* | -0.11 | 157.35 | 3.60 | -2.65 |
| 55. | 27A × SRF 330 | 7.06 | 0.78 | 0.74* | 9.46 | 1.62** | -0.10 | 100.72 | 2.49 | -4.14 |
| 56. | 27A × SRF 331 | 9.78 | 0.71 | 3.37** | 9.85 | 1.57** | -0.10 | 140.53 | 1.65 | -8.11 |
| 57. | 27A × SRF 332 | 8.25 | 0.83 | 0.82** | 8.05 | 2.47 | 0.45* | 119.58 | 0.35 | -8.64 |
| 58. | 27A × SRF 334 | 9.37 | 1.34* | 0.67* | 9.16 | 1.87* | 0.03 | 143.91 | 1.26* | -9.70 |
| 59. | 27A × SRF 335 | 9.30 | 1.18 | 2.54** | 8.32 | 3.16* | 0.28* | 133.51 | 1.59 | -9.04 |
| 60. | 27A × SRF 336 | 10.86 | 0.73 | 2.07** | 7.57 | 1.52** | -0.12 | 117.34 | 2.52 | -2.16 |
| 61. | 27A × SRF 337 | 8.08 | 1.03** | 0.00 | 9.20 | 4.46* | 0.79** | 138.42 | 0.35* | -9.75 |
| 62. | 27A × CSV 15 | 12.54 | 0.90* | 0.09 | 10.31 | 1.59** | -0.09 | 129.59 | 1.02 | -9.33 |
| 63. | 27A × SPV 1616 | 10.61 | 0.60 | 1.12** | 8.65 | -2.12 | 1.49** | 98.51 | 0.77 | -9.58 |
| 64. | 27A × SPV 2113 | 9.54 | 0.17 | 21.34** | 7.17 | -1.43* | -0.09 | 109.12 | 1.84 | -8.07 |
| 65. | 104A × SRF 317 | 8.31 | 1.13* | 0.26 | 10.22 | 0.02 | 0.01 | 119.41 | 2.59 | -6.96 |
| 66. | 104A × SRF 321 | 8.63 | 1.19* | 0.45* | 10.17 | 1.49* | -0.09 | 103.99 | 1.25 | -9.09 |
| 67. | 104A × SRF 323 | 11.23 | 0.90 | 5.67** | 9.13 | -2.71 | 1.01** | 108.77 | 0.87** | -9.77 |
| 68. | 104A × SRF 327 | 8.38 | 1.49 | 5.24** | 11.35 | -0.40 | 0.20 | 122.28 | 1.18* | -9.58 |
| 69. | 104A × SRF 328 | 7.88 | 1.13** | -0.08 | 11.71 | -1.55 | 1.92** | 151.22 | 0.32 | -9.29 |
| 70. | 104A × SRF 330 | 9.42 | 1.52 | 5.83** | 8.70 | 1.45* | -0.04 | 116.08 | -5.29 | 13.27 |
| 71. | 104A × SRF 331 | 8.50 | 1.09** | -0.12 | 12.76 | -2.06 | 0.45* | 125.54 | 3.27 | -1.36 |
| 72. | 104A × SRF 332 | 9.70 | 1.30* | 1.51** | 9.03 | -0.71 | 0.02 | 135.49 | 1.35 | 2.03 |
| 73. | 104A × SRF 334 | 9.28 | 1.47 | 5.54** | 8.31 | 0.11 | 0.03 | 139.61 | 1.50 | -8.59 |
| 74. | 104A × SRF 335 | 6.45 | 1.03** | -0.21 | 9.65 | -0.90* | -0.11 | 133.17 | 0.01 | -9.54 |
| 75. | 104A × SRF 336 | 8.27 | 0.99** | -0.13 | 9.94 | -1.57* | -0.08 | 124.47 | 1.04 | -8.61 |
| 76. | 104A × SRF 337 | 9.14 | 1.27 | 2.23** | 17.07 | 0.12 | 0.64** | 148.51 | -0.05 | -9.28 |
| 77. | 104A × CSV 15 | 11.10 | 0.64 | 0.62* | 11.56 | 2.68** | -0.10 | 123.34 | 1.63 | -7.25 |
| 78. | 104A × SPV 1616 | 13.58 | 0.86 | 5.79** | 11.75 | 4.33** | -0.01 | 102.54 | 1.04* | -9.61 |
| 79. | 104A × SPV 2113 | 11.14 | 0.71 | 3.11** | 12.13 | 2.06** | -0.12 | 111.10 | 2.42 | -1.49 |
| 80. | GFS 4 check | 10.39 | 0.94** | -0.15 | 6.27 | -0.04 | -0.07 | 111.48 | 0.76 | -9.59 |
| 81. | GFS 5 check | 6.86 | 0.97** | -0.19 | 10.04 | 0.12 | 0.06 | 159.16 | 2.51 | -3.60 |
| 82. | CSV 21F check | 6.87 | 0.88* | 0.34 | 8.33 | 0.54* | -0.11 | 121.70 | -3.43 | -3.58 |
| | Mean | 9.59 | 1.00 | - | 9.36 | 1.00 | - | 118.71 | 1.00 | - |
| | S.Em.± | 0.10 | 0.35 | - | 0.37 | 0.55 | - | 0.12 | 0.96 | - |

