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Genetic Variation in Dry Lowland Sorghum Landraces of Abergelle, Northern Ethiopia

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Abstract

Even though sorghum is dominant cereal crop in Tigray region of Ethiopia, a limited study has been undertaken on existing sorghum landraces variability. Thus, the objectives of this study were to assess the presence and degree of variability among ýfteen sorghum landraces for desired agro-morphological traits at Abergelle Agricultural Research Center, northern Ethiopia during 2020 cropping season. The ýeld experiment was conducted in randomized complete block design (RCBD) with three replications. Data were collected and analyzed variance for days to emergence, days to þowering, days to maturity, plant height, panicle length, number of seeds per panicle, thousand grain weight, grain yield and striga count at harvesting of sorghum under random stress conditions. Analysis of variance revealed signiýcant genetic di erence among sorghum landraces for most of the l races c ¯ M $^{-1}$), Woitozira (3500 kg ha^{-1}), Tewzale (3260 kg ha^{-1}), Daka (3000 kg ha^{-1}) and Amsel (2700 kg ha^{-1}) were found superior over check variety Chare. The phenotypic coe cient of variation (PCV) had exceeded the genotypic coe cient of variation (GCV) for all the variables studied, suggesting certain degree of interaction with the environment. Moreover, high heritability coupled with high genetic advance as percent of mean (GAM) were recorded for grain yield, panicle length, number of seeds per panicle, thousand grain weight and plant height, reþecting the presence of additive gene action for the expression of these traits and improvement of these traits could be done through selection. In conclusion, the high yield performing of sorghum landraces screened in this study could be exploited as source of breeding materials for further sorghum improvement to enhanced grain yield.

Table 3: Mean squares of agronomic traits from analysis of variance, estimates of phenotypic and genotypic variances and coe cient of variations, heritability in broad sense, genetic advance and genetic advance as percent of mean.

Traits	MSg (df=14)	MSe (σ^2e) (df=28)	Mean	σ^2g	σ^2p	GCV%	PCV%	H²%	GA	GAM%
DF	81.85**	0.72	86.3	18	18.7	4.9	5	96.2	8.6	9.95
DM	237.7**	1.47	138.4	78.7	80.2	6.4	6.5	98.2	18.1	13.1
PH	2813.3**	32.66	262.4	926.9	959.5	11.6	11.8	96.6	61.7	23.5
PL	83.05**	0.614	22	27.5	28.1	23.8	24.1	97.8	10.7	48.6
NSPP	356522**	4020	1966.9	1E+05	121521	17.4	17.7	96.7	695.4	35.4
TGW	83.05**	0.614	31.4	27.5	28.1	16.7	16.9	97.8	10.7	34.1
GY	1390834**	4282	2460	5E+05	466466	27.6	27.8	99.1	1396.1	56.8

*, ** = signiýcant at PÒ 0.05 and PÒ 0.01, respectively.
Where: df= degree of freedom, DF= days to þowering, DM = days to maturity, PH = plant height, PL = panicle length, NSPP = number of seeds per panicle, GY = grain yield, TGW = thousand grain weight; MSg = mean square of genotypes, MSe = mean square of error (environmental variance, ŭ2e), ů2g = genotypic variance, ů2p = phenotypic variance, PCV = phenotypic coe cient of variance (%), GCV = genotypic coe cient of variance (%), H2 = broad sense heritability (%), GA = Genetic advance and GAM = genetic advance as percent of mean (%).

Authors Contribution