

GENETIC VARIABILITY AND HERITABILITY OF VEGETATIVE AND GENERATIVE TRAITS OF DIFFERENT SORGHUM GENOTYPES

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ABSTRACT

The development of sorghum varieties have been conducted with several purposes such as to obtain grain sorghum, sweet sorghum, forage sorghum, and biomass sorghum. Recently, sorghum breeders try to develop sorghum type for bioenergy. Unfortunately, there is a little information on genetic variability especially that of biomass sorghum. The objectives of this study were to evaluate the genetic components of 20 different sorghum genotypes, to estimate the broad sense of heritability value, and to assess the economic yield for biofuel and feed. There were 20 sorghum genotypes as GH-1, GH-2, GH-3, GH-6, GH-7, GH 9, GH 10, GH 11, GHP-1, GHP-3, GHP-11, P/I WHP, P/F 5-193-C, PF 10-90-A, P/I 150-21-A CYMMIT, Mandau, Numbu, Pahat, Talaga Bodas, UPCA. Treatments were arranged in randomized block design with 3 reps. Variables observed in this study were root dry weight, leaf number, leaf dry weight, stem dry weight, inflorescence length, and yield components as seed size and seed weight. Data were analysed by using analysis of variance and broad sense heritability. Analysis of variance showed that genotypes were significantly different based on the variables observed. Plant height, panicle length, and seed size showed high broad sense heritability i.e. 90.2, 92.6, and 92.3% respectively. On the other hand, stem diameter, seed number and seed weight have low broad sense heritability i.e. 52.3, 54.5, and 55.7% respectively.

Keywords: biomass, broad sense heritability, genetic variability, sorghum

INTRODUCTION

The development of breeding program in sorghum (*Sorghum bicolor* (L) Moench) have been conducted with aims of obtaining different type of sorghum such as grain sorghum, sweet sorghum, forage sorghum, and biomass sorghum. It is well documented that sorghum has a genome size of 736 Mb and is diploid. Its relatively small genome makes it a suitable model for other related crops with much larger genomes or polyploidy, such as sugar cane.

Sorghum has 25 species with the chromosome number of $2n=2x=20$ (Wang *et.al.* 2015). Recently, breeders tend to focus on developing sorghum for feed and biofuel. They have also been developing sorghum variety not only for high sugar content but also for cellulose content. The information regarding the social economic (Amosson, *et.al.* 2013; Saptoadi. 2015), agronomic (Bakheit, 1990; Fujii, *et.al.* 2014; Hoffmann and Rooney. 2014; Pabendon *et.al.* 2012; Purnomohadi. 2006; Rocateli *et.al.* 2012; Hadi *et.al.* 2016; Setiawan *et.al.* 2016), physiological (Barbanti *et.al.* 2015; Beheshti and Fard. 2010) and genetic (Setyowati *et.al.* 2005; DeLacya *et.al.* 2010; Singh *et.al.* 2012) characters of sorghum has already been published. DeLacya *et.al.* (2010) reported that the trait for high grain yield tended to associate with early flowering, whereas high stover yield would associate with plant height. Kong *et.al.* (2014) showed that based on identified QTL of sorghum population, the genetic determinants of branching might contribute to components of vegetative branching in sorghum. It seems that trait of stem characters is concomitant with stem improvement for biofuel and feed. However, the published papers on genetic characters of selected sorghum genotypes for biomass production are still rare. The objectives of this study were to evaluate the genetic components of 20 different sorghum genotypes, to estimate the broad sense of heritability value, and to assess the economic yield for biofuel and feed. What it means by the economic yield this paper is seed number, seed size, and seed weight, harvest index and biomass index.

MATERIALS AND METHODS

This study was conducted from April to July 2015 in dry land of South Lampung with planting materials of 20 sorghum genotypes. Treatments were arranged in randomized block design with 3 reps. Three seeds per hole were planted with space of 80 cm x 20 cm. Fertilizers as urea, TSP and KCl were used in this study with the dosage of 150 kg/ha, 100 kg/ha, and 150 kg/ha, respectively. Fertilizers of urea and KCl were applied twice in 30 day after planting (DAP) and 60 DAP for half dosage, while TSP was applied once in 30 DAP.

Variables observed in this study were root dry weight (RDW), leaf dry weight (LDW), stem dry weight (SDW), panicle length (PL), panicle dry weight (PDW), and yield components as seed size (SS), seed number (SN), seed weight per panicle (SW), leaf number (LN), plant height (PH), stem diameter (SD). Photoassimilate allocation was determined by harvest index (HI) and biomass index (BI). Seed size was calculated from 100 seeds (g). HI

was based on ratio between SW and total of RDW, LDW, SDW, PDW and SW. Biomass index (BI) was calculated as SDW divided by RDW, LDW, SDW, PDW and SW. The grouping for sorghum biomass production type was based on intensity of the value of BI that is ≥ 50 . Data was analysed by using SAS 9.0 including analysis of variance.