*, ** Significant at 5 and 1 per cent levels of significance, respectively.

Brix, HCN and crude protein content are the three most important parameters of fodder quality. These three parameters were found to be stable (non-significant $S^2d_i$ and $b_i$ near unity for most of the genotypes). For brix per cent parental line, SRF 334 and three hybrids 104A × SRF 327, 104A × SRF 317, 14A × SRF 330 and 14A × SRF 317 were average stable with high mean because they had non-significant $b_i$ values near unity, non-significant deviation from regression and the average score higher than the general mean. A non-significant correlation between the deviation from regression ($S^2d_i$) and mean performance or regression coefficient ($b_i$) indicated that these stability parameters might be under the control of different genes located on different chromosomes as also discussed by Reddy and Chaudhary, 1991. The parents 104A, SRF 327 and SPV 1616, while the hybrids 104A × SPV 2113, 14A × CSV 15, 104A × SPV 1616, 104A × CSV 15 and 14A × SRF 337 were below average stable with high mean, significant regression coefficient more than unity and non-significant deviation from regression specifically suited to good farming condition for brix per cent. The hybrids that showed stability under poor environments were 104A × SRF 336 and 104A × SRF 335 and they had high mean, significant regression coefficient ($b_i < 1$) and least deviation from regression and was considered as above average stable for brix per cent. Low mean, non-significant regression coefficient ($b_i = 1$) and non-significant deviation from regression for HCN content observed for six parental lines, SRF 317, SRF 330, SRF 327, 9A, SPV 1616 and SRF 328 and hybrids viz.,

*Table 3. Stability of performance of parents and their hybrids for different characters in forage sorghum*

