

Performance of Elite Sesame Genotypes (*Sesamum Indicum* L.) Collected from Western Ethiopia

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Abstract

Sesame is an important agricultural commodity in earning foreign currency for Ethiopia. However, its productivity in Western Ethiopia has been constrained due to harsh weather conditions and severe diseases. Hence local landraces are better adaptable to environmental conditions in which they were evolved, collection and evaluation of landraces is the preliminary plant breeding task to develop high yielding and adaptable variety. Thus, the experiment was conducted at Kamashi and Pawe during 2014-2016 to evaluate 18 sesame genotypes consisted of 17 landraces screened from collections of Western Ethiopia, and one check. The experiment was laid out on randomized complete block design with three replications. Data was collected on days to 50% flowering, bacterial blight disease severity, days to maturity, plant height, plant height to first branch, number of branches/plant number of capsules/plant, number of seeds/capsule, 1000 seeds weight and seed yield/plot. Analysis of variance on combined data revealed significance difference among environments for all traits while the genotypes were significantly different for days to flowering, bacterial blight disease severity, number of branches/plant 1000 seeds weight and seed yield. Combined analysis indicates that mean seed yield of sesame genotypes was ranged from 220 kg ha⁻¹ to 1065 kg ha⁻¹ across environments. Seed yielding potential of Ass-acc-64 and Ass-acc-29 reached about 1100 kg ha⁻¹-1400 kg ha⁻¹ and 1200-1400 kg ha⁻¹ respectively. Ass-acc-64 and Ass-acc-29 were high seed yielding genotypes with combined mean seed yield of 715 kg ha⁻¹ and 706 kg ha⁻¹ respectively. Minimum bacterial blight disease severity was recorded on high yielding genotypes Ass-acc-64 (24.76%) and Ass-acc-29 (30.86%). Therefore, Ass-acc-64 and Ass-acc-29 are proposed as candidate variety based on their seed yielding performance and resistance against bacterial blight. However, temporal deviation in productivity of sesame genotypes indicates that achieving high and stable seed yield in sesame needs interdisciplinary research.

Keywords: Bacterial blight; Collection; High rainfall areas; Seed yield

Introduction

Sesame (*Sesamum indicum* L. 2n=26) which belongs to the Pedaliaceae family is the most ancient oilseed crop where *Sesamum indicum* is the most widely cultivated one [1]. Since most of wild species of the genus *Sesamum* exist only in Africa, sesame has been thought to be originated from Africa [2]. Five major centers of diversity have been proposed for sesame including Ethiopia, India, China, Central Asia and the Middle East [3]. Due to the presence of diverse wild relatives in Africa, Africa is considered the primary centre of origin, while India and Japan are considered as the two secondary centers of origin of this crop [4,5].

Sesame is highly drought tolerant, and it can adapt and produce seed well under fairly high temperatures [1]. In Ethiopia sesame grows well in semi-arid areas of Amhara, Tigray, lowlands of Oromia, Benishangul Gumuz, Gambella and Somali regions. The Ethiopian government has indicated that the oil seeds such as sesame, Niger and safflower seeds as a high priority export crops and ranks the second highest export earner [6]. Sesame is also a suitable crop for poverty alleviation for small holders in Benishangul Gumuz in which farmers can achieve high profits without significant upfront investments [7].

Despite suitable agro-ecologies and established market opportunities for Ethiopian sesame production, farmers still grow cultivars with low yielding performance and undesirable characteristics. The national average yield of Ethiopian sesame is 600 kg/ha [8]. The low yield is attributed by numerous abiotic and biotic factors including lack of widely adapted improved varieties, poor agronomic practices, attack by many pests, soil and climatic conditions, insufficient seed supply and

poor extension coverage. Bacterial blight disease causes complete crop failure in areas such as Wellega and Assosa where its incidence and severity may reach up to 100% due to high humidity and water logging. Bacterial blight disease mainly develops in the rainy season with high relative humidity which causes defoliation and sterility under severe conditions [9]. Higher seed yield accompanied by desirable seed quality, resistance to major diseases and insect pests are the breeding objectives of sesame breeders. Even though several improved sesame varieties released in Ethiopia, non-adaptability of these varieties limited the productivity of sesame in high rainfall areas of Western Ethiopia. Water logging and severe bacterial blight disease constrains sesame productivity as result of high and prolonged rainfall. Collection

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Received: 05-May-2022, Manuscript No. ACST-22-62937; **Editor assigned:** 09-May-2022, PreQC No. ACST-22-62937 (PQ); **Reviewed:** 23-May-2022, QC No. ACST-22-62937; **Revised:** 04-Jul-2022, Manuscript No. ACST-22-62937 (R); **Published:** 11-Jul-2022, DOI: 10.4172/2329-8863.1000531

Citation: Gedifew S, Robsa A (2022) Performance of Elite Sesame Genotypes (*Sesamum Indicum* L.) Collected from Western Ethiopia. Adv Crop Sci Tech 10:531.