Broad sense heritability (H^2_{bs}) was calculated and modified from Stansfield (1991) as the followings: $(H^2_{bs}) = (\sigma^2_g / \sigma^2_f) \times 100\%$ where $40\% < H^2_{bs} < 55\%$ is small; $55\% < H^2_{bs} < 70\%$ is medium and $H^2_{bs} > 70\%$ is high.

σ^2_g (variance of genetics) = $\{(MSG - MSE)/n\}$ and then

σ^2_f (variance of phenotype) = $\sigma^2_g + \sigma^2_e$

σ^2_e is the same as MSE

Standard deviation of genetic variance is followed:

$\sigma \sigma^2_g = \sqrt{(2/r^2)\{(MSG/dfg) + 2\} + (MSE/dfe) + 2\}}$ where dfg is degree freedom of genetic and dfe is degree freedom of error.

The Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were determined to indicate the variation performance in the field by formula as followed:

$(GCV) = \sqrt{(\sigma^2_g/X)} \times 100\%$ and $(PCV) = \sqrt{(\sigma^2_f/X)} \times 100\%$ where X = general means

$CV < 30\%$ is narrow; $30 < CV < 40\%$ is medium and $CV > 40\%$ is wide

RESULTS AND DISCUSSION

Based on vegetative and generative variables of 20 sorghum genotypes used in this study, the genetic variance was considered to be high. According to Ng'Uni et.al (2011) by using simple sequence repeat (SSR), genetic variation was revealed according to the sites of sorghum collection. Additionally, the range values of H^2_{bs} were 52-93% (Table 1). Most of the traits observed in this study showed high H^2_{bs} except for SD, SN, and SW. Three traits of SD, SN, and SW had the values of H^2_{bs} as 52.3, 54.5, and 55.7%, respectively. It implies that most of the characters that showed high H^2_{bs} were under genetic control. The variable of SD showed low value of H^2_{bs} as 52.3% compared to plant height that was 90.2%, suggesting that trait for plant height of sorghum would be more heritable than that for SD. This result was similar to the DeLacy *et.al.*'s study in 2010 who reported that the heavier stover production was closely related to taller sorghum type. Moreover, this result was also associated with the previous result (Setiawan *et.al.* 2016) that plant height was significantly correlated with SDM

of unselected sorghum genotypes based on the best performance of biomass production group as $r=0.61^*$. However, this correlation would not be significantly different for sorghum genotypes which were selected for the best performance of biomass production group. This condition was probably caused by highly homogenous vegetative characters selected for the best performance of biomass. This inferred that stem characters as length and internode seem suitable trait for selection for improvement of biomass sorghum. On the contrary, SD does not appear to be a proper trait for selection for biomass sorghum. Besides, SD showed low H^2_{bs} (52.3%) and seemed to be influenced by environmental factors.

Three traits of SD, SN, and SW having low H^2_{bs} are under environmental factors. It means that such traits would be influenced by environmental factors. Three generative traits (PH, PL and SS) showed high H^2_{bs} i.e. 90.2, 92.6 and 92.3%, respectively, suggesting that these traits were mostly controlled by genetic factors. Two sorghum genotypes of GH-2 and GH-6 revealed high BI (0.51). This infers that these sorghum genotypes have heavier biomass compared to other sorghum genotypes in this study. Accordingly, these genotypes could be used as a donor to improve biomass traits especially plant height. Two traits of PL and SS seem directly contribute to seed number and seed weight that lead to influence HI. Seed number and seed weight were two traits that as individual variable do not directly affect the HI because many factor affected HI as SDW, LDW, PDW, and RDW.

Among variables observed in this study, SN had high SDGV and this would directly affect very high CV of both phenotype and genotype (Table 2). It seems that such condition was influenced by high range of SN that was 1200-3086 (Table 3). The very high difference between GCV and PCV was revealed in SN as 46.08 (141.43-95.35). The cause of this is still not very clear yet. However, high SDGV of SN might contribute to high differences between GCV and PCV as 82.01. It means that 20 sorghum genotypes tested in this study produced high variation in SN. The result of this study was not the same as that of Jain and Patel (2013) who reported that stem girth showed highly different between GCV and PCV.

Two sorghum genotypes that produced high biomass were GH-2 and GH-6 as 0.51 (Table 3). Both of these sorghum genotypes produced low yield of SW that was less than 70 g per panicle. The lowest biomass production was revealed by GHP-3 as 0.05 yet this sorghum genotype is able to produce high yield (SW= 97.8 g per panicle). Based on this, GH-2 and GH-6 could be used for biomass production yet GHP-3 would be suitable for grain sorghum.