| Characters | No. of parents/ hybrids showed stability | Best parents and hybrids (Ideal genotypes) having general adaptability $ | Specific adaptability favorable environments | Specific adaptability unfavorable environments |
|---|---|---|---|---|
| Green fodder yield plant$^{-1}$ | 4 (P)<br>4 (H) | 14A × SPV 1616 | SRF 327<br>27A × SRF 323* | 9A, 27A, SRF 328<br>27A × SRF 330<br>27A × SPV 2113* |
| Dry fodder yield plant$^{-1}$ | 3 (P)<br>6 (H) | SRF 328<br>14A × SPV 1616 | SRF 327, 9A × SRF 334*, 27A × SRF 323* | 27A, 27A × SRF 327*<br>27A × SRF 330<br>27A × SPV 2113 |
| Crude protein content (%) | 19 (P)<br>58 (H) | 104A*, SRF 321*, SRF 332*, SRF 335*<br>104A × SRF 332*, 9A × SRF 331*, 104A × SRF 321*, 104A × SPV 2113*, 104A × SRF 328*, 104A × SRF 332*, 27A × SRF 334* | 9A × SRF 328*, 9A × SRF 337*, 27A × SRF 327*, 27A × SRF 330*, 27A × SPV 2113*, 104A × SRF 323*, 104A × SRF 331* | 14A, 14A × SRF 323*<br>14A × SRF 334*,14A × SPV 1616* |
| Shoot fly dead heart percentage | 6 (P)<br>19 (H) | | 104A*, SRF 334*, SRF 335*, SRF 336*, 9A × SRF 323*, 9A × SPV 2113*, 14A × SRF 317*, 14A × SRF 336, 14A × SRF 327<br>27A × SRF 321*, 27A × SRF 323*, 27A × SRF 337*, 104A × SRF 317*, 104A × SRF 328*, 104A × SRF 331*, 104A × SRF 335* | 9A*, SPV 2113, 9A × SRF 321*, 9A × SRF 335*, 14A × SRF 321*, 14A × SRF 332, 27A × CSV 15, 104A × SRF 336* |
| Brix per cent | 14 (P)<br>39 (H) | 9A, SRF 334*, SRF 335, 14A × SRF 317*<br>14A × SRF 330*, 104A × SRF 317*, 104A × SRF 327* | 14A, 104A*, SRF 327*, SRF 331, SPV 1616*, 14A × SRF 323*, 14A × SRF 328*, 14A × SRF 332*, 14A × SRF 337*, 14A × CSV 15*, 14A × SPV 2113*, 27A × SRF 330*, 27A × SRF 331*, 27A × CSV 15*, 104A × SRF 321*, 104A × CSV 15*, 104A × SPV 1616*, 104A × SPV 2113* | 27A, SRF 317, SRF 321, SRF 323, SPV 2113, 27A × SRF 328, 27A × SPV 2113, 104A × SRF 335*, 104A × SRF 336* |

[$] Stable parents and hybrids; *Genotype's mean value is higher than population mean.

9A × SRF 331, 9A × SRF 336, 27A × SRF 327, 27A × SPV 1616, 27A × SRF 323, 9A × SRF 330, 9A × CSV 15 and 104A × SPV 2113 were desirable. These genotypes exhibited stability under changing environments. However, the genotypes 27A, SRF 336, 9A × SRF 327, 104A × SPV 1616 and 27A × SRF 317 had low mean, significant regression coefficient ($b_i > 1$) and non-significant $S^2d_i$ reflecting below average stability and was found to be specifically adapted to favorable farming situations. The cross combinations, 104A × SRF 323, 14A × SPV 2113 and 9A × SRF 332 were stable under poor farming situations as they depicted low mean, significant regression coefficient ($b_i < 1$) and non-significant $S^2$di as discussed by Rajashekhar, 2007 and Narayan, 2009.

For crude protein content, the parents 104A, SRF 321, SRF 332 and SRF 335 and seven stable hybrids were 104A × SRF 332, 9A × SRF 331, 104A × SRF 321, 104A × SPV 2113, 104A × SRF 328, 104A × SRF 332 and 27A × SRF 334. They possessed higher protein content, non-significant deviation from regression and non-significant regression coefficient ($b_i = 1$) suggesting their stability for crude protein content. The cross, 14A × SRF 334, 14A × SPV 1616 and 14A × SRF 323 exhibited $b_i$ value significantly less than one, high mean and non-significant deviation from regression showing above average stability suitable for poor environments. Whereas, the seven hybrids (104A × SRF 331,9A × SRF 337, 27A × SRF 330, 27A × SRF 327, 27A × SPV 2113, 9A × SRF 328 and 104A × SRF 323) due to high mean, $b_i$ value significantly more than one and $S^2d_i$ value non significantly deviating from zero, showed below average stability which were suitable in good environments for crude protein content. The results are in line with the findings of Het Ram *et al*. (1993); Sankarpandian (2000); Patel and Patel (2010).

Considering highest mean values, regression around unity and least deviation from regression, it was observed that none of the genotypes was stable for all the characters in the present study. But the hybrid 27A × SRF 323 was more suitable specifically under good farming conditions for green and dry fodder yield plant$^{-1}$. While, hybrids 27A × SPV 2113 and 27A × SRF 327 were more suitable specifically under poor farming situation for green and dry fodder yield plant$^{-1}$. For quality characters viz., HCN content and crude protein content, hybrids 9A × SRF 331 and 104A × SPV 2113 were found stable. Thus, these hybrids can be exploited commercially for high quality fodder after testing in wide range of environments.

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