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and characterization followed by evaluation of local landraces for their performance might enable to develop locally adaptable and high yielding sesame varieties. Thus, to meet crop improvement goals of sesame in high rainfall areas, it is a prerequisite to collect and evaluate local landraces for their performance based on seed yield and seed yield related traits. Therefore, the objective of the experiment was to evaluate elite sesame genotypes those have been screened from collections of Western Wollega and Assosa based on their performance for their seed yield and seed yield related traits across locations and years at high rainfall areas of Western Ethiopia.

Materials and Methods

Experimental materials and design

The experiment was conducted at Kamashi research station of Asossa Agricultural Research Center, and Pawe Agricultural Research Center during 2014-2016 cropping season. A total of 18 experimental materials which consisted of 17 elite sesame landraces screened from collections of Western Ethiopia and Abasena (check) were the experimental materials of the study. The experiment was laid out on Randomized Complete Block Design (RCBD) with three replications. Each experimental material was planted on a plot consisted of 5 rows of 5 m length. The spacing between rows was 40 cm while spacing of 10 cm between plants was maintained by thinning at 3-4 leaves stage. Thinning, weeding and other agronomic practices were carried out appropriately and uniformly to raise optimum population and good crop condition.

Data collection

Data were recorded on Days to 50% Flowering (DF), Days to 90% Maturity (DM), Bacterial Blight Disease Severity (BBDS), Plant Height (PH) in cm, Plant Height to First Branching (PHFB) in cm, number of Branches/Plant (BPP), number of Capsules/Plant (CPP), number of Seeds/Capsule (SPC), Seed Yield/Plot (SYPP) and 1000 Seed Weight (TSW) in gram (g). Data on Days to Flowering (DF), Days to Maturity (DM), seed yield and thousand seeds weight were recorded on plot basis while data on bacterial blight disease severity, plant height, plant height to first branching, number of branches/plant, number of capsules/plant, and number of seeds/capsule were recorded on plant basis from five randomly taken plants. At flowering stage, resistance of genotypes against bacterial blight was scored in 0-6 disease susceptibility scale [10], where 0=0% (immune), 1=0.1-5% (highly resistant); 2=5.1-10% (resistant); 3=10.1-20% (moderately resistant); 4=20.1-50% (moderately susceptible); 5=50.1-70% (susceptible) and 6=>70% (highly susceptible). Disease susceptibility scales recorded in 0-6 scale were converted to Percentage of Severity Index (PSI) according to Wheeler [11] as follows:

$$PSI (\%) = \frac{\text{Sum of all disease scores}}{\text{Number of ratings} \times \text{Maximum disease grade}} \times 100$$

Data analysis

Analysis of Variance (ANOVA): Analysis of variance was carried out by using "PROC GLM" procedure of SAS University Edition [12]. Hence the data was collected from the trial conducted in three years at and two locations; environments were defined as combinations of years and locations. Therefore, environments which composed of as combinations of two locations (Kamashi and Pawe) and three years (2014, 2015 and 2016); replications within environments; genotypes and genotype by environment interaction were the terms of the model used for testing the performance of sesame genotypes. The generalized linear model used in analysis of variance was:

$$Y_{ijk} = \mu + E_k + R(E)_{jk} + G_i + GE_{ik} + e_{ijk}$$

where Y_{ijk} is the observation of the i^{th} genotype (G) in the k^{th} replication (R) in the j^{th} environment (E); μ is the overall mean; E is the k^{th} environment effect; R (E) $_{jk}$ is the j^{th} replication effect within k^{th} environment; G_i is the i^{th} genotype effect; GE_{ik} is the interaction effect of i^{th} genotype and k^{th} environment, and e_{ijk} is the associated error term.

Mean performance of sesame genotypes: Combined mean performance of sesame genotypes for seed yield and seed yield related traits were determined to identify promising sesame genotypes. Least Significant Difference (LSD) value at 5% of probability was used to compare genotype means for traits considered based on combined data.

Result and Discussion

Analysis of Variance (ANOVA)

The combined analysis of variance for seed yield and seed yield related traits revealed that there was significant variation among environments for all traits (Table 1). The ANOVA also confirmed that sesame genotypes showed significant variation for days to flowering, bacterial blight disease severity, number of branches/plant, 1000 seeds weight and seed yield. Significance difference among sesame genotypes for these traits revealed the presence of genetic variability that can be exploited for improvement of seed yield and seed yield related traits of sesame through collection, characterization and evaluation of local landraces. Besides, ANOVA on combined data revealed that genotype by environment interaction effect was non-significant for all traits considered except for number of branches/plant. Hence the environments in the study are the combinations of locations and years; the absence of genotype by environment interaction indicates that sesame genotypes included in the study equally respond to favorability or unfavorability of environments. Therefore, it is reasonable to suggest that the testing sites can represent each other in multi-environment trials of future sesame breeding programs.