Genetic variation of 20 sorghum genotypes was high. Three phenotypic traits showing high H^2_{bs} were height (90.2%), panicle length (92.6%), and seed size (92.3%). Stem diameter, seed number, and seed weight tended to have low broad sense heritability i.e. 52.3, 54.5, and 55.7%, respectively. The value of standard deviation of genetic variance for seed number was very high (82.01) and this would lead to associate with high CV of phenotype and genotype. This study would recommend that GH-2 and GH-6 have good economic values because these sorghum genotypes could be used for biomass production for both biofuel and feeds. Therefore, both of GH-2 and GH-6 are sorghum genotypes that could be used as parents for biomass trait improvement in a breeding program.

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Table 1. Mean square of genotype (MSG), mean square of error (MSE), variance of genetics, and heritability of broad sense (H^2_{bs}) of 20 sorghum genotypes.

Variables	MSE	MSG	Variance of Genetics	H^2_{bs} (%)
RDW	71.295	11.162	20.04	64.23
SDW	3911.450	185.917	1241.84	86.98
LDW	44.925	7.816	12.37	61.28
Plant Height	12767.441	445.916	4107.17	90.21
LN	3.683	0.253	1.14	81.91
SD	0.080	0.019	0.02	52.32
PDW	15.081	1.227	4.62	79.01
PL	47.444	1.226	15.41	92.63
SS	0.960	0.026	0.31	92.30
SN	798190.710	173533.720	208219.00	54.54
SW	908.735	190.167	239.52	55.74
HI	0.046	0.003	0.01	83.74

RDW= root dry weight, SDW= stem dry weight, LDW= leaf dry weight, LN= leaf number, SD= stem diameter, PDW= panicle dry weight, PL= panicle length, SS= seed size, SW= seed weight, HI= harvest index

Table 2. Standard deviation of genetics variance (SDGV), general means, coefficient of variation (GCV) for genetics, and coefficient of variation (PCV) for phenotype of 20 sorghum genotypes.

Variables	SDGV	Means	CV of Phenotype	CV of Genotype
RDW	2.264	11.932	16.17	9.67
SDW	7.392	66.644	46.29	16.70
LDW	2.175	23.140	9.34	5.81
Height	12.848	209.613	46.61	14.59
LN	2.012	12.173	3.39	1.44
SD	2.000	1.804	1.47	1.02
PDW	2.052	7.447	8.86	4.06
PL	2.142	22.161	8.66	2.35
SS	2.003	3.791	2.98	0.83
SN	117.925	1908.567	141.43	95.35
SW	4.431	71.143	24.58	16.35
HI	2.000	0.432	2.00	0.80

Tabel 3. The means of generative variables as seed size (SS), seed number (SN), seed weight (SW), harvest index (HI), and biomass index (BI) form 20 sorghum genotypes

Genotype	SS (g)	SN	SW (g)	IP	BI
GH-10	3,67fg	2242,7b-e	100,1ab	0,34d-f	0,45abc
GH-7	4,10cd	1821,7c-g	74,8b-f	0,31efg	0,47ab
P/F5-193	3,33bc	3086,7a	107,5a	0,40cd	0,39b-e
GH-2	4,30bc	1355,2fg	56,9d-g	0,27g	0,51a
GH-1	4,07cde	1471,0efg	58,2d-g	0,30fg	0,48ab
Mandau	3,90def	1690,5d-g	72,4c-g	0,34d-g	0,44a-d
GH-6	3,80ef	2827,7ab	46,5g	0,26g	0,51a
P/IWHP	4,50ab	1207,2g	51,0fg	0,28g	0,48ab
GH-3	4,50ab	1620,3d-g	70,6d-g	0,37c-f	0,38b-e
GH-9	4,17cd	2053,2b-f	81,1b-e	0,44c	0,34cde
Talaga Bodas	4,60a	1772,3d-g	78,8b-e	0,43cd	0,47cde
Numbu	4,57ab	1560,3d-g	72,2c-g	0,40cde	0,34de
GH-11	2,80j	2109,5b-f	61,2d-g	0,37c-f	0,37b-e
P/F10-90	3,10i	1722,8d-g	54,0efg	0,39c-f	0,36cde
UPCA	4,05cde	1523,0efg	63,2d-g	0,42cd	0,30ef
Pahat	3,41gh	2371,7a-d	83,4a-d	0,53b	0,22fg
GHP-11	3,08i	2075,0b-f	80,4b-e	0,60c-f	0,17g
P/I150-2	3,08i	1207,0g	46,5g	0,54b	0,16g
GHP-1	3,32hi	1865,0c-g	66,1d-g	0,56b	0,13gh
GHP-3	3,47gh	2588,7abc	97,9abc	0,68a	0,05h

Number in the same column followed by the same letter indicated not significantly difference under Tukey's procedure in the level of 5%