	Source of variation				
	Environment	Replication (Environment)	Genotype	Genotype x Environment	Residual
Degree of freedom/Traits	5	12	17	85	204

Days to flowering	1643.83**	8.39	10.53**	3.62 ^{ns}	3.45
Bacterial blight disease severity (%)	305.08**	145.48	194.89**	64.00 ^{ns}	59.73
Days to maturity	2321.57**	12.57	12.33 ^{ns}	5.47 ^{ns}	8.4
Plant height (cm)	42430.12**	644.26	113.12 ^{ns}	86.91 ^{ns}	137.22
Plant height to first branching (cm)	19949.15**	295.33	128.4 ^{ns}	53.74 ^{ns}	119.83
Number of branches/plant	124.25**	14.79	3.59*	2.72**	1.78
Number of capsules/plant	16784.57**	1555.36	290.93 ^{ns}	166.81 ^{ns}	193.43
Number of seeds/capsule	7873.42**	267.07	9.85 ^{ns}	30.83 ^{ns}	31.9
1000 seeds weight (gm)	0.0085**	0.0089**	0.068**	0.0042 ^{ns}	0.0032
Seed yield (kg ha ⁻¹)	7198082.83**	105399.4	64694.17**	32440.15 ^{ns}	30608.55

** =significant at 1% of probability and * =significant at 5% of probability

Table 1: Analysis of variance on agro-morphological traits of sesame genotypes at Kamashi and Pawe during 2014-2016 cropping year.

Mean performance of sesame genotypes

The highest mean seed yield was recorded during 2015 (environment two and five), in which mean yield of these environments had 70% and 45.28% of yield advantage than mean yield recorded in 2014 (environment one and four) and 2016 (environment three and six), respectively (Figure 1). This indicates that genetic potential of sesame genotypes was determined by the influence of temporal variation such as water logging and aggravated bacterial blight disease severity as result of the occasions of suitable weather conditions for disease development. The analysis of variance confirmed that bacterial blight disease infection was highly significant among environments. Bacterial blight disease which caused by *Xanthomonas campestris* *pv.* *sesami* is the major problem in sesame production in high rainfall areas of Western Ethiopia like Western Wollega, Gambella, Kamashi, Assosa and Pawe. In occasions of prolonged rainfall, bacterial blight results a total crop failure in some local cultivars and non-adaptable varieties in high rainfall areas of Western Ethiopia. Bacterial blight disease mainly develops in the rainy season with high relative humidity which would cause defoliation and sterility under severe conditions [9]. Bacterial blight disease incidence reaches up to 100% in Wellega, Gambella and Pawe where high humidity persists and water logging assist the spread of bacterial blight [13]. Therefore, increment of sesame productivity in the study area can be achieved through evaluation of local landraces and selection of promising sesame genotypes for their adaptability and seed yielding performance accompanied by improved agronomic practices.

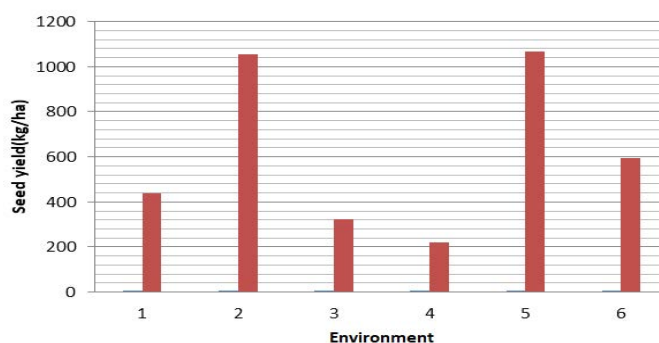


Figure 1: Mean seed yield of 18 sesame genotypes at six environments

Combined mean performance of sesame genotypes in terms of seed yield and seed yield related traits showed the possibility to select promising sesame genotypes for their improved agronomic performance (Table 2). Minimum and maximum number of days to 50% flowering was recorded on Ass-acc-17 (59 days) and Ass-acc-5 (62 days), respectively. All sesame genotypes showed moderate susceptibility (20-50%) against bacterial blight disease severity. Minimum bacterial blight disease severity was recorded from high seed yielding sesame genotypes such as Ass-acc-64 (24.76%) followed by Ass-acc-29 (30.86%). Maximum combined mean seed yield was obtained from Ass-acc-64 (715 kg ha⁻¹) and Ass-acc-29 (706 kg ha⁻¹) whereas the least seed yielding genotype was Ass-acc-17 with mean seed yield of 512 kg ha⁻¹. Among the highest yielding sesame genotypes; Ass-acc-29 gave 1200 kg ha⁻¹ and 1400 kg ha⁻¹ seed yield at environment two and environment five, respectively whereas 1100 kg ha⁻¹ and 1400 kg ha⁻¹ seed yield was obtained from Ass-acc-64 at environment two and environment five, respectively. As a result, hence Ass-acc-64 and Ass-acc-29 gave higher combined seed yield, these genotypes can be suggested as potential candidate to be grown in high rainfall areas of Western Ethiopia.

Genotype	DF	BBDS	DM	PH	PHFB	BPP	CPP	SPC	TSW	SY
Abasena	60.17	31.43	112.83	115.06	57.87	4.04	48.73	61.96	2.28	687.77
Ass-acc-105	60.11	32.43	111.22	108.84	51.87	3.24	40.22	63.92	2.19	538.18
Ass-acc-11	59.94	32.8	111.22	108.99	51.68	4.39	48.74	61.28	2.08	591.73
Ass-acc-127	61.39	34.41	113.06	113.48	56.49	3.67	47.89	65.73	2.22	655.66
Ass-acc-128	60.22	37.69	112.67	110.05	53.53	3.93	50.66	63.69	2.13	581.18
Ass-acc-17	59.11	35.01	111.33	109.76	55.05	3.77	46.09	62.93	2.18	512.96
Ass-acc-25	59.61	35.89	111.83	108.22	49.92	4.52	48.73	62.84	2.12	625.48
Ass-acc-29	60.22	30.86	111.72	109.27	50.47	3.95	42.59	63.89	2.19	706.64
Ass-acc-3	60.33	35.84	112.94	109.52	48.92	4.59	54.16	63.73	2.18	679.38
Ass-acc-35	60.22	36.86	113.11	110.53	53.68	3.88	41.01	64.94	2.17	565.89
Ass-acc-36	60.67	31.84	112.78	105.51	54.1	3.16	42.26	62.56	2.19	529.17
Ass-acc-48	59.89	35.18	111.78	111.98	52.83	4.16	46.95	65.17	2.09	598.3
Ass-acc-5	61.83	34.27	114.22	111.14	56.93	3.14	40.43	62.13	2.21	592.13
Ass-acc-64	59.78	24.76	112.17	109.78	53.21	4.24	49.72	62.73	2.14	715.97
Ass-acc-71	61.39	34.39	111.89	114.12	58.39	3.77	49.62	66.98	2.07	639.81
Ass-acc-74	59.44	33.96	113.11	108.26	53.95	3.55	47.01	64.93	2.28	658.79
Ass-acc-78	60.28	40.34	113.22	110.18	56.09	3.89	46.09	63.81	2.19	599.96
Ass-acc-85	61.67	35.43	112.06	105.87	53.94	3.3	41.76	62.08	2.1	616.54
Mean	60.35	34.08	112.39	110.03	53.82	3.84	46.26	63.63	2.17	616.42
Least Significant Difference (5%)	1.22	5.07	ns	ns	ns	0.51	ns	ns	0.037	114.98
Coefficient of Variation (%)	3.08	22.26	2.58	10.64	20.33	34.73	30.06	8.87	2.63	28.38

DF: Days to 50% of Flowering; DM: Days to 90% of Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branching in cm; BPP: number of capsule Bearing Branches/Plant; CPP: number of Capsules/Plant; SPC: number of Seeds/Capsule; TSW: Thousand Seeds Weight in g; SY: Seed Yield kg/ha and ns: non-significant

Table 2: Combined mean performance of elite sesame genotypes for different traits at Kamashi and Pawe during 2014-2016 cropping year.

Conclusion

Analysis of variance on combined data revealed the presence of significant difference among environments and genotypes for seed yield and seed yield related traits. The significant difference among environments for seed yield and seed yield related traits in sesame indicated the presence of environmental influence on genetic potential of sesame genotypes. Mean seed yield was higher at environment two and five and sesame landraces Ass-acc-64 and Ass-acc-29 were the highest yielders. Besides, low productivity of sesame genotypes during 2014 and 2016 at both locations indicates undetermined effect of weather condition such as prolonged rainfall and water logging during these cropping years. Significance difference among sesame genotypes for seed yield and seed yield related traits confirmed the possibility of selecting sesame genotypes with desirable traits like high seed yielding performance in high rainfall areas. Sesame genotypes such as Ass-acc-29 and Ass-acc-64 were recommended based on their relatively better resistance against bacterial blight disease and seed yielding potential. However, sesame crop improvement through plant breeding tasks for higher yield and adaptability need to be accompanied by improved agronomic and crop protection practices.